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(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.



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METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF
SCREENING FOR MODULATORS OF CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS

5 This application claims priority to USSN 60/340,376, filed December 14, 2001;
Attorney Docket Number 018501-006400US, filed February 8, 2002; USSN 60/347,211, filed
January 8, 2002; USSN 60/334,393, filed November 29, 2001; USSN 60/335,394, filed
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July 16, 2002; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April
15 12, 2002; each of which is incorporated herein by reference for all purposes. The application
also incorporates by reference PCT/US02/29560; PCT/US02/02242; and PCT/US02/17594.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles
and nucleic acids, products, and antibodies thereto that are involved in cancer and other
20 diseases; and to the use of such expression profiles and compositions in the diagnosis,
prognosis, and therapy of these conditions. The invention further relates to methods for
identifying and using agents and/or targets that modulate these conditions.

BACKGROUND OF THE INVENTION

Cancer is a major cause of morbidity in the United States. For example, in 1996, the
25 American Cancer Society estimated that 1,359,150 people were diagnosed with a malignant
neoplasm and 554,740 died from one of these diseases. Cancer is responsible for 23.9 percent
of all American deaths and is exceeded only by heart disease as a cause of mortality (33
percent). Unfortunately, cancer mortality is increasing and sometime early in this century,
cancer is expected to become the leading cause of mortality in the United States as it already is
30 in Japan.

Cancers share the characteristic of disordered control over normal cell division, growth,
and differentiation. Their initial clinical manifestations are extremely heterogeneous, with over

70 types of cancer arising in virtually every organ and tissue of the body. Moreover, some of those similarly classified cancer types may represent multiple different molecular diseases. Unfortunately, some cancers may be virtually asymptomatic until late in the disease course, when treatment is more difficult, and prognosis grim.

5 Treatment for cancer typically includes surgery, chemotherapy, and/or radiation therapy. Although nearly 50 percent of cancer patients can be effectively treated using these methods, the current therapies all induce serious side effects which diminish quality of life. The identification of novel therapeutic targets and diagnostic markers will be important for improving the diagnosis, prognosis, and treatment of cancer patients.

10 Recent advances in molecular medicine have increased the interest in tumor-specific antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues, preferably accessible from the vasculature and at the cell surface, and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be
15 tolerated, e.g., reproductive organs, especially those absent in one sex. Examples of antigens that are currently available for the detection and treatment of certain cancers include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. See Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies
20 (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. See Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

 The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is valuable for improving the current treatment of cancer patients. Accordingly, provided herein are molecular targets for therapeutic
25 intervention in various defined cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate cancer.

SUMMARY OF THE INVENTION

 The present invention provides methods for determining the presence or absence of a
30 pathological cell in a patient, the method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a biological sample from the patient, thereby determining the presence or absence of the pathological cell.

In certain embodiments of the method, the pathology is described in Table 1, including a cancer; the biological sample comprises isolated nucleic acids; the nucleic acids are mRNA; the biological sample is tissue from an organ which is affected by the pathology of Table 1, including a cancer; a further step is used of amplifying nucleic acids before the step of detecting the nucleic acid; the detecting is of a protein encoded by the nucleic acid; the nucleic acid comprises a sequence as described in Tables 2A-80; the detecting step is carried out by using a labeled nucleic acid probe, utilizing a biochip comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80, or detecting a polypeptide encoded by the nucleic acid; or the patient is undergoing a therapeutic regimen to treat the pathology of Table 1, or is suspected of having the pathology or cancer.

Compositions are also provided, e.g., an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80, including, e.g., those which are labeled; an expression vector comprising such nucleic acid; a host cell comprising such expression vector; an isolated polypeptide which is encoded by such a nucleic acid molecule comprising a sequence as described in Tables 2A-80; or an antibody that specifically binds the polypeptide. In particular embodiments, the antibody is: conjugated to an effector component, is conjugated to a detectable label (including, e.g., a fluorescent label, a radioisotope, or a cytotoxic chemical), an antibody fragment, or is a humanized antibody.

Additional methods are provided, including methods for specifically targeting a compound to a pathological cell in a patient, the method comprising administering to the patient an antibody, as described, thereby providing the targetting. Others include, e.g., methods for determining the presence or absence of a pathological cell in a patient, the methods comprising contacting a biological sample with an antibody, as described. In more particular methods, the antibody is: conjugated to an effector component, or to a fluorescent label; or the biological sample is a blood, serum, urine, or stool sample.

Further methods include those for identifying a compound that modulates a pathology-associated polypeptide, the method comprising steps of: contacting the compound with a pathology-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80; and determining the functional effect of the compound upon the polypeptide. Another drug screening assay method comprises steps of: administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and comparing the level of gene expression

of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of the pathology.

5 DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for various disorders, e.g., angiogenesis, fibrosis, and various defined forms of cancer, including metastatic cancer, as well as methods for screening for compositions which modulate such conditions. Also provided are methods for

10 treating such disorders or cancers. See, e.g., American Society of Clinical Oncology (ed. 2001) ASCO Curriculum: Symptom Management Kendall/Hunt, ISBN: 0787277851; Bonadonna, et al. (2001) Textbook of Breast Cancer (2d ed.) Dunitz Martin, ISBN: 1853178241; Devita and Hellman (eds. 2001) Cancer Principles and Practice of Oncology (2 vols.), Lippincott Williams, ISBN: 0781723876; Howell, et al. (2001) Breast Cancer Isis Medical Media, ISBN:

15 1901865584; Kaye and Laws (2001) Brain Tumours: An Encyclopedic Approach (2d ed.) Churchill Livingstone, ISBN: 0443064261; Mihm, et al. (2001) The Melanocytic Proliferation: A Comprehensive Textbook of Pigmented Lesions Wiley-Liss, ISBN: 0471252719; Montgomery and Aaron (2001) Clinical Pathology of Soft-Tissue Tumors Marcel Dekker, ISBN: 0824702905; Petrovich, et al. (eds. 2001) Combined Modality of Central Nervous

20 System Tumors (Medical Radiology) Springer Verlag, ISBN: 3540660534; Rosen (2001) Rosen's Breast Pathology Lippincott Williams and Wilkins, ISBN: 0781723795; Shah, et al. (2001) Oral Cancer Isis Medical Media, ISBN: 189906687X; Weiss and Goldblum (2001) Enzinger and Weiss's Soft Tissue Tumors (4th ed.) Mosby, ISBN: 0323012000; Abeloff, et al. (eds. 2000) Clinical Oncology (2d ed.) Churchill Livingstone, ISBN: 044307545X; American

25 Society of Clinical Oncology (ed. 2000) Cancer Genetics and Cancer Predisposition Testing Kendall/Hunt, ISBN: 0787276154; Fletcher (2000) Diagnostic Histopathology of Tumors (2 vols. 2d ed.) Churchill Livingstone, ISBN: 0443079927; Vogelzang (ed. 2000) Comprehensive Textbook of Genitourinary Oncology (2d ed.) Lippincott Williams and Wilkins, ISBN: 0683306456; Holland, et al. (eds. 2000) Holland-Frei Cancer Medicine (Book with CD-ROM

30 5th ed.) Decker, ISBN: 1550091131; Turrisi, et al. (2000) Lung Cancer Isis Medical Media, ISBN: 1901865428; Bartolozzi and Lencioni (eds. 1999) Liver Malignancies: Diagnostic and Interventional Radiology (Medical Radiology) Springer Verlag, ISBN: 3540647562; Gasparini

- (ed. 1999) Prognostic Variables in Node-Negative and Node-Positive Breast Cancer Kluwer, ISBN: 0792384474; Hansen (ed. 1999) The LASLC Textbook of Lung Cancer: International Association for the Study of Lung Cancer Dunitz Martin, ISBN: 1853177083; Raghavan, et al. (eds. 1999) Textbook of Uncommon Cancer (2nd ed.) Wiley, ISBN: 0471929212; Thawley, et al. (eds. 1999) Comprehensive Management of Head and Neck Tumors (2 vols.) Saunders, ISBN: 0721655823; Whittaker and Holmes (eds. 1999) Leukemia and Related Disorders (3d ed.) Blackwell Science, ISBN: 0865426074; Aapro (ed. 1998) OncoMedia: Medical Oncology (CD-ROM) Elsevier Science, ISBN: 0080427480; Abeloff (1998) Clinical Oncology (Library Version 2 CD-ROM Individual Version 2.0 Windows and Macintosh) Harcourt Brace, ISBN: 0443075557; Benson (ed. 1998) Gastrointestinal Oncology (Cancer Treatment and Research, CTAR 98) Kluwer, ISBN: 0792382056; Brambilla and Brambilla (eds. 1998) Lung Tumors: Fundamental Biology and Clinical Management (Vol 124) Marcel Dekker, ISBN: 0824701607; Canellos, et al. (eds. 1998) The Lymphomas Saunders, ISBN: 0721650309; Greenspan and Remagen (1998) Differential Diagnosis of Tumors and Tumor-Like Lesions of Bones and Joints Lippincott Williams and Wilkins Publishers, ISBN: 0397517106; Hiddemann (ed. 1998) Acute Leukemias VII: Experimental Approaches and Novel Therapies (Haematologie Und Bluttransfusion, Vol 39), Springer Verlag, ISBN: 3540635041; Husband and Reznick (1998) Imaging in Oncology (2 vols.) Mosby, ISBN: 1899066489; Leibel and Phillips (eds. 1998) Textbook of Radiation Oncology Saunders, ISBN: 0721653367; Maloney and Miller (eds. 1998) Cutaneous Oncology: Pathophysiology, Diagnosis, and Management Blackwell Science, ISBN: 0865425175; Mittal, et al. (eds. 1998) Advances in Radiation Therapy Kluwer, ISBN: 0792399811; Oldham (ed. 1998) Principles of Cancer Biotherapy (3d ed.) Kluwer, ISBN: 0792335074; Ozols (ed. 1998) Gynecologic Oncology Kluwer, ISBN: 0792380703; Parkin, et al. (eds. 1998) Cancer Incidence in Five Continents (Iarc Scientific Publications, No 143) Oxford University Press, ISBN: 9283221435; Perez and Brady (eds. 1998) Principles and Practice of Radiation Oncology Lippincott Williams and Wilkins, ISBN: 0397584164; Black, et al. (eds. 1997) Cancer of the Nervous System Blackwell Science, ISBN: 0865423849; Bonadonna, et al. (1997) Textbook of Breast Cancer: A Clinical Guide to Therapy Blackwell Science, ISBN: 1853173487; Pollock (ed. 1997) Surgical Oncology Kluwer, ISBN: 0792399005; Sheaves, et al. (eds. 1997) Clinical Endocrine Oncology Blackwell Science, ISBN: 086542862X; Vahrson (1997) Radiation Oncology of Gynecological Cancers Springer Verlag, ISBN: 0387567682; Walterhouse and Cohn (eds. 1997) Diagnostic and Therapeutic

Advances in Pediatric Oncology Kluwer, ISBN: 0792399781; Aisner (ed. 1996) Comprehensive Textbook of Thoracic Oncology Lippincott, Williams and Wilkins, ISBN: 0683000624; Bertino, et al. (eds. 1996) Encyclopedia of Cancer (3 vols.) Academic, ISBN: 012093230X; Cavalli, et al. (1996) Textbook of Medical Oncology Dunitz Martin, ISBN: 1853172901;

5 Peckham, et al. (eds. 1995) Oxford Textbook of Oncology (2-Vols.) Oxford University Press, ISBN: 0192616854; and Freireich and Kantarjian (eds. 1996) Molecular Genetics and Therapy of Leukemia (Cancer Treatment and Research, V. 84) Kluwer, ISBN: 0792339126.

In particular, identification of markers selectively expressed on defined cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the

10 invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g.,

15 using antisense or RNAi. The markers may be useful for molecular characterization of subsets of the diseases, e.g., as provided in Table 1, which subsets may actually require very different treatments. Moreover, the markers may also be important in related diseases to the specific disorders and cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also

20 be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

25 Tables 2B-76B provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in diseased samples (see Tables 1-3), particularly sequences involved in angiogenesis, arthritis, prostate cancer, breast cancer, colorectal cancer, cervical cancer, bladder cancer, head and neck cancer, esophageal cancer, lung cancer, ovarian cancer, pancreatic cancer, renal cancer, stomach cancer, skin

30 cancer, testicular cancer, uterine cancer, glioblastoma, Ewing sarcoma, soft tissue sarcoma, and lung fibrosis. Tables 2A-80 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

The term "cancer protein" or "cancer polynucleotide" or "cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably about 92%, 94%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-80; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-80, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-80 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, preferably 90%, 91%, 93%, 95%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-80. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "cancer polypeptide" and a "cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" cancer protein or nucleic acid refers to a cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains elements normally contained in one or more naturally occurring, wild type cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival samples, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is

typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of interest.

5 "Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

10 The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 93%, 95%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over
15 a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes
20 sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is about 50-100 amino acids or nucleotides in length.

25 For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison
30 algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from about 20 to 600, usually about 50 to 200, more usually about 100 to 150, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Wiley).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-

scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=4 and a comparison of both strands. For amino acid sequences, the BLASTP
5 program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1992) Proc. Natl. Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences. See, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787.

10 One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than
15 about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a
20 polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

25 A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site,
30 www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its

native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetic refers to a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variant" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts,

et al. (eds. 2001) Molecular Biology of the Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein;

Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805, Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986) Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucleic Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-2322), O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach, Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-1897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature 365:566-568; Carlsson, et al. (1996) Nature 380:207, all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Natl. Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141, and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Letsinger, et al. (1994) Nucleoside and Nucleotide 13:1597; Chapters 2 and 3 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp 169-176). Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in at least two advantages. The PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively

insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies, antigens, or epitope tags; and c) colored or fluorescent dyes. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , electron-dense reagents, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable such as alkaline phosphatase, beta-galactosidase, or horseradish peroxidase. Methods are known for conjugating the antibody to the label. See, e.g., Hunter, et al. (1962) *Nature* 144:945; David, et al. (1974) *Biochemistry* 13:1014-1021; Pain, et al. (1981) *J. Immunol. Meth.* 40:219-230; and Nygren (1982) *J. Histochem. and Cytochem.* 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including

radioactive compounds, fluorescent compounds, enzymes or substrates, tags such as epitope tags, toxins; activatable moieties, chemotherapeutic agents; lipases; antibiotics; chemoattracting moieties, immune modulators (micA/B), or radioisotopes, e.g., emitting "hard" beta, radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, e.g., covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, methods using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein, or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is

achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. The protein may be isolated or purified away from some or most of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. An isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a cancer protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid

sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01-1.0 M sodium ion concentration (or other salts) at pH 7.0 to

8.3 and the temperature is at least about 30° C for short probes (e.g., about 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32°-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press, NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is typically at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. (eds. 1991 and supplements) Current Protocols in Molecular Biology Wiley.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the cancer protein or nucleic acid, e.g., a physiological, functional, physical, or chemical effect, such as the ability to decrease cancer. It includes ligand binding activity; cell viability; cell growth on soft agar; anchorage dependence; contact

inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis; and other characteristics of cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the cancer protein, measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring growth, cellular proliferation, cell viability, cellular transformation, growth factor or serum dependence, tumor specific marker levels, invasiveness into Matrigel, tumor growth and metastasis in vivo, mRNA and protein expression, and other characteristics of cancer cells. The functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators," and "modulators" of cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Such assays for

inhibitors and activators include, e.g., expressing the cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of cancer can also be identified by incubating cancer cells with the test compound and determining increases or decreases in the expression of 1 or more cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more cancer proteins, such as cancer proteins encoded by the sequences set out in Tables 2A-80.

Samples or assays comprising cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is about 110%, more preferably 150%, more preferably 200-500% (e.g., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (2d ed.) Wiley-Liss.

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes.

5 Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

10 An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these
15 light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H - CH_1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild
20 conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant
25 DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies,
30 many techniques known. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985) pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in

Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, effector function, chemoattractant, immune modulator, etc.; or (b) the variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or cancer tissue or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

The identification of sequences that are differentially expressed in cancer versus non-cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis

and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression
5 profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the cancer expression profile. This may be done by making biochips comprising sets of the important cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the cancer proteins can be
10 evaluated for diagnostic purposes or to screen candidate agents. In addition, the cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are
15 differentially expressed in cancer relative to normal tissues and/or non-malignant disease, or in different types of related diseases, herein termed "cancer sequences." As outlined below, cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the cancer sequences are from humans; however, cancer sequences from other
20 organisms may be useful in animal models of disease and drug evaluation; thus, other cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Cancer sequences from other organisms may be obtained using the techniques outlined below.

25 Cancer sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the skin cancer sequences are recombinant nucleic acids. These nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the cancer
30 sequences.

A cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the cancer sequences outlined herein. Such homology can be based

upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying cancer-associated sequences, the cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing cancer samples with metastatic cancer samples from other cancers, such as lung, stomach, gastrointestinal cancers, etc. Samples of different stages of cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, and not limited to lung, heart, brain, liver, stomach, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the cancer screen that are expressed in a significant amount in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensible, e.g., female or male specific). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs were there expression.

In a preferred embodiment, cancer sequences are those that are up-regulated in cancer; that is, the expression of these genes is higher in the cancer tissue as compared to non-cancer or non-malignant tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Uniformity among relevant samples is also preferred.

Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is available, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7; and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases,

e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH. See Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have
5 been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, cancer sequences are those that are down-regulated in the cancer; that is, the expression of these genes is lower in cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher
10 being preferred.

Informatics

The ability to identify genes that are over or under expressed in cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development,
15 and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with cancer or related diseases. See Tables 1-3. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA).

Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).
20

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access
25 to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.
30

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. Similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing cancer, e.g., the identification of cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others.

Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is available. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures. See also Baxevanis, et al. (2001) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins Wiley; Mount (2001)

- Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999)
Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge University Press; Baxévanis and Oeullette (eds. 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Rashidi and Buehler (1999)
 5 Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds. 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford University Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the
 10 Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with
 15 data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another
 20 tissue specimen to be analyzed for cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in
 25 a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of
 30 magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention

provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method
5 for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount
10 of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed,
15 Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line,
20 wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes
25 generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a
30 query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute

the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

5 The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can
10 be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal
15 comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

 The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be
20 stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values. See, e.g., Ewens and Grant (2001) Statistical Methods in Bioinformatics: An Introduction Springer-Verlag. Mathematical approaches can also be used to conclude whether similarities or differences in the gene expression exhibited by different
25 samples are significant. See, e.g., Golub, et al. (1999) Science 286:531-537; Duda, et al. (2001) Pattern Classification Wiley; and Hastie, et al. (2001) The Elements of Statistical Learning: Data Mining, Inference, and Prediction Springer-Verlag. One approach to determine whether a sample is more similar to or has maximum similarity with a given condition between the sample and one or more pools representing different conditions for comparison; the pool with the
30 smallest vector angle is then chosen as the most similar to the biological sample among the pools compared.

Characteristics of cancer-associated proteins

Cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus.

5 Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase

10 activity, polymerase activity, and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In

15 addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH

20 domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. These motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.

25 One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420 ; Bateman, et al. (1999) Nuc.

30 Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may

have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors, and the like. Extracellular domains also bind to cell-associated

molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

5 Cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are
10 typically permeabilized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated that a transmembrane protein can be made soluble by
15 removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal
20 sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion
25 into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic
30 markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of cancer nucleic acids

As described above, cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally
5 determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

As detailed elsewhere, percent identity can be determined using an algorithm such as BLAST. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. Alignment
10 may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids described, the percentage of homology may be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, e.g., homology of sequences shorter than those of the sequences identified will be determined using the number of nucleosides in the
15 shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, e.g., nucleic acids which hybridize under high stringency to a described nucleic acid, or its complement, or is also found on naturally occurring mRNAs is considered a cancer sequence. In another embodiment, less stringent hybridization conditions are used; e.g.,
20 moderate or low stringency conditions may be used; see Ausubel, supra, and Tijssen, supra.

The cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-80, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, using the sequences provided herein, extended sequences, in either direction, of
25 the cancer genes can be obtained, using techniques well known for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent
30 parts recombined to form the entire cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant cancer nucleic acid can

be further used as a probe to identify and isolate other cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant cancer nucleic acids and proteins.

The cancer nucleic acids of the present invention are used in several ways. In one embodiment, nucleic acid probes to the cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, cancer nucleic acids that include coding regions of cancer proteins can be put into expression vectors for the expression of cancer proteins, again for screening purposes or for administration to a patient.

10 In a preferred embodiment, nucleic acid probes to cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8-100 bases long, with from about 10-80 bases being preferred, and from about 30-50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

Nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or
5 binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, e.g., streptavidin to the support and
10 the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds, and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid
15 support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

20 The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often, the substrate may contain discrete individual sites appropriate for individual partitioning and identification. The number of possible substrates is very large, and include, but
25 are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably
30 fluoresce. See WO 0055627.

Generally the substrate is planar, although other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube for flow-

through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is
5 derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups, and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers; e.g., homo-or hetero-bifunctional linkers as are well known
10 (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or
15 attachment may be via linkage to an internal nucleoside. In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface. For example,
20 photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix
25 GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative
30 amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of cancer-associated RNA. Methods of quantitative amplification are well known.

Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569, Landegren, et al. (1988) Science 241:1077-1080, and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Natl. Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of cancer proteins from nucleic acids

In a preferred embodiment, cancer nucleic acids, e.g., encoding cancer proteins, are used to make a variety of expression vectors to express cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in

the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the cancer protein. Numerous types of appropriate expression vectors and suitable regulatory sequences are known for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known, and are useful in the present invention.

An expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, *supra*; and Kitamura, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:9146-9150.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known and will vary with the host cell used.

The cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a cancer protein, under the appropriate conditions to induce or cause expression of the cancer protein. Conditions appropriate for cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line), and various other human cells and cell lines.

In a preferred embodiment, the cancer proteins are expressed in mammalian cells. Mammalian expression systems may be used, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

Methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, are available, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques such as calcium chloride treatment, electroporation, and others.

In one embodiment, cancer proteins are produced in insect cells using, e.g., expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors.

In a preferred embodiment, a cancer protein is produced in yeast cells. Yeast expression systems are well known, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The cancer protein may also be made as a fusion protein, using available techniques. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the cancer protein is a cancer peptide, the nucleic acid encoding the peptide may

be linked to other nucleic acid for expression purposes. Fusion with detection epitope tags can be made, e.g., with FLAG, His6, myc, HA, etc.

In a preferred embodiment, the cancer protein is purified or isolated after expression. Cancer proteins may be isolated or purified in a variety of ways depending on what other components are present in the sample and the requirements for purified product, e.g., natural conformation or denatured. Standard purification methods include ammonium sulfate precipitations, electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the cancer protein may be purified using a standard anti-cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. See, e.g., Walsh (2002) Proteins: Biochemistry and Biotechnology Wiley; Hardin, et al. (eds. 2001) Cloning, Gene Expression and Protein Purification Oxford Univ. Press; Wilson, et al. (eds. 2000) Encyclopedia of Separation Science Academic Press; and Scopes (1993) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

Variants of cancer proteins

Also included within one embodiment of cancer proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85%, and most preferably greater than 90%. In some embodiments the homology will be as high as about 93-95% or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques, as are outlined above for nucleic acid homologies.

Cancer proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of cancer proteins are portions or fragments of the wild type sequences herein. In addition, as

outlined above, the cancer nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence.

In one embodiment, the cancer proteins are derivative or variant cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at many residue positions within the cancer peptide.

Also included within one embodiment of cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as a naturally occurring analogue, although variants can also be selected which have modified characteristics.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1-20 amino acids, although considerably larger insertions may be tolerated. Deletions generally range from about 1-20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions, or combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the

alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships described.

The variants typically exhibit essentially the same qualitative biological activity and will
5 elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of cancer proteins as needed. Alternatively, the variant may be designed such that a biological activity of the cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Substantial changes in function or immunological identity are sometimes made by
10 selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which generally are expected to produce the greatest changes in the polypeptide's
15 properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain,
20 e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Variants typically exhibit a similar qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to
25 modify the characteristics of the skin cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of
30 a cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking cancer polypeptides to a water-

insoluble support matrix or surface for use in a method for purifying anti-cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional
5 imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutamyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine,
10 phosphorylation of hydroxyl groups of serinyl, threonyl, or tyrosyl residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1992) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the cancer polypeptide included within the
15 scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence cancer polypeptide. Glycosylation patterns can be altered in many ways. Different cell types to express cancer-
20 associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence cancer polypeptide (for O-linked glycosylation sites). The cancer amino acid sequence may optionally
25 be altered through changes at the DNA level, particularly by mutating the DNA encoding the cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g.,
30 WO 87/05330; pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem.

Removal of carbohydrate moieties present on the cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for

amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) Arch. Biochem. Biophys. 259:52-57 and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases.

5 See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

Another type of covalent modification of cancer comprises linking the cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

10 Cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl-
15 terminus of the cancer polypeptide. The presence of such epitope-tagged forms of a cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a cancer polypeptide
20 with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are available. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Natl. Acad. Sci. USA 87:6393-6397).

Also included are other cancer proteins of the cancer family, and cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related cancer proteins from humans or other organisms. Particularly useful probe and/or PCR primer
5 sequences include the unique areas of the cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for PCR reaction have been well described (e.g., Innis, PCR Protocols, supra).

In addition, cancer proteins can be made that are longer than those encoded by the
10 nucleic acids of the Tables, e.g., by the elucidation of extended sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Cancer proteins may also be identified as being encoded by cancer nucleic acids. Thus, cancer proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

15 Antibodies to cancer proteins

In a preferred embodiment, when the cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell
20 receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from a protein sequence set out in the tables.

25 Methods of preparing polyclonal antibodies exist (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 2A-80 or
30 fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum

albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). Various immunization protocols may be used.

- 5 The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent.
- 10 Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line
- 15 using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine, or human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or
- 20 more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.
- 25 In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for another antigen, and
- 30 preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to cancer protein are capable of reducing or eliminating a biological function of a cancer protein, in a naked form or conjugated to an effector moiety, as is described below. That is, the addition of anti-cancer protein antibodies (either polyclonal or preferably monoclonal) to cancer tissue (or cells containing cancer) may
5 reduce or eliminate the cancer. Generally, at least a 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.)
10 Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the
15 recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized
20 antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human
25 immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be essentially performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding
30 sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human antibodies can also be produced using phage display libraries (Hoogenboom and Winter (1992) J. Mol. Biol. 227:381-388; Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95).

- 5 Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-851; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

- 15 By immunotherapy is meant treatment of cancer with an antibody raised against cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are
20 desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

- In a preferred embodiment the cancer proteins against which antibodies are raised are
25 secreted proteins as described above. Without being bound by theory, antibodies used for treatment may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted cancer protein, e.g., in autocrine signaling.

- In another preferred embodiment, the cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may
30 bind the extracellular domain of the cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane cancer protein. The antibody may be a competitive, non-

competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the cancer protein. The antibody may also be an antagonist of the cancer protein. Further, the antibody may prevent activation of the transmembrane cancer protein, or may induce or suppress a particular cellular pathway. In one aspect, when the antibody prevents the binding of other molecules to the cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, cancer may be treated by administering to a patient antibodies directed against the transmembrane cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, target a drug loaded liposome, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a cancer protein. In another aspect the therapeutic moiety may modulate the activity of molecules associated with or in close proximity to a cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase or protein kinase activity associated with cancer, or be an attractant of other cells, such as NK cells. See, e.g., USSN 09/544,494.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane cancer proteins not only serves to increase the local concentration of therapeutic moiety in the cancer afflicted area, but also serves to reduce

deleterious side effects that may be associated with the untargeted therapeutic moiety.

Antibody fragments may be used to target toxin loaded liposomes.

In another preferred embodiment, the cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto may contain a signal for that target localization, e.g., a nuclear localization signal.

10 The cancer antibodies of the invention specifically bind to cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related sequences is often also important.

15 Detection of cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing cancer) and in cancer tissue (and in some cases, for varying severities of cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus

permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to cancer genes, e.g., those identified as being important in a cancer or disease phenotype, can be evaluated in a cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the cancer protein are detected. Although DNA or RNA encoding the cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA, or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after

immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method, detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably
5 labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl
10 phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane, or intracellular proteins) are used in diagnostic assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in diagnostic assays. This can be performed on an individual gene or
15 corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of cancer, e.g., for prognostic or
20 diagnostic purposes. Detection of these proteins in putative cancer tissue allows for detection, prognosis, or diagnosis of cancer or similar disease, and for selection of therapeutic strategy. In one embodiment, antibodies are used to detect cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following
25 separation of proteins, the cancer protein is detected, e.g., by immunoblotting with antibodies raised against the cancer protein.

In another preferred method, antibodies to the cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai, et al. (eds. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. In this method, cells are contacted with
30 from one to many antibodies to the cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a

detectable label. In another method the primary antibody to the cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of cancer proteins.

5 Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

10 In another preferred embodiment, antibodies find use in diagnosing cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of cancer proteins. Antibodies can be used to detect a cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIAcore technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous cancer protein.

15 In a preferred embodiment, in situ hybridization of labeled cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, a diagnosis, a prognosis, or a prediction may be based on the findings. It is further understood that the genes
20 which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in prognosis assays. As above, gene
25 expression profiles can be generated that correlate to cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, cancer probes may be attached to biochips for the detection and quantification of cancer sequences in a tissue or patient. The assays proceed as outlined
30 above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in drug screening assays or
5 by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-88; Heid (1996) Genome Res. 6:986-994.

10 In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the cancer phenotype or an identified physiological function of a cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of
15 drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be
20 performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal
25 versus tissue undergoing cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

30 The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be

monitored, e.g., through the use of antibodies to the cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically
5 involve a plurality of those entities described herein.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for
10 each well.

Modulators of cancer

Expression monitoring can be performed to identify compounds that modify the expression of one or more cancer-associated sequences, e.g., a polynucleotide sequence set out
15 in the tables. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate cancer, modulate cancer proteins, bind to a cancer protein, or interfere with the binding of a cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical
20 equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator
25 suppresses a cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced a cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

30 Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or

less than 1500, or less than 1000, or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or
5 heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs, or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a cancer protein. By "neutralize"
10 is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity,
15 creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis. See, e.g., Janzen (2002) High Throughput Screening: Methods and Protocols Humana; Devlin (ed. 1997) High Throughput Screening: The Discovery of Bioactive Substances Dekker; and Mei and Czarnik (eds. 2002) Integrated Drug Discovery Techniques
20 Dekker.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired
25 characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical
30 library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be

synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37:1233-1251).

Preparation and screening of combinatorial chemical libraries is well known. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6909-6913, vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-1305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33 Baum (Jan 18, 1993) C&EN; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and

implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek
5 Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of cancer gene transcription, inhibition, or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of
10 particular nucleic acids or protein products are well known. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody
15 binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including sample and reagent pipetting, liquid dispensing, timed
20 incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding,
25 and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in
30 this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test

compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines, or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of prokaryotic or eukaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in

vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

These assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246, and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate, and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used

to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

5 The assay data are analyzed to determine the expression levels, and changes in expression levels as between states of individual genes, forming a gene expression profile.

 Screens are performed to identify modulators of the cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another
10 embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially
15 expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

 In addition, screens can be done for genes that are induced in response to a candidate agent or treatment process. After identifying a modulator based upon its ability to suppress a cancer expression pattern leading to a normal expression pattern (or its converse), or to
20 modulate a single cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated cancer tissue reveals genes that are not expressed in normal tissue or cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be
25 identified and used by methods described herein for cancer genes or proteins. In particular, these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics, e.g., toxin loaded liposomes, to the treated cancer tissue sample.

 Thus, in one embodiment, a test compound is administered to a population of cancer
30 cells that have an associated cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell

surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

5 Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

 Thus, e.g., cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on cancer activity. By defining such a signature for the cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

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 In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins" or a "cancer modulatory protein". The cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the cancer modulatory protein is a fragment. In a preferred embodiment, the cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of the Tables. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

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 Preferably, the cancer modulatory protein is a fragment of about 14-24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

30

In one embodiment the cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the cancer protein is conjugated to BSA.

Measurements of cancer polypeptide activity, or of cancer or the cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5-48 hours. In one embodiment, the cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA, and the like with an antibody that selectively binds to the cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or

the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins." The cancer protein may be a fragment, or alternatively, the full length protein to a fragment shown herein.

5 In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

10 In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the cancer proteins can be used in the assays.

15 Thus, in a preferred embodiment, the methods comprise combining a cancer protein and a candidate compound, and determining the binding of the compound to the cancer protein. Preferred embodiments utilize the human cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative cancer proteins may be used.

20 Generally, in a preferred embodiment of the methods herein, the cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface
25 of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes, and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular
30 manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not

sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked
5 through incubation with bovine serum albumin (BSA), casein, or other innocuous protein or other moiety.

In a preferred embodiment, the cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the cancer protein is added. Novel binding agents include specific antibodies, non-natural
10 binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.), and the like.

15 The determination of the binding of the test modulating compound to the cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and
20 washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

25 In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (e.g., a cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test
30 compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between about 4-40° C. Incubation

periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1-1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

5 In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the cancer protein and thus is capable of binding to, and potentially modulating, the activity of the cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent.

10 Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

 In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the cancer protein with a higher affinity. Thus, if the test
15 compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the cancer protein.

 In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the cancer proteins. In one embodiment, the methods comprise combining a cancer protein and a competitor in a first sample. A second
20 sample comprises a test compound, a cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the cancer protein.

25 Alternatively, differential screening is used to identify drug candidates that bind to the native cancer protein, but cannot bind to modified cancer proteins. The structure of the cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

30 Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein.

Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

5 A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may
10 be added in an order that provides for the requisite binding.

 In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a
15 cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

 In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including
20 chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

 In this way, compounds that modulate cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the
25 compound.

 In one embodiment, a method of inhibiting cancer cell division is provided. The method comprises administration of a cancer inhibitor. In another embodiment, a method of inhibiting cancer is provided. The method may comprise administration of a cancer inhibitor. In a further embodiment, methods of treating cells or individuals with cancer are provided, e.g., comprising
30 administration of a cancer inhibitor.

 In one embodiment, a cancer inhibitor is an antibody as discussed above. In another embodiment, the cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are available, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are
5 transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of cancer
10 sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described, e.g., in Freshney (1998) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-
15 Liss; Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss; and Garkavtsev, et al. (1996) Nature Genet. 14:415-20.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop
20 growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can
25 be used to measure density limitation of growth. See Freshney (2000), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with
30 a cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1998), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Inst. 37:167-175; Eagle, et al.(1970) J. Exp. Med. 131:836-879); Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem. Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1998), supra. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum; Freshney (1985) Anticancer Res. 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved,

or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

Tumor growth in vivo

Effects of cancer-associated sequences on cell growth can be tested in transgenic or
5 immune-suppressed mice. Knock-out transgenic mice can be made, in which the cancer gene is disrupted or in which a cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous cancer gene with a mutated version of the cancer gene, or by mutating the
10 endogenous cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the
15 chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288-1292). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

20 Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected
25 into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably about 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction
30 (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a cancer-associated protein is down-regulated, or entirely inhibited, by the use of an inhibitory or antisense polynucleotide, e.g., a nucleic acid
5 complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their
10 close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. Analogs are comprehended by this invention so long as they function effectively to hybridize with the cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

15 Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense
20 oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for cancer molecules. A preferred antisense molecule is for a cancer sequences in the Tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to
25 the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14-30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific
30 manner. See, e.g., Brumelkamp, et al. (2002) Scienceexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be

effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

5 In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general
10 review of the properties of different ribozymes).

 The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparation are described in, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-
15 45; Leavitt, et al.(1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

 Polynucleotide modulators of cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface
20 receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of cancer may be introduced into a cell containing the
25 target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

 Thus, in one embodiment, methods of modulating cancer in cells or organisms are
30 provided. In one embodiment, the methods comprise administering to a cell an anti-cancer antibody that reduces or eliminates the biological activity of an endogenous cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic

acid encoding a cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the cancer sequence is down-regulated in cancer, such state may be reversed by increasing the amount of cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous cancer gene or administering a gene encoding the cancer sequence, using known gene-therapy techniques. In a preferred
5 embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/0386. Alternatively, e.g., when the cancer sequence is up-regulated in cancer, the activity of the endogenous cancer gene is decreased, e.g., by the administration of a cancer antisense or other
10 inhibitor, e.g., RNAi.

In one embodiment, the cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to cancer proteins. Similarly, the cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify cancer antibodies useful for production, diagnostic, or therapeutic
15 purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The cancer antibodies may be coupled to standard affinity chromatography columns and used to purify cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the cancer protein.

20 Methods of identifying variant cancer-associated sequences

Without being bound by theory, expression of various cancer sequences is correlated with cancer. Accordingly, disorders based on mutant or variant cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant cancer genes, e.g., determining all or part of the sequence of at least one
25 endogenous cancer gene in a cell. In a preferred embodiment, the invention provides methods of identifying the cancer genotype of an individual, e.g., determining all or part of the sequence of at least one cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced cancer gene to
30 a known cancer gene, e.g., a wild-type gene.

The sequence of all or part of the cancer gene can then be compared to the sequence of a known cancer gene to determine if any differences exist. This can be done using known

homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the cancer gene of the patient and the known cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the cancer genes are used as probes to determine the number
5 of copies of the cancer gene in the genome.

In another preferred embodiment, the cancer genes are used as probes to determine the chromosomal localization of the cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the cancer gene locus.

10 Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable using known techniques. See, e.g., Ansel, et al. (1999)
15 Pharmaceutical Dosage Forms and Drug Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceut. Assn.; and Pickar (1998) Dosage Calculations Thomson. Adjustments for cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as
20 the age, body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the condition may be necessary. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in cancer.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and
25 veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary,
30 vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts, and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are available.

The compositions for administration will commonly comprise a cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by
5 conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents, and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate, and the like. The concentration of active agent in these formulations can vary widely, and will be
10 selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., (1980) Remington's Pharmaceutical Science (18th ed.) Mack, and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill.

Thus, a typical pharmaceutical composition for intravenous administration would be
15 about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent.

20 The compositions containing modulators of cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend
25 upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a
30 mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender,

administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present cancer protein-modulating compounds can be administered alone or in combination with additional cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the Tables, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA, or other foreign genetic material into a host cell (see, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the cancer coding regions) can be administered in a gene therapy application. These cancer genes can include inhibitory applications, e.g., as inhibitory RNA, gene therapy (e.g., for incorporation into the genome), or antisense compositions.

Cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can

include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341-349), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294.; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in
5 immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p.
10 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kieny, et al. (1986) Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al.
15 (1995) Nature Med. 1:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de
20 Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance
25 designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham,
30 Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron, or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes;

biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient.

5 This approach is described, for instance, in Wolff et. al. (1990) Science 247:1465-1468, as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S.

10 Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode cancer polypeptides or polypeptide

15 fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors are available for therapeutic

20 administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing a

25 cancer gene or portion of a cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a cancer patient. The cancer gene used for DNA vaccines can encode full-length cancer proteins, but more preferably encodes portions of the cancer proteins including peptides derived from the cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a

30 cancer gene. For example, cancer-associated genes or sequence encoding subfragments of a cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure

provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment, cancer genes find use in generating animal models of cancer. When the cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein inhibitory or antisense RNA directed to the cancer gene will also diminish or repress expression of the gene. Animal models of cancer find use in screening for modulators of a cancer-associated sequence or modulators of cancer. Similarly, transgenic animal technology, including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the cancer protein. When desired, tissue-specific expression or knockout of the cancer protein may be necessary.

It is also possible that the cancer protein is overexpressed in cancer. As such, transgenic animals can be generated that overexpress the cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods will find use as animal models of cancer and are additionally useful in screening for modulators to treat cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications, such kits may include at least one of the following: assay reagents, buffers, cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative cancer polypeptides or polynucleotides, small molecule inhibitors of cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials

typically comprise written or printed materials, they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to, electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may
5 include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing cancer-associated
10 activity. Optionally, the kit contains biologically active cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will typically be selected based on correlations with important parameters in disease which may be identified in historical or
15 outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and
20 analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynn, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Table 1 lists medical conditions, abnormalities, or organs affected by disease, referred to in Tables 2A and 3A, for which markers have been identified, and other related medical conditions (including various stages and/or metastases) in which those markers will also be useful, e.g., in therapeutic, diagnostic, prognostic, subsetting, vaccine, and other uses.

- 5 blood vessels/angiogenesis: hemangiomas, lymphangiomas, angiosarcoma, lymphangiosarcoma, Kaposi's sarcoma, wound healing, tissue remodeling, psoriasis, ischemic heart disease, inflammatory diseases (e.g., arthritis, asthma, chronic bronchitis), atherosclerosis, endometriosis, presumed ocular histoplasmosis syndrome, hypoxia, solid tumors, lymphomas, lymphadenitis, lymphangitis, autoimmune diseases (e.g., RA, SLE, juvenile chronic arthritis, pigmented villonodular synovitis, etc.), retinal neovascularization syndromes (e.g., diabetic retinopathy, macular degeneration, presumed ocular histoplasmosis syndrome, etc.), scleritis/conjunctivitis, hypertrophic scars (keloid), birth control, uterine fibroids
- 10 bladder: carcinoma in situ, papillary carcinomas, transitional cell carcinoma, squamous cell carcinoma
bone: Ewing sarcoma, sarcomas arising from skeletal and extraskeletal connective tissues, including the peripheral nervous system (e.g. chondrosarcoma, osteosarcoma)
brain: glioblastoma, oligodendroglioma, anaplastic astrocytoma, meningioma, medulloblastoma, neuroblastoma, ependymoma, schwannoma, craniopharyngioma, pineoblastoma, pineocytoma, neurofibroma, neurofibrosarcoma, malignant peripheral nerve sheath tumors, granular cell tumors, plexosarcoma, ganglioneuroblastoma, neuroepithelioma, neuroma, ganglioneuroma
- 15 breast: ductal carcinoma in situ, lobular carcinoma in situ
cervix: cancer of the cervix, vagina, or vulva
colon/rectum: precancerous colorectal disease (e.g., neoplastic polyps (adenomas), familial adenomatous polyposis, ulcerative colitis), colon cancer, e.g., epithelial tumor (e.g., adenocarcinoma, mucinous adenocarcinoma, signet-ring cell adenocarcinoma, squamous cell carcinoma, adenosquamous carcinoma, undifferentiated carcinoma, unclassified carcinoma), carcinoid tumor (e.g., argentaffin, nonargentaffin, composite), non-epithelial tumor (e.g., leiomyosarcoma, others), inflammatory bowel disease (e.g., ulcerative colitis, Crohn's disease (granulomatous colitis), dysplasia), rectal cancer, cancer of the anal region (e.g., squamous cell carcinoma, transitional carcinoma, adenocarcinoma, carcinoma, papillary villous carcinoma, mucinous adenocarcinoma, melanoma)
- 20 esophagus: premalignant or predisposing conditions (e.g., esophagitis), squamous cell cancers (e.g., cancers of the head and neck, lung, or cervix), gastrointestinal carcinomas (e.g., cancers of the stomach, colon, or rectum)
fibrosis: lung fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, cirrhosis (liver fibrosis), renal fibrosis, scleroderma, wound healing
- 25 head and neck: tumors of the nasal cavity, paranasal sinuses, nasopharynx, oral cavity, oral pharynx, lip, larynx, hypopharynx, salivary glands, paragangliomas, esophagus
kidney: clear cell (nonpapillary) carcinoma, papillary carcinoma, chromophobe renal carcinoma, hypernephroma, adenocarcinoma, sporadic renal carcinomas, hereditary renal carcinomas (von Hippel-Lindau disease), carcinoma of the renal pelvis, ureteral carcinoma, fibroma, papillary adenoma, angiomylipoma, oncocytoma
leukocytes: acute lymphoblastic leukemia/lymphoma, chronic lymphocytic leukemia, follicular lymphoma, large B-cell lymphoma, Burkitt lymphoma, plasma cell neoplasms, mantle cell lymphoma, lymphoplasmacytic lymphoma, peripheral T-cell lymphoma, adult T-cell leukemia/lymphoma, Hodgkin disease, acute myelogenous leukemia, chronic myelogenous leukemia, thymic hyperplasia, hairy cell leukemia, malignant transformation, inappropriate activation or abnormalities of leukocytes (e.g., immature, precursor B (pre-B) or precursor T (pre-T) lymphocytes, monocytes, neutrophils, eosinophils, basophils, dendritic cells, lymphoblasts), arthritis, inflammation, leukocytosis, lymphadenitis, lymphangitis, bacteremia, chronic nonspecific lymphadenitis, psoriasis, wound healing
- 30 liver: hepatitis (e.g., types A, B, C), benign epithelial tumors and tumor like conditions, primary malignant epithelial tumors, primary malignant mesenchymal tumors, tumors of the gallbladder or bile duct
- 35 lung: lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, esophageal cancer
ovary: ovarian carcinoma (e.g., epithelial (serous tumors, mucinous tumors, endometrioid tumors), germ cell (e.g., teratomas, choriocarcinomas, polyembryomas, embryonal carcinoma, endodermal sinus tumor, dysgerminoma, gonadoblastoma), stromal carcinomas (e.g., granulosa stromal cell tumors)), fallopian tube carcinoma, peritoneal carcinoma, leiomyoma
- 40 pancreas: adenocarcinoma, ductal adenocarcinoma, mucinous cyst adenocarcinoma, acinar cell carcinoma, unclassified large cell carcinoma, small cell carcinoma, pancreatoblastoma, duct-ectatic mucin-hypersecreting tumor, mucinous cyst adenoma, papillary cystic neoplasm, serous cyst adenoma, diabetes mellitus, chronic pancreatitis
prostate: epithelial neoplasms (e.g., adenocarcinoma, small cell tumors, transitional cell carcinoma, carcinoma in situ, and basal cell carcinoma), carcinosarcoma, non-epithelial neoplasms (e.g., mesenchymal and lymphoma), germ cell tumors, prostatic intraepithelial neoplasia (PIN), hormone independent prostate cancer, benign prostate hyperplasia, prostatitis
- 45 skin/melanoma: melanoma, lentigo (common benign localized hyperplasia of melanocytes), nevocellular nevi (congenital or acquired neoplasm of melanocytes), actinic keratosis (overgrowth of outer layers of skin), basal cell carcinoma, Merkel cell carcinoma, benign fibrous histiocytoma (dermal neoplasms of fibroblasts and histiocytes), dermatofibrosarcoma protuberans (well differentiated fibrosarcoma of the skin), xanthomas (tumor-like collections of foamy histiocytes within the dermis), dermal vascular tumors, seborrheic keratoses (benign tumor), acanthosis nigricans (benign or malignant hyperplasia and hyperpigmentation of skin), and squamous cell carcinomas of the skin, lung, cervix, esophagus, uterus, head, neck, or bladder
- 50 soft tissue: soft tissue tumors (e.g., fibrosarcoma, liposarcoma, leiomyosarcoma, histiocytoma, fibrohistiocytic sarcoma) smooth muscle tumors (e.g., rhabdomyoma, rhabdomyosarcoma) tumors of the blood and lymph vessels (e.g., angiosarcoma, lymphangiosarcoma, lymphangiosarcoma, Kaposi's sarcoma), perivascular tumors (e.g., glomus tumors, hemangiopericytoma), synovial tumors (e.g., mesothelioma), neural tumors (e.g., neurofibroma, neurofibrosarcoma, malignant peripheral nerve sheath tumors, granular cell tumors, plexosarcoma, ganglioneuroblastoma, neuroepithelioma, extraskeletal Ewing's sarcoma, schwannoma, neuroma, ganglioneuroma), paraganglioma, extraskeletal cartilaginous and osseous tumors (e.g., chondrosarcoma, osteosarcoma), pluripotential mesenchymal tumors, epithelioid sarcomas, rhabdoid tumors, desmoplastic small cell tumors, alveolar sarcoma
- 55 stomach: adenocarcinoma, squamous cell carcinoma, adenocanthoma, carcinoid, leiomyosarcoma, gastritis (chronic atrophic, H. pylori associated), hyperplastic polyps, lipoma, leiomyoma, esophageal adenocarcinomas
testicles: germ cell tumors (including seminomas, embryonal carcinomas, teratomas, choriocarcinomas, yolk sac tumors), sex chord stromal tumors (including Leydig cell tumors, Sertoli cell tumors, and Granulosa cell tumors), germ cell and gonadal stromal elements (e.g., gonadoblastomas), adnexal and paratesticular tumors (e.g., mesotheliomas, soft tissue sarcomas, and adnexal of the rete testes), miscellaneous neoplasms (including carcinoid, lymphoma, and cysts)
uterus: epithelial tumors (e.g., endometrioid, papillary endometrioid, papillary serous, clear cell, mucinous), mesenchymal tumors (e.g., endometrial stromal sarcoma, leiomyosarcoma, nonspecific sarcomas), mixed tumors (e.g., malignant mixed müllerian tumors, adenosarcoma)

70 Tables 2B-72B, 76B, and 79B list accession numbers for Pkeys lacking UnigeneID's for Tables 2A-72A, 76A, and 79A, respectively. For each probeset is listed gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

75 Tables 2C-72C, 76C, and 79C list genomic positioning for Pkeys lacking Unigene ID's and accession numbers in Tables 2A-72A, 76A, and 79A, respectively. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Table 2A, Disease Indications and Preferred Utilities for Selected Genes

80 Table 2A provides preferred disease indications and preferred utilities for about 413 selected genes. These genes were identified using Eos/Affymetrix Genechip arrays.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number
UnigeneID: Unigene ID number

5	<p>Unigene Title: Unigene gene title</p> <p>Disease: preferred diseases indicated for selected gene as described in table 1 and abbreviated as follows: blad (bladder diseases), angio (blood vessel diseases), EWS (bone diseases), glio (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrosis diseases), headnk (head & neck diseases), lei (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), omuc (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), sarc (soft tissue and bone diseases), mela (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)</p> <p>Utility: preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)</p>
10	<p>Pkey; ExAccn; UnigenID; Unigene Title; Disease; Utility</p>
15	<p>102892; BE440042; Hs.83326; matrix metalloproteinase 3 (st; headnk; mAb+diag+s.m.</p> <p>104865; T79340; Hs.22575; B-cell CLL/lymphoma 6, member; angio; CTL</p> <p>104978; A1199268; Hs.19322; Homo sapiens, Similar to RIKEN; colon, lung, pros, blad, stom; CTL</p> <p>109424; NM_005328; Hs.85962; hyaluronan synthase 3; blad, lung; mAb+s.m.</p> <p>110765; AK000322; Hs.18457; hypothetical protein FLJ20315; colon, pros, stom, uter; mAb+diag</p> <p>110906; AA035211; Hs.17404; SOX7 SRY (sex determining reg); angio, blad; CTL</p> <p>115522; BE614387; Hs.333893; c-Myc target JPO1; colon, lung, blad, panc; CTL</p> <p>116176; AA311152; Hs.288708; hypothetical protein FLJ21562; colon; CTL</p>
20	<p>118695; AK000465; Hs.50081; KIAA1199 protein; colon, lung; diag</p> <p>123049; BE047680; Hs.211869; dickkopf (Xenopus laevis) homo; EWS; mAb+diag</p> <p>131486; F06972; Hs.27372; endothelial tyrosine kinase (E; angio; CTL+s.m.</p> <p>133370; AF245505; Hs.72157; Adican; breast, lung, panc; diag</p> <p>310016; AW449612; Hs.152475; ESTs; colon; CTL</p>
25	<p>322305; AJ357412; Hs.157801; ESTs; colon, pros, fibro, breast; CTL+diag</p> <p>400289; X07820; Hs.2258; matrix metalloproteinase 10 (s; angio, blad, lung, cerv, ovar, headnk, esoph; mAb+diag+s.m.</p> <p>400297; A1127076; Hs.288381; hypothetical protein DKFZp564O; breast, blad, colon, pros; mAb</p> <p>400303; AA242758; Hs.79136; LIV-1 protein, estrogen regula; breast, ovar, pros, stom, uter, blad, lung, headnk; mAb</p> <p>400843; ; NM_003105; Homo sapiens sortil; blad; s.m.</p>
30	<p>402075; ; ENSP00000251056; Plasma membra; blad, lung, headnk, cerv, mela, esoph; mAb+diag</p> <p>402901; ; NM_025206; Homo sapiens hypoth; blad; CTL</p> <p>404287; ; FGENESH predicted novel CUB-do; panc, lung, colon, uter, esoph; mAb+s.m.</p> <p>404682; ; ortholog of mouse polydomain p; panc; diag</p> <p>404875; ; NM_022819; Homo sapiens phosph; blad; CTL+s.m.</p>
35	<p>404977; ; Insulin-like growth factor 2 (; blad, ovar, sarc; mAb+diag</p> <p>405033; ; C1002652; gij544327[sp]Q04799; blad; s.m.</p> <p>406400; ; kallikrein 8 (neurotrophin/ovasin; ovar, uter; diag</p> <p>406964; M21305; ; FGENES predicted novel secrete; angio, blad, fibro, sarc; diag</p> <p>407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE:4299; glio, blad; CTL</p>
40	<p>407792; A1077715; Hs.39384; putative secreted ligand homol; ovar, uter, cerv, panc; mAb+diag</p> <p>407811; AW190902; Hs.40098; cysteine knot superfamily 1, B; blad, panc, stom, uter, lung, esoph; diag</p> <p>407836; T79340; Hs.22575; B-cell CLL/lymphoma 6, member; angio; CTL</p> <p>407975; X89426; Hs.41716; endothelial cell-specific mole; angio, renal; diag</p> <p>408243; Y00787; Hs.624; Interleukin 8; blad, stom, headnk, cerv, lung, angio, esoph, panc; diag</p>
45	<p>408367; AK001178; Hs.44424; Homo sapiens orphan neurotrans; mela; mAb+s.m.</p> <p>408369; R38438; Hs.118747; SLC15A2 Solute carrier family; pros, lung, fibro, uter, glio, cerv, ovar; mAb</p> <p>408380; AF123050; Hs.44532; diubiquitin; lung, blad, headnk, panc, stom, fibro, esoph, mela; CTL</p> <p>408482; NM_000676; Hs.45743; adenosine A2b receptor; lung, esoph, headnk, colon; mAb+s.m.</p> <p>408562; A436323; Hs.31141; roundabout (axon guidance rece; uter, fibro, sarc; mAb+s.m.</p>
50	<p>408790; AW580227; Hs.47860; neurotrophic tyrosine kinase; lung; mAb+s.m.</p> <p>408908; BE296227; Hs.250822; serine/threonine kinase 15; blad, lung, headnk, stom, colon; s.m.</p> <p>409041; AB033025; Hs.50081; Hypothetical protein, XP_05186; uter, ovar, lung, colon, stom, headnk, breast, panc; CTL+diag</p> <p>409079; W87707; Hs.82065; interleukin 6 signal transduce; breast, pros; mAb+s.m.</p> <p>409103; AF251237; Hs.112208; XAGE-1 protein; lung; CTL</p>
55	<p>409178; BE393948; Hs.50915; kallikrein 5; ovar, breast, mela; diag</p> <p>409220; BE243323; Hs.51233; tumor necrosis factor receptor; angio, renal, colon, stom; mAb+s.m.</p> <p>409420; Z15008; Hs.54451; laminin, gamma 2 (niclin (100k; lung, headnk, panc, stom, cerv, esoph, blad; diag</p> <p>409632; W74001; Hs.55279; serine (or cysteine) proteinase; lung, blad, headnk; diag</p> <p>409663; A1743750; Hs.98306; KIAA1862 protein; renal; CTL</p>
60	<p>409757; NM_001898; Hs.123114; cystatin SN; panc, stom, lung, blad; diag</p> <p>409889; AW630041; Hs.56937; suppression of tumorigenicity; colon, ovar, pros; mAb+s.m.</p> <p>409893; AW247090; Hs.57101; minichromosome maintenance def; lung, cerv, blad, test, esoph; CTL+s.m.</p> <p>409956; AW103364; Hs.727; inhibin, beta A (activin A, ac; breast, panc, ovar, colon, headnk, lung, blad, esoph; diag</p> <p>410001; AB041036; Hs.57771; kallikrein 11; ovar, pros, uter, cerv, lung; diag</p>
65	<p>410055; AJ250839; Hs.58241; gene for serine/threonine prot; renal; s.m.</p> <p>410153; BE311926; Hs.15830; hypothetical protein FLJ12691; renal, blad; CTL</p> <p>410274; AA381807; Hs.336402; hypoxia-inducible protein 2; lung, renal; CTL</p> <p>410309; BE043077; Hs.278153; alpha-2,8-sialyltransferase II; panc; s.m.</p> <p>410407; X66839; Hs.63287; carbonic anhydrase IX; renal, lung, colon, stom, ovar, uter, blad, sarc; mAb+s.m.</p>
70	<p>410418; D31382; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.</p> <p>411274; NM_002776; Hs.69423; kallikrein 10; colon, ovar, uter, cerv, headk, panc; diag</p> <p>411411; AA345241; Hs.55950; ESTs, Weakly similar to KIAA13; renal; mAb+s.m.</p> <p>411773; NM_006799; Hs.72026; protease, serine, 21 (testisin; ovar; diag</p> <p>411975; A1916058; Hs.144583; 3'UTR of: dead ringer (Drosoph; test, colon; CTL</p>
75	<p>412078; X69699; Hs.73149; paired box gene 8; ovar; CTL</p> <p>412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like; lung, blad, headnk, breast, ovar, panc, angio, test, mela; s.m.</p> <p>412314; AA825247; Hs.356084; G protein-coupled receptor 27; ovar, uter, test; mAb+s.m.</p> <p>412609; Z48804; Hs.74124; ocular albinism 1 (Nettleship; mela; s.m.</p> <p>412628; A1972402; Hs.306051; hypothetical protein MGC2648; pros; diag</p>
80	<p>412709; AL022327; Hs.74518; KIAA0027 protein; glio, sarc; mAb+s.m.</p> <p>412719; AWO16610; Hs.816; ESTs; lung, headnk, blad, glio, cerv, sarc; s.m.</p> <p>412959; D87458; Hs.75090; KIAA0282 protein; glio; CTL+s.m.</p> <p>413048; M93221; Hs.75182; mannose receptor, C type 1; fibro, panc; mAb</p>

- 413063; AL035737; Hs.75184; chitinase 3-like 1 (cartilage); glio, ovar, blad, lung; diag
 413278; BE563085; Hs.833; Interferon-stimulated protein; panc, lung, blad, breast, cerv, ovar, headnk, esoph, mel; CTL+s.m.
 413324; V00571; Hs.75294; corticotropin releasing hormon; blad; diag
 413385; M34455; Hs.840; indoleamine-pyrrole 2,3 dioxyg; blad, lung, mel, fibro, uter, sarc; s.m.
 413554; AA319148; Hs.75426; secretogranin II (chromogranin); panc, glio; diag
 413719; BE439580; Hs.75498; small inducible cytokine subfa; leuk, panc, lung, headnk, cerv, colon, uter, stom, esoph; diag
 414555; N88569; Hs.76422; phospholipase A2, group IIA (p; pros; s.m.
 414577; A056548; Hs.378938; hypothetical protein FLJ20992; angio; CTL+diag
 414774; X02419; Hs.77274; plasminogen activator, urokin; lung, blad, headnk, panc, stom, ovar, esoph; diag
 414812; X72755; Hs.77367; monokine induced by gamma int; breast, blad, lung, fibro, panc, colon, headnk, cerv, stom, renal, ovar, test, mel, esoph; diag
 414883; AA926960; Hs.348669; CDC28 protein kinase 1; lung, ovar, stom, colon, cerv, headnk, test; s.m.
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; blad, lung, ovar, test; s.m.
 414991; C17898; ; Homo sapiens up-regulated by 8; fibro, lung; mAb+diag
 415138; C18358; Hs.295944; tissue factor pathway inhibitor; angio, panc, stom, lung, uter; CTL+diag
 415539; A1733881; Hs.72472; NAME OMITTED ... receptor kinase; breast; mAb+s.m.
 415668; AW957684; Hs.306814; Homo sapiens lysyl oxidase-like; mel; diag
 415669; NM_005025; Hs.78589; serine (or cysteine) proteinase; lung; mAb+diag+s.m.
 415817; U88967; Hs.78867; protein tyrosine phosphatase; ; lung, glio, headnk, cerv, mel, esoph, fibro; mAb+s.m.
 415929; AA724373; Hs.304950; Homo sapiens mucolin-3 (MCO3); mel; mAb
 416091; AF295370; Hs.283082; defensin, beta 3; headnk, esoph, mel; CTL+diag
 416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient; lung, headnk, colon, uter, stom; CTL+s.m.
 416250; AA581386; Hs.73452; Kremen 2; esoph, lung, cerv, ovar; mAb+s.m.
 416530; U62801; Hs.79381; kallikrein 6 (neurosin, zyme); ovar, uter; diag
 416636; N32536; Hs.42645; solute carrier family 16 (mono; breast, panc, uter, mel; mAb+s.m.
 416658; U03272; Hs.79432; fibrillin 2 (congenital contra; lung, ovar, uter, blad, angio, test, sarc; diag
 416836; D54745; Hs.80247; cholecystokinin; pros, EWS, glio; diag
 416857; AA188775; Hs.292453; FGENSESH predicted TM containin; glio; mAb+s.m.
 416965; N26223; Hs.160436; MDAC1; fibro, ovar, uter; mAb
 417034; NM_006183; Hs.80962; neurotensin; lung, headnk, cerv; diag
 417079; U65590; Hs.81134; interleukin 1 receptor antagon; blad, lung, headnk, cerv, esoph; diag
 417166; AA431323; Hs.42146; Paired box protein Pax-3; mel, sarc; CTL
 417389; BE260964; Hs.82045; midkine (neurite growth-promot; ovar, lung, blad, uter, cerv, panc, stom, mel, test, colon, sarc; mAb+diag
 417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glyco; panc, breast, blad, lung, headnk, cerv, uter, ovar, stom, renal; mAb
 417771; AA804698; Hs.82547; retinoic acid receptor respond; blad, cerv, panc, pros, ovar; mAb
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; lung, panc, breast, ovar, headnk, stom, sarc; CTL
 417931; W95642; Hs.82961; trefol factor 3 (intestinal); ovar, panc, stom, colon, uter, pros; diag
 417933; X02308; Hs.82962; thymidylate synthetase; blad, lung, angio, colon, panc, esoph; s.m.
 418007; M13509; Hs.83169; matrix metalloproteinase 1 (in; lung, blad, fibro, headnk, panc, stom, colon, ovar, esoph, mel; mAb+diag+s.m.
 418030; BE207573; Hs.83321; neuromedin B; glio, panc; diag
 418064; BE387287; Hs.83384; S100 calcium-binding protein; ; mel; diag
 418281; U09550; Hs.11554; oviductal glycoprotein 1, 120k; uter, ovar; CTL+diag
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibi; lung, blad, ovar, headnk, panc, cerv, mel, sarc; s.m.
 418500; AA084248; Hs.372651; Unknown protein for MGC:29643; angio, ovar, glio, uter, lung, blad, panc, mel, sarc; mAb+diag
 418526; BE019020; Hs.85838; solute carrier family 16 (mono; lung, blad, renal, panc, stom, colon, ovar; mAb+s.m.
 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via d; esoph, headnk; s.m.
 418678; NM_001327; Hs.87225; cancer/testis antigen (NY-ESO-1); lung, blad, stom, ovar, panc, esoph, cerv, sarc; CTL
 418738; AW388633; Hs.6682; solute carrier family 7, (cat; angio, lung, ovar, blad, colon, stom, panc, uter, leuk; mAb+s.m.
 418830; BE513731; Hs.348874; hypothetical protein MGC4816; lung; CTL
 418867; D31771; Hs.89404; msh (Drosophila) homeo box hom; blad; s.m.
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), recepr; leuk, ovar, breast, blad, renal; mAb+s.m.
 419080; AW150835; Hs.18878; hypothetical protein FLJ21620; renal, lower uter, lung; CTL
 419121; AA374372; Hs.89626; parathyroid hormone-like hormo; lung, esoph, headnk, blad; diag
 419171; NM_002846; Hs.89655; protein tyrosine phosphatase; ; lung; mAb+s.m.
 419172; AW338625; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio, renal; mAb+s.m.
 419183; U06669; Hs.89663; cytochrome P450, subfamily X0; blad, lung, headnk, panc; CTL+s.m.
 419216; AU076718; Hs.164021; small inducible cytokine subfa; panc, lung, stom, cerv, pros, headnk, esoph; diag
 419235; AW470411; Hs.288433; neurotrophin; panc, fibro, headnk, lung; mAb+diag
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ovar, pros, lung, breast, uter, test, panc, stom, sarc; mAb+s.m.
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-fam; glio, omuc, stom, lung, panc, colon, renal, uter; mAb+s.m.
 419556; U29615; Hs.91093; chitinase 1 (chitinotriidase); lung, fibro, test; mAb+diag
 419704; AA429104; Hs.45057; ESTs; glio; CTL+s.m.
 419723; AL120193; Hs.339810; longevity assurance (LAG1, S; ; glio; mAb+diag
 419741; NM_007019; Hs.93002; ubiquitin carrier protein E2-C; blad, lung, colon, ovar, test, esoph, mel, sarc; CTL+s.m.
 419833; AA251131; Hs.220697; Homo sapiens tryptophanyl-IRNA; fibro, stom, blad, esoph, uter; diag
 420159; A1572490; Hs.99785; Homo sapiens cDNA: FLJ21245 f; blad, stom; mAb
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; lung, mel, sarc; s.m.
 420370; Y13645; Hs.97234; uroplakin 2; blad; mAb
 420440; NM_002407; Hs.97644; mammaglobin 2; ovar, uter, cerv; diag
 420602; AF060877; Hs.99236; regulator of G-protein signal; headnk, glio, cerv, mel; CTL+s.m.
 420610; A1683183; Hs.99348; distal-less homeo box 5; uter, endo, lung; CTL
 420737; U08096; Hs.99899; CD70; tumor necrosis factor; renal; mAb+s.m.
 420876; AA918425; Hs.177744; FGENSES predicted novel protein; panc, blad; s.m.
 421066; AU076725; Hs.101408; branched chain aminotransferase; blad, lung; CTL+s.m.
 421110; A1250717; Hs.1355; cathepsin E; blad, panc, stom, lung, fibro, ovar, esoph; sm+diag
 421340; F07783; Hs.1369; decay accelerating factor for; angio, panc, stom; diag
 421379; Y15221; Hs.103982; small inducible cytokine subfa; breast, panc, headnk, lung, stom, blad, cerv, colon, leuk, fibro, test, mel, esoph; diag
 421471; U80545; Hs.327179; solute carrier family 17 (sodi; renal; mAb+s.m.
 421474; U76362; Hs.104637; solute carrier family 1 (gluta; lung; mAb+s.m.
 421524; AA312082; Hs.105445; GDNF family receptor alpha 1; breast; mAb+s.m.
 421552; AF026692; Hs.105700; secreted frizzled-related prot; breast, ovar, panc, cerv, uter, pros, lung, stom, headnk; diag
 421563; NM_006433; Hs.105806; granulysin; fibro; diag
 421574; AJ000152; Hs.105924; defensin, beta 2; headnk, lung; CTL+diag
 421582; A1910275; Hs.350470; trefol factor 1 (breast cancer; breast, panc, lung, omuc; diag

- 421659; NM_014459; Hs.106511; protocadherin 17; fibro; mAb
- 421753; BE314828; Hs.107911; ATP-binding cassette, sub-fam1; lung; mAb+s.m.
- 421817; AF146074; Hs.108660; ATP-binding cassette, sub-fam1; lung, cerv, headnk, blad; mAb+s.m.
- 421829; AB018330; Hs.108708; calcium/calmodulin-dependent p; pros; s.m.
- 5 422048; NM_012445; Hs.288126; spondin 2, extracellular matr; panc, pros, sarc; diag
- 422083; NM_001141; Hs.111256; arachidonate 15-lipoxygenase; ; pros; s.m.
- 422109; S73265; Hs.1473; gastrin-releasing peptide; panc, lung, colon, fibro; diag
- 422158; L10343; Hs.112341; protease inhibitor 3, skin-der; headnk, blad, lung, cerv, stom, esoph; diag
- 422192; AA305159; Hs.113019; fts485; mela; s.m.
- 10 422260; AA315993; Hs.105484; regenerating gene type IV; colon, omuc, stom, panc; mAb+diag
- 422282; AF019225; Hs.114309; apolipoprotein L; blad, lung, headnk, renal; diag
- 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45; lung, blad, test, cerv, headnk, esoph; s.m.
- 422330; D30783; Hs.115263; epiregulin; panc, colon, blad; mAb+diag
- 15 422397; AJ223366; Hs.116051; MYEOV Myeloma overexpressed ge; panc, stom, colon, esoph, renal, blad; CTL+s.m.
- 422424; A186431; Hs.296638; prostate differentiation factor; blad, panc, pros, angio, colon, stom, lung, mela; diag
- 422578; AF239666; Hs.1545; caudal type homeo box transcr; colon; CTL
- 422627; BE336857; Hs.118787; transforming growth factor, be; colon, renal, sarc; mAb+diag
- 422765; AW409701; Hs.1578; baculoviral IAP repeat-contain; lung, blad; s.m.
- 20 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; blad, cer, lung, uter, angio, stom, test; s.m.
- 422867; L32137; Hs.1584; cartilage oligomeric matrix pr; breast, ovar, pros, panc, lung, colon, uter, sarc; diag
- 422956; BE545072; Hs.122579; ECT2 protein (Epithelial cell; ovar, blad, panc, lung, headnk, colon, stom; CTL+s.m.
- 423161; AL049227; Hs.124776; downstream of cadherin 6 (by 3; renal, ovar, blad; mAb+s.m.
- 423184; NM_004428; Hs.1624; ephrin-A1; pros, panc, renal, colon; mAb+s.m.
- 25 423242; AL039402; Hs.125783; DEME-6 protein; breast, renal, ovar, pros, colon; CTL
- 423508; AW604297; Hs.129711; hepatitis A virus cellular rec; renal, colon; mAb
- 423583; AL122055; Hs.129838; KIAA1028 protein; pros; s.m.
- 423634; AW959908; Hs.1690; heparin-binding growth factor; lung, blad, headnk, panc; diag
- 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (m; blad, lung, headnk, ovar, panc, colon, stom, uter, cerv, esoph, test; mAb+diag+s.m.
- 30 423936; U77629; Hs.135639; achaete-scute complex (Drosoph; colon, stom, ovar; CTL
- 423961; D13666; Hs.136348; periostin (OSF-2os); breast, colon, blad, lung, fibro, panc, headnk, ovar, mela, sarc; mAb+diag
- 424008; R02740; Hs.137555; putative chemokine receptor; G; blad, headnk, stom, cerv, esoph; mAb+s.m.
- 424046; AF027866; Hs.138202; serine (or cysteine) proteinase; headnk, lung, cerv; diag
- 424321; W74048; Hs.1765; lymphocyte-specific protein ty; mela, fibro; s.m.
- 35 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); lung, colon, test; s.m.
- 424411; NM_005209; Hs.146549; crystallin, beta A2; panc, sarc; s.m.
- 424502; AF242388; Hs.149585; lensin; lung; s.m.
- 424503; NM_002205; Hs.149609; Integrin, alpha 5 (fibronectin; panc, pros, angio, blad, lung; mAb+s.m.
- 424620; AA101043; Hs.151254; kallikrein 7 (chymotryptic, st; ovar; diag
- 40 424687; J05070; Hs.151738; matrix metalloproteinase 9 (ge; headnk, panc, lung, blad, uter, cerv, colon, stom, test, mela, sarc; diag
- 424735; U31875; Hs.272499; short-chain alcohol dehydrogen; blad, breast; CTL+s.m.
- 424825; AF207069; Hs.153357; procollagen-lysine, 2-oxogluta; mela; CTL+s.m.
- 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a); ovar, blad, lung, headnk, panc, stom; s.m.
- 424917; A1636208; Hs.96901; hypothetical protein FLJ23043; fibro, uter, ovar; CTL
- 424943; AU077260; Hs.153924; death-associated protein kinase; fibro; s.m.
- 45 425009; X58288; Hs.154151; protein tyrosine phosphatase; ; renal, fibro; mAb+s.m.
- 425071; NM_013989; Hs.154424; deiodinase, iodothyronine, typ; pros, colon, stom, uter, cerv, headnk, esoph, panc; diag
- 425115; R44664; Hs.123956; downstream of: G protein-coup; gli; mAb+s.m.
- 425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (s; breast, ovar, lung, colon, panc, headnk, stom, uter, cerv, blad, esoph, sarc; mAb+diag+s.m.
- 50 425263; NM_001197; Hs.155419; BCL2-interacting killer (apopt; pros; s.m.
- 425322; U63630; Hs.155637; protein kinase, DNA-activated; lung, headnk; s.m.
- 425335; AB007937; Hs.158287; syndecan 3; mela, gli; mAb+s.m.
- 425650; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgar; lung, headnk, cerv, esoph, blad; mAb
- 425721; AC002115; Hs.159309; uroplakin 1A; blad; mAb
- 55 425723; NM_014420; Hs.159311; dickkopf (Xenopus laevis) homo; endo, uter, colon; CTL+diag
- 425734; AF056209; Hs.159396; peptidylglycine alpha-amidatin; lung; s.m.
- 425776; U25128; Hs.159499; parathyroid hormone receptor 2; ovar, uter, lung; mAb+diag
- 425842; A1587490; Hs.159623; NK-2 (Drosophila) homolog B; panc, gli; s.m.
- 425852; AK001504; Hs.159651; death receptor 6, TNF superfam; blad, lung, headnk; mAb+s.m.
- 60 425883; AL137708; Hs.161031; Homo sapiens mRNA; cDNA DKFZp4; blad, panc; mAb
- 425998; AU076629; Hs.165950; fibroblast growth factor recep; renal; mAb+s.m.
- 426028; NM_001110; Hs.172028; a disintegrin and metalloprote; blad; mAb+diag
- 426215; AW963419; Hs.155223; stanniocalcin 2; breast, lung, renal, colon, ovar, uter; mAb+diag
- 426227; U67058; Hs.154299; Human proteinase activated rec; panc, lung, colon, esoph, stom; mAb+s.m.
- 65 426322; J05068; Hs.2012; transcobalamin I (vitamin B12; panc, blad, stom; diag
- 426344; H41821; Hs.322489; transcriptional activator of t; gli; CTL+s.m.
- 426427; M86699; Hs.169840; TTK protein kinase; ovar, lung, headnk, cerv, colon, uter, stom, test; CTL+s.m.
- 426451; A1908165; Hs.169946; GATA-binding protein 3 (T-cell; blad, breast; s.m.
- 426514; BE616633; Hs.170195; bone morphogenetic protein 7 (; ovar, colon, blad, lung, cerv; mAb+diag
- 70 426600; NM_003378; Hs.171014; VGF nerve growth factor induc; mela, sarc; diag
- 426761; A1015709; Hs.172089; PORIMIN Pro-oncosis receptor t; lung, esoph, pros, uter, panc, colon, ovar, headnk; mAb+s.m.
- 426812; AF105365; Hs.172613; solute carrier family 12 (pota; renal; mAb+s.m.
- 426890; AA393167; Hs.41294; ESTs; renal, colon, ovar, uter, stom; CTL
- 427239; BE270447; Hs.356512; ubiquitin carrier protein; lung, blad, test, mela, sarc; CTL+s.m.
- 75 427335; AA448542; Hs.278444; G antigen 7B; lung, headnk, blad, mela, esoph, sarc; CTL
- 427343; A1880044; Hs.176977; protein kinase C binding prote; gli; CTL+s.m.
- 427722; AK000123; Hs.180479; hypothetical protein FLJ20116; colon, stom, panc; CTL
- 427747; AW411425; Hs.180655; serine/threonine kinase 12; blad, lung, ovar, stom, test, esoph, sarc; s.m.
- 427923; AW274357; Hs.301406; FGENSEH predicted 11 TM prota; mela; mAb
- 427969; NM_001963; Hs.2230; epidermal growth factor (beta-; panc; mAb+diag
- 80 428093; AW594508; Hs.104830; ESTs; ovar, panc; CTL
- 428179; A1127772; Hs.380877; serum/glucocorticoid regulated; breast; s.m.
- 428187; A1687303; Hs.285529; G protein-coupled receptor 49; ovar, uter, colon, stom; mAb+s.m.
- 428242; H55709; Hs.2250; leukemia inhibitory factor (ch; ovar, panc, leuk, lung; diag

- 428296; NM_003058; Hs.183572; solute carrier family 22 (orga; renal; mAb+s.m.
 428330; U22524; Hs.2256; matrix metalloproteinase 7 (ma; uter, ovar, fibro, pros, panc, lung, blad, headnk, esoph, mela; mAb+diag+s.m.
 428368; BE440042; Hs.83326; matrix metalloproteinase 3 (st; headnk, stom, esoph, colon; diag
 428392; H10233; Hs.2265; secretory granule, neuroendocr; panc; diag
 428450; NM_014791; Hs.184339; KIAA0175 gene product; ovar, cerv, panc, lung, blad, mela; s.m.
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S; lung, blad, colon, uter, ovar; s.m.
 428484; AF104032; Hs.184601; solute carrier family 7 (catio; lung, blad, headnk, cerv, esoph, glio, uter, stom, colon, mela; mAb+s.m.
 428486; AW583497; Hs.184604; pancreatic polypeptide; panc; diag
 428505; AL035461; Hs.2281; chromogranin B (secretogranin; panc, lung; diag
 428513; BE220806; Hs.184697; plexin C1; mela, panc, breast stom, headnk; mAb
 428579; NM_005756; Hs.184942; G protein-coupled receptor 64; ovar, EWS, uter; mAb+s.m.
 428664; AK001666; Hs.189095; similar to SALL1 (sal (Drosoph; blad, ovar, pros, lung, stom, test; CTL+s.m.
 428698; AAB52773; Hs.334838; KIAA1866 protein; breast, colon, lung, panc, stom, headnk, ovar; EWS; mAb
 428748; AW593206; Hs.98785; Ksp37 protein; lung, sarc; diag
 428758; AA433988; Hs.98502; CA125 antigen; much 16; ovar, cerv, lung, panc, stom, renal; diag
 428778; AK000530; Hs.193326; fibroblast growth factor recept; ovar; mAb+s.m.
 428953; AA306610; Hs.348183; tumor necrosis factor receptor; cerv, panc, colon, stom, headnk, renal; mAb+diag
 428969; AF120274; Hs.194689; artemin; lung, cerv; diag
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG; stom, panc, colon, ovar, fibro; mAb+s.m.
 429149; AW193360; Hs.197962; Homolog of mouse ADP-ribosylat; glio; mAb+s.m.
 429211; AF052693; Hs.198249; gap junction protein, beta 5 (j; lung, blad, headnk, cerv, esoph, stom, mela; mAb+s.m.
 429263; AA019004; Hs.198396; ATP-binding cassette, sub-fam1; lung; mAb+s.m.
 429276; AF056085; Hs.198612; G protein-coupled receptor 51; angio, blad, glio; mAb+s.m.
 429353; AL117406; Hs.335891; ATP-binding cassette transport; breast, pros; mAb+s.m.
 429547; AW009166; Hs.99376; FGENSESH predicted novel secret; panc, headnk, lung, ovar; diag
 429610; AB024937; Hs.211092; LUNX protein; PLUNC (palate l; lung, fibro; mAb+diag
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, reg; lung, mela; s.m.
 429910; NM_000867; Hs.2507; 5-hydroxytryptamine (serotonin); leio; mAb+s.m.
 430147; R60704; Hs.234434; hairy/enhancer-of-split relata; glio; s.m.
 430178; AW449612; Hs.152475; 3'UTR of. achaete-scute comple; colon, stom, ovar; CTL
 430377; NM_001922; Hs.301865; dopachrome tautomerase (dopach; mela; CTL
 430413; AW842182; Hs.241392; small inducible cytokine A5 (R; fibro, esoph, mela; diag
 430486; BE062109; Hs.241551; chloride channel, calcium acti; lung, blad, headnk, cerv, esoph; mAb+s.m.
 430822; AJ005371; Hs.248017; glyceraldehyde-3-phosphate deh; mela, sarc; s.m.
 431130; NM_006103; Hs.2719; HE4; epididymis-specific, whey; ovar, uter; diag
 431462; AW583672; Hs.256311; granin-like neuroendocrine pep; panc, lung, glio, test; diag
 431515; NM_012152; Hs.258583; EDG-7 (endothelial different; ovar, pros, lung, blad; mAb+s.m.
 431620; AA126109; Hs.264981; 2'-5'-oligoadenylate synthetas; esoph, cerv; CTL+s.m.
 431629; AU077025; Hs.265827; interferon, alpha-inducible pr; panc, uter, cerv, stom, esoph, mela; mAb+diag
 431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD4; ovar, panc, blad, headnk, mela, renal; mAb+s.m.
 431745; AW972448; Hs.163425; Novel FGENSESH predicted cadher; fibro, ovar, uter; mAb
 431840; AA534908; Hs.2860; POU domain, class 5, transcrip; test, renal, blad; CTL
 431846; BE019924; Hs.271580; uroplakin 1B; lung, blad, headnk, uter, cerv, stom, ovar; mAb+diag
 431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin; lung, blad, cerv, headnk, ovar, colon, pros, panc, breast, esoph, test, mela; mAb+diag
 432101; A1918950; Hs.123642; EphA3; pros, panc, EWS sarc; s.m.
 432179; X75208; Hs.2913; EphB3; ovar, colon; mAb+s.m.
 432196; AW300888; Hs.273230; hypothetical protein FLJ10830; renal; CTL
 432201; A1538613; Hs.298241; Transmembrane protease, serine; breast, colon, ovar, stom, panc, uter, cerv, lung; mAb+diag+s.m.
 432578; AF043244; Hs.278439; nucleolar protein 3 (apoptosis; renal; CTL
 432596; AJ224741; Hs.278461; matrilin 3; panc, breast, sarc; diag
 432606; NM_002104; Hs.3066; granzyme K (serine protease, g; renal, breast, lung, stom, hepC, fibro, leuk; CTL
 432828; W60377; Hs.57772; ESTs; blad; CTL+s.m.
 432874; W94322; Hs.278651; melanoma inhibitory activity; panc, stom, mela, sarc; diag
 432990; AL036071; Hs.279899; tumor necrosis factor receptor; pros, renal; mAb+s.m.
 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; colon, breast, lung, blad, cerv, uter, test, mela; s.m.
 433447; U29195; Hs.3281; neuronal pentraxin II; mela, esoph, colon, renal; diag
 433848; AF095719; Hs.93764; carboxypeptidase A4; headnk, esoph, lung; s.m.
 433867; AK000596; Hs.3618; hippocalcin-like 1; renal; CTL
 434206; AW136973; Hs.362915; ESTs, Weakly similar to S69890; colon, lung, stom; CTL+s.m.
 434276; AF123659; Hs.93605; leucine zipper, putative tumor; mela; s.m.
 434293; NM_004445; Hs.3796; EphB6; blad, pros; s.m.
 435013; H19123; Hs.110024; NM_020142; Homo sapiens NADHtub; renal, lung, sarc; CTL
 435472; AW972330; Hs.283022; triggering receptor expressed; glio; mAb
 435505; AF200492; Hs.211238; interleukin-1 homolog 1; lung, headnk; diag
 436456; AW292677; Hs.248122; melanin-concentrating hormone; mela, glio; mAb+s.m.
 436480; AJ271643; Hs.87469; putative acid-sensing ion chan; glio; mAb+s.m.
 436481; AA378597; Hs.6199; HSPC150 protein similar to ubt; lung, blad, colon, ovar, uter, headnk, test; s.m.
 436576; AJ458213; Hs.77542; ESTs; renal, panc, headnk, lung; mAb+s.m.
 436608; AA626980; Hs.192371; down syndrome critical region; blad, lung, sarc; CTL+s.m.
 436895; AF037335; Hs.5338; carbonic anhydrase XII; breast, renal, ovar, glio; mAb+s.m.
 436961; AW375974; Hs.156704; ESTs; lung, panc, renal, uter, colon; CTL
 436982; AB018305; Hs.6378; spondin 1, (I-spondin) extrace; ovar, fibro; diag
 437016; AU076916; Hs.5398; guanine monophosphate synthetas; lung, blad, cerv, esoph, colon, headnk; s.m.
 437044; AL035864; Hs.69517; differentially expressed in Fa; headnk, cerv, lung, blad, breast, pros, ovar, stom, esoph; CTL
 437789; AJ581344; Hs.127812; ESTs, Weakly similar to T17330; lung; CTL
 437852; BE001836; Hs.256897; putative GPCR; blad, lung; mAb+s.m.
 438380; T06430; Hs.6194; chondroitin sulfate proteoglyc; glio, mela; diag
 438549; BE386801; Hs.21856; trinucleotide repeat containin; mela, sarc; CTL+diag
 439018; AW300887; Hs.26638; membrane-spanning 4-domains, s; uter, stom, pros, fibro; mAb
 439223; AW238299; Hs.250618; UL16 binding protein 2; lung, headnk, cerv, esoph, leuk, blad, colon; mAb
 439477; W69813; Hs.58042; ESTs, Moderately similar to GF; lung; mAb+s.m.
 439569; AW602166; Hs.222399; CEGP1 protein; breast, pros, blad; diag
 439606; W79123; Hs.58561; G protein-coupled receptor 87; lung, blad, headnk, cerv, esoph; mAb+s.m.

- 439738; BE246502; Hs.9598; sema domain, immunoglobulin do; blad, lung, cerv, renal; mAb+s.m.
 439979; AW600291; Hs.6823; hypothetical protein FLJ10430; renal, cerv, pros, headnk, colon, test, sarc; mAb
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing; blad, ovar, lung, headnk, test; s.m.
 440065; W03476; Hs.266331; Homo sapiens Fc receptor homot; mela; diag
 440304; BE159984; Hs.125395; hepatitis A virus cellular rec; renal, colon, blad; mAb+s.m.
 440516; S42303; Hs.161; cadherin 2, type 1, N-cadherin; glo, ovar, uter, renal, hepC; mAb+diag
 440672; AF083811; Hs.7345; MAD1 (mitotic arrest deficient; mela; s.m.
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog; lung, blad, headnk, test, mela, esoph; s.m.
 442117; AW664964; Hs.128899; ESTs; hypothetical protein for; breast, lung, blad, panc, headnk, stom, ovar, pros, sarc; mAb+s.m.
 442133; AW874138; Hs.129017; ESTs; type Ia transmembrane p; ovar, uter; mAb
 442275; AW449467; Hs.54795; Homo sapiens secretogloblin, fa; fibro; diag
 442652; AI005163; Hs.201378; Homo sapiens cDNA FLJ40427 fis; fibro, ovar, uter; CTL
 443105; X95753; Hs.9004; chondroitin sulfate proteoglyc; mela; mAb+diag
 443247; BE614387; Hs.333893; c-Myc target JPO1; colon, lung, blad, panc; CTL
 443324; R44013; Hs.164225; ESTs; fibro; mAb+diag
 443426; AF098158; Hs.9329; chromosome 20 open reading fra; colon, lung, blad, stom, test, mela, sarc; CTL
 443595; AF169312; Hs.9613; PPAR(gamma) angiotensin relat; renal; diag
 443646; AI085198; Hs.164226; Thrombospondin 1; angio, panc, uter; diag
 443859; NM_013409; Hs.9914; follistatin; lung, cerv, headnk, blad, esoph; diag
 443987; AW163123; Hs.10071; seven transmembrane protein TM; renal; mAb+s.m.
 444006; BE395085; Hs.334762; type I transmembrane protein F; panc, colon, lung, ovar, renal, esoph, mela, blad, stom, cerv; mAb
 444090; S69115; Hs.10306; natural killer cell group 7 se; fibro, renal, mela; diag
 444371; BE540274; Hs.239; forkhead box M1; lung, headnk, blad, glo, test, mela; s.m.
 444381; BE387335; Hs.283713; hypothetical protein BC014245; breast, colon, blad, lung, panc, headnk, ovar, stom, uter, renal, angio, test, mela, esoph, sarc; CTL+diag
 444486; AW192879; Hs.355660; ancient conserved domain prote; renal; mAb+s.m.
 444527; NM_005408; Hs.11383; small inducible cytokine subfa; fibro, esoph; diag
 444781; NM_014400; Hs.11950; GPI-anchored metastasis-associ; lung, blad, headnk, cerv; mAb+diag
 444783; AK001468; Hs.62180; anillin (Drosophila Scrapes hom; ovar, lung, blad, headnk, panc, cerv, stom, uter, colon, esoph; CTL+s.m.
 445417; AK001058; Hs.12680; a disintegrin-like and metallo; panc, headnk, stom, lung, esoph, sarc, colon; diag
 445537; AJ245671; Hs.12844; EGF-like domain, multiple 6; ovar, blad, uter, breast, lung, headnk, renal, fibro, panc, cerv, sarc; mAb+diag
 445891; AW391342; Hs.199460; DPCR1 protein; stom, panc, esoph, omuc; esoph; mAb
 445895; D29954; Hs.13421; KIAA0056 protein; pros; CTL
 446051; BE048061; Hs.37054; ephrin-A3; colon, breast; mAb+diag
 446163; AA026880; Hs.25252; prolactin receptor; breast, cerv, uter; mAb+s.m.
 446341; AL040763; Hs.310735; FGENESH prediction similar to; mela; mAb+s.m.
 446619; AU076643; Hs.313; secreted phosphoprotein 1 (ost; ovar, fibro, panc, headnk, lung, colon, blad, mela, esoph, uter, sarc; diag
 446650; AB016625; Hs.15813; solute carrier family 22 (orga; renal; mAb+s.m.
 446921; AB012113; Hs.18530; small inducible cytokine subfa; breast, panc, headnk, lung, fibro, mela; diag
 447033; AJ357412; Hs.157601; Predicted gene: Eos cloned; se; colon, pros, fibro, breast, ovar, lung, panc, sarc; CTL+diag
 447072; D61594; Hs.17279; tyrosylprotein sulfotransferas; glo, panc; CTL+s.m.
 447131; NM_004585; Hs.17466; retinoic acid receptor respond; renal, breast, stom, lung, mela, ovar; mAb+s.m.
 447208; BE315291; Hs.237971; hypothetical protein MGC5627; esoph, stom, colon; CTL+diag
 447269; NM_004861; Hs.17958; cerebroside (3'-phosphoadenyly; renal; CTL
 447342; AI199268; Hs.19322; Homo sapiens, Similar to RIKEN; colon, blad, pros, lung, stom, ovar; CTL
 447400; AK000322; Hs.18457; hypothetical protein FLJ20315; colon, pros, stom, uter; mAb+diag
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; mela; s.m.
 448243; AW369771; Hs.367688; Integrin, beta 8; ovar, uter, lung, stom, headnk, glo, panc; mAb+s.m.
 448610; NM_008157; Hs.21602; nei (chicken)-like 1; mela, sarc; diag
 448733; NM_005629; Hs.187958; solute carrier family 6 (neuro; lung, renal; mAb+s.m.
 448844; AI581519; Hs.177164; FGENESH predicted novel cell s; panc, lung, stom, omuc; mAb+s.m.
 449032; AA045573; Hs.22900; nuclear factor (erythroid-der; colon, test, stom; CTL+s.m.
 449048; Z45051; Hs.22920; similar to S68401 (cattle) glu; panc, ovar, uter, glo, headnk, lung, sarc; mAb
 449444; AW818436; Hs.351306; solute carrier family 16 (mono; renal, panc; mAb+s.m.
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor; lung, panc, renal, stom, hepC, fibro, leuk, mela; mAb+s.m.
 449720; AA311152; Hs.288708; hypothetical protein FLJ21562; colon; CTL
 449722; BE280074; Hs.23960; cyclin B1; headnk, blad, lung, panc, angio, test, mela, esoph; s.m.
 450001; NM_001044; Hs.406; solute carrier family 6 (neuro; renal; mAb+s.m.
 450375; AA009647; Hs.352537; a disintegrin and metalloprote; breast, ovar, headnk, panc, lung, esoph, colon, sarc; mAb+diag+s.m.
 450531; AW301032; Hs.203800; (BC017500) Similar to hypothet; colon; CTL
 450701; H39960; Hs.288467; hypothetical protein XP_098151; lung, headnk, panc, breast, stom, ovar, esoph, colon, sarc; mAb+diag
 450726; AW204600; Hs.355462; HUMPSPBA Human pulmonary surfac; fibro, lung; s.m.
 450931; N25166; Hs.25648; tumor necrosis factor receptor; lung, renal; mAb+s.m.
 450983; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; blad, lung, ovar, panc; diag
 451310; AW250651; Hs.26213; Human DNA sequence from clone; colon, panc; CTL
 451527; AF022813; Hs.26518; transmembrane 4 superfamily me; renal; mAb
 451537; R56631; Hs.26550; retinoid X receptor, gamma; mela; CTL+s.m.
 451668; Z43948; Hs.326444; cartilage acidic protein 1; blad, ovar, lung; mAb+diag
 451939; U80456; Hs.27311; single-minded (Drosophila) hom; pros; CTL
 451979; F06972; Hs.27372; endothelial tyrosine kinase (E; angio; CTL+s.m.
 451988; AF263928; Hs.27410; papillomavirus regulatory fact; renal; CTL
 452017; AF109302; Hs.27495; prostate cancer associated pro; pros; s.m.
 452097; AB002364; Hs.27916; a disintegrin-like and metallo; ovar; mAb+s.m.+diag
 452190; H26735; Hs.91668; Homo sapiens clone PP1498 unk; breast, stom, panc; mAb
 452194; AI694413; Hs.373599; olfactory receptor, family 2; stom, panc, renal, colon, mela, fibro; mAb+s.m.
 452203; X57522; Hs.352018; transporter 1, ATP-binding cas; cerv, esoph, blad, stom, mela, renal; mAb+s.m.
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis; breast, headnk, panc, stom, lung, esoph, fibro; diag
 452401; NM_007115; Hs.29352; tumor necrosis factor, alpha-t; blad, breast, panc, headnk, stom, lung, leuk, renal, esoph; diag
 452431; U88879; Hs.29499; toll-like receptor 3; renal, hepC; mAb
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; breast, blad, lung, headnk, ovar, stom, uter, panc; mAb
 452838; U65011; Hs.30743; preferentially expressed antig; lung, ovar, breast, mela, test, esoph, renal, sarc; CTL
 452862; AW378065; Hs.8687; ADAMTS2 (a disintegrin-like a; headnk, breast, colon, leuk, lung, blad, esoph, stom, sarc; mAb+diag
 453195; BE241876; Hs.32352; hypothetical protein DKFZp434K; renal; CTL
 453496; AA442103; Hs.33084; solute carrier family 2 (facil; renal, pros; mAb+s.m.

453837; AL138387; Hs.256126; baculoviral IAP repeat-contains; renal, meta, sarc; s.m.
 453968; AA847843; Hs.62711; High mobility group (nonhistone); lung, uter, blad, test; CTL+s.m.
 456546; AI690321; Hs.203845; KCNK15 potassium channel, subf; ovar; mAb+s.m.
 456662; NM_002448; Hs.1494; msh (Drosophila) homeo box hom; uter, ovar; CTL
 457133; M54968; Hs.351221; v-Ki-ras2 Kirsten rat sarcoma; panc; s.m.
 457489; AI693815; Hs.127179; cryptic gene; panc, pros, lung; diag
 457819; AA057484; Hs.35406; FLJ20522 Hypothetical protein; lung, cerv, headnrc; mAb+diag
 458079; AI796870; Hs.381220; Homo sapiens similar to RIKEN; meta, fibro, sarc; mAb
 458627; AW086642; Hs.97984; SRY (sex determining region Y); ovar, uter, test; CTL

TABLE 2B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

414991 1785136_1 D78831 C17898 D78863

TABLE 2C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
402901	8894222	Minus	175426-175667
404287	2326514	Plus	53134-53281
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404977	3738341	Minus	43081-43229
405033	7107731	Minus	142358-142546
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 3A. Disease Indications and Preferred Utilities for Selected Genes

Table 3A provides preferred disease indications and preferred utilities for about 2709 selected genes. These genes were identified using Eos/Affymetrix Genechip arrays.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number
 UnigenelD: Unigene ID number
 Unigene Title: Unigene gene title
 Disease: preferred diseases indicated for selected gene as described in table 1 and abbreviated as follows: blad (bladder diseases), angio (blood vessel diseases), EWS (bone diseases), glio (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrosis diseases), headnrc (head & neck diseases), lei (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), omuc (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), sarc (soft tissue and bone diseases), meta (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)
 Utility: preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)

Pkey; ExAccn; UnigenelD; Unigene Title; Disease; Utility

100125; R02740; Hs.137555; putative chemokine receptor; G; blad; mAb+s.m.
 100131; D12485; Hs.11951; ectonucleotide pyrophosphatase; breast; mAb
 100147; D13666; Hs.136348; periostin (OSF-2os); breast, colon, blad, lung, fibro, panc; mAb+diag
 100241; BE273648; Hs.32963; cadherin 6, type 2, K-cadherin; blad; mAb
 100299; D49493; Hs.2171; growth differentiation factor; EWS; diag
 100335; AW247529; Hs.6793; platelet-activating factor ace; breast, lung, blad; s.m.
 100365; AI878927; Hs.79284; mesoderm specific transcript; colon, pros; diag
 100372; NM_014791; Hs.184339; KIAA0175 gene product; ovar, lung, cerv, panc; s.m.
 100405; AW291587; Hs.82733; nidogen 2; angio; diag
 100420; D86983; Hs.118893; Melanoma associated gene; breast, pros, lung, colon, angio, leuk; diag
 100448; AF234887; Hs.57652; cadherin, EGF LAG seven-pass G; breast; mAb+s.m.
 100452; D87742; Hs.241552; KIAA0268 protein; pros; diag
 100559; NM_000094; Hs.1640; collagen, type VII, alpha 1 (ex); lung; CTL+s.m.
 100654; A03758; Hs.184411; NM_000477; Homo sapiens albumin; pros; diag
 100655; A03758; Hs.184411; Empirically selected from AFFX; pros; diag
 100668; L05424; Hs.169610; CD44 antigen (homing function); lung, breast; mAb
 100824; AI393237; Hs.193989; runt-related transcription fac; ovar; CTL+s.m.
 100930; J04129; Hs.82269; progesterone-associated endomet; lung; diag
 101063; D54745; Hs.80247; cholecystokinin; pros, EWS; diag
 101097; BE245301; Hs.89414; chemokine (C-X-C motif), recep; leuk, ovar, breast, blad; mAb+s.m.
 101104; AW862258; Hs.169266; neuropeptide Y receptor Y1; breast, EWS; mAb
 101192; BE247295; Hs.78452; solute carrier family 20 (phos); angio; mAb+s.m.
 101193; L20861; Hs.152213; wingless-type MMTV Integration; blad, lung; diag
 101249; L18964; Hs.1904; protein kinase C, iota; ovar; s.m.

- 101261; D30857; Hs.82353; protein C receptor, endothelia; angio; mAb+s.m.
 101389; AW951430; Hs.78888; diazepam binding inhibitor (GA); pros; mAb+s.m.
 101431; BE185289; Hs.1076; small proline-rich protein 1B; lung, blad; diag
 101447; M21305; ; gbHuman alpha satellite and s; angio, blad; diag
 5 101481; N98569; Hs.76422; phospholipase A2, group IIA (p); pros; diag
 101485; AA296520; Hs.89546; selectin E (endothelial adhesi; pros, ovar; mAb
 101506; J02931; Hs.62192; coagulation factor III (thromb; pros; mAb
 101526; NM_002197; Hs.220529; aconitase 1, soluble; lung, colon, headnk, panc; mAb
 101543; M31166; Hs.2050; pentaxin-related gene, rapidly; angio, ovar; diag
 10 101545; BE246154; Hs.154210; endothelial differentiation, s; angio; mAb+s.m.
 101560; AW9568272; Hs.347326; intercellular adhesion molecu; angio; mAb
 101626; M57399; Hs.44; pleiotrophin (heparin binding; lung; diag
 101649; AW959908; Hs.1690; heparin-binding growth factor; lung, blad; diag
 101714; M68874; Hs.211587; phospholipase A2, group IVA (c; angio; s.m.
 15 101724; L11690; Hs.198689; bullous pemphigoid antigen 1 (c; breast, pros, blad, lung; mAb+CTL
 101741; NM_003199; Hs.326198; transcription factor 4; angio; CTL+s.m.
 101748; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgar; lung, blad, headnk, cerv; mAb
 101759; M80244; Hs.184601; solute carrier family 7 (catio; lung, glio, blad, headnk; mAb+s.m.
 101791; M83822; Hs.62354; cell division cycle 4-like; pros; s.m.
 20 101804; M86699; Hs.169840; TTK protein kinase; ovar, lung, blad, cerv; CTL+s.m.
 101806; AA586894; Hs.112408; S100 calcium-binding protein A; lung, breast, blad; diag
 101809; M86849; Hs.323733; gap junction protein, beta 2, ; colon, blad, lung, panc, headnk; mAb
 101839; AA446644; Hs.692; GA733-2 antigen; epithelial gl; ovar, pros; mAb
 25 101845; U88967; Hs.78867; protein tyrosine phosphatase, ; lung, glio, headnk, cerv; mAb+s.m.
 101851; BE260964; Hs.82045; midkine (neurite growth-promot; lung, blad, ovar, breast, panc; mAb+diag
 102009; BE245149; Hs.82643; protein tyrosine kinase 9; ovar; s.m.
 102012; BE259035; Hs.118400; singed (Drosophila)-like (sea; angio; diag
 102024; AA301867; Hs.76224; EGF-containing fibulin-like ex; angio; diag
 102048; U07225; Hs.339; purinergic receptor P2Y, G-pro; blad; mAb
 30 102076; BE299197; Hs.179665; cyclin-dependent kinase inhibi; pros; CTL+s.m.
 102125; NM_006456; Hs.288215; slalytransferase; breast, lung, ovar, s.m.
 102136; AA300576; Hs.85769; acidic 82 kDa protein mRNA; ovar; diag
 102151; T27013; Hs.3132; steroidogenic acute regulatory; ovar; diag
 35 102154; U17760; Hs.75517; laminin, beta 3 (nicel (125kD; lung, blad, headnk; diag
 102178; AW178761; Hs.227948; serine (or cysteine) proteinas; blad; mAb+diag
 102187; U20325; Hs.1707; cocaine- and amphetamine-regul; breast; diag
 102193; AL036335; Hs.313; secreted phosphoprotein 1 (ost; ovar, lung, fibro; diag
 102200; AA232362; Hs.317432; branched chain aminotransferas; ovar; s.m.
 40 102208; U22961; Hs.184411; gbHuman mRNA clone with simil; pros; diag
 102211; BE314524; Hs.78776; putative transmembrane protein; breast, blad; mAb
 102283; AW161552; Hs.83381; guanine nucleotide binding pro; angio; CTL+s.m.
 102297; NM_001504; Hs.198252; G protein-coupled receptor 9; breast; mAb
 102304; AF015224; Hs.46452; mammaglobin 1; breast; diag
 45 102305; AL043202; Hs.90073; chromosome segregation 1 (yeas; ovar, lung, blad; diag
 102348; U37519; Hs.87639; aldehyde dehydrogenase 3 famil; lung, blad; s.m.
 102380; U40434; Hs.155981; mesothelin; ovar; diag
 102394; NM_003816; Hs.2442; a disintegrin and metalloprota; panc; s.m.
 102455; U48705; Hs.75562; discoidin domain receptor fam; breast; mAb
 50 102457; NM_001394; Hs.2359; dual specificity phosphatase 4; breast; s.m.
 102522; BE250944; Hs.183556; solute carrier family 1 (neur; pros; mAb
 102581; AU077228; Hs.77256; enhancer of zeste (Drosophila); blad, EWS, leuk; CTL+s.m.
 102610; U65011; Hs.30743; preferentially expressed antig; lung, ovar; CTL
 102623; AW249285; Hs.37110; melanoma antigen, family A, 9; lung, blad; mAb+CTL
 102669; U71207; Hs.29279; eyes absent (Drosophila) homol; lung, pros; CTL+s.m.
 55 102696; BE540274; Hs.239; forkhead box M1; lung, blad; s.m.
 102725; AB026187; Hs.374280; protocadherin 11; EWS; mAb
 102742; U79293; Hs.159264; Human clone 23948 mRNA sequenc; breast, ovar; diag
 102745; AW753865; Hs.74376; olfactomedin related ER local; EWS; diag
 102803; H48299; Hs.26126; claudin 10; ovar; mAb
 60 102829; NM_006183; Hs.80962; neurolensin; lung, ovar, headnk; diag
 102836; U94320; Hs.158330; neuropeptide Y receptor Y5; EWS; mAb
 102852; V00571; Hs.75294; corticotropin releasing hormon; blad; diag
 102898; NM_002205; Hs.149609; integrin, alpha 5 (fibronectin; angio, blad, lung, pros; mAb+s.m.
 102915; X07820; Hs.2258; matrix metalloproteinase 10 (s; angio, blad, lung, ovar; mAb+diag+s.m.
 65 102917; AJ016712; Hs.287797; integrin, beta 1 (fibronectin; angio; mAb
 102927; BE512730; Hs.65114; keratin 18; ovar; diag
 102968; AU076611; Hs.154672; methylene tetrahydrofolate deh; ovar; s.m.
 102994; X51730; Hs.2905; progesterone receptor; blad; mAb+s.m.
 70 103003; AJ910275; Hs.350470; trefol factor 1 (breast cancer; breast, panc; diag
 103021; BE001596; Hs.85266; integrin, beta 4; lung blad; mAb
 103036; M13509; Hs.83169; matrix metalloproteinase 1 (in; angio, colon, blad, lung, leuk, ovar, headnk, fibro, panc, stom; mAb+diag+s.m.
 103037; BE018302; Hs.2894; placental growth factor, vascu; angio; diag
 103060; NM_005940; Hs.155324; matrix metalloproteinase 11 (s; breast, lung, ovar, panc; mAb+diag+s.m.
 103080; AU077231; Hs.82932; cyclin D1 (PRAD1; parathyroid; breast, EWS; diag
 75 103095; NM_005424; Hs.78824; tyrosine kinase with immunoglo; angio; mAb
 103111; NM_006103; Hs.2719; epididymis-specific, whey-acid; ovar, uter; diag
 103119; X63629; Hs.2877; cadherin 3, type 1, P-cadherin; lung, blad, ovar, colon, pros, panc, breast; mAb+diag
 103206; X72755; Hs.77367; monokine induced by gamma inte; breast, lung; diag
 80 103210; X72925; Hs.69752; desmocollin 1; pros; mAb
 103280; U84722; Hs.76205; cadherin 5, type 2, VE-cadheri; angio, fibro; mAb+s.m.
 103299; NM_005756; Hs.184942; G protein-coupled receptor 64; ovar; mAb+s.m.
 103312; Y12642; Hs.3185; lysosomal; lung, blad; mAb
 103365; X90908; Hs.74126; fatty acid binding protein 6, ; blad; diag

- 103408; NM_001504; Hs.198252; G protein-coupled receptor 9; breast; mAb
 103478; BE514982; Hs.38991; S100 calcium-binding protein A; lung, blad, headnk; diag
 103587; BE270266; Hs.82128; 5T4 oncofetal trophoblast glyco; breast, blad, lung; mAb
 103594; A1368680; Hs.816; SRY (sex determining region Y); lung, glio; s.m.
 103692; AW137912; Hs.227583; Homo sapiens chromosome X map; angio; mAb+s.m.
 103739; AA115173; ; gbzn30d02.s1 Stratagene neuro; pros; s.m.
 103767; BE244667; Hs.348996; CGI-100 protein; angio; diag
 103989; AA315993; Hs.105484; regenerating gene type IV; colon, omuc; mAb+diag
 104052; NM_002407; Hs.97644; mammaglobin 2; ovar; diag
 104115; AF183810; Hs.26102; opposite strand of trichorh; breast; mAb
 104252; AF002246; Hs.210863; cell adhesion molecule with ho; ovar; diag
 104301; AA768491; Hs.6783; hypothetical protein FLJ22724; ovar; diag
 104308; N25117; Hs.355957; ribosomal protein S26; pros; diag
 104394; AA129551; Hs.172129; Homo sapiens cDNA: FLJ21409 f; colon; diag
 104542; R29657; ; gbF1-1179D 22 week old human; pros; diag
 104608; AF143867; Hs.337588; ESTs, Moderately similar to S6; blad; mAb
 104659; AW969769; Hs.100343; ESTs; EWS; diag
 104660; BE298665; Hs.14846; Homo sapiens mRNA; cDNA DKFZp5; uter, colon, pros; mAb
 104667; A1239923; Hs.63931; dachshund (Drosophila) homolog; breast, pros, colon; diag
 104689; AA420450; Hs.380088; Plakophilin; lung; diag
 104691; U29690; Hs.37744; Homo sapiens beta-1 adrenergic; pros, EWS; mAb+s.m.
 104755; T49951; Hs.9029; DKFZP434G032 protein; breast, colon; diag
 104764; A1039243; Hs.278585; ESTs; angio; diag
 104786; AA027167; Hs.380438; KIAA0955 protein; angio; CTL+s.m.
 104877; A138635; Hs.22968; intron of VEGFR; renal; diag
 104888; AW939591; Hs.5940; mucin 13, epithelial transmembr; colon, stom, uter; mAb+s.m.
 104919; AA026880; Hs.25252; Homo sapiens cDNA FLJ13603 f; breast, cerv, uter; mAb+s.m.
 104943; AF072873; Hs.114218; frizzled (Drosophila) homolog; ovar; mAb+s.m.
 104954; AW250651; Hs.26213; Human DNA sequence from clone; colon; diag
 104971; BE311926; Hs.15830; hypothetical protein FLJ12691; blad; CTL
 105012; AF098158; Hs.9329; chromosome 20 open reading fra; colon, lung, blad; CTL
 105038; AW503733; Hs.9414; KIAA1488 protein; breast, angio; CTL+s.m.
 105039; AA507305; Hs.36475; ESTs; breast; diag
 105093; A137566; Hs.32405; Homo sapiens mRNA; cDNA DKFZp5; blad; diag
 105149; BE089288; Hs.8958; Homo sapiens cDNA FLJ12024 f; pros; diag
 105175; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; colon, lung; mAb
 105263; AW388633; Hs.6682; solute carrier family 7, (cat; angio, lung, ovar, blad, panc; mAb+s.m.
 105298; BE387790; Hs.26369; hypothetical protein FLJ20287; ovar, lung; diag
 105301; AW352357; Hs.7457; MAGE1 protein; EWS; diag
 105316; A1671245; Hs.24835; hypothetical protein FLJ14594; EWS; mAb
 105329; AA234561; Hs.22862; ESTs; breast, pros; CTL+s.m.
 105330; AW338625; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio; mAb+s.m.
 105370; AF179274; Hs.22791; transmembrane protein with EGF; pros; mAb+s.m.
 105500; AW602166; Hs.222399; CEGP1 protein; breast, pros; diag
 105503; AW963624; Hs.31707; ESTs, Weakly similar to YEW4_Y; pros, breast, colon; CTL+s.m.
 105507; BE268348; Hs.380963; CCR4-NOT transcription complex; colon; diag
 105516; AK001269; Hs.30738; hypothetical protein FLJ10407; ovar; diag
 105564; BE616694; Hs.288042; hypothetical protein FLJ14299; breast; diag
 105645; AW294631; Hs.351270; ESTs; pros; diag
 105715; BE621800; Hs.29444; putative small membrane protei; colon; diag
 105743; BE246502; Hs.9598; sema domain, immunoglobulin do; breast, lung; mAb+s.m.
 105746; AW151952; Hs.46679; hypothetical protein FLJ20739; breast; CTL+s.m.
 105777; R42765; Hs.23096; ESTs; breast; diag
 105782; H09748; Hs.67987; B-cell CLL/lymphoma 11B (zinc); EWS; CTL+s.m.
 105826; AA478756; Hs.194477; E3 ubiquitin ligase SMURF2; angio; s.m.
 105990; A1690586; Hs.29403; hypothetical protein FLJ22060; breast; diag
 106000; AW194426; Hs.20726; ESTs; breast; diag
 106012; A1240665; Hs.352537; ESTs; breast, lung; diag
 106014; AF123094; Hs.180566; mucosa associated lymphoid tis; leuk; diag
 106063; BE260415; Hs.348198; hypothetical protein FLJ20262; pros; diag
 106066; AW274357; Hs.301408; hypothetical protein PP3501; meta; CTL+s.m.
 106111; AW875398; Hs.6451; PRO0659 protein; EWS; CTL+s.m.
 106124; H93366; Hs.7567; branched chain aminotransferas; angio; s.m.
 106155; AA25414; Hs.33287; nuclear factor I/B; breast, pros, angio; diag
 106373; AW503807; Hs.21907; histone acetyltransferase; breast; s.m.
 106400; BE397649; Hs.279607; Homo sapiens cDNA FLJ13634 f; colon; diag
 106414; BE568205; Hs.28827; mitogen-activated protein kin; breast; s.m.
 106448; Z42061; Hs.27004; ESTs; pros; diag
 106533; A134708; Hs.145998; ESTs; EWS; diag
 106574; BE044325; Hs.227280; U6 snRNA-associated Sm-like pr; colon; diag
 106579; AA456135; Hs.23023; ESTs; pros; diag
 106632; NM_014400; Hs.11950; GPI-anchored metastasis-associ; lung, blad, headnk; mAb+diag
 106738; AW149266; Hs.25130; Homo sapiens cDNA FLJ14923 f; ovar; diag
 106793; H94997; Hs.16450; ESTs; angio; diag
 106844; AA485055; Hs.158213; sperm associated antigen 6; breast; mAb+CTL
 106906; AA861271; Hs.222024; transcription factor BMAL2; lung, blad; diag
 106990; AA280722; Hs.24758; ESTs, Weakly similar to I38022; breast; diag
 107036; A1973016; Hs.15725; hypothetical protein SBB148; pros; diag
 107102; AB037765; Hs.30652; KIAA1344 protein; pros, breast; diag
 107105; AW963419; Hs.155223; stannocalcin 2; breast; diag
 107136; AV661958; Hs.8207; GK001 protein; breast, colon; diag
 107151; AW378065; Hs.8687; ADAMTS2 (a disintegrin-like a; breast, colon, leuk, lung, blad; mAb+diag
 107216; D51069; Hs.211579; melanoma cell adhesion molecu; angio; diag

- 107246; AW263124; Hs.350547; nuclear receptor co-repressor; breast, colon, pros; mAb+s.m.
 107284; NM_005629; Hs.187958; solute carrier family 6 (neuro; lung; mAb+s.m.
 107385; NM_005397; Hs.16426; podocalyxin-like; angio; diag
 107901; L42612; Hs.335952; keratin 6B; breast, blad, lung; diag
 107922; BE153855; Hs.51460; Ig superfamily receptor LNIR; breast, blad, lung; mAb
 107932; AW392555; Hs.18878; hypothetical protein FLJ21620; lung; CTL
 108055; AJ404672; Hs.334483; hypothetical protein FLJ23571; breast, ovar; diag
 108059; S69002; Hs.234773; Homo sapiens cDNA: FLJ22281 f; ovar; CTL+s.m.
 108153; AW519204; Hs.40808; ESTs; pros; diag
 108186; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 108242; AA062746; Hs.355244; gbzm03g12s1 Stratagene come; pros; diag
 108282; AA065142; gbzm50h11.1 Stratagene fibro; pros; diag
 108505; AA083376; gbzm09g08.s1 Stratagene hNT n; pros; diag
 108579; AA115963; Hs.323423; ESTs, Moderately similar to B; pros; diag
 108695; AB029000; Hs.70823; KIAA1077 protein; breast, colon, lung; diag
 108732; AA258888; Hs.107476; ATP synthase, H⁺ transporting.; pros; s.m.
 108778; AF133123; Hs.90847; general transcription factor I; ovar; diag
 108828; AK001693; Hs.273344; DKFZP564O0463 protein; breast; diag
 108860; AA133334; Hs.816; ESTs; lung; s.m.
 109001; AI056548; Hs.72116; hypothetical protein FLJ20992; angio; CTL+diag
 109032; AI219207; Hs.72222; hypothetical protein FLJ13459; blad; CTL
 109077; AI732617; Hs.182362; ESTs; blad; diag
 109112; AW419196; Hs.257924; hypothetical protein FLJ13782; breast, pros, blad; diag
 109141; AF174600; Hs.5978; ESTs, Highly similar to AF1746; colon; CTL+s.m.
 109166; AA219691; Hs.73625; RAB6 interacting, kinesin-like; lung, blad, breast, colon, ovar, headnk, EWS; s.m.
 109220; AW958181; Hs.189998; ESTs; pros; diag
 109273; AA375752; Hs.348140; Homo sapiens mRNA; cDNA DKFZp5; breast; diag
 109292; AW975746; Hs.188662; KIAA1702 protein; breast; diag
 109454; AA232255; Hs.295232; ESTs, Moderately similar to A4; ovar; diag
 109456; AW956580; Hs.42699; ESTs; angio, panc; diag
 109514; AA234087; Hs.262346; ESTs, Weakly similar to S72482; breast; diag
 109530; AA908645; Hs.19597; KIAA1694 protein; pros; CTL+s.m.
 109548; H17800; Hs.7154; ESTs; ovar; diag
 109680; AB037734; Hs.4993; KIAA1313 protein; ovar; diag
 110009; BE075297; Hs.6814; ESTs, Weakly similar to A43932; breast, colon; diag
 110151; H18835; Hs.31608; hypothetical protein FLJ20041; pros, EWS; diag
 110156; AA581322; Hs.4213; hypothetical protein MGC16207; lung, blad; diag
 110240; AI668594; Hs.176588; ESTs, Weakly similar to CP4Y_H; breast; diag
 110278; AF061573; Hs.19492; protocadherin 8; EWS; mAb+s.m.
 110675; H89355; Hs.249159; adrenergic, alpha-2A-, recepto; pros; mAb+s.m.
 110728; AA737106; Hs.32250; ESTs, Moderately similar to I7; EWS; s.m.
 110844; AI740792; Hs.167531; methylcrotonoyl-Coenzyme A car; pros, pros; s.m.
 110915; BE092285; Hs.29724; hypothetical protein FLJ13187; breast, pros; diag
 110971; AJ760098; Hs.21411; ESTs; pros; diag
 111157; AL109729; Hs.99364; putative transmembrane protein; pros; mAb+s.m.
 111179; AK000136; Hs.10760; asporin (LRR class 1); breast, colon; CTL+s.m.
 111185; AJ245671; Hs.12844; EGF-like-domain, multiple 6; ovar, blad; mAb+diag
 111223; AA852773; Hs.334838; KIAA1866 protein; breast, colon, lung, EWS; mAb
 111299; AB033091; Hs.355925; KIAA1265 protein; ovar; diag
 111357; BE314949; Hs.87128; hypothetical protein FLJ23309; breast; diag
 111384; N94606; Hs.288969; HSCARG protein; breast; diag
 111900; AF131784; Hs.25318; Homo sapiens clone 25194 mRNA; breast; diag
 111929; AF027208; Hs.112360; prominin (mouse)-like 1; colon, breast, fibro; mAb
 112134; R41823; Hs.7413; ESTs, calyntenin-2; breast, EWS; diag
 112244; AB029000; Hs.70823; KIAA1077 protein; breast, colon, blad, lung; diag
 112280; AA863360; Hs.26040; ESTs, Weakly similar to fatty; breast; s.m.
 112283; L14561; Hs.20952; ATPase, Ca⁺⁺ transporting, pla; ovar; mAb
 112287; AB033064; Hs.236463; KIAA1238 protein; breast; diag
 112971; Z42387; Hs.83883; transmembrane, prostate androg; colon, pros, pros; mAb+s.m.
 113003; AW292315; Hs.7215; ESTs; EWS; diag
 113021; AL122055; Hs.129836; KIAA1028 protein; pros; s.m.
 113047; AI571940; Hs.7549; ESTs; breast, colon; diag
 113073; N39342; Hs.103042; microtubule-associated protein; pros; CTL+s.m.
 113168; AW002393; Hs.337629; gb:wu61d05.x1 NCL_CGAP_GC6 Hom; ovar; diag
 113195; H83265; Hs.8881; ESTs, Weakly similar to S41044; angio, lung; diag
 113230; T61430; gb:yc06a03.s1 Stratagene lung; blad; diag
 113361; T79589; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 113374; T79925; Hs.269165; ESTs, Weakly similar to ALU1_H; leuk; diag
 113443; AW083920; Hs.16098; claudin 2; colon, panc; mAb
 113471; AI765890; Hs.16341; MAWD binding protein; pros; diag
 113490; BE178110; Hs.173374; Homo sapiens cDNA FLJ10500 f; colon; diag
 113950; AI267652; Hs.246107; Homo sapiens mRNA; cDNA DKFZp4; breast, pros; diag
 113970; W27249; Hs.8109; hypothetical protein FLJ21080; breast, lung, stom, uter; diag
 114124; W57554; Hs.125019; lymphoid nuclear protein (LAF-; breast; diag
 114251; H15261; Hs.21948; ESTs; breast; diag
 114292; AI815395; Hs.184641; fatty acid desaturase 2; breast; s.m.
 114334; AB037784; Hs.22941; KIAA1363 protein; ovar; diag
 114407; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp4; breast, colon, lung; diag
 114452; AJ369275; Hs.243010; Homo sapiens cDNA FLJ14445 f; angio; diag
 114480; BE066778; Hs.151678; UDP-N-acetyl-alpha-D-galactose; breast; s.m.
 114531; AA053033; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 114540; AI904232; Hs.75323; prohibitin; breast; diag
 114542; AW970128; Hs.91011; anterior gradient 2 (Xenopus t; breast, pros; diag

- 114587; AF086009; Hs.296398; gb:Homo sapiens full length ltr; colon; diag
- 114724; R64730.comp; Hs.155986; DEAD/H (Asp-Glu-Ala-Asp/His) h; ovar; CTL+s.m.
- 114768; AF212848; Hs.182339; ets homologous factor; pros; breast; colon; CTL+s.m.
- 114788; AA159181; Hs.54900; serologically defined colon ca; pros; CTL+s.m.
- 114908; AA454985; Hs.54973; cadherin-like protein VR20; pros; diag
- 114918; BE165762; Hs.23518; hypothetical protein from BCRA; pros; diag
- 114965; AJ733881; Hs.72472; NAME OMITTED ... receptor kinase; breast; mAb
- 115060; AF052693; Hs.198249; gap junction protein, beta 5 (-); lung, blad, headnk; mAb+s.m.
- 115221; AW365434; Hs.79741; hypothetical protein FLJ10116; ovar; diag
- 115239; BE251328; Hs.73291; hypothetical protein FLJ10881; colon; diag
- 115291; BE545072; Hs.122579; hypothetical protein FLJ10461; ovar; lung; CTL+s.m.
- 115412; AW131168; Hs.372382; ESTs, Weakly similar to I38022; pros; diag
- 115536; AK001468; Hs.62180; anillin (Drosophila Scraps hom; ovar; lung, blad, headnk, panc, cerv, stom, uter; colon; CTL+s.m.
- 115674; AW992356; Hs.380760; Homo sapiens pyruvate dehydrog; ovar; s.m.
- 115675; W87707; Hs.82065; interleukin 6 signal transduce; breast; pros; mAb+s.m.
- 115683; AF255910; Hs.54650; junctional adhesion molecule 2; angio; glio; mAb
- 115697; D31382; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
- 115719; AW992405; Hs.352406; Homo sapiens, clone IMAGE:3507; pros; breast; colon; CTL+s.m.
- 115819; AA486620; Hs.41135; endomucin-2; angio; diag
- 115827; AA428000; Hs.283072; actin related protein 2/3 comp; angio; diag
- 115844; AJ373062; Hs.332938; hypothetical protein MGC5370; pros; diag
- 115881; NM_005756; Hs.184942; G protein-coupled receptor 64; ovar; EWS, uter; mAb+s.m.
- 115892; AA291377; Hs.50831; ESTs; ovar; blad, lung; diag
- 115909; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_H; ovar; lung; diag
- 115947; R47479; Hs.94761; KIAA1691 protein; colon; diag
- 115978; AL035864; Hs.69517; cDNA for differentially expres; lung, blad, breast, pros, ovar, headnk; CTL
- 116003; BE275469; Hs.66493; Down syndrome critical region ; colon; mAb
- 116011; AL359053; Hs.57664; Homo sapiens mRNA full length ; breast; diag
- 116028; H59799; Hs.42644; thioredoxin-like; ovar; lung; diag
- 116107; AL133916; Hs.47860; hypothetical protein FLJ20093; lung, breast; diag
- 116202; BE159395; Hs.284092; ESTs; pros; diag
- 116238; AV660717; Hs.47144; DKFZP586N0819 protein; ovar; diag
- 116301; AW969706; Hs.293332; ESTs; EWS; diag
- 116334; AL038450; Hs.48948; ESTs; pros; diag
- 116335; AK001100; Hs.41690; desmocollin 3; lung, blad, headnk; diag
- 116393; AJ972402; Hs.306051; hypothetical protein MGC2648; pros; diag
- 116399; AA889120; Hs.110637; homeo box A10; pros; CTL+s.m.
- 116401; AW893940; Hs.59698; ESTs; ovar; diag
- 116416; AW753676; Hs.39982; ESTs; ovar; diag
- 116470; AJ272141; Hs.351928; SRY (sex determining region Y); colon, breast, angio, blad; diag
- 116483; AJ346201; Hs.76118; ubiquitin carboxyl-terminal est; angio, lung; s.m.
- 116610; D80449; Hs.184841; ESTs; pros; diag
- 116732; AW152226; Hs.165909; ESTs, Weakly similar to I38022; colon; diag
- 116787; AW362955; Hs.356547; Homo sapiens cDNA FLJ14415 fis; pros, breast, colon, pros; mAb
- 116962; H79677; ; gb:yu76g10.s1 Soares fetal liv; pros; diag
- 117027; AW085208; Hs.130093; ESTs; breast; diag
- 117280; M18217; Hs.172129; Homo sapiens cDNA: FLJ21409 ft; breast, colon, pros; diag
- 117284; AK001701; Hs.183779; Homo sapiens cDNA FLJ10590 fis; pros; diag
- 117320; AB024937; Hs.211092; LUNX protein; PLUNC (palate tu; lung; mAb+diag
- 117367; AI041793; Hs.42502; ESTs; breast; diag
- 117412; N32538; Hs.42645; solute carrier family 16 (mono; breast, ovar; mAb+s.m.
- 117425; AK000028; Hs.356100; ribosomal protein S24; pros; diag
- 117563; AF055634; Hs.44553; unc5 (C.elegans homolog) c; leuk; diag
- 117602; N35020; Hs.44685; C3HC4-like zinc finger protein; EWS; CTL+s.m.
- 117921; AA021459; Hs.306480; Homo sapiens mRNA; cDNA DKFZp7; pros; diag
- 117984; AF189723; Hs.106778; ATPase, Ca++ transporting, typ; pros, breast, colon; mAb
- 118049; N53145; ; gb:yyv5509.s1 Soares fetal liv; pros; diag
- 118314; N48580; Hs.46692; ESTs; blad, lung; diag
- 118336; BE327311; Hs.47166; HT021; breast, ovar, blad, pros; CTL+s.m.
- 118368; N64339; Hs.48956; gap junction protein, beta 6 (-); lung, blad; mAb
- 118417; AF080229; ; gb:Human endogenous retrovirus; pros; s.m.
- 118472; AL157545; Hs.173179; bromodomain and PHD finger con; breast; diag
- 118511; N75620; Hs.43157; ESTs; angio; diag
- 118901; AW292577; Hs.94445; ESTs; breast; diag
- 118905; AW973708; Hs.201925; Homo sapiens cDNA FLJ13446 fis; breast; diag
- 119018; AA631143; Hs.278695; Homo sapiens protein mRNA, co; pros, pros; diag
- 119036; R95872; Hs.117572; chemokine binding protein 2; breast, ovar; mAb
- 119073; BE245360; Hs.45514; v-ets erythroblastosis virus E; angio, pros; CTL+s.m.
- 119082; AF252297; Hs.81546; cytochrome P450 retinoid metab; EWS; diag
- 119126; R45175; Hs.117183; ESTs; pros, breast, colon; diag
- 119279; N57568; Hs.48028; EST; breast; diag
- 119307; BE048081; Hs.37054; ephrin-A3; colon, breast; mAb+diag
- 119478; AJ624342; Hs.179082; ESTs; breast; diag
- 119617; AA516531; Hs.55999; NK homeobox (Drosophila), fami; pros; diag
- 119743; AA947552; Hs.58086; branched chain aminotransferase; ovar; s.m.
- 119771; AJ905687; Hs.348419; AJ905687-IL-BT095-190199-019 B; breast; diag
- 119780; NM_016625; Hs.191381; hypothetical protein; ovar, lung; CTL+s.m.
- 119789; BE393948; Hs.50915; kallikrein 5; ovar; diag
- 119845; W79123; Hs.58551; G protein-coupled receptor 87; lung, blad, headnk, cerv; mAb+s.m.
- 119940; AL050097; Hs.272531; DKFZP586B0319 protein; pros; diag
- 120104; AK000123; Hs.180479; hypothetical protein FLJ20116; colon, lung; diag
- 120132; W57554; Hs.125019; lymphoid nuclear protein (LAF-; pros, breast; diag
- 120147; AI917116; Hs.348941; hemoglobin, beta; EWS; diag

- 120206; H26735; Hs.91668; Homo sapiens clone PP1498 unkn; breast; mAb
 120242; AW969587; Hs.86366; ESTs; blad; diag
 120328; AA923278; Hs.290905; ESTs, Weakly similar to protea; pros; s.m.
 120438; AW015242; Hs.99488; ESTs, Weakly similar to YK54_Y; ovar; diag
 120471; AA251944; Hs.104058; CGI-29 protein; colon; diag
 120486; AW368377; Hs.137669; tumor protein 63 kDa with stro; lung, blad, headnk; diag
 120588; AA703228; Hs.16193; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 120624; AW407987; Hs.173518; M-phase phosphoprotein homolog; breast; s.m.
 120830; AI568170; Hs.96886; ESTs; EWS; diag
 120977; AA398155; Hs.97600; ESTs; breast, ovar; diag
 121027; AI572490; Hs.99785; Homo sapiens cDNA: FLJ21245 f; blad; mAb
 121231; AA814948; Hs.96343; ESTs, Weakly similar to ALUC_H; EWS; diag
 121335; AA404418; ; gb:zw37e02.s1 Soares_totalet; angio; diag
 121362; AF050147; Hs.97932; chondromodulin I precursor; EWS; mAb
 121457; W07404; Hs.102558; hypothetical protein FLJ22055; colon; diag
 121619; AA528339; Hs.178062; ESTs, Weakly similar to phosph; EWS; s.m.
 121710; AF163474; Hs.96744; prostate androgen-regulated tr; pros; diag
 121721; AL047051; Hs.199961; ESTs, Weakly similar to ALU7_H; pros; diag
 121723; AA243499; Hs.104800; hypothetical protein FLJ10134; breast; diag
 121748; BE536911; Hs.234545; hypothetical protein NUF2R; breast; diag
 121779; AW513143; Hs.98367; SRY (sex determining region Y); ovar; diag
 121791; AA815378; Hs.293317; ESTs, Weakly similar to GGC1_H; blad, headnk, lung, ovar; mAb+CTL
 121792; AW969726; Hs.98381; ESTs, Weakly similar to serine; EWS; diag
 121913; AI249368; Hs.98558; ESTs; protease inhibitor 15 f; breast, pros; s.m.
 121920; AA428300; ; gb:zw18b02.s1 Soares ovary tum; ovar, uter, cerv; diag
 122041; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
 122520; AW951324; Hs.173609; pregnancy specific beta-1-glyc; colon; diag
 122797; AJ251027; Hs.99526; odorant-binding protein 2B (OB; breast; diag
 122802; AI687303; Hs.285529; G protein-coupled receptor 49; ovar, uter; mAb+s.m.
 122969; AW821252; Hs.104336; hypothetical protein; ovar; diag
 123005; AW369771; Hs.367688; integrin, beta 8; ovar, lung, headnk, glio; mAb+s.m.
 123044; AK001035; Hs.130881; B-cell CLL/lymphoma 11A (zinc; lung; diag
 123137; AI073913; Hs.100686; ESTs, Weakly similar to JE0350; breast, colon, ovar, uter, lung, stom; diag
 123158; AF161426; Hs.218329; hypothetical protein; breast; diag
 123160; AA488687; Hs.284235; ESTs, Weakly similar to 138022; lung; diag
 123169; AI950087; Hs.369628; gb:wg05c02.x1 NCL CGAP_Kid12 H; ovar; diag
 123209; AW968543; Hs.203270; ESTs, Weakly similar to ALU1_H; pros; diag
 123308; C14187; Hs.157208; ESTs; EWS; diag
 123339; AW188464; Hs.101515; ESTs; ovar; diag
 123475; BE439553; Hs.12329; Homo sapiens, clone IMAGE:4098; pros; diag
 123494; AW179019; Hs.112110; mitochondrial ribosomal prot; ovar; diag
 123520; AA608550; ; gb:cae5d12.s1 Stragene lung; pros; s.m.
 123533; AA608751; ; gb:cae56h07.s1 Stragene lung; colon; diag
 123619; AA602964; Hs.366318; gb:nc097c02.s1 NCL CGAP_Pr2 Hom; breast; CTL+s.m.
 123689; AA399323; Hs.285130; Homo sapiens pinch-2 protein m; ovar; diag
 123709; AA706910; Hs.112742; ESTs; breast; diag
 123828; AF251237; Hs.112208; XAGE-1 protein; lung, blad, test; CTL
 123972; T46848; Hs.70337; immunoglobulin superfamily, m; ovar; diag
 124006; AI147155; Hs.279727; ESTs; homologue of PEM-3 (Cion; breast, angio, lung, ovar, EWS; diag
 124059; BE387335; Hs.283713; ESTs, Weakly similar to S64054; breast, colon, blad, lung; CTL+diag
 124153; AU077333; Hs.160483; erythrocyte membrane protein b; pros; mAb
 124352; AA640891; Hs.102406; ESTs; breast, pros, ovar, lung; diag
 124526; N62096; Hs.293185; ESTs, Weakly similar to JC7328; pros; mAb+s.m.
 124579; AI693815; Hs.127179; cryptic gene; panc; diag
 124777; R41933; Hs.140237; ESTs, Weakly similar to ALU1_H; pros, breast; diag
 125103; AA570056; Hs.122730; ESTs, Moderately similar to K1; colon; mAb
 125154; W38419; ; gb:zc78a07.s1 Pancreatic Islet; ovar; diag
 125250; W26524; Hs.356686; protein phosphatase 4 regulato; ovar; CTL+s.m.
 125266; W90022; Hs.186809; ESTs, Highly similar to LCT2_H; angio; diag
 125453; BE385523; Hs.18048; melanoma antigen, family A, 10; blad; mAb+CTL
 125666; AL390172; Hs.317432; Homo sapiens cDNA: FLJ21270 f; ovar; diag
 125770; AA143045; Hs.81665; v-kit Hardy-Zuckerman 4 feline; EWS; diag
 125976; AA436760; Hs.35552; gb:zv67d11.r1 Soares_totalet; pros; diag
 126399; AA088767; Hs.83883; transmembrane, prostate androg; panc; mAb+s.m.
 126645; AA316181; Hs.61635; six transmembrane epithelial a; pros, breast, lung, panc, headnk, EWS; mAb+CTL
 126758; AI559444; Hs.104679; ESTs; pros, breast; mAb
 126799; AW753865; Hs.74376; olfactomedin related ER local; EWS; diag
 126872; AW450979; ; gb:LI-H-B13-ala-a-12-Q-ULs1 N; blad; diag
 126892; AF121856; Hs.284291; sorting nexin 6; ovar; diag
 126980; AL390172; Hs.317432; branched chain aminotransferas; ovar; s.m.
 126966; R38438; Hs.118747; solute carrier family 15 (H+); pros; mAb
 127003; AW816515; Hs.173540; ATPase, Class V, type 10D; pros; mAb
 127221; BE062108; Hs.241551; chloride channel, calcium act; lung, blad, headnk, cerv; mAb+s.m.
 127240; AJ005683; Hs.86998; nuclear factor of activated T-; pros; CTL+s.m.
 127425; AF183810; Hs.26102; trichorhinophalangeal syndrome; breast; mAb
 127479; D31152; Hs.179729; collagen, type X, alpha 1 (Sch; breast, lung, headnk, panc; diag
 127537; AI926047; Hs.162859; ESTs; pros; diag
 127664; AA806164; Hs.116502; ESTs; EWS; diag
 128046; AA873285; Hs.357313; gb:zh68h05.s1 NCL CGAP_Kid5 Ho; pros, breast, colon; diag
 128305; AI954968; Hs.365706; matrix Gla protein; breast; diag
 128478; AA708205; Hs.100343; ESTs; EWS; CTL+s.m.
 128515; BE395085; Hs.334762; type I transmembrane protein F; panc; mAb
 128595; U31875; Hs.272499; short-chain alcohol dehydrogen; blad, breast; CTL+s.m.

- 128610; N48373; Hs.10247; activated leucocyte cell adhes; breast, pros, lung, ovar; diag
 128734; AB008390; Hs.104570; kallikrein 8 (neuropsin/ovasin); ovar; diag
 128790; AF026692; Hs.105700; secreted frizzled-related prot; breast, colon, pros, ovar, uter, panc; diag
 128797; NM_002975; Hs.105927; stem cell growth factor; lymph; EWS; leuk; diag
 128854; BE159181; Hs.168232; hypothetical protein FLJ13855; breast; diag
 128925; R67418; Hs.21851; Homo sapiens cDNA FLJ12900 fis; breast; diag
 128949; AA009647; Hs.352537; a disintegrin and metalloprote; breast, ovar, headnk, panc; mAb+diag+s.m.
 128959; Z42047; Hs.107479; Homo sapiens PRO2751 mRNA, com; pros; diag
 129041; BE382756; Hs.169902; solute carrier family 2 (facil; lung, blad; mAb+s.m.
 129097; BE243933; Hs.108642; zinc finger protein 22 (KOX 15; ovar, CTL+s.m.
 129099; AF146074; Hs.108660; ATP-binding cassette, sub-fam; lung, blad, headnk; mAb+s.m.
 129184; AW161450; Hs.109201; CGI-86 protein; pros; mAb
 129260; AF077200; Hs.279813; hypothetical protein; colon; diag
 129284; AA318224; Hs.296141; ESTs; colon; diag
 129362; U30246; Hs.110736; solute carrier family 12 (sodi; colon, breast, pros; mAb
 129366; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA; breast; diag
 129389; NM_012445; Hs.288126; spondin 2, extracellular matric; colon, pros; diag
 129404; AJ267700; Hs.351201; ESTs; pros, ovar, lung, blad, headnk, panc; diag
 129466; L42583; Hs.334309; keratin 6A; lung, blad; diag
 129482; AA188185; Hs.289043; spindlin; breast; diag
 129534; AK002126; Hs.11260; hypothetical protein FLJ11284; pros; diag
 129571; X51630; Hs.1145; Wilms tumor 1; ovar, CTL+s.m.
 129605; AF061812; Hs.115947; keratin 16 (focal non-epidermo; lung, blad, headnk; diag
 129620; D79338; Hs.239720; CCR4-NOT transcription complex; breast, angio; diag
 129628; U36945; Hs.1174; cyclin-dependent kinase inhibi; lung, blad, ovar, headnk s.m.
 129650; AF109298; Hs.118258; prostate cancer associated pro; pros, EWS; diag
 129689; AW748482; Hs.77873; B7 homolog 3; breast; diag
 129703; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457; EWS, leuk; diag
 129720; AA156214; Hs.12152; APMCF1 protein; breast; diag
 129750; AF056085; Hs.198612; G protein-coupled receptor 51; angio, blad; mAb+s.m.
 129869; AJ222069; Hs.13015; hypothetical protein similar t; breast; diag
 129912; AF155096; Hs.107213; hypothetical protein FLJ20585; ovar, CTL+s.m.
 129936; AJ250717; Hs.1355; cathepsin E; blad; sm+diag
 129953; AA412195; Hs.13740; ESTs; breast; diag
 129977; NM_000399; Hs.1395; early growth response 2 (Krox-; EWS; CTL+s.m.
 130010; AA301116; Hs.142638; nucleolar phosphoprotein Nopp3; ovar; diag
 130057; AF027153; Hs.324787; solute carrier family 5 (inos; breast; mAb
 130095; AK001635; Hs.14838; hypothetical protein FLJ10773; breast; diag
 130155; AA101043; Hs.151254; kallikrein 7 (chymotryptic, st; ovar; diag
 130181; AF052119; Hs.151608; Homo sapiens clone 23622 mRNA; pros; diag
 130184; H58306; Hs.15165; retinoic acid induced 14; angio; diag
 130262; D63216; Hs.153684; frizzled-related protein; panc, EWS, stom, renat; diag
 130343; AB040914; Hs.278628; KIAA1481 protein; breast; diag
 130376; R40873; Hs.155174; CDC5 (cell division cycle 5, S; ovar; CTL+s.m.
 130385; AW067800; Hs.155223; stannocalcin 2; breast, lung; mAb+diag
 130455; D80041; Hs.155956; N-acetyltransferase 1 (arylami; breast; s.m.
 130511; L32137; Hs.1584; cartilage oligomeric matrix pr; breast, ovar; diag
 130558; BE564937; Hs.15984; pp21 homolog; pros; CTL+s.m.
 130577; M69241; Hs.162; insulin-like growth factor bin; ovar; diag
 130604; AA383256; Hs.1657; estrogen receptor 1; breast; mAb+s.m.
 130627; BE003054; Hs.1695; matrix metalloproteinase 12 (m; lung, colon, blad, headnk, ovar, panc; mAb+diag+s.m.
 130637; AA356764; Hs.17109; Integral membrane protein 2A; EWS; mAb+s.m.
 130648; AJ458165; Hs.17296; hypothetical protein MGC2376; colon; diag
 130667; BE246961; Hs.17639; Homo sapiens ubiquitin protein; breast; s.m.
 130690; AB006625; Hs.139033; paternally expressed 3; ovar; diag
 130714; AJ348274; Hs.18212; DNA segment on chromosome X (u; breast; diag
 130760; AW379130; Hs.18953; phosphodiesterase 9A; pros; CTL+s.m.
 130800; AJ187292; Hs.19574; hypothetical protein MGC5469; colon, lung; diag
 130839; AB011169; Hs.380875; similar to S. cerevisiae SSM4; angio; diag
 130844; U76248; Hs.20191; seven in absentia (Drosophila); breast; diag
 130892; AL120837; Hs.20993; high-glucose-regulated protein; breast; CTL+s.m.
 130941; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin; ovar; mAb
 130967; AA393071; Hs.182579; leucine aminopeptidase; ovar; s.m.
 130972; D81866; Hs.374468; Homo sapiens mRNA; cDNA DKFZp5; angio; diag
 130987; BE613269; Hs.21893; hypothetical protein DKFZp761N; colon; diag
 131046; AA321649; Hs.2248; small inducible cytokine subfa; breast, lung, blad, ovar, fibro; diag
 131080; NM_001955; Hs.2271; endothelin 1; angio; diag
 131083; Y09763; Hs.22785; gamma-aminobutyric acid (GABA); pros; mAb
 131148; AW953575; Hs.303125; p53-induced protein PIGPC1; breast, colon, angio; diag
 131216; AJ815486; Hs.243901; Homo sapiens cDNA FLJ20738 fis; colon, breast; diag
 131228; AW207469; Hs.24485; chondroitin sulfate proteoglyc; ovar; diag
 131244; AJ638429; Hs.24763; RAN binding protein 1; lung, blad, headnk; CTL+s.m.
 131288; AA278482; Hs.25328; ESTs, Moderately similar to AL; pros; diag
 131289; AA296696; Hs.333418; FYD domain-containing ion tra; colon; diag
 131307; NM_000025; Hs.2549; adrenergic, beta-3-, receptor; EWS; mAb
 131313; R96290; Hs.75874; ribosomal protein L44; EWS; diag
 131492; AJ452601; Hs.288869; nuclear receptor subfamily 2, ; pros; mAb+s.m.
 131544; AL355715; Hs.28555; programmed cell death 9 (PDCD9; breast; diag
 131559; AL078599; Hs.10784; hypothetical protein FLJ20037; breast; diag
 131564; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis; breast; diag
 131603; X81334; Hs.2936; matrix metalloproteinase 13 (c; blad; s.m.
 131643; AW410601; Hs.30026; HSPC182 protein; breast; diag
 131739; AF017986; Hs.31386; secreted frizzled-related prot; breast; mAb+s.m.

- 131817; U20536; Hs.3280; caspase 6, apoptosis-related c; fibro, breast, cerv, lung, blad, panc, gli; s.m.
 131885; BE502341; Hs.3402; ESTs; breast; diag
 131919; T15803; Hs.272458; protein phosphatase 3 (formet; pros, breast; s.m.
 131925; AF151048; Hs.183180; anaphase promoting complex sub; breast; diag
 131965; W79283; Hs.35962; ESTs; lung, ovar; diag
 131985; AA503020; Hs.36563; hypothetical protein FLJ22418; breast, ovar; diag
 132050; AI267615; Hs.38022; ESTs; angio; diag
 132173; X89426; Hs.41716; endothelial cell-specific mole; angio; diag
 132180; NM_004460; Hs.418; fibroblast activation protein; colon, panc, esoph; mAb
 132191; AA507576; Hs.288361; Homo sapiens cDNA: FLJ22698 f; ovar; diag
 132349; AW975654; Hs.181286; serine protease inhibitor, Kaz; pros, blad; s.m.
 132354; BE185289; Hs.1076; small proline-rich protein 1B; lung; diag
 132358; NM_003542; Hs.46423; H4 histone family, member G; pros; CTL+s.m.
 132371; AA235448; Hs.222088; PRO2000 protein; breast; diag
 132454; BE296227; Hs.250822; serine/threonine kinase 15; blad, breast; s.m.
 132490; NM_001290; Hs.4980; LIM domain binding 2; angio; diag
 132520; AA257992; Hs.50651; Janus kinase 1 (a protein tyro; EWS; s.m.
 132528; T78736; Hs.50758; SMC4 (structural maintenance o; ovar; CTL+s.m.
 132543; BE568452; Hs.344037; protein regulator of cytokines; colon, lung; diag
 132572; AI929659; Hs.237825; signal recognition particle 72; ovar; diag
 132592; AW803564; Hs.288850; Homo sapiens cDNA: FLJ22528 f; colon; diag
 132624; AA326108; Hs.33829; bHLH protein DEC2; ovar; diag
 132632; AU076916; Hs.5398; guanine monophosphate synthetas; ovar, lung; s.m.
 132669; W38586; Hs.380933; guanine nucleotide binding pro; colon; diag
 132710; W74001; Hs.55279; serine (or cysteine) proteinases; lung, blad, colon, headnk; diag
 132725; NM_006276; Hs.184167; splicing factor, arginine/ser; ovar; CTL+s.m.
 132767; BE182592; Hs.11281; small proline-rich protein 2A; lung; diag
 132791; AB029551; Hs.7910; RING1 and YY1 binding protein; pros; CTL+s.m.
 132837; AA370362; Hs.57958; EGF-TM7-latrophilin-related pr; angio; diag
 132856; NM_001448; Hs.58367; glypican 4; breast, colon, pros; mAb
 132888; NM_005476; Hs.5920; UDP-N-acetylglucosamine-2-epim; pros; s.m.
 132902; AI936442; Hs.59838; hypothetical protein FLJ10808; colon; diag
 132939; AB009284; Hs.61152; exostosins (multiple)-like 2; ovar; diag
 132964; AI362575; Hs.303171; ESTs; pros; diag
 132967; AA316181; Hs.61635; six transmembrane epithelial a; pros, pros; mAb+CTL
 132990; X77343; Hs.334334; transcription factor AP-2 alph; breast, lung; CTL+s.m.
 132994; AA112748; Hs.279905; clone HQ0310 PRO0310p1; colon, breast; s.m.
 133006; AW978436; Hs.62516; KIAA0494 gene product; colon; diag
 133015; AJ002744; Hs.246315; UDP-N-acetyl-alpha-D-galactosa; breast, colon, pros; s.m.
 133016; AI439688; Hs.6289; hypothetical protein FLJ20886; breast; diag
 133051; AI186431; Hs.296636; prostate differentiation factor; angio, pros, blad; diag
 133063; AI654133; Hs.356247; thyroid receptor interacting p; pros; mAb+s.m.
 133070; U92649; Hs.380136; a disintegrin and metalloprote; leuk; diag
 133179; U81599; Hs.66731; homeo box B13; pros; CTL+s.m.
 133199; AF231981; Hs.250175; homolog of yeast long chain po; breast, angio; CTL+s.m.
 133260; AA403045; Hs.6906; Homo sapiens cDNA: FLJ23197 f; angio; diag
 133272; NM_002776; Hs.69423; kallikrein 10; colon, ovar; diag
 133314; AA102670; Hs.70725; gamma-aminobutyric acid (GABA); breast, panc; mAb
 133321; T79526; Hs.179516; integral type I protein; breast; diag
 133391; AW103384; Hs.727; inhibin, beta A (activin A, ac; breast, blad, lung; diag
 133415; X69699; Hs.73149; paired box gene 8; ovar; CTL
 133477; AW502935; Hs.740; PTK2 protein tyrosine kinase 2; breast; s.m.
 133579; X76346; Hs.75074; mitogen-activated protein kina; pros; diag
 133626; AW836130; Hs.75277; hypothetical protein FLJ13910; pros; diag
 133736; D49958; Hs.75819; glycoprotein M6A; pros; mAb
 133829; AW630088; Hs.76550; Homo sapiens mRNA: cDNA DKFZp5; ovar; diag
 133860; S78296; Hs.76888; hypothetical protein MGC12702; blad; diag
 133944; AW068579; Hs.7780; Homo sapiens mRNA: cDNA DKFZp5; pros; diag
 133975; C18356; Hs.295944; tissue factor pathway inhibitor; angio, panc; CTL+diag
 133976; AI908165; Hs.169946; GATA-binding protein 3 (T-cell; breast, blad; mAb+s.m.
 134100; AA460085; Hs.171075; replication factor C (activato; pros; diag
 134110; U41060; Hs.79136; LIV-1 protein, estrogen regula; breast, blad, ovar, pros; mAb
 134169; AI690916; Hs.178137; transducer of ERBB2, 1; breast; CTL+s.m.
 134219; NM_000402; Hs.80206; glucose-6-phosphate dehydrogen; breast; s.m.
 134319; BE304999; Hs.285754; fumarate hydratase; colon; s.m.
 134326; AW903838; Hs.81800; chondroitin sulfate proteoglyc; ovar, breast, panc, lung; diag
 134348; AW291946; Hs.82065; interleukin 6 signal transduce; breast; mAb+s.m.
 134374; N22687; Hs.8236; ESTs; pros; diag
 134390; R35528; Hs.8258; DKFZP434D1335 protein; pros; CTL+s.m.
 134401; AI916662; Hs.211577; kinesin 1 (kinesin receptor); pros, breast; mAb+s.m.
 134405; AW067903; Hs.82772; collagen, type XI, alpha 1; breast, lung, ovar, headnk; CTL
 134470; X54942; Hs.83758; CDC28 protein kinase 2; lung, blad, headnk; s.m.
 134520; BE091005; Hs.349506; activated RNA polymerase II tr; ovar; s.m.
 134529; AW411479; Hs.848; FK506-binding protein 4 (59kD); breast; diag
 134570; U66615; Hs.172280; SWI/SNF related, matrix associ; EWS; CTL+s.m.
 134654; AK001741; Hs.8739; hypothetical protein FLJ10873; breast; diag
 134666; BE391929; Hs.8752; transmembrane protein 4; breast; mAb+s.m.
 134691; AW382967; Hs.88474; prostaglandin-endoperoxide synt; ovar; s.m.
 134727; X80507; Hs.84520; yes-associated protein 65 kDa; blad; diag
 134731; D89377; Hs.89404; msh (Drosophila) homeo box hom; blad; s.m.
 134786; T29618; Hs.89640; TEK tyrosine kinase, endotheli; angio; s.m.
 134824; S78723; Hs.298623; 5-hydroxytryptamine (serotonin); blad; mAb
 134856; BE281128; Hs.9030; TONDU; blad; CTL+s.m.

- 134868; AB020689; Hs.90419; KIAA0882 protein; breast; diag
 134924; BE294029; Hs.279903; Ras homolog enriched in brain ; breast; mAb
 134972; AL033527; Hs.169252; v-myc avian myelocytomatosis v; ovar; CTL+s.m.
 134975; R50333; Hs.92186; Leman coiled-coil protein; breast; diag
 134989; AW968058; Hs.92381; nudix (nucleoside diphosphate); colon; diag
 135073; W55956; Hs.94030; Homo sapiens mRNA; cDNA DKFZp5; angio; diag
 135117; W52493; Hs.94694; Homo sapiens cDNA FLJ10561 fis; breast; diag
 135166; AA135867; Hs.280858; ESTs, Highly similar to A35661; pros; diag
 135235; AW298244; Hs.266195; ESTs; angio; diag
 135242; AI583187; Hs.9700; cyclin E1; ovar; CTL+s.m.
 135243; BE463721; Hs.97101; putative G protein-coupled rec; colon; mAb+s.m.
 135255; Y13645; Hs.97234; uroplakin 2; blad; mAb
 135309; AI564123; Hs.355689; ADP-ribosylation factor-like 5; pros; diag
 135315; H81136; Hs.334604; Homo sapiens mRNA for KIAA1870; pros; diag
 135389; U05237; Hs.99872; fetal Alzheimer antigen; pros; breast; colon; CTL+s.m.
 135400; X78592; Hs.99915; androgen receptor (dihydrotest; pros; mAb+s.m.
 300254; AW183618; Hs.55610; solute carrier family 30 (zinc; pros; breast; mAb+s.m.
 300256; AW591433; Hs.298241; Transmembrane protease, serine; breast; colon, lung, ovar; mAb+diag+s.m.
 300318; AW444502; Hs.256982; ESTs, Weakly similar to NEL1_H; angio; CTL+diag
 300605; AI218847; Hs.152670; ESTs; pros; diag
 300921; AF146747; Hs.232165; polycythemia rubra vera 1; cel; pros; mAb+s.m.
 300923; AW136372; Hs.1852; acid phosphatase, prostate; pros; s.m.
 301042; AI659131; Hs.366053; hypothetical protein MGC2849; pros; mAb
 301043; AI160316; Hs.149155; voltage-dependent anion channel; pros; mAb+s.m.
 301050; AW136973; Hs.362915; ESTs, Weakly similar to S69890; colon, lung; CTL+s.m.
 301341; AA887801; Hs.208229; G protein-coupled receptor; breast; lung; mAb+s.m.
 302001; AB020711; Hs.374965; KIAA0904 protein; breast; CTL+s.m.
 302005; BE252922; Hs.123119; MAD (mothers against decapentap; pros; diag
 302067; BE542708; Hs.222399; CEGP1 protein; breast; diag
 302167; NM_006227; Hs.283007; phospholipid transfer protein; pros; mAb
 302225; NM_007231; Hs.162211; solute carrier family 6 (neuro; panc; mAb+s.m.
 302276; AW057736; Hs.323910; HER2 receptor tyrosine kinase ; breast; mAb+s.m.
 302280; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp5; pros; breast; diag
 302372; AL117406; Hs.335891; ATP-binding cassette transport; breast; pros ; mAb+s.m.
 302384; AI678059; Hs.202676; synaptonemal complex protein 2; breast; cerv; diag
 302410; NM_004917; Hs.218366; kallikrein 4 (protease, enamel; pros; diag
 302468; AL133561; Hs.380155; DKFZP4348061 protein; pros; diag
 302562; BE149762; Hs.48958; gap junction protein, beta 6 (; lung, blad; mAb
 302881; AA508353; Hs.105314; relaxin 1 (H1); pros; diag
 303285; AA205625; Hs.208067; ESTs; blad; diag
 303380; AW952764; Hs.303171; olfactory receptor, family 51.; pros; mAb
 303506; AA340605; Hs.105887; ESTs, Weakly similar to Homolo; pros; breast; colon ; diag
 303699; BE143707; Hs.19525; hypothetical protein FLJ22794; pros; diag
 303753; AW503733; Hs.9414; KIAA1488 protein; pros; breast; colon; CTL+s.m.
 305503; AA759177; Hs.298148; ESTs, Weakly similar to KIAA05; pros; diag
 306273; AA936290; ; gb:ov70a01.s1 Soares_NFL_T_GBC; pros; diag
 306676; AI005603; ; gb:ov15c10.s1 NCI_CGAP_GC3 Hom; lung; diag
 306840; AI077477; Hs.307912; ESTs; angio; diag
 309177; AI951118; Hs.326738; Homo sapiens breast cancer ant; breast; pros; mAb+CTL
 309583; AW170035; Hs.326738; Homo sapiens breast cancer ant; breast; mAb+CTL
 309931; AW341683; Hs.343663; gb:hd13d01.x1 Soares_NFL_T_GBC; lung; mAb
 310382; AI734009; Hs.127699; KIAA1603 protein; pros; diag
 310431; AI420227; Hs.366053; ESTs, Weakly similar to A46010; pros; diag
 310573; AW292180; Hs.156142; ESTs; pros; diag
 310636; AI814373; Hs.164175; ESTs; lung; diag
 310781; AI380797; Hs.158992; ESTs; breast ; diag
 310955; AI476732; Hs.263912; ESTs; breast; angio; diag
 311034; BE567130; Hs.311389; ESTs, Highly similar to NKGD_H; lung; mAb+s.m.
 311166; AI821005; Hs.118599; intron of BFF9 (GDNFRa); breast ; diag
 311251; AI655662; Hs.197698; ESTs; pros; diag
 311557; AF200492; Hs.211238; Interleukin-1 homolog 1; lung; diag
 311596; AI682088; Hs.79375; single-minded (Drosophila) hom; pros; CTL
 311630; AI915444; Hs.372037; ESTs; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 311877; AA084248; Hs.372651; G protein-coupled receptor 39; ovar; angio, glio; mAb+s.m.
 311911; R19175; Hs.169793; ribosomal protein L32; pros; diag
 311928; T62216; Hs.378028; ESTs; pros; diag
 312182; T94344; Hs.326263; ESTs; pros; diag
 312252; AI128388; Hs.143655; ESTs; blad; diag
 312319; AA906997; Hs.180780; TERA protein; colon; CTL+s.m.
 312521; AI263307; Hs.356901; H2B histone family, member L; pros; breast; lung; diag
 312544; AA516420; Hs.352340; ESTs, Weakly similar to I38022; breast; diag
 312742; AI650363; Hs.116462; ESTs; colon; diag
 312795; AW975014; Hs.26; ferrochelatase (protoporphyrin; pros; s.m.
 312857; BE083868; Hs.126914; KIAA1430 protein; colon; pros; CTL+s.m.
 312922; AA329256; Hs.378739; ESTs, Moderately similar to et; pros; diag
 313328; AW449211; Hs.105445; GDNF family receptor alpha 1; breast ; mAb+s.m.
 313513; AW298600; Hs.64313; ESTs, Weakly similar to S59501; angio; mAb+s.m.
 313556; AA628517; Hs.118502; ESTs; angio; diag
 313665; AW751201; Hs.120932; ESTs; angio; diag
 313774; AI916058; Hs.144583; ESTs; colon; CTL
 313915; C18863; Hs.163443; intron of pericostin (OSF-2os); breast; diag
 313978; AI870175; Hs.13957; ESTs; angio; diag
 314078; AW129357; Hs.329700; ESTs; breast; diag

- 314097; AA648744; Hs.269493; ESTs; breast; diag
 314121; A1732083; Hs.187619; ESTs; pros; breast; diag
 314171; A1821895; Hs.193481; ESTs; pros; diag
 314506; AA833655; Hs.206868; Homo sapiens cDNA FLJ14056 fis; breast; diag
 314547; AA399272; Hs.144341; ESTs; breast; diag
 314558; A1873274; Hs.370280; ESTs; breast; pros; diag
 314589; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis; lung, blad; diag
 314691; AW207206; Hs.356962; ESTs; breast; pros; diag
 314785; A1538226; Hs.32976; guanine nucleotide binding pro; colon; pros; diag
 314907; AW971082; Hs.222886; ESTs, Weakly similar to TRHY_H; pros; diag
 315006; A1538613; Hs.298241; Transmembrane protease, serine; breast, colon, lung, ovar; mAb+diag+s.m.
 315033; A1493046; Hs.146133; ESTs; colon; diag
 315051; AW292425; Hs.163484; ESTs; breast, pros, blad; diag
 315052; AA876910; Hs.134427; ESTs; pros; breast; diag
 315196; A1367347; Hs.44898; Homo sapiens clone TCCCTA00151; breast; diag
 315368; AB037745; Hs.104696; KIAA1324 protein; pros; diag
 315408; AW273261; Hs.216292; ESTs; pros; diag
 315634; AA837085; Hs.372254; ESTs; breast; pros; diag
 315720; AA292998; Hs.163900; ESTs; blad; diag
 316177; A1904982; Hs.293102; downstream of breast cancer an; breast; mAb+CTL
 316442; AA760894; Hs.125350; ESTs; pros; diag
 316580; AA938198; Hs.146123; poly(A) polymerase gamma; breast, angio; s.m.
 316886; AA836331; Hs.170261; ESTs; breast; diag
 316943; AW014875; Hs.137007; ESTs; blad; diag
 317079; BE159984; Hs.125395; ESTs; blad; mAb+s.m.
 317140; AA885430; Hs.201925; Homo sapiens cDNA FLJ13446 fis; breast; diag
 317224; X73608; Hs.93029; spondyloneurin, cwcv and ka; pros, angio; diag
 317548; BE568568; Hs.159066; ESTs; pros; CTL+s.m.
 317803; AW684964; Hs.128899; ESTs; breast, lung, ovar, pros; mAb+s.m.
 317881; A1827248; Hs.224398; Homo sapiens cDNA FLJ11469 fis; breast, lung; diag
 318240; A1085377; Hs.143610; ESTs; lung; diag
 318524; AK001050; Hs.159066; hypothetical protein FLJ10188; pros, colon; CTL+s.m.
 318532; AW139377; Hs.127179; cryptic gene; panc; diag
 318744; A1793124; Hs.144479; ESTs; breast; diag
 318754; W21423; Hs.44222; CGI-90 protein; pros; diag
 319080; AW967646; Hs.23023; ESTs; pros; diag
 319795; AB037821; Hs.146858; protocadherin 10; pros, glio; mAb+s.m.
 320066; BE305242; Hs.16098; claudin 2; colon, panc; diag
 320167; AA984373; Hs.90790; Homo sapiens cDNA: FLJ22930 ft; breast, pros; diag
 320203; AL049227; Hs.124776; downstream of cadherin 6 (by 3; renal, ovar; mAb+s.m.
 320211; AL039402; Hs.125783; DEME-6 protein; breast, pros; CTL
 320322; AF077374; Hs.139322; small proline-rich protein 3; lung; diag
 320324; AF071202; Hs.139336; ATP-binding cassette, sub-fam1; pros; mAb
 320561; AF085808; Hs.159330; uroplakin 3; pros, blad; diag
 320590; U67058; Hs.154259; Human proteinase activated rec; pros; mAb+s.m.
 320635; N50617; Hs.80506; small nuclear ribonucleoprotein; angio lung; diag
 320736; AA315361; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag
 320796; AK001541; Hs.31218; secretory carrier membrane pro; pros, colon; diag
 320896; BE019924; Hs.271580; uroplakin 1B; lung, blad, ovar, headnk; mAb+diag
 321023; AW294316; Hs.125608; ESTs; colon; diag
 321107; A1732643; Hs.144151; downstream of breast cancer an; breast; mAb+CTL
 321412; A1674383; Hs.22891; solute carrier family 7 (calio; pros; mAb+s.m.
 321441; AF107493; Hs.201676; Homo sapiens L15CA-15 protein m; pros, breast; diag
 321644; AW975944; Hs.237396; ESTs; breast, pros; diag
 321717; AW956580; Hs.42699; ESTs; angio; diag
 321908; AW270608; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag
 321911; AF026944; Hs.293797; ESTs; angio, lung, blad; diag
 322035; AL137517; Hs.306201; hypothetical protein DKFZp554C; breast, blad; mAb
 322521; AF147347; ; gb:Homo sapiens full length in; breast; diag
 322706; AA018899; Hs.127179; cryptic gene; panc; diag
 322782; AA056060; Hs.202577; Homo sapiens cDNA FLJ12166 fis; pros; diag
 322818; AW043782; Hs.293616; ESTs; pros, breast, angio, glio; diag
 322882; AW248508; Hs.279727; Homo sapiens cDNA FLJ14035 fis; breast, lung, ovar, angio, blad; diag
 322975; C16391; ; Intron of breast cancer antigen; breast; mAb+CTL
 323168; AL120862; Hs.124165; programmed cell death 9 (PDCD9; breast; diag
 323226; AF055019; Hs.355278; Homo sapiens clone 24670 mRNA; pros; diag
 323262; AL133990; Hs.190642; CEGP1 protein; breast, pros, blad; diag
 323287; AA639902; Hs.104215; ESTs, Moderately similar to SP; pros; diag
 323332; A1829520; ; gb:W19c06.x1 NCL_CGAP_U11 Hom; breast; diag
 323335; A1655499; Hs.161712; ESTs; pros, breast; mAb
 323587; A1299709; Hs.131886; Homo sapiens cDNA: FLJ22113 ft; colon; diag
 323817; AA410943; ; NAME OMITTED ... receptor kinase; breast; mAb
 324261; BE069341; ; gb:QV3-BT0381-270100-073-c08 B; breast; diag
 324295; AA434579; Hs.143691; ESTs; pros; diag
 324338; AA927668; Hs.145078; regulator of differentiation (; colon; diag
 324430; AA464018; Hs.335798; Homo sapiens cDNA: FLJ23241 ft; pros, colon; diag
 324432; AA464510; Hs.152812; ESTs; breast, lung, panc; diag
 324603; AW993522; Hs.299867; ESTs; pros, breast; diag
 324617; AA508552; Hs.228274; ESTs, Weakly similar to 138022; pros; diag
 324658; A1694767; Hs.129179; Homo sapiens cDNA FLJ13581 fis; pros; diag
 324718; A1557019; Hs.116467; small nuclear protein PRAC; colon, pros; diag
 324866; A1541214; Hs.46320; Small proline-rich protein SPR; lung, blad; diag
 324871; A1890347; Hs.271923; Homo sapiens cDNA: FLJ22785 ft; colon; diag

- 324987; AI375572; Hs.172634; ESTs; breast; diag
 325372; ; Phase 2 & 3 Exons; breast; CTL+s.m.
 325544; ; Phase 2 & 3 Exons; breast; angio; diag
 327036; ; Phase 2 & 3 Exons; lung; angio; diag
 327075; ; Phase 2 & 3 Exons; breast; lung; diag
 327414; ; Phase 2 & 3 Exons; angio; diag
 328700; ; Phase 2 & 3 Exons; breast; angio; diag
 330211; ; Phase 2 & 3 Exons; pros; CTL+s.m.
 330468; L10343; Hs.112341; protease inhibitor 3; skin-der; lung; colon; blad; diag
 330493; M27826; Hs.334372; endogenous retroviral protease; lung; colon; s.m.
 330630; NM_002902; Hs.79088; reticulocalbin 2; EF-hand calc; pros; diag
 330762; AW407332; Hs.13014; ADP-ribosylation factor GTPase; pros; CTL+s.m.
 330790; AI660243; Hs.318545; Hu01 Chip Redos; pros; blad; diag
 330814; AI955040; Hs.265398; PAR-6 beta (partitioning def; breast; diag
 330827; AI961486; Hs.249196; ESTs; lung; uter; diag
 330892; AF109298; Hs.118258; prostate cancer associated pro; pros; diag
 331014; AW770994; Hs.30340; hypothetical protein KIAA1165; colon; diag
 331151; R82331; Hs.121602; ESTs; pros; breast; diag
 331183; T40769; Hs.8469; ESTs; colon; diag
 331237; W87874; Hs.25277; Homo sapiens cDNA FLJ10717 fis; angio; diag
 331490; AF216751; Hs.26813; CDA14; pros; diag
 331578; AI246482; Hs.243010; ESTs; angio; diag
 331614; N92283; Hs.206832; EST; Moderately similar to ALU; breast; diag
 331811; AW885727; Hs.9914; Hu01 Chip Redos; lung; diag
 331889; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
 331969; AA526911; Hs.82772; collagen; type XI; alpha 1; breast; lung; CTL
 332180; AF134160; Hs.7327; claudin 1; lung; mAb
 332247; AA669097; ; ESTs; pros; breast; diag
 332396; AW579842; Hs.380730; hypothetical protein FLJ10697; pros; diag
 332453; L42583; Hs.334309; Hu01 Chip Redos; lung; diag
 332466; AB018259; Hs.118140; KIAA0716 gene product; angio; diag
 332530; M31669; Hs.1735; inhibin; beta B (activin AB be; ovar; pros; diag
 332535; AF167706; Hs.19280; cysteine-rich repeat-containing; angio; diag
 332640; BE568452; Hs.344037; protein regulator of cytokines; blad; headnk; diag
 332645; AA284371; Hs.118064; ESTs; breast; colon; diag
 332686; X69699; Hs.73149; paired box gene 8; ovar; CTL+s.m.
 332697; X51405; Hs.75360; carboxypeptidase E; pros; diag
 332740; BE409869; Hs.286241; Homo sapiens cDNA: FLJ22698 ft; pros; diag
 332798; ; C22000007:gl|12314195|emb|CAB9; pros; breast; diag
 333769; ; NM_005940; Homo sapiens matrix; breast; colon; lung; mAb+diag+s.m.
 333904; ; Chromosome 22; pros; diag
 334223; ; NM_005080; Homo sapiens X-box; pros; breast; diag
 334447; ; NM_012429; Homo sapiens SEC14; pros; diag
 335115; ; NM_006498; Homo sapiens lectin; pros; CTL+s.m.
 335809; ; NM_014509; Homo sapiens kraken; breast; CTL+s.m.
 335824; ; ENSP00000249072; DJ222E13.1 (N; breast; pros; CTL+s.m.
 335825; ; ENSP00000249072; DJ222E13.1 (N; breast; diag
 335936; ; Chromosome 22; lung; diag
 336034; ; NM_007172; Homo sapiens nudeop; breast; angio; CTL+s.m.
 336152; ; NM_014246; Homo sapiens cadher; breast; mAb
 336636; ; C220000024:gl|10645308|gb|AAG2; lung; breast; CTL+s.m.
 338008; ; NM_005940; Homo sapiens matrix; lung; breast; colon; mAb+diag+s.m.
 338033; ; Chromosome 22; lung; angio; diag
 338158; ; NM_012399; Homo sapiens phosph; lung; angio; diag
 338255; ; NM_014323; Homo sapiens zinc f; pros; breast; colon; CTL+s.m.
 400195; ; Hs.42650; NM_007057; Homo sapiens ZW10 f; lung; CTL+s.m.
 400269; ; Hs.253495; Eos Control; fibro; diag
 400285; ; Eos Control; lung; diag
 400287; S39329; Hs.181350; kallikrein 2; prostatic; pros; diag
 400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin; panc; pros; angio; blad; lung; mAb+s.m.
 400290; H18836; Hs.31608; hypothetical protein FLJ20041; pros; colon; EWS; mAb
 400294; N95796; Hs.276695; Homo sapiens protein mRNA; co; pros; pros; mAb
 400295; W72838; Hs.348419; AI905687; IL-BT095-190199-019 B; breast; diag
 400298; AA032279; Hs.61635; six transmembrane epithelial a; panc; lung; headnk; stom; EWS; ovar; mAb+CTL
 400328; X87344; transporter 2, ATP-binding cas; lung; mAb+s.m.
 400409; AF153341; ; Homo sapiens winged helix/fork; blad; CTL+s.m.
 400419; AF084545; ; Target; lung; sarc; diag
 400440; X83957; Hs.83870; nebulin; sarc; diag
 400494; ; ENSP00000238970; CIG30 (Fragma; angio; mAb
 400517; ; lensin; stom; cerv; uter; lung; pros; colon; hepC; diag
 400651; ; ENSP00000228031; COPPER CHAPER; sarc; s.m.
 400665; ; NM_002425; Homo sapiens matrix; lung; mAb+diag+s.m.
 400773; ; NM_003105; Homo sapiens sortit; blad; mAb
 400844; ; NM_003105; Homo sapiens sortit; blad; s.m.
 400846; ; sortilin-related receptor, L(D; blad; mAb+s.m.
 400881; ; NM_025080; Homo sapiens hypothe; ovar; diag
 401093; ; C12000586; gl|6330167|dbj|BAAB; blad; lung; CTL+s.m.
 401234; ; mitogen-activated protein kinase; angio; diag
 401424; ; NM_001172; Homo sapiens arginas; pros; s.m.
 401486; ; C4000647; gl|4758508|ref|NP_00; headnk; mAb
 401704; ; NM_021195; Homo sapiens claud; test; mAb
 401732; ; NM_001176; Homo sapiens Rho G; panc; diag
 401747; ; Homo sapiens keratin 17 (KRT17; blad; lung; headnk; melz; diag

- 401760; ; Target Exon; blad, lung, headnk, esoph; diag
 401780; ; NM_005557*:Homo sapiens kerat1; lung, blad, headnk, esoph, mela; diag
 401781; ; Target Exon; lung, blad, headnk, esoph, cerv; diag
 401785; ; NM_002275*:Homo sapiens kerat1; lung; diag
 401797; ; Target Exon; sarc; diag
 401994; ; Target Exon; lung; diag
 402145; ; Target Exon; test; CTL+s.m.
 402199; ; Target Exon; test; CTL+s.m.
 402230; ; Fgenesh predicted: CYTOCHROME ; blad; diag
 402239; ; Target Exon; blad; diag
 402260; ; NM_001436*:Homo sapiens fibril; blad; CTL+s.m.
 402265; ; Target Exon; lung; diag
 402305; ; C19000735*:gi14508027[ref]NP_0; blad; CTL+s.m.
 402420; ; C1000823*:gi10432400[emb]CAC1; lung; diag
 402424; ; NM_024901:Homo sapiens hypothe; blad; CTL+s.m.
 402447; ; C1000201:gi1204416[gb]AAA02627; esoph; mAb
 402474; ; NM_004079:Homo sapiens catheps; lung, colon, stom, fibro; diag
 402550; ; Target Exon; fibro; diag
 402604; ; Target Exon; glio; diag
 402605; ; Target Exon; glio; diag
 402606; ; NM_024626:Homo sapiens hypothe; ovar, breast; mAb
 402680; ; Target Exon; test; mAb
 402777; ; C1002652*:gi1544327[sp]Q04799; blad; diag
 402860; ; ENSP00000239210:DJ50024.4 (nov; mela; CTL+s.m.
 402888; ; Target Exon; sarc; diag
 402992; ; Target Exon; sarc; diag
 402994; ; NM_002463*:Homo sapiens myxovir; esoph; diag
 403046; ; NM_005656*:Homo sapiens transm; pros; mAb
 403047; ; NM_005656*:Homo sapiens transm; pros, blad, colon; mAb
 403071; ; NM_003319*:Homo sapiens tiin ; sarc; diag
 403088; ; NM_003319*:Homo sapiens tiin ; sarc; diag
 403171; ; C2001472*:gi15809678[gb]AAB418; test; diag
 403328; ; Target Exon; mela; diag
 403329; ; unnamed protein product [Homo ; lung; diag
 403381; ; ENSP00000231844*:Ecotropic vir; blad; CTL+s.m.
 403409; ; NM_005929:Homo sapiens antigen; mela; mAb
 403433; ; NM_001622:Homo sapiens alpha-2; hepC; diag
 403478; ; NM_022342:Homo sapiens kinesin; lung; CTL+s.m.
 403715; ; Target Exon; lung; diag
 403740; ; NM_001076*:Homo sapiens UDP gl; pros, hepC; s.m.
 403776; ; ENSP00000226542*:Small inducib; panc; diag
 403903; ; C5001632*:gi10645308[gb]AAG21; blad; CTL+s.m.
 404029; ; NM_018936*:Homo sapiens protoc; glio; mAb
 404049; ; NM_018937*:Homo sapiens protoc; glio; mAb
 404210; ; NM_005936:Homo sapiens myeloid; panc, uter, cerv, lung, ovar, pros, colon, stom; diag
 404240; ; NM_018950:Homo sapiens major h; fibro; mAb
 404263; ; NM_021058*:Homo sapiens H2B h1; lung; CTL+s.m.
 404286; ; C6001909:gi1704441[db]BAA1890; panc; diag
 404298; ; C6001238*:gi121715[sp]P26697; lung; s.m.
 404403; ; Target Exon; blad; diag
 404440; ; NM_021048:Homo sapiens melanom; lung, blad; mAb+CTL
 404866; ; ENSP00000251112*:Sodium/potass; panc; s.m.
 404877; ; NM_005365:Homo sapiens melanom; lung, blad; CTL+s.m.
 404927; ; Target Exon; lung, headnk; diag
 404996; ; Target Exon; lung, headnk, esoph; diag
 405001; ; Interleukin enhancer binding f; sarc; diag
 405025; ; Homo sapiens bone morphogenetic; angio; diag
 405121; ; mitogen-activated protein kin; angio, renat; s.m.
 405238; ; Target Exon; glio; diag
 405239; ; oxidative 3 alpha hydroxyster; glio; s.m.
 405451; ; Homo sapiens glutaminy-peptid; mela; s.m.
 405545; ; Target Exon; cerv; mAb
 405546; ; NM_018833*:Homo sapiens transp; cerv; mAb
 405547; ; NM_018833*:Homo sapiens transp; cerv, mela; mAb
 405646; ; C12000200:gi14557225[ref]NP_00; lung; diag
 405704; ; NM_001844*:Homo sapiens collag; sarc; diag
 405770; ; NM_002362:Homo sapiens melanom; lung, esoph; mAb+CTL
 405849; ; Target Exon; panc; diag
 405932; ; C15000305:gi3806122[gb]AAC691; blad, lung, headnk, cerv; CTL+s.m.
 406081; ; Target Exon; blad; diag
 406137; ; NM_000179*:Homo sapiens mulS (; lung; CTL+s.m.
 406173; ; ENSP00000250148*:Growth hormon; panc; CTL+s.m.
 406348; ; Target Exon; breast; CTL+s.m.
 406360; ; Target Exon; lung, headnk; diag
 406399; ; NM_003122*:Homo sapiens serine; blad; diag
 406434; ; NM_030579*:Homo sapiens cytoch; blad; diag
 406467; ; Target Exon; lung, headnk, blad; diag
 406506; ; Target Exon; angio; diag
 406547; ; Target Exon; test; diag
 406627; T64904; Hs.163780; ESTs; angio; CTL+s.m.
 406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte; panc; mAb
 406672; M26041; Hs.198253; major histocompatibility compl; fibro; mAb
 406685; M18728; ; gb:Human nonspecific crossreac; panc, colon, blad, headnk, stom, lung; mAb+CTL

- 406687; M31126; Hs.352054; matrix metalloproteinase 11 (s; breast, lung, ovar, cerv, uter, panc, esoph, mela, sarc; mAb+diag+s.m.
 406690; M29540; Hs.220529; carcinoembryonic antigen-relat; lung, headnk, panc, stom, blad, colon, cerv; mAb+CTL
 406706; X03740; Hs.231581; myosin, heavy polypeptide 1, s; sarc; diag
 406850; A1624300; Hs.172928; collagen, type I, alpha 1; sarc; CTL+s.m.
 406906; Z25424; ; gb:Hsapiens protein-serine/th; blad, lung; s.m.
 406937; U14622; ; gb:Human transketolase-like pr; test; s.m.
 406967; M24349; ; gb:Human parathyroid hormone-r; lung; CTL+s.m.
 406974; M57293; ; gb:Human parathyroid hormone-r; lung, blad; diag
 407013; U35637; Hs.83870; gb:Human nebulin mRNA, partial; sarc; diag
 407034; U84540; ; gb:Human dystrobrevin isoform ; glio; diag
 407103; AA424881; Hs.256301; hypothetical protein MGC13170; pros; diag
 407116; AA156790; Hs.262036; ESTs, Weakly similar to Z223_1t; pros; diag
 407122; H20276; Hs.31742; ESTs; pros; diag
 407137; T97307; ; gb:ye53h05.s1 Soares fetal liv; lung, blad, ovar, pros, panc, headnk; diag
 407168; A45175; Hs.117183; ESTs; pros, breast, colon; diag
 407178; AA195651; Hs.352312; AP-2 beta transcription factor; breast; CTL+s.m.
 407202; N58172; Hs.109370; ESTs; pros; diag
 407216; N91773; Hs.348385; lysyl oxidase; panc; diag
 407242; M18728; ; gb:Human nonspecific crossreac; panc, colon, blad, headnk, stom, lung, ovar, cerv; mAb
 407244; M10014; ; fibrinogen, gamma polypeptide; lung; diag
 407245; X90568; Hs.172004; tlin; sarc; diag
 407251; U67611; Mm.29182; transaldolase 1; pros; s.m.
 407252; AA659037; Hs.163780; ESTs; angio; CTL+s.m.
 407276; A1951118; Hs.326736; Homo sapiens breast cancer ant; breast; mAb+CTL
 407289; AA135159; Hs.203349; Homo sapiens cDNA FLJ12149 fis; lung; diag
 407366; AF026942; Hs.17518; gb:Homo sapiens cig33 mRNA, pa; ovar, hepC, stom, mela, esoph; diag
 407581; R48402; Hs.173508; P3ECSL; blad; CTL+s.m.
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gat; blad; mAb
 407619; AL050341; Hs.37165; collagen, type IX, alpha 2; sarc; diag
 407634; AW016569; Hs.136414; UDP-GlcNAc:betaGal beta-1,3-N-; lung, headnk; s.m.
 407710; AW022727; Hs.23616; ESTs; test; diag
 407720; AB037776; Hs.38002; KIAA1355 protein; lung; mAb
 407746; AK001962; Hs.38114; hypothetical protein FLJ11100; lung; diag
 407756; AA116021; Hs.38260; ubiquitin specific protease 18; panc, lung, esoph, fibro, mela; CTL+s.m.
 407758; D50915; Hs.38365; KIAA0125 gene product; lung; diag
 407777; AA161071; Hs.71465; squalene epoxidase; panc, esoph; s.m.
 407782; AA608956; Hs.112619; ESTs, Moderately similar to PU; lung; diag
 407786; AA687538; Hs.38972; tetraspan 1; pros, colon, uter, stom, ovar, cerv; mAb
 407788; BE514982; Hs.38991; S100 calcium-binding protein A; headnk, panc, blad, lung, fibro; diag
 407818; AL021938; Hs.40154; jumonji (mouse) homolog; test; CTL+s.m.
 407824; AA147884; Hs.9812; Homo sapiens cDNA FLJ14388 fis; sarc; diag
 407839; AA045144; Hs.161566; ESTs; blad, headnk; mAb
 407846; AA426202; Hs.40403; Cbplp300-interacting transacti; meta; diag
 407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homo; colon, stom, renal, breast, ovar, uter, cerv; diag
 407856; AA045281; Hs.266175; phosphoprotein associated with; mela; diag
 407872; AB039723; Hs.40735; frizzled (Drosophila) homolog ; ovar; mAb
 407881; AW072003; Hs.40968; heparan sulfate (glucosamine) ; panc; s.m.
 407910; AA650274; Hs.41298; fibronectin leucine rich trans; fibro; mAb
 407944; R34008; Hs.239727; desmocollin 2; lung, headnk, esoph; mAb
 407949; W21874; Hs.247057; ESTs, Weakly similar to 210926; fibro, blad; diag
 407962; A1133530; Hs.62930; ESTs, Weakly similar to S59501; angio; mAb+s.m.
 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (; breast, pros, blad, lung, headnk, cerv, esoph; mAb+CTL
 408015; AW136771; Hs.244349; epidermal differentiation comp; mela, sarc; diag
 408045; AW138959; Hs.245123; ESTs; breast; diag
 408056; AA312329; Hs.42331; ephrin-A4; ovar; diag
 408063; BE086548; Hs.381047; calcineurin-binding protein ca; pros, lung; diag
 408081; AW451597; Hs.187409; Intron of basic-helix-loop-hel; ovar, glio; diag
 408101; AW968504; Hs.278346; CDC2-related protein kinase 7; breast, lung, stom; s.m.
 408122; A1432652; Hs.42824; hypothetical protein FLJ10718; lung; diag
 408209; NM_004454; Hs.43697; ets variant gene 5 (ets-relata; mela; CTL+s.m.
 408296; AL117452; Hs.44155; DKFZP586G1517 protein; angio; diag
 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D; panc, renal, colon; mAb
 408353; BE439838; Hs.44298; mitochondrial ribosomal protel; lung; diag
 408430; S79876; Hs.44926; dipeptidylpeptidase IV (CD26, ; pros; mAb
 408522; A1541214; Hs.46320; Small protine-rich protein SPR; lung, blad, headnk, esoph, cerv; diag
 408561; A1308037; Hs.84120; hypothetical protein MGC13018; mela; CTL+s.m.
 408570; ALD48406; Hs.103483; KIAA1798 protein; angio; CTL+s.m.
 408572; AA055611; Hs.226568; ESTs, Moderately similar to AL; lung; diag
 408591; AF015224; Hs.46452; mammaglobin 1; breast, cerv; diag
 408611; NM_004367; Hs.46468; chemokine (C-C motif) receptor; mela; mAb
 408633; AW963377; Hs.222088; PRO2000 protein; blad, lung, headnk, pros; diag
 408660; AA525775; Hs.89040; ESTs, Moderately similar to PC; ovar, panc, pros, esoph, sarc; diag
 408728; AL137379; Hs.47125; hypothetical protein FLJ13912; test; diag
 408758; NM_003686; Hs.47504; exonuclease 1; mela; CTL+s.m.
 408770; AW270608; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag
 408771; AW732573; Hs.47584; potassium voltage-gated channel; lung; mAb
 408780; D31797; Hs.662; tumor necrosis factor (ligand); leuk; diag
 408795; AW749126; Hs.170345; hypothetical protein FLJ13710; ovar; diag
 408826; AF216077; Hs.48376; Homo sapiens clone HB-2 mRNA s; panc, pros; diag
 408833; AW612232; Hs.254835; ESTs; pros; diag
 408877; AA479033; Hs.130315; ESTs, Weakly similar to A47582; breast; diag
 408915; NM_016651; Hs.48950; hepatocellular carcinoma novel ; panc, sarc; diag
 408930; AA146721; Hs.334686; hypothetical protein FLJ21588; blad; CTL+s.m.

- 408962; BE386436; Hs.44317; SRY (sex determining region Y); mela; diag
 408992; AA059325; Hs.30114; guanine nucleotide binding pro; lung; diag
 408996; AI979168; Hs.82226; glycoprotein (transmembrane) n; mela; mAb+s.m.
 409012; AL117435; Hs.49725; DKFZP434I216 protein; sarc; CTL+s.m.
 409036; T97490; Hs.50002; small inducible cytokine subfa; mela; diag
 409051; AA080912; ; gb:zn04d03.r1 Stratagene hNT n; pros; s.m.
 409077; AA063037; Hs.66803; ESTs; lung; diag
 409093; BE243834; Hs.50441; CGI-04 protein; lung; diag
 409123; AA063403; ; gb:zn04d12.s1 Stratagene come; pros; s.m.
 409142; AL136877; Hs.50758; SMC4 (structural maintenance o; ovar, lung, mela; diag
 409153; W03754; Hs.50813; hypothetical protein FLJ20022; fibro; diag
 409200; AL042914; Hs.51039; KIAA0076 gene product; sarc; CTL+s.m.
 409203; AA780473; Hs.687; cytochrome P450, subfamily IVB; fibro, blad, ovar; diag
 409228; R16811; Hs.22010; ESTs, Weakly similar to 210926; lung; mAb
 409231; AA446644; Hs.692; GA733-2 antigen; epithelial gl; pros, ovar, breast, uter, panc, colon, stom; mAb
 409243; AB037761; Hs.51743; KIAA1340 protein; test; diag
 409262; AK000631; Hs.52256; hypothetical protein FLJ20624; pros; CTL+s.m.
 409264; NM_014937; Hs.52463; KIAA0966 protein; mela; CTL+s.m.
 409269; AA576953; Hs.22972; steroid 5 alpha-reductase 2-ii; breast, ovar, lung, panc, uter; mAb
 409327; AL1162; Hs.53563; collagen, type IX, alpha 3; colon, panc, sarc; CTL+s.m.
 409340; BE174629; Hs.321130; hypothetical protein MGC2771; mela; CTL+s.m.
 409342; AU077058; Hs.54089; BRCA1 associated RING domain 1; test; CTL+s.m.
 409348; AI401535; Hs.146090; ESTs; renal, glio; diag
 409361; NM_005982; Hs.54416; sine oculis homeobox (Drosophi; blad, lung, pros; CTL+s.m.
 409389; AB007979; Hs.301281; Homo sapiens mRNA, chromosome 1; glio; diag
 409395; U46745; Hs.336678; dystrobrevin, alpha; glio; diag
 409402; AF208234; Hs.695; cystatin B (stefin B); blad; diag
 409415; AA579258; Hs.6083; Homo sapiens cDNA: FLJ21028 f; mela; diag
 409421; AA199883; Hs.67624; ESTs; test; diag
 409430; R21945; Hs.346735; splicing factor, arginine/ser; mela; diag
 409432; D49372; Hs.54460; small inducible cytokine subfa; stom, esoph; diag
 409433; AA074382; Hs.135255; ESTs; glio, sarc; diag
 409509; AL036923; Hs.322710; ESTs; angio; diag
 409512; AW979187; Hs.293591; melanoma differentiation assoc; mela, esoph; CTL+s.m.
 409542; AA503020; Hs.36563; hypothetical protein FLJ22418; breast, ovar; diag
 409582; R27430; Hs.271565; ESTs; lung; diag
 409601; AF237621; Hs.80828; keratin 1 (epidermolytic hyper; headnk, mela, sarc; CTL+s.m.
 409633; AW449822; Hs.65200; ESTs; sarc; diag
 409637; AA323948; Hs.55407; Homo sapiens mRNA; cDNA DKFZp4; renat; diag
 409638; AW450420; Hs.21335; ESTs; glio; diag
 409670; AI368109; Hs.381163; KIAA1856 protein; test; CTL+s.m.
 409703; NM_006187; Hs.56009; 2'-5'-oligoadenylate synthetas; panc, esoph, mela; s.m.
 409705; M37762; Hs.56023; brain-derived neurotrophic fac; lung; diag
 409719; AI769160; Hs.108681; Homo sapiens brain tumor assoc; lung; diag
 409731; AA125985; Hs.56145; thymosin, beta, identified in ; pros, sarc; CTL+s.m.
 409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal ; ovar, renat; CTL+s.m.
 409935; AW511413; Hs.187393; ESTs; lung; diag
 409958; NM_001523; Hs.57697; hyaluronan synthase 1; panc, ovar; mAb
 409988; N27687; Hs.334334; transcription factor AP-2 alph; mela; diag
 410008; AW732308; Hs.57783; eukaryotic translation initiat; test; diag
 410037; AB020725; Hs.58009; KIAA0918 protein; pros; diag
 410044; BE566742; Hs.58169; highly expressed in cancer, ri; blad; diag
 410048; W76467; Hs.343874; proline oxidase homolog; test; s.m.
 410076; T05387; Hs.7991; ESTs; lung, pros; diag
 410079; U94382; Hs.380757; glycogenin 2; mela; diag
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; pros; diag
 410102; AW248508; Hs.279727; ESTs; homologous of PEM-3 (Cion; ovar, breast, blad, lung, angio, sarc; diag
 410174; AA306007; Hs.59461; DKFZP434C245 protein; mela; diag
 410240; AL157424; Hs.61289; synaptotagmin 2; angio; diag
 410247; AF181721; Hs.61345; RU2S; ovar; CTL+s.m.
 410268; AA316181; Hs.61635; six transmembrane epithelial a; panc, pros, EWS; mAb+CTL
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A; mela; diag
 410310; J02931; Hs.62192; coagulation factor III (thromb; pros, panc; mAb
 410361; BE391804; Hs.62661; guanylate binding protein 1, i; mela, esoph, hepC, fibro, uter; diag
 410438; AW748012; Hs.45207; hypothetical protein KIAA1335; lung; CTL+s.m.
 410467; AF102546; Hs.63931; dachshund (Drosophila) homolog; breast, colon, uter, stom; diag
 410480; R97457; Hs.63984; cadherin 13, H-cadherin (heart; angio; mAb
 410491; AA465131; Hs.64001; Homo sapiens clone 25218 mRNA ; mela, esoph; diag
 410530; M25809; Hs.64173; ATPase, H transporting, lysoso; ovar; mAb
 410553; AW016824; Hs.272068; hypothetical protein MGC14128; blad, lung; diag
 410555; U92649; Hs.380136; a disintegrin and metalloprote; leuk, lung; mAb
 410561; BE540255; Hs.6994; Homo sapiens cDNA: FLJ22044 f; lung; diag
 410566; AA373210; Hs.43047; Homo sapiens cDNA FLJ13585 f; panc; diag
 410600; AW575742; Hs.351676; ESTs, Moderately similar to S6; mela; mAb+s.m.
 410621; AA194329; Hs.172004; titin; sarc; diag
 410681; AW246890; Hs.65425; calbindin 1, (28kD); lung; diag
 410687; U24389; Hs.65436; lysyl oxidase-like 1; panc; diag
 410733; D84284; Hs.66052; CD38 antigen (p45); pros; mAb+CTL
 410763; AF279145; Hs.8966; hypothetical protein FLJ21776; panc; mAb
 410855; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; test; CTL+s.m.
 410867; X63556; Hs.750; fibrillin 1 (Marfan syndrome); panc; diag
 410870; U81599; Hs.66731; homeo box B13; pros; CTL+s.m.
 410883; D43767; Hs.66742; CCL17 chemokine (TARC) (SCYA1; leuk; diag

- 410889; X91662; Hs.66744; *twist* (*Drosophila*) homolog (ac; sarc; CTL+s.m.
 410929; H47233; Hs.30643; ESTs; ovar; test; diag
 411078; A1222020; Hs.182364; *Coccolisp*; pros; glio; breast; diag
 411089; AA456454; Hs.214291; cell division cycle 2-like 1 (); lung; fibro; CTL+s.m.
 411243; AB039886; Hs.69319; CA11; esoph; diag
 411248; AA551538; Hs.69321; Homo sapiens cDNA FLJ14408 fis; blad; diag
 411257; AA628967; Hs.115274; Indian hedgehog protein (IHH); ovar; diag
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic cent; lung; blad; headnk; CTL+s.m.
 411296; BE207307; Hs.10114; growth suppressor 1; sarc; diag
 411358; R47479; Hs.94761; KIAA1691 protein; meta; renal; sarc; mAb
 411388; X72925; Hs.69752; desmocollin 1; headnk; meta; mAb
 411393; AW797437; Hs.69771; B-factor, properdin (COMPLEMEN; ovar; diag
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA); panc; pros; stom; breast; uter; cerv; ovar; mAb
 411573; AB029000; Hs.70823; KIAA1077 protein; panc; headnk; lung; stom; diag
 411579; AC005258; Hs.70830; U6 snRNA-associated Sm-like pr; lung; diag
 411732; U47924; Hs.71642; guanine nucleotide binding pro; lung; diag
 411768; NM_013371; Hs.71979; interleukin 19; ovar; uter; cerv; diag
 411789; AF245505; Hs.72157; Adilcan; breast; panc; lung; stom; headnk; ovar; uter; esoph; sarc; diag
 411825; AK000334; Hs.352415; solute carrier family 39 (zinc; colon; ovar; mAb
 411828; AW161449; Hs.72290; wingless-type MMTV integration; ovar; diag
 411869; W20027; Hs.23439; ESTs; angio; diag
 411874; AA096106; Hs.20403; ESTs; blad; diag
 411880; AW872477; gb:hm30f03.x1 NCL_CGAP_Thy4 Hs; blad; diag
 411945; AL033527; Hs.92137; L-myo-2 protein (MYCL2); blad; ovar; CTL+s.m.
 412006; AW451618; Hs.380683; ESTs; sarc; diag
 412026; AA383618; Hs.73073; testis-specific ankyrin motif; test; diag
 412045; AA099802; Hs.83883; transmembrana, prostate androg; pros; mAb+s.m.
 412099; U64198; Hs.73165; Interleukin 12 receptor, beta; leuk; meta; mAb
 412104; AW205197; Hs.240951; Homo sapiens, Similar to RIKEN; panc; fibro; diag
 412115; AK001763; Hs.73239; hypothetical protein FLJ10901; lung; blad; CTL+s.m.
 412116; AW402166; Hs.784; Epstein-Barr virus induced gen; panc; mAb
 412133; U83460; Hs.380728; solute carrier family 31 (copp; pros; mAb
 412228; AW503785; Hs.73792; complement component (3d/Epste; meta; mAb
 412247; AF022375; Hs.73793; vascular endothelial growth fa; renal; glio; blad; colon; diag
 412265; AA101325; Hs.86154; hypothetical protein FLJ12457; test; CTL+s.m.
 412326; R07566; Hs.73817; small inducible cytokine A3 (h; pros; leuk; diag
 412351; AL135960; Hs.73828; T-cell acute lymphocytic leuke; angio; CTL+s.m.
 412420; AL035668; Hs.73853; bone morphogenetic protein 2; blad; glio; lung; stom; angio; diag
 412448; L12964; Hs.73895; tumor necrosis factor receptor; leuk; mAb
 412471; M53193; Hs.73946; endothelial cell growth factor; cerv; meta; esoph; diag
 412490; AW803564; Hs.288850; Homo sapiens cDNA: FLJ22528 fi; meta; diag
 412519; AA196241; Hs.73980; troponin T1, skeletal, slow; sarc; diag
 412530; AA766268; Hs.266273; hypothetical protein FLJ13346; blad; lung; diag
 412564; X83703; Hs.355934; cardiac ankyrin repeat protein; angio; diag
 412580; AA113262; Hs.17901; similar to CABLES [Homo sapien; meta; diag
 412610; X90608; Hs.74126; fatty acid binding protein 6; ; blad; diag
 412661; N32860; Hs.24611; ESTs, Weakly similar to I54374; blad; CTL+s.m.
 412715; NM_000947; Hs.74519; primase, polypeptide 2A (58kD); pros; s.m.
 412723; AA648459; Hs.335951; hypothetical protein AF301222; lung; blad; headnk; colon; stom; uter; diag
 412755; BE144306; Hs.179891; ESTs, Weakly similar to P4HA_H; angio; s.m.
 412811; H06382; Hs.349705; ESTs; lung; diag
 412817; AL037159; Hs.74619; proteasome (prosome, macropain; lung; s.m.
 412843; AF007555; Hs.74624; protein tyrosine phosphatase; ; pros; mAb
 412856; BE386745; Hs.74631; basigin (OK blood group); meta; mAb
 412926; AI879076; Hs.75061; macrophage myristoylated alan; meta; CTL+s.m.
 412939; AW411491; Hs.75069; eukaryotic translation elongat; meta; renal; diag
 412970; AB026436; Hs.177534; dual specificity phosphatase 1; breast; meta; s.m.
 412986; X81120; Hs.75110; cannabinoid receptor 1 (brain); glio; mAb
 413004; T35901; Hs.75117; interleukin enhancer binding f; lung; diag
 413011; AW068115; Hs.821; biglycan; lung; CTL+s.m.
 413049; NM_002151; Hs.823; hepsin (transmembrane protease; pros; mAb
 413095; AA494359; Hs.30715; potassium voltage-gated channe; panc; stom; renal; colon; mAb+s.m.
 413125; BE244589; Hs.75207; glyoxalase I; pros; s.m.
 413126; AW419203; Hs.174174; ESTs; angio; diag
 413129; AF292100; Hs.104613; RP42 homolog; lung; diag
 413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent; angio; CTL+s.m.
 413142; M81740; Hs.75212; ornithine decarboxylase 1; lung; s.m.
 413163; Y00815; Hs.75216; protein tyrosine phosphatase; ; pros; mAb
 413171; AA318325; Hs.75219; tyrosinase-related protein 1; meta; mAb
 413190; AA151802; Hs.40368; adaptor-related protein compo; meta; diag
 413219; AA878200; Hs.116727; Homo sapiens cDNA FLJ13692 fis; esoph; cerv; diag
 413223; AI732182; Hs.191866; ESTs; lung; diag
 413268; AL039079; Hs.75256; regulator of G-protein signal; headnk; CTL+s.m.
 413281; AA861271; Hs.222024; transcription factor BMAL2; lung; blad; headnk; panc; angio; diag
 413313; NM_002047; Hs.293885; glycyl-tRNA synthetase; test; s.m.
 413328; Y15723; Hs.75295; guanylate cyclase 1, soluble; ; pros; s.m.
 413335; AI613318; Hs.48442; ESTs; ovar; diag
 413364; BE536218; Hs.137516; fidgulin-like 1; lung; diag
 413372; H55532; Hs.349695; tubulin, alpha 2; test; diag
 413435; X51405; Hs.75360; carboxypeptidase E; pros; glio; panc; sarc; diag
 413436; AF238083; Hs.68061; sphingosine kinase 1; sarc; s.m.
 413472; BE242870; Hs.75379; solute carrier family 1 (glut; glio; mAb
 413566; AW604451; Hs.381153; sprouty (*Drosophila*) homolog 4; sarc; CTL+s.m.

- 413573; A1733859; Hs.149089; ESTs; lung; diag
 413582; AW295647; Hs.71331; hypothetical protein MGC5350; lung; diag
 413597; AW302885; Hs.117183; ESTs; pros; diag
 413623; AA825721; Hs.246973; Intron of Bicaudal D homolog 1; ovar; pros; diag
 413691; AB023173; Hs.75478; ATPase, Class VI, type 11B; lung; mAb
 413711; AW291765; Hs.75486; heat shock transcription factor; renal; diag
 413753; U17760; Hs.75517; laminin, beta 3 (nicotin (125kD); lung, blad, headnk, panc, cerv, esoph, colon; diag
 413762; AW411479; Hs.848; FK506-binding protein 4 (59kD); test; diag
 413778; AA090235; Hs.75535; myosin, light polypeptide 2, r; sarc; diag
 413794; AF234532; Hs.61638; myosin X; mela; diag
 413804; T64682; gb:yc48b02.r1 Stratagene liver; blad; diag
 413808; J00287; Hs.350038; Homo sapiens mRNA for caldesmo; esoph; diag
 413813; M96956; Hs.75561; teratocarcinoma-derived growth; colon; diag
 413833; Z15005; Hs.75573; centromere protein E (312kD); lung; CTL+s.m.
 413842; M29383; Hs.856; interferon, gamma; leuk; diag
 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; fibro, renal; mAb
 413880; A1650842; Hs.110915; Interleukin 22 receptor; panc, colon; mAb+s.m.
 413924; AL119964; Hs.75616; seladin-1; pros, breast, ovar; diag
 413943; AW294416; Hs.144687; Homo sapiens cDNA FLJ12981 fis; blad, lung; CTL+s.m.
 413985; A1018668; Hs.75667; synaptophysin; glio, sarc; mAb
 414004; AA737033; Hs.7155; ESTs, Moderately similar to 21; panc, mela; diag
 414020; NM_002984; Hs.75703; CCL4 Chemokine (C-C motif) lig; pros; diag
 414034; U89277; Hs.305985; early development regulator 1; test; CTL+s.m.
 414035; Y00630; Hs.75716; serine (or cysteine) proteinase; lung, cerv, headnk, blad; s.m.
 414053; BE391635; Hs.75725; transgelin 2; blad; diag
 414061; NM_000699; Hs.300280; amylase, alpha 2A; pancreatic; ovar; diag
 414065; AW515373; Hs.271249; Homo sapiens cDNA FLJ13580 fis; pros; diag
 414085; AA114016; Hs.75746; aldehyde dehydrogenase 1 family; pros, panc, sarc; s.m.
 414142; AW368397; Hs.334485; hemocentin (fibulin 6); fibro, panc, sarc; diag
 414161; AA136106; Hs.184852; KIAA1553 protein; test; diag
 414166; AW888941; Hs.75789; N-myc downstream regulated; pros, renal; diag
 414217; A1309298; Hs.278898; Homo sapiens cDNA: FLJ23165 fi; glio; diag
 414219; W20010; Hs.76823; ALL1-fused gene from chromosome; sarc; diag
 414221; AW450979; gb:U1-H-B13-ela-a-12-O-U1.s1 N; blad; diag
 414251; AL042306; Hs.97689; VASA protein; test; CTL+s.m.
 414259; W44633; Hs.301296; Integrin, beta-like 1 (with EG; panc; diag
 414334; AA824298; Hs.21331; hypothetical protein FLJ10036; test; diag
 414359; M62194; Hs.75929; cadherin 11, type 2, OB-cadher; breast, ovar, uter, pros, colon, panc, sarc; mAb
 414368; W70171; Hs.75939; uridine monophosphate kinase; lung; s.m.
 414386; X00442; Hs.75990; haploglobin; ovar; diag
 414416; AW409985; Hs.76084; hypothetical protein MGC2721; blad, lung; CTL+s.m.
 414420; AA043424; Hs.76095; Immediate early response 3; panc, colon; diag
 414430; A1348201; Hs.76118; ubiquitin carboxyl-terminal es; lung; s.m.
 414443; AU077268; Hs.76144; platelet-derived growth factor; sarc, panc, headnk; mAb
 414476; AA301867; Hs.76224; EGF-containing fibulin-like ex; angio; diag
 414477; U41635; Hs.76228; amplified in osteosarcoma; sarc; diag
 414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 anti; mela; mAb
 414521; D28124; Hs.76307; neuroblastoma, suppression of; breast, ovar, uter, pros, blad, panc, colon, stom, fib; diag
 414565; AA502972; Hs.183390; hypothetical protein FLJ13590; pros; diag
 414569; AF109298; Hs.118258; prostate cancer associated pro; pros, EWS; diag
 414575; H11257; Hs.375743; Homo sapiens clone IMAGE:45193; renal; diag
 414595; AA641726; Hs.289015; hypothetical protein MGC4171; blad; diag
 414602; AW630088; Hs.76550; Homo sapiens mRNA; cDNA DKFZp5; pros; mAb
 414683; S78296; Hs.76888; hypothetical protein MGC12702; blad, lung, test; diag
 414732; AW410976; Hs.77152; minichromosome maintenance def; test, blad; diag
 414761; AU077228; Hs.77256; enhancer of zeste (Drosophila); lung, blad, test; CTL+s.m.
 414776; AA155598; Hs.212839; hypothetical protein FLJ14195; angio; diag
 414786; A1246482; Hs.243010; Homo sapiens cDNA FLJ14372 lis; angio; diag
 414799; A1752416; Hs.77326; insulin-like growth factor bin; renal; diag
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; lung; mAb
 414807; A1738616; Hs.77348; hydroxyprostaglandin dehydroge; blad; s.m.
 414809; A1434699; Hs.77356; transferrin receptor (p90, CD7; lung; mAb+s.m.
 414825; X06370; Hs.77432; epidermal growth factor recept; glio, lung, renal, esoph, panc, headnk, leuk; mAb+s.m.
 414915; NM_002462; Hs.76391; myxovirus (Influenza) resistanc; esoph; diag
 414918; A1219207; Hs.72222; hypothetical protein FLJ13459; blad; CTL
 414921; BE390551; Hs.77628; steroidogenic acute regulatory; breast; diag
 414945; BE076358; Hs.77667; lymphocyte antigen 6 complex; mela; mAb
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; blad, panc, esoph; diag
 414998; NM_002543; Hs.77729; oxidised low density lipoprote; fibro, ovar, panc, colon; mAb
 415003; M11437; Hs.77741; kininogen; panc; diag
 415025; AW207091; Hs.72307; ESTs; blad; diag
 415091; AL044872; Hs.77910; 3-hydroxy-3-methylglutaryl-CoA; lung, headnk; s.m.
 415178; D80503; Hs.46692; ESTs; blad; diag
 415214; A1445236; Hs.125124; EphB2; colon, stom; mAb
 415314; N88802; Hs.5422; glycoprotein M6B; mela; mAb
 415457; AW081710; Hs.7369; Homo sapiens testes specific A; fibro, ovar, uter; CTL+s.m.
 415511; A1732617; Hs.182362; ESTs; blad, ovar, renal; diag
 415542; R13474; Hs.290263; ESTs, Weakly similar to f38022; blad; diag
 415724; NM_003580; Hs.78687; neutral sphingomyelinase (N-SM; test; CTL+s.m.
 415752; BE314524; Hs.78776; putative transmembrane protein; endo, uter, breast, stom, blad, mela; mAb
 415786; AW419196; Hs.257924; hypothetical protein FLJ13782; breast, pros, blad; diag
 415787; H01463; Hs.93534; ESTs; pros; diag
 415819; AU077330; Hs.360791; transcription elongation factor; test; CTL+s.m.

- 415829; AW450198; Hs.163742; ESTs; test; diag
 415857; AA866115; Hs.127797; Homo sapiens cDNA FLJ11381 fis; lung, test; diag
 415910; U20350; Hs.78913; chemokine (C-X3-C) receptor 1; glio; mAb
 415947; U04045; Hs.78934; mutS (E. coli) homolog 2 (colo; test; diag
 415989; AJ267700; Hs.351201; ESTs; pros, ovar, blad, lung, headnk, panc, colon, sarc; diag
 415992; C05837; Hs.145807; hypothetical protein FLJ13593; pros, fibro; mAb
 415999; AA172179; Hs.294029; ESTs; pros, uter; diag
 416018; AW138239; Hs.78977; proprotein convertase subtilisin; colon, panc, lung; diag
 416030; H16261; Hs.21948; ESTs; breast, fibro; diag
 416065; BE267931; Hs.78996; proliferating cell nuclear ant; blad, lung, headnk, mela; CTL+s.m.
 416111; AA033813; Hs.79018; chromatin assembly factor 1, s; lung, stom; CTL+s.m.
 416188; BE157260; Hs.79070; v-myc avian myelocytomatosis v; pros; diag
 416201; AA467752; Hs.195161; ESTs; test; diag
 416208; AW291168; Hs.41295; ESTs, Weakly similar to MUC2_H; lung; diag
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calc; ovar; diag
 416225; AA577730; Hs.188684; ESTs, Weakly similar to PC4259; pros, blad; diag
 416350; AF188625; Hs.189507; phospholipase A2, group IID; test, mela, fibro; diag
 416370; N90470; Hs.203697; CD38 antigen (p45); pros, glio; mAb+CTL
 416373; AA195845; Hs.73680; ESTs, Weakly similar to S12658; sarc; diag
 416402; NM_000715; Hs.1012; complement component 4-binding; fibro; diag
 416448; L13210; Hs.79339; lectin, galactoside-binding, s; ovar, colon, stom; diag
 416498; U33632; Hs.79351; potassium channel, subfamily K; panc, stom, breast, ovar, colon; mAb
 416539; Y07909; Hs.79368; epithelial membrane protein 1; pros, headnk; diag
 416602; NM_006159; Hs.367895; Protein kinase C-binding prote; breast; diag
 416640; BE262478; Hs.13406; neuron-specific protein; mela; diag
 416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; blad, lung, headnk, cerv, panc, angio; diag
 416773; AK000340; Hs.79828; hypothetical protein FLJ20333; test; CTL+s.m.
 416815; U41514; Hs.80120; UDP-N-acetyl-alpha-D-galactose; angio; s.m.
 416819; U77735; Hs.80205; pim-2 oncogene; lung, test; diag
 416881; N32520; Hs.141358; ESTs; mela; diag
 416929; N20535; Hs.43265; metastatin 1; mela; diag
 416975; NM_004131; Hs.1051; granzyme B (granzyme 2, cytol; mela; s.m.
 417003; AL038170; Hs.80756; betaine-homocysteine methyltra; blad; s.m.
 417070; Z19077; Hs.172004; titin; sarc; diag
 417105; X60992; Hs.81226; CD6 antigen; fibro; mAb
 417115; AW952792; Hs.334612; small nuclear ribonucleoprote; test; CTL+s.m.
 417124; BE122762; Hs.25338; ESTs; angio; diag
 417148; AA359896; Hs.374554; hypothetical protein FLJ14902; panc; diag
 417151; AA194055; Hs.293858; ESTs; blad; diag
 417153; X57010; Hs.81343; collagen, type II, alpha 1 (pr; pros, sarc; diag
 417218; AA005247; Hs.285754; met proto-oncogene (hepatocyte; lung; mAb+s.m.
 417237; H86385; Hs.81737; palmitoyl-protein thioesterase; mela; s.m.
 417259; AW903838; Hs.81800; chondroitin sulfate proteoglyc; panc, breast; diag
 417275; X63578; Hs.295449; parvalbumin; blad; diag
 417295; AW993524; Hs.43148; epithelial membrane protein 1; pros; diag
 417308; H60720; Hs.81892; KIAA0101 gene product; lung, headnk, blad, cerv, angio, mela, sarc; diag
 417312; AW888411; Hs.250811; leukemia-associated phosphopro; blad; CTL+s.m.
 417333; AL157645; Hs.173179; bromodomain and PHD finger con; breast; diag
 417355; D13168; Hs.82002; endothelin receptor type B; glio, mela; mAb
 417365; D50683; Hs.82028; transforming growth factor, br; fibro, angio; mAb
 417366; BE185289; Hs.1076; small proline-rich protein 1B; lung, blad, headnk, panc, esoph, mela; diag
 417370; T28651; Hs.374466; tryptophanyl-tRNA synthetase; fibro, mela; diag
 417391; AW291946; Hs.82065; interleukin 6 signal transducer; breast; mAb+s.m.
 417400; AA663486; Hs.123072; RAB3B, member RAS oncogene fam; pros; diag
 417407; AA923278; Hs.290905; ESTs, Weakly similar to protea; test, pros; s.m.
 417409; BE272506; Hs.82109; syndecan 1; blad; diag
 417412; X16896; Hs.82112; interleukin 1 receptor, type I; fibro, pros, panc; mAb
 417426; NM_002291; Hs.82124; laminin, beta 1; angio; diag
 417437; U52682; Hs.82132; interferon regulatory factor 4; mela; CTL+s.m.
 417512; X76534; Hs.82226; glycoprotein (transmembrane) n; lung, mela, headnk, panc, breast; mAb
 417516; L24203; Hs.82237; ataxia-telangiectasia group D; lung, headnk, blad; diag
 417542; J04129; Hs.82269; progesterone-associated endomet; lung, mela; diag
 417592; AA204664; Hs.182437; ESTs, Weakly similar to I54383; test; diag
 417599; AA204688; Hs.62954; ESTs; blad, esoph; diag
 417621; AV654694; Hs.82316; interferon-induced, hepatitis; esoph; diag
 417698; BE241624; Hs.82401; CD69 antigen (p60, early T-cell; pros; mAb
 417705; AW134952; Hs.175220; hypothetical protein FLJ14541; test; mAb
 417715; AW959587; Hs.86366; ESTs; blad, lung, headnk; diag
 417720; AA205625; Hs.208067; ESTs; blad, lung, esoph, headnk; diag
 417750; AJ267720; Hs.260523; synovial sarcoma, translocated; sarc; diag
 417777; AJ823763; Hs.7055; ESTs, Weakly similar to I78885; test; s.m.
 417791; AW965339; Hs.44269; ESTs; ovar, blad, lung, headnk; CTL+s.m.
 417801; AA417383; Hs.82582; integrin, beta-like 1 (with EG; panc, fibro; diag
 417805; U38545; Hs.82587; phospholipase D1, phosphatidyl; angio; s.m.
 417831; H16423; Hs.82685; CD47 antigen (Rb-related ant; ovar; mAb
 417843; W07361; Hs.22545; Homo sapiens cDNA FLJ12935 fis; pros; diag
 417847; AI521558; Hs.7331; hypothetical protein FLJ22316; ovar; diag
 417849; AW291587; Hs.82733; nidogen 2; angio, headnk; diag
 417874; BE618160; Hs.82829; protein tyrosine phosphatase, ; panc; mAb+s.m.
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesio; mela; mAb
 417886; AA214584; ; ESTs; test, ovar; diag
 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20; lung, stom, test, blad, headnk, cerv, esoph; CTL+s.m.
 417911; AA333387; Hs.82916; chaperonin containing TCP1, su; test; diag

- 417944; AU077196; Hs.82985; collagen, type V, alpha 2; sarc; diag
 417976; AA641836; Hs.30085; hypothetical protein FLJ23186; colon, stom, lung; mAb
 417976; BE565892; Hs.83077; interleukin 18 (interferon-gam; colon, stom, fibro; diag
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 fami; lung, headnk, esoph; s.m.
 5 418036; Z37978; Hs.83337; latent transforming growth fac; angio; diag
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; lung, angio, test, sarc; diag
 418067; AI127958; Hs.83393; cystatin E/M; headnk, panc, blad; diag
 418068; AW971155; Hs.293902; ESTs, Weakly similar to ISHUS; blad; s.m.
 10 418113; AI272141; Hs.83484; SRY (sex determining region Y); blad, breast, uter, colon, lung, ovar, glio, test, sarc; CTL+s.m.
 418134; AA397769; Hs.86617; ESTs; test; diag
 418140; BE613836; Hs.83551; microfibrillar-associated prot; lung, headnk, esoph, ovar, sarc; diag
 418156; W17056; Hs.83623; nuclear receptor subfamily 1, ; fibro; mAb+s.m.
 418203; X54942; Hs.83758; CDC28 protein kinase 2; lung, blad, test, mela, stom; s.m.
 15 418216; AA662240; Hs.283099; AF15q14 protein; headnk, lung, blad; diag
 418245; AA088767; Hs.83883; transmembrane, prostate androg; panc; mAb+s.m.
 418283; S79895; Hs.83942; cathepsin K (pseudosclerosis); breast, cerv, ovar, uter, pros, headnk, lung, panc, colon, stom; diag
 418318; U47732; Hs.84072; transmembrane 4 superfamily me; panc, pros, colon, stom, omuc; mAb
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibi; headnk, lung, blad; s.m.
 20 418338; NM_002522; Hs.84154; neuronal pentraxin I; sarc; diag
 418339; AA639902; Hs.104215; ESTs, Moderately similar to SP; pros; diag
 418345; AJ001696; Hs.241407; serine (or cysteine) proteinase; cerv, lung; s.m.
 418371; M13560; Hs.84298; CD74 antigen (invariant polype; renal; mAb
 418379; AA218940; Hs.137516; fidgetin-like 1; lung; diag
 25 418394; AF132818; Hs.84728; Kruppel-like factor 5 (intest; panc; CTL+s.m.
 418396; AI765805; Hs.26591; SLC2A12 Solute carrier family 1; pros; mAb
 418397; NM_001269; Hs.84746; chromosome condensation 1; lung; diag
 418399; AF131781; Hs.84753; hypothetical protein FLJ12442; test, blad, sarc; diag
 418406; X73501; Hs.84905; cytokeratin 20; blad, colon; diag
 30 418432; M14156; Hs.85112; insulin-like growth factor 1 (; pros, fibro; diag
 418460; M26315; Hs.85258; CD8 antigen, alpha polypeptide; fibro; mAb
 418462; BE001596; Hs.85266; integrin, beta 4; lung, blad, cerv, headnk, ovar; mAb
 418543; NM_005329; Hs.85962; hyaluronan synthase 3; blad, lung; mAb
 418576; AW968159; Hs.302740; Epithelial calcium channel 2, ; pros; mAb+s.m.
 35 418610; AW245993; Hs.32417; hypothetical protein MGC2742; pros; diag
 418641; BE243136; Hs.86947; a disintegrin and metalloprote; cerv, lung, panc, blad, headnk, stom; mAb
 418655; AA226354; Hs.111240; ESTs; pros; diag
 418661; NM_001949; Hs.1189; E2F transcription factor 3; ovar, lung, mela; CTL+s.m.
 418663; AK001100; Hs.41690; desmocollin 3; lung, blad, headnk, cerv, esoph; mAb
 418683; U90908; Hs.87241; hypothetical protein from clon; angio; CTL+s.m.
 40 418686; Z36830; Hs.87268; annexin A8; blad, lung; diag
 418693; AI750878; Hs.87409; thrombospondin 1; angio, panc; diag
 418696; AW959433; Hs.326290; hypothetical protein FLJ12581; test; diag
 418739; AA310964; Hs.88012; SHP2 interacting transmembrane; mela; diag
 418756; AA252254; Hs.226949; ESTs; test; diag
 45 418825; AA228881; Hs.22394; hypothetical protein FLJ10893; angio; diag
 418829; AA516531; Hs.55999; NK homeobox (Drosophila), fami; pros; diag
 418882; NM_004996; Hs.89433; ATP-binding cassette, sub-fam; ovar, pros, breast, lung; diag
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate r; fibro; s.m.
 50 418888; AU076801; Hs.89436; cadherin 17, LI cadherin (live; colon, stom, ovar, uter, panc; mAb+s.m.
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red b; mela, fibro; mAb
 418932; L34059; Hs.89484; cadherin 4, type 1, R-cadherin; glio; mAb
 418941; AA452970; Hs.239527; E1B-55kDa-associated protein 5; angio, blad; diag
 418968; NM_000078; Hs.89538; cholesteryl ester transfer pro; mela; diag
 418994; AA296520; Hs.89546; selectin E (endothelial adhesi; pros, angio; mAb
 55 419038; AW134924; Hs.68290; ESTs; pros; diag
 419073; AW372170; Hs.183918; transmembrane receptor Unc5H2 ; ovar, renal, blad, lung; mAb
 419078; M93119; Hs.89584; insulinoma-associated 1; blad, lung, panc, sarc; diag
 419079; AW014836; Hs.18844; ESTs; esoph, lung, stom, colon; diag
 419086; NM_000216; Hs.89591; Kallmann syndrome 1 sequence; fibro; diag
 60 419092; J05581; Hs.89603; mucin 1, transmembrane; breast, panc, lung, blad, fibro; mAb
 419222; AD001528; Hs.89718; spermine synthase; pros; s.m.
 419223; X60111; Hs.1244; CD9 antigen (p24); breast, pros, ovar; mAb
 419231; AL046294; Hs.136245; ESTs, Weakly similar to T17227; fibro; diag
 419261; X07876; Hs.89791; wingless-type MMTV Integration; panc; diag
 65 419264; AA877104; Hs.293672; ESTs, Weakly similar to ALUB_H; pros; diag
 419290; AI128114; Hs.112885; spinal cord-derived growth fac; panc; diag
 419356; AI658166; Hs.7331; hypothetical protein FLJ22316; uter, ovar; diag
 419359; AL043202; Hs.90073; chromosome segregation 1 (yeas; lung, blad, test; diag
 419440; AB020689; Hs.90419; KIAA0882 protein; breast; diag
 70 419485; AA489023; Hs.99807; ESTs, Weakly similar to unname; mela; diag
 419490; NM_006144; Hs.90708; granzyme A (granzyme 1, cyto; fibro; s.m.
 419519; AI198719; Hs.176376; ESTs; mela; diag
 419551; AW582256; Hs.91011; anterior gradient 2 (Xenopus I; panc, pros, breast; diag
 419559; Y07828; Hs.91096; ring finger protein; blad, colon, stom; CTL+s.m.
 75 419568; AB026116; Hs.283078; hOAT4; renal; mAb
 419569; AI971651; Hs.91143; jagged 1 (Alagille syndrome); headnk, lung; diag
 419626; H67546; Hs.49768; ESTs; mela, sarc; diag
 419667; AU077005; Hs.92208; a disintegrin and metalloprote; breast, cerv, angio; mAb
 419693; AA133749; Hs.301350; FXRD domain-containing ion tra; pros, breast, ovar, panc, lung; mAb
 80 419721; NM_001650; Hs.315359; aquaporin 4; glio, lung, fibro; mAb
 419743; AW408762; Hs.5957; Homo sapiens clone 24416 mRNA; blad, headnk; diag
 419749; X73608; Hs.93029; sparco osteonectin, cwcw and ka; pros, panc, lung; diag
 419752; AA249573; Hs.152618; ESTs, Moderately similar to ZN; lung; diag

- 419839; U24577; Hs.93304; phospholipase A2, group VII (p; pros; lung; diag
419870; AW403911; Hs.266175; phosphoprotein associated with; meta; diag
419875; AA853410; Hs.93557; proenkephalin; sarc; diag
5 419948; AB041035; Hs.93847; NM_016931: Homo sapiens NADPH α; angio; mAb
419956; AL137939; Hs.40096; cadherin 19, type 2; meta; mAb
419968; X04430; Hs.93913; interleukin 6 (interferon, beta; lung, panc, esoph; diag
419981; AA897581; Hs.128773; ESTs; angio; diag
420005; AW271106; Hs.133294; ESTs; lung, test, blad, colon; diag
10 420062; AW411096; Hs.94785; TGF(beta)-induced transcriptio; test; CTL+s.m.
420067; T52431; Hs.94795; Homo sapiens mRNA; cDNA DKFZp5; sarc; diag
420137; AA306478; Hs.95327; CD3D antigen, delta polypeptid; fibro; mAb
420154; AI093155; Hs.95420; G antigen family C 1 protein (; pros, lelo; CTL+s.m.
420174; AI824144; Hs.199749; ESTs; angio; CTL+s.m.
15 420208; BE276055; Hs.95972; silver (mouse homolog) like; meta, sarc; mAb
420209; AA256444; Hs.125485; hypothetical protein FLJ12604; angio; diag
420218; AW958037; Hs.381105; ribosomal protein L4; meta, pros; diag
420255; NM_007289; Hs.1298; membrane metallo-endopeptidase; pros; mAb
420256; U84722; Hs.76206; cadherin 5, type 2, VE-cadheri; angio, fibro; mAb
20 420267; N37030; Hs.173337; ESTs; meta, sarc; diag
420281; AI823693; Hs.323494; Predicted cation efflux pump; lung, blad, ovar, panc; mAb
420301; AA767526; Hs.22030; paired box gene 5 (B-cell line; meta; diag
420338; AA825595; Hs.88269; Homo sapiens, clone MGC:17339; meta; mAb
420340; NM_000734; Hs.97087; CD32 antigen, zeta polypeptid; fibro; mAb
25 420344; BE463721; Hs.97101; putative G protein-coupled rec; colon, pros, blad, headnk, panc, stom, ovar; mAb
420347; AL033539; Hs.97124; Human DNA sequence from clone ; test; diag
420360; U83171; Hs.97203; small inducible cytokine subfa; leuk; diag
420367; AA259090; Hs.257028; ESTs; test; diag
420376; AL137471; Hs.97266; protocadherin 18; sarc; mAb+s.m.
30 420378; NM_014143; Hs.97269; B7-H1 protein; leuk; mAb
420380; AA640891; Hs.102406; ESTs; lung; diag
420424; AB033036; Hs.97594; KIAA1210 protein; pros; diag
420462; AF050147; Hs.97932; chondromodulin I precursor; lung, EWS, sarc; mAb
420474; L09753; Hs.1313; tumor necrosis factor (ligand); leuk; mAb
35 420544; AA677577; Hs.380213; Homo sapiens Chromosome 18 BAC; pros; diag
420576; AA297634; Hs.54925; KIAA1858 protein; sarc; diag
420598; NM_002692; Hs.99185; polymerase (DNA directed), eps; test; CTL+s.m.
420633; NM_014581; Hs.274480; odorant-binding protein 2B (OB; breast, endo; diag
420656; AA279098; Hs.187638; ESTs; fibro; diag
40 420710; NM_007009; Hs.99875; zona pellucida binding protein; test; diag
420729; AW964897; Hs.290825; ESTs; pros; diag
420757; X78592; Hs.99916; androgen receptor (dihydrotest; pros; mAb+s.m.
420759; T11832; Hs.127787; Homo sapiens cDNA FLJ11381 f1; test; diag
420783; AI659838; Hs.99923; lectin, galactoside-binding, s; lung, blad, headnk; diag
45 420789; AI670057; Hs.199882; ESTs; renal; diag
420859; AW468397; Hs.100000; S100 calcium-binding protein A; sarc; diag
420908; AL049974; Hs.100261; Homo sapiens mRNA; cDNA DKFZp5; panc; diag
420923; AF097021; Hs.273321; differentially expressed in he; blad, colon; diag
50 420931; AF044197; Hs.100431; small inducible cytokine B sub; breast, lung, meta; diag
420981; L40904; Hs.100724; peroxisome proliferative activ; colon; mAb+s.m.
421016; AA504583; Hs.101047; transcription factor 3 (E2A im; test; CTL+s.m.
421044; AF061871; Hs.101302; Human DNA sequence from clone ; panc; diag
421059; AI654133; Hs.356247; thyroid receptor interacting p; pros; mAb+s.m.
421064; AI245432; Hs.101382; tumor necrosis factor, alpha-i; blad, uter; diag
55 421070; AA283185; Hs.19327; ESTs; blad; diag
421100; AW351839; Hs.124660; Homo sapiens cDNA: FLJ21763 f1; blad; diag
421133; AA814971; Hs.26410; ESTs; lung; diag
421154; AA284333; Hs.287631; Homo sapiens cDNA FLJ14269 f1; BPH; diag
421155; H87879; Hs.102267; lysyl oxidase; headnk, panc, renal, sarc; diag
60 421218; NM_000499; Hs.72912; cytochrome P450, subfamily I (; blad, angio; diag
421233; AA209534; Hs.284243; tetraspan NET-8 protein; pros, breast, ovar; mAb
421241; X91817; Hs.102866; transketolase-like 1; test; s.m.
421302; T34462; Hs.103291; neuritin; uter, endo ; diag
421305; BE397354; Hs.324830; diphtheria toxin resistance pro; ovar; diag
65 421307; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp4; breast, lung, angio, test, sarc; diag
421341; AJ243212; Hs.279611; deleted in malignant brain tum; panc, lung; diag
421350; AW301608; Hs.278188; ESTs, Moderately similar to I5; test; diag
421373; AA808229; Hs.222088; ESTs; blad; diag
421433; AI829192; Hs.22380; ESTs; pros; diag
70 421451; AA291377; Hs.60831; ESTs; ovar, blad, lung; diag
421458; NM_003654; Hs.104576; carbohydrate (keratan sulfate ; sarc; s.m.
421478; AI683243; Hs.97258; ESTs, Moderately similar to S2; ovar, blad, renal, uter; diag
421481; AW391972; Hs.104696; KIAA1324 protein; pros; diag
421502; AF111856; Hs.105039; solute carrier family 34 (sodi; ovar, fibro; mAb
75 421508; BE302796; Hs.105097; thymidine kinase 1, soluble; lung, headnk, esoph; s.m.
421508; NM_004833; Hs.105115; absent in melanoma 2; blad, esoph, lung, meta; CTL+s.m.
421535; AB002359; Hs.105478; phosphoribosylformylglycinamid; test; s.m.
421537; BE383488; Hs.105547; neural proliferation, differen; pros; diag
421566; NM_000399; Hs.1395; early growth response 2 (Krox-; pros; CTL+s.m.
80 421579; NM_002975; Hs.105927; stem cell growth factor; lymph; sarc; mAb
421633; AF121860; Hs.106260; sorting nexin 10; meta; diag
421650; AA781795; Hs.343800; ESTs; meta; diag
421666; AL035250; Hs.1408; endothelin 3; meta; diag
421727; Y13153; Hs.107318; kynurenine 3-monooxygenase (ky; breast; s.m.

- 5 421773; W69233; Hs.112457; ESTs; mela, esoph, sarc; diag
 421777; BE552088; Hs.108196; HSPC037 protein; esoph, cerv, lung; diag
 421779; A1879159; Hs.108219; wingless-type MMTV Integration; colon, ovar; diag
 421798; N74880; Hs.355462; N-acylsphingosine amidohydrolase; fibro; s.m.
 421814; L12350; Hs.108623; thrombospondin 2; panc; diag
 421831; AA298836; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio; mAb+s.m.
 421887; AW161450; Hs.109201; CGI-86 protein; pros; mAb
 421896; N62293; Hs.45107; ESTs; pros; diag
 10 421917; AB028943; Hs.109445; KIAA1020 protein; test; diag
 421920; BE551245; Hs.1438; gamma-aminobutyric acid (GABA); sarc; mAb
 421924; BE514514; Hs.109606; coronin, actin-binding protein; fibro; diag
 421948; L42583; Hs.334309; keratin 6A; lung, headnk, blad, esoph, cerv, mela; diag
 421952; AA300900; Hs.98849; dynein light chain 2B (DNL2B); fibro; diag
 421991; NM_014918; Hs.110486; KIAA0990 protein; panc; diag
 15 421996; AW583807; Hs.1460; glucagon; panc; diag
 422002; X70070; Hs.110642; neurotensin receptor 1 (high a; colon; mAb
 422027; AL043100; Hs.288828; fatty acid amide hydrolase; pros; s.m.
 422033; AW245805; Hs.110903; claudin 5 (transmembrane prote; glio; mAb
 422087; X58968; Hs.111301; matrix metalloproteinase 2 (ge; sarc; diag
 20 422089; AS23172; Hs.103135; ESTs, Weakly similar to SFR4_H; pros; diag
 422094; AF129535; Hs.272027; F-box only protein 5; blad, lung; CTL+s.m.
 422095; A1868872; Hs.282804; hypothetical protein FLJ22704; lung, panc, ovar, breast; CTL+s.m.
 422099; AA156022; Hs.111518; hypothetical protein; angio; CTL+s.m.
 25 422100; A1096988; Hs.111554; ADP-ribosylation factor-like 7; lung, esoph; CTL+s.m.
 422110; A1376736; Hs.121555; secreted protein, acidic, cyst; panc; diag
 422119; A1277829; Hs.111862; KIAA0590 gene product; blad; diag
 422134; AW179019; Hs.112110; mitochondrial ribosomal prote; lung; diag
 422152; AA909249; Hs.112282; solute carrier family 30 (zinc; blad; mAb+s.m.
 30 422163; AF027208; Hs.112360; prominin (mouse)-like 1; colon, breast, fibro; mAb
 422164; NM_014312; Hs.112377; cortic al thymocyte receptor (l; blad; mAb+s.m.
 422168; AA586894; Hs.112408; S100 calcium-binding protein A; lung, blad, headnk, breast, mela, esoph, sarc, cerv; CTL+s.m.
 422170; A1791949; Hs.112432; anti-Mullerian hormone; uter; blad; diag
 422173; BE385828; Hs.250619; phorbol-like protein MDS019; mela; diag
 35 422247; U18244; Hs.113602; solute carrier family 1 (high; blad; mAb
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog; ovar, headnk, blad, cerv, lung, panc, stom; mAb
 422309; U79745; Hs.114924; solute carrier family 16 (mono; mela; mAb+s.m.
 422311; AF073515; Hs.114948; cytokine receptor-like factor; lung, fibro; diag
 422355; AW403724; Hs.300697; coagulation factor VII (serum; fibro; diag
 40 422363; T55979; Hs.115474; replication factor C (activator; mela, colon; diag
 422398; A1476149; Hs.334489; hypothetical protein FLJ21992; fibro; CTL+s.m.
 422406; AF025441; Hs.116206; Opa-Interacting protein 5; blad, lung; diag
 422420; U03398; Hs.1524; tumor necrosis factor (ligand); colon, panc, stom, leuk; mAb
 422423; AF283777; Hs.116481; CD72 antigen; spleen, leuk; mAb
 45 422440; NM_004812; Hs.116724; aldo-keto reductase family 1, ; lung, headnk; s.m.
 422487; A1010901; Hs.198267; mucin 4, tracheobronchial; lung, headnk, panc, sarc; diag
 422532; AL008726; Hs.118126; protective protein for beta-ga; renal, mela; s.m.
 422565; BE259035; Hs.118400; singed (Drosophila)-like (sea; panc, test, mela; diag
 422573; AW297985; Hs.295726; integrin, alpha V (vitronectin; panc; mAb+s.m.
 50 422596; AF063611; Hs.118633; 2'-5'-oligoadenylate synthetase; esoph, mela; s.m.
 422603; BE242587; Hs.118651; hematopoietically expressed ho; angio; CTL+s.m.
 422633; X56832; Hs.118804; enolase 3, (beta, muscle); sarc; s.m.
 422658; AF231981; Hs.250175; homolog of yeast long chain po; pros; diag
 422689; AW856666; Hs.299797; gb:RC3-CT0297-290100-013-d03 C; test; diag
 55 422726; U11690; Hs.1572; facio-genital dysplasia (Aarskog; test; diag
 422728; AW937826; Hs.103262; MAD (mothers against decapenta; pros; diag
 422789; AK001113; Hs.120842; hypothetical protein FLJ10251; test; CTL+s.m.
 422835; BE218705; Hs.121378; metallothionein-like 5, testis; breast; diag
 422871; AL031228; Hs.121509; collagen, type XI, alpha 2; sarc; diag
 60 422887; A1751848; Hs.49215; ESTs; sarc; CTL+s.m.
 422938; NM_001809; Hs.1594; centromere protein A (17kD); lung, test; CTL+s.m.
 422963; M79141; Hs.13234; ESTs; lung, panc; diag
 422997; BE018212; Hs.122908; DNA replication factor; test; CTL+s.m.
 423017; AW178761; Hs.227948; serine (or cysteine) proteinase; blad, headnk, mela; mAb+diag
 65 423052; M28214; Hs.123072; RAB38, member RAS oncogene fam; pros; diag
 423189; M59371; Hs.171596; EphA2; colon, ovar; mAb
 423196; AK001866; Hs.125139; hypothetical protein FLJ11004; fibro; CTL+s.m.
 423198; M81933; Hs.1634; cell division cycle 25A; test; CTL+s.m.
 423201; NM_000163; Hs.125180; growth hormone receptor; pros; mAb
 70 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (e; lung, esoph; diag
 423271; W47225; Hs.126256; interleukin 1, beta; blad, stom, esoph; diag
 423309; BE006775; Hs.126782; sushi-repeat protein; lung, colon; diag
 423354; AB011130; Hs.127436; calcium channel, voltage-depend; test, fibro; mAb
 423387; AJ012074; Hs.348500; vasoactive intestinal peptide; pros; mAb
 75 423397; NM_001838; Hs.1652; chemokine (C-C motif) receptor; blad, mela; mAb
 423412; AF109300; Hs.351615; prostate cancer associated pro; pros; diag
 423422; AC005175; Hs.128425; NY-REN-24 antigen; glio; mAb+CTL
 423445; NM_014324; Hs.128749; alpha-methylacyl-CoA racemase; pros; s.m.
 423453; AW450737; Hs.128791; CGI-09 protein; lung; CTL+s.m.
 80 423458; A1204212; Hs.351113; ESTs; test; CTL+s.m.
 423511; AF036329; Hs.129715; gonadotropin-releasing hormone; lung; diag
 423515; AA327017; Hs.176594; ESTs; ovar; diag
 423541; AA296922; Hs.129778; serine protease inhibitor, Kaz; colon, panc; diag
 423575; C18863; Hs.163443; Intron of periostin (OSF-2os); headnk, breast, panc, lung, fibro, esoph; diag

- 423605; AF047826; Hs.129887; cadherin 19, type 2; meta; mAb
 423642; AW452650; Hs.157148; hypothetical protein MGC13204; lung; diag
 423662; AK001035; Hs.130881; B-cell CLL/lymphoma 11A (zinc); lung; diag
 423685; BE350494; Hs.49753; uveal autoantigen with coiled; panc, uter, colon; CTL+s.m.
 423725; AJ403108; Hs.132127; hypothetical protein LOC57822; lung, headnk, blad; diag
 423739; AA398155; Hs.97600; ESTs; breast, ovar, panc; diag
 423761; NM_006194; Hs.132576; paired box gene 9; headnk; CTL+s.m.
 423765; R23858; Hs.143375; Homo sapiens, clone IMAGE:3840; test; diag
 423778; Y09267; Hs.132821; flavin containing monooxygenase; fibro; s.m.
 423779; AW071837; Hs.57971; TRANSCRIPTION FACTOR HES-5; glio; diag
 423787; AJ295745; Hs.236204; nuclear pore complex protein; test; esoph; diag
 423798; AF047033; Hs.132904; solute carrier family 4, sodium; angio; mAb
 423799; AW026300; Hs.132906; 19A24 protein; meta; mAb
 423849; AL157425; Hs.133315; Homo sapiens mRNA; cDNA DKFZp7; lung; diag
 423887; AL080207; Hs.134585; DKFZP434G232 protein; headnk, lung; diag
 423899; NM_001427; Hs.134989; engrailed homolog 2; meta; CTL+s.m.
 423905; AW579960; Hs.135150; lung type-I cell membrane-asso; test; mAb
 423909; AJ223183; Hs.135194; immunoglobulin superfamily, mc; test; diag
 423934; U89995; Hs.159234; forkhead box E1 (thyroid trans; lung; CTL+s.m.
 424001; W67883; Hs.137476; paternally expressed 10; breast, ovar, diag
 424012; AW368377; Hs.137569; tumor protein 63 kDa with stro; lung, blad, headnk, esoph; diag
 424036; AA770688; Hs.348495; H2A histone family, member L; panc, ovar; CTL+s.m.
 424054; AA334511; Hs.26638; membrane-spanning 4-domains, s; pros, fibro; mAb
 424078; AB006625; Hs.139033; paternally expressed 3; ovar, uter; CTL+s.m.
 424081; NM_006413; Hs.139120; ribonuclease P (30K); test; s.m.
 424098; AF077374; Hs.139322; small proline-rich protein 3; lung, blad, headnk, esoph, cerv; diag
 424125; M31669; Hs.1735; inhibin, beta B (activin AB bc; ovar, pros; diag
 424144; AA454033; Hs.41644; AKAP-associated sperm protein; fibro; diag
 424153; AA451737; Hs.141496; MAGE-like 2; meta; CTL+s.m.
 424165; AW582904; Hs.142255; islet amyloid polypeptide; panc; mAb
 424212; NM_005814; Hs.143131; glycoprotein A33 (transmembran; colon, stom, ovar; mAb
 424218; AF031824; Hs.143212; cystatin F (leukocystatin); meta, fibro; diag
 424244; AV647184; Hs.143601; hypothetical protein hCLA-iso; blad; diag
 424252; AK000520; Hs.143811; hypothetical protein FLJ20513; colon, stom; diag
 424264; D80400; Hs.239388; Human DNA sequence from clone; blad; mAb
 424308; AW975531; Hs.154443; minichromosome maintenance def; blad, lung, test; diag
 424310; AA338648; Hs.50334; testes development-related NYD; fibro; diag
 424332; AA338919; Hs.101615; ESTs; pros; diag
 424339; BE257148; Hs.145416; endoglycan; pros, lung; diag
 424343; AW956360; Hs.4748; adenylate cyclase activating p; glio, ovar, uter; mAb
 424364; AW383226; Hs.163834; ESTs, Weakly similar to G01763; lung, blad, headnk, cerv; diag
 424399; AI905687; Hs.348419; AI905687:IL-BT095-190199-019 B; breast, uter, headnk; diag
 424420; BE614743; Hs.146688; prostaglandin E synthase; lung, blad; s.m.
 424440; AA340743; Hs.133208; ESTs; sarc; diag
 424441; X14850; Hs.147097; H2A histone family, member X; lung; diag
 424450; AL137526; Hs.147472; dynein intermediate chain 2; fibro; diag
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 9; breast, cerv, ovar, uter, blad, colon, stom; s.m.
 424527; AW138558; Hs.334873; ESTs, Weakly similar to I54374; fibro; diag
 424578; AK001973; Hs.150890; hypothetical protein; test; CTL+s.m.
 424581; M52062; Hs.150917; catenin (cadherin-associated p; glio, ovar, uter; mAb+s.m.
 424586; NM_003401; Hs.150930; X-ray repair complementing def; panc; CTL+s.m.
 424629; M90656; Hs.151393; glutamate-cysteine ligase, cat; lung; CTL+s.m.
 424635; AA420687; Hs.115455; Homo sapiens cDNA FLJ14259 f1; glio; diag
 424676; Y08565; Hs.151678; UDP-N-acetyl-alpha-D-galactose; breast; s.m.
 424704; AI263293; Hs.152056; cytochrome P450, subfamily II; renal; s.m.
 424711; NM_005795; Hs.152176; calcitonin receptor-like; angio; mAb
 424717; H03754; Hs.152213; wingless-type MMTV integration; blad, lung, headnk; diag
 424800; AL035588; Hs.153203; MyoD family inhibitor; test, pros; diag
 424806; AA382523; Hs.105689; MSTP031 protein; angio; mAb
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 f1; lung, blad, ovar, headnk, esoph, cerv, uter; diag
 424846; AU077324; Hs.1832; neuropeptide Y; pros; diag
 424897; D63216; Hs.153684; frizzled-related protein; panc, EWS, stom, renal; diag
 424902; NM_003866; Hs.153687; inositol polyphosphate-4-phosph; panc, leuk, meta; CTL+s.m.
 424954; NM_000546; Hs.1846; tumor protein p53 (Lj-Fraumeni; meta, colon; CTL+s.m.
 424971; AA479005; Hs.154036; tumor suppressing subtransfer; panc, meta; CTL+s.m.
 424998; U58515; Hs.154138; chitinase 3-like 2; glio; diag
 425023; AW956889; Hs.154210; EDG-1 (endothelial differenti; angio; mAb
 425048; H05468; Hs.164502; ESTs; lung, blad; diag
 425057; AA826434; Hs.1619; achaete-scute complex (Drosoph; glio, lung; CTL+s.m.
 425088; AA663372; Hs.169395; hypothetical protein FLJ12015; glio, meta; diag
 425154; NM_001851; Hs.154850; collagen, type IX, alpha 1; sarc; diag
 425159; NM_004341; Hs.154868; carbamoyl-phosphate synthetase; lung, test; s.m.
 425200; BE255203.comp; Hs.155101; ATP synthase, H transporting,; panc; s.m.
 425206; NM_002153; Hs.155109; hydroxysteroid (17-beta) dehyd; blad; mAb
 425211; M18667; Hs.1867; progastrin (pepsinogen C); fibro, esoph, pros; diag
 425234; AW152225; Hs.165909; ESTs, Weakly similar to I38022; lung, angio, blad, meta; diag
 425235; AA353113; Hs.105468; Homo sapiens cDNA: FLJ22743 f1; angio; diag
 425237; U07695; Hs.155227; EphB4; test; mAb
 425245; AI751768; Hs.155314; KIAA0095 gene product; lung; diag
 425259; AL049280; Hs.145010; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 425262; D87118; Hs.155418; GS3355 protein; meta, renal; CTL+s.m.
 425266; J00077; Hs.155421; alpha-fetoprotein; lung; diag
 425274; BE281191; Hs.155462; minichromosome maintenance def; test; diag

- 425289; AW139342; Hs.155530; Interferon, gamma-inducible pr; mela; CTL+s.m.
 425308; M97639; Hs.155585; receptor tyrosine kinase-like; pros; sarc; mAb
 425367; BE271188; Hs.155975; protein tyrosine phosphatase; ; fibro; diag
 425371; D49441; Hs.155981; masothelin; ovar; lung; fibro; mAb
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (i); lung, blad, panc, angio, test, mela, esoph; CTL+s.m.
 425427; A1652662; Hs.317432; branched chain aminotransferase; test; s.m.
 425428; AL110261; Hs.157211; DKFZP586B0621 protein; panc; diag
 425465; L18964; Hs.1904; protein kinase C, iota; ovar; pros; colon; s.m.
 425525; AA358883; Hs.23871; ESTs; sarc; diag
 425545; N98529; Hs.158295; Homo sapiens, clone MGC12401; ; sarc; diag
 425555; AA359291; Hs.130767; Homo sapiens cDNA: FLJ23553 f; fibro; CTL+s.m.
 425572; AB011076; Hs.158307; undifferentiated embryonic cel; test; CTL+s.m.
 425601; AW629485; Hs.140720; GSK-3 binding protein FRAT2; test; CTL+s.m.
 425606; U52112; Hs.158331; renin-binding protein; mela; diag
 425628; NM_004476; Hs.1915; folate hydrolase (prostate-spe; pros; s.m.
 425638; NM_012337; Hs.158450; nasopharyngeal epithelium spec; fibro; CTL+s.m.
 425679; X05997; Hs.159177; lipase, gastric; esoph; s.m.
 425692; D90041; Hs.155956; N-acetyltransferase 1 (arylami; breast; s.m.
 425695; NM_005401; Hs.159238; protein tyrosine phosphatase; ; lung; mAb+s.m.
 425709; AA383076; Hs.159274; outer dense fibre of sperm tail; test; diag
 425710; AF030880; Hs.159275; solute carrier family, member; pros; mAb
 425722; A1659076; Hs.97031; hypothetical protein MGC13047; mela; diag
 425726; AF085808; Hs.159330; uropilin 3; pros; blad; diag
 425769; U72513; Hs.159486; Human RPL13-2 pseudogene mRNA; ; test; diag
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort; test; diag
 425849; AJ000512; Hs.296323; serum/glucocorticoid regulated; lung, headnk; s.m.
 425921; NM_007231; Hs.162211; solute carrier family 6 (neuro; stom, panc; mAb
 425976; C75094; Hs.334514; NG22 protein; pros; ovar; mAb
 426027; NM_002608; Hs.1976; platelet-derived growth factor; sarc; diag
 426050; AF017307; Hs.166096; E74-like factor 3 (ets domain; ovar, blad, stom; CTL+s.m.
 426059; BE292842; Hs.166120; interferon regulatory factor 7; esoph, cerv; CTL+s.m.
 426067; AW654691; Hs.97053; ESTs; lung; diag
 426088; AF038007; Hs.166196; ATPase, Class I, type 8B, memb; blad, lung; mAb
 426094; AF034611; Hs.166206; cubilin (intrinsic factor-cofactor; renal; diag
 426116; AA868729; Hs.144694; ESTs; fibro; diag
 426125; X87241; Hs.156994; FAT tumor suppressor (Drosophila; colon, stom, panc, pros, renal, fibro, cerv; mAb
 426158; BE244537; Hs.167382; natriuretic peptide receptor A; ovar; mAb
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic; breast, ovar, uter, pros, blad, panc, colon, fibro, mela; diag
 426172; AA371307; Hs.125056; ESTs; pros; diag
 426174; AA547959; Hs.115838; Homo sapiens similar to Echin; breast, pros, fibro; diag
 426212; S71824; Hs.167988; neural cell adhesion molecule; ; glio; mAb
 426271; AF026547; Hs.169047; chondroitin sulfate proteoglyc; glio; diag
 426274; D38122; Hs.2007; tumor necrosis factor (ligand); fibro, mela; mAb
 426300; U15979; Hs.169228; delta-like homolog (Drosophila; ovar, sarc; mAb
 426310; NM_003909; Hs.169266; neuropeptide Y receptor Y1; breast; mAb
 426312; AF026939; Hs.181874; interferon-induced protein wit; esoph, mela; diag
 426320; W47595; Hs.169300; transforming growth factor, be; ovar, pros, blad, panc; diag
 426350; NM_003245; Hs.2022; transglutaminase 3 (E polypept; cerv; s.m.
 426363; M58524; Hs.2025; transforming growth factor, be; pros; diag
 426370; R98288; Hs.281706; sortilin 1; sarc; diag
 426416; AW612744; Hs.169824; killer cell lectin-like recept; fibro; mAb
 426440; BE382758; Hs.169902; solute carrier family 2 (facit; lung, panc, ovar, blad, headnk, esoph; mAb
 426462; U59111; Hs.169993; dermatan sulphate proteoglycan; sarc; diag
 426470; AA528794; Hs.128644; ESTs; mela; diag
 426471; M22440; Hs.170009; transforming growth factor, al; headnk, renal, panc; diag
 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; panc; mAb+s.m.
 426501; AW043782; Hs.293616; ESTs; pros, breast, glio, lung, mela; mAb
 426502; Y07759; Hs.170157; myosin VA (heavy polypeptide 1; mela; diag
 426534; U58096; Hs.2051; testis specific protein, Y-lin; test; CTL+s.m.
 426535; AU077012; Hs.170279; ESTs, Weakly similar to ubiquit; angio; diag
 426555; NM_000372; Hs.2053; tyrosinase (oculocutaneous alb; mela, sarc; mAb
 426559; AB001914; Hs.170414; paired basic amino acid cleav; hepC, breast, ovar, renal; diag
 426575; M74828; Hs.170808; glutamate decarboxylase 2 (pan; panc; s.m.
 426627; AF012359; Hs.195685; ESTs; test; diag
 426635; BE395109; Hs.129327; hypothetical protein MGC13057; ovar; CTL+s.m.
 426682; AV660038; Hs.2056; UDP glycosyltransferase 1 fami; blad, lung; s.m.
 426691; NM_005201; Hs.171834; PCTAIRE protein kinase 1; ovar; CTL+s.m.
 426696; AW363332; Hs.171844; Homo sapiens cDNA: FLJ22296 f; angio; mAb
 426721; AA383588; Hs.288545; ESTs, Weakly similar to T29012; fibro; diag
 426726; AA488915; Hs.171955; trophinin associated protein (i; test; diag
 426747; AA535210; Hs.171995; kallikrein 3, (prostate specif; pros; diag
 426752; X69490; Hs.172004; titin; sarc; diag
 426759; AI590401; Hs.21213; ESTs; mela; diag
 426793; X89887; Hs.172350; HIR (histone cell cycle regula; pros; CTL+s.m.
 426826; NM_000020; Hs.172670; activin A receptor type II-B; angio; mAb
 426866; U02330; Hs.172816; neuregulin 1; esoph; CTL+s.m.
 426897; AW976570; Hs.97387; ESTs; lung; diag
 426900; AW163564; Hs.142375; ESTs; blad, pros; mAb
 426935; NM_000088; Hs.172928; collagen, type I, alpha 1; test, sarc; CTL+s.m.
 426966; AI493134; Hs.349204; sclerostin; lung; diag
 426968; U07616; Hs.173034; amphiphysin (Stiff-Mann syndro; blad; mAb+CTL
 426991; AK001536; Hs.214410; Homo sapiens cDNA FLJ10674 f; ovar, sarc; diag
 427080; AW068287; Hs.301175; ras-related C3 botulinum toxin; mela; diag

- 427059; AB032953; Hs.173560; odd Oz/ten-m homolog 2 (Drosop; headnk, esoph; diag
427122; AW057736; Hs.323910; HER2 receptor tyrosine kinase; breast; mAb
427244; AA402400; Hs.178045; ESTs; esoph; diag
5 427260; AA663848; gb:ae70b06.s1 Stratagene schiz; lung; diag
427274; NM_005211; Hs.174142; colony stimulating factor 1 re; pros, sarc; mAb
427298; AA400495; ESTs; test; diag
427318; AF186081; Hs.175783; zinc transporter; pros; mAb
427333; AF067797; Hs.176658; aquaporin 8; panc, colon; mAb
10 427344; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin; ovar; mAb
427356; AW023482; Hs.97849; ESTs; ovar, breast, pros, blad, lung; diag
427398; AW390020; Hs.20415; chromosome 21 open reading fra; pros; diag
427427; AF077345; Hs.177936; lectin, superfamily member 1 (); breast; diag
427441; AA412605; Hs.293266; SPANX family, member C; lung, esoph; CTL+s.m.
15 427461; AA531527; Hs.332040; hypothetical protein MGC13010; pros; mAb
427474; U13192; Hs.2159; aggrecan 1 (chondroitin sulfat; sarc; diag
427486; AA974433; Hs.362432; fibroblast growth factor 4 (he; test; diag
427510; Z47542; Hs.179312; small nuclear RNA activating c; lung; CTL+s.m.
427515; T79526; Hs.179516; integral type I protein; pros; diag
20 427521; AW973352; ESTs; test; diag
427528; AU077143; Hs.179565; minichromosome maintenance def; mela; CTL+s.m.
427535; R29543; Hs.2164; pro-platelet basic protein (in; fibro; diag
427546; AA405280; Hs.36793; hypothetical protein FLJ23188; lung; diag
427550; BE242818; Hs.311609; nuclear RNA helicase, DECD var; mela; CTL+s.m.
25 427557; NM_002659; Hs.179657; plasminogen activator, urokin; panc, colon, stom, ovar, cerv, blad, lung, headnk, esoph; mAb
427578; AI591305; Hs.169084; ESTs, Highly similar to TUL3_H; test; diag
427583; M82962; Hs.179704; meprin A, alpha (PABA peptide; colon; mAb
427584; BE410293; Hs.179718; v-myb avian myeloblastosis vir; test; CTL+s.m.
427585; D31152; Hs.179729; collagen, type X, alpha 1 (Sch; breast, lung, headnk, panc, stom, colon, ovar, cerv, sarc; diag
30 427615; BE410107; Hs.179817; CGI-82 protein, PSDR1; pros; diag
427634; AI399745; Hs.18449; hypothetical protein MGC10820; mela, sarc; diag
427647; W19744; Hs.180059; Homo sapiens cDNA FLJ20653 fis; sarc; diag
427666; AI791495; Hs.180142; calmodulin-like skin protein (); breast, cerv, blad, lung, headnk, esoph; diag
427667; AK001279; Hs.180171; Homo sapiens cDNA FLJ10417 fis; test; diag
35 427668; AA298760; Hs.180191; hypothetical protein FLJ14904; lung, test; diag
427681; AB018263; Hs.284232; tumor necrosis factor receptor; ovar; mAb+s.m.
427698; AW972594; Hs.335499; ESTs; fibro; CTL+s.m.
427701; AA411101; Hs.243686; nuclear autoantigenic sperm pr; lung; mAb+CTL
427715; BE245274; Hs.180428; KIAA1181 protein; pros; diag
40 427719; AI393122; Hs.134726; ESTs; test; blad; diag
427730; AW250549; Hs.180577; granulin; mela; diag
427786; BE407863; Hs.256871; ESTs; esoph, blad; diag
427809; M26380; Hs.180878; lipoprotein lipase; ovar; mAb
427811; M81057; Hs.180884; carboxypeptidase B1 (tissue); breast s.m.
45 427897; NM_017413; Hs.303084; apelin; peptide ligand for APJ; angio, renal, pros; diag
427912; AL022310; Hs.181097; tumor necrosis factor (ligand); angio; mAb
427958; AA418000; Hs.376771; potassium intermediate/small c; pros, glio; mAb
427961; AW293165; Hs.143134; ESTs; lung, sarc; diag
50 428001; H97428; Hs.219907; ESTs, Moderately similar to Tr; mela; diag
428004; AA449563; Hs.151393; glutamate-cysteine ligase, cat; lung; s.m.
428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 ft; lung; diag
428046; AW812795; Hs.337534; ESTs, Moderately similar to I3; lung, colon; diag
428062; AA420683; Hs.98321; hypothetical protein FLJ14103; angio; diag
55 428087; AA100573; Hs.182421; troponin C2, fast; sarc; CTL+s.m.
428141; D50402; Hs.182611; solute carrier family 11 (prot; glio; mAb
428153; AW513143; Hs.98367; SRY (sex determining region Y); ovar; diag
428169; AI928984; Hs.182793; golgi phosphoprotein 2; pros; diag
428182; BE386042; Hs.293317; ESTs, Weakly similar to GGC1_H; blad, headnk, lung, ovar, sarc; CTL+s.m.
60 428183; AW969726; Hs.98381; ESTs, Weakly similar to serine; EWS; diag
428206; AB020643; Hs.183006; KIAA0836 protein; angio; mAb
428221; U95781; Hs.183075; ATPase, Ca transporting, cardf; sarc; s.m.
428227; AA321649; Hs.2248; small inducible cytokine subta; breast, lung, blad, ovar, headnk, fibro, colon, stom, cerv, leuk, renal, test, mela, esoph, hepC; diag
65 428248; AI126772; Hs.40479; ESTs; sarc; diag
428293; BE250944; Hs.183558; solute carrier family 1 (neut; pros; mAb
428305; AA446628; Hs.2799; cartilage linking protein 1; sarc; diag
428329; AA426091; Hs.98453; ESTs, Moderately similar to R2; test; diag
428338; AA503115; Hs.183752; microseminoprotein, beta-; pros; diag
428355; BE256452; Hs.2257; vitronectin (serum spreading f; colon; diag
70 428398; AI249368; Hs.98558; ESTs; pros, breast; diag
428405; Y00762; Hs.2266; cholinergic receptor, nicotin; esoph, sarc; mAb
428423; AU076517; Hs.184276; solute carrier family 9 (sodiu; ovar; CTL+s.m.
428434; AW363590; Hs.65551; Homo sapiens, Similar to DNA s; lung, fibro; diag
428467; AK002121; Hs.184465; hypothetical protein FLJ11259; fibro; mAb
428471; X57348; Hs.184510; stratifin; lung, headnk, colon, panc; diag
75 428645; AA431400; Hs.98729; ESTs, Weakly similar to 201720; lung; s.m.
428651; AF198478; Hs.188401; annexin A10; blad, stom, panc; diag
428667; AI375550; Hs.346868; nucleolar protein p40; homolog; fibro, uter; diag
428722; U76456; Hs.190787; tissue inhibitor of metallopro; glio; diag
428728; NM_016625; Hs.191381; hypothetical protein; ovar, lung, BPH; CTL+s.m.
80 428771; AB026992; Hs.193143; KIAA1069 protein; lung; CTL+s.m.
428784; Y12851; Hs.193470; purinergic receptor P2X, ligand; glio, mela; mAb
428800; M57627; Hs.193717; interleukin 10; fibro; diag
428801; AW277121; Hs.254881; ESTs; pros; diag
428804; AK000713; Hs.193736; hypothetical protein FLJ20706; mela; diag

- 428810; AF068236; Hs.193788; nitric oxide synthase 2A (indu; lung; s.m.
 428819; AL135623; Hs.193914; KIAA0575 gene product; pros; CTL+s.m.
 428824; W23624; Hs.173059; ESTs; panc; diag
 428832; AA578229; Hs.324239; ESTs, Moderately similar to ZN; panc, uter; diag
 5 428841; AJ18430; Hs.104935; ESTs; renal; diag
 428848; NM_000230; Hs.194236; leptin (murine obesity homolog; sarc; diag
 428862; NM_000346; Hs.2316; SRY (sex determining region Y); pros; sarc; CTL+s.m.
 428927; AA441837; Hs.90250; Homo sapiens hypothetical prot; fibro; mAb+diag
 10 428928; BE408838; Hs.194657; cadherin 1, type 1, E-cadherin; pros; breast, stom, blad; mAb
 428949; AA442153; Hs.104744; hypothetical protein DKFZp434J; sarc; diag
 428957; NM_003881; Hs.194679; WNT1 inducible signaling pathw; cerv; diag
 428959; AF100779; Hs.194680; WNT1 inducible signaling pathw; sarc; diag
 428977; AK001404; Hs.194698; cyclin B2; test; CTL+s.m.
 15 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2_H; sarc; diag
 429002; AW248438; Hs.2340; junction plakoglobin; blad; CTL+s.m.
 429010; Y18198; Hs.194725; one cut domain, family member; panc; diag
 429038; AL023513; Hs.194766; seizure related gene 6 (mouse); lung; mAb
 429058; AF138863; Hs.35254; hypothetical protein FLB6421; esoph; diag
 20 429065; AI753247; Hs.29643; Homo sapiens cDNA FLJ13103 f1s; lung; diag
 429083; Y09397; Hs.227817; BCL2-related protein A1; mela; diag
 429113; D28235; Hs.196384; prostaglandin-endoperoxide syn; angio, blad, stom; s.m.
 429120; AK001673; Hs.196530; hypothetical protein FLJ10811; test; diag
 429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; ovar; mAb
 25 429163; AA884766; ; gb:am20a10.s1 Soares_NFL_T_GBC; pros; diag
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; breast, panc, stom, lung, mela; s.m.
 429201; X03178; Hs.198246; group-specific component (vita; panc; diag
 429220; AW207206; Hs.356962; ESTs; breast, pros, BPH; diag
 429228; AI553633; Hs.356828; ESTs; lung, fibro, headnk, esoph; diag
 30 429259; AA420450; Hs.380088; Plakophilin; lung, headnk; diag
 429280; AF203032; Hs.198760; neurofilament, heavy polypept; pros; CTL+s.m.
 429299; AI620463; Hs.347408; hypothetical protein MGC13102; pros, cerv; diag
 429329; AA466140; Hs.99235; Homo sapiens pannexin 3 (PANX3; sarc; mAb
 429345; R11141; Hs.199695; hypothetical protein; blad; diag
 35 429359; W00482; Hs.2399; matrix metalloproteinase 14 (m; headnk, breast, cerv, ovar, blad, lung, esoph, mela, sarc; mAb
 429413; NM_014058; Hs.201877; DESC1 protein; lung, blad; diag
 429415; NM_002593; Hs.202097; procollagen C-endopeptidase en; sarc; diag
 429423; AJ016712; Hs.380983; integrin, beta 1 (fibronectin; angio; mAb
 429432; AJ678059; Hs.202676; synaptonemal complex protein 2; breast, cerv; diag
 40 429441; AJ224172; Hs.204096; lipophilin B (uteroglobin fami; breast, pros, ovar; diag
 429468; M85835; Hs.12827; ESTs; glio, uter; CTL+s.m.
 429469; M64590; Hs.380791; glycine dehydrogenase (decarbo; test; s.m.
 429486; AF155827; Hs.203963; hypothetical protein FLJ10339; blad, lung, headnk, test; diag
 429500; X78565; Hs.289114; hexabrachion (tenascin C, cyto; lung, glio, headnk, mela, sarc; diag
 45 429504; X99133; Hs.204238; lipocalin 2 (oncogene 24p3) (N; ovar, lung, blad; diag
 429505; AW820035; Hs.278679; a disintegrin and metalloprote; colon, leuk; mAb
 429538; BE182592; Hs.139322; small proline-rich protein 2A; lung, esoph; diag
 429563; BE619413; Hs.2437; eukaryotic translation Initiat; lung; diag
 429586; T73510; Hs.209153; angiotensin-like 3; hepC; CTL+s.m.
 50 429597; NM_003816; Hs.2442; a disintegrin and metalloprote; panc, colon, stom, lung; mAb
 429609; AF002246; Hs.210863; cell adhesion molecule with ho; ovar, mela; diag
 429612; AF062649; Hs.252587; pituitary tumor-transforming 1; lung, blad, headnk; diag
 429655; U48959; Hs.211582; myosin, light polypeptide kin; pros; s.m.
 429663; M68874; Hs.211587; phospholipase A2, group IVA (c; angio, lung; s.m.
 55 429664; L20433; Hs.211588; POU domain, class 4, transcript; sarc; CTL+s.m.
 429736; AF125304; Hs.212680; tumor necrosis factor receptor; lung; mAb
 429747; M87507; Hs.2490; caspase 1, apoptosis-related c; colon, stom, fibro; s.m.
 429764; BE245076; Hs.216958; KIAA0194 protein; pros; mAb
 429769; NM_004917; Hs.218366; kallikrein 4 (prostase, enamel; pros; s.m.
 60 429784; M89796; Hs.30; membrane-spanning 4-domains, s; fibro; mAb
 429823; AA459443; Hs.181400; ESTs; sarc; diag
 429859; NM_007050; Hs.225952; protein tyrosine phosphatase; breast; mAb+s.m.
 429918; AW873986; Hs.119383; ESTs; pros; glio; diag
 429921; AA526911; Hs.82772; collagen, type XI, alpha 1; headnk, panc, sarc; CTL
 65 429983; W92620; Hs.260855; ESTs; blad; diag
 429986; AF092047; Hs.227277; sine oculis homeobox (Drosophi; lung; CTL+s.m.
 430014; H59354; Hs.374303; actinin, alpha 4; renal; diag
 430016; NM_004736; Hs.227656; xenotropic and polytropic retr; ovar; mAb
 430044; AA464510; Hs.152812; ESTs; breast, lung, panc, headnk, ovar, stom, esoph; diag
 70 430056; X97548; Hs.228059; KRAB-associated protein 1; test; CTL+s.m.
 430129; BE301708; Hs.233955; hypothetical protein FLJ20401; angio; diag
 430130; AL137311; Hs.234074; Homo sapiens mRNA; cDNA DKFZp7; pros; mAb
 430144; AI732722; Hs.98927; ERGL protein; ERGIC-53-like pr; pros; diag
 430152; AB001325; Hs.234642; aquaporin 3; blad, fibro; mAb
 75 430154; AW583058; Hs.234726; serine (or cysteine) proteinases; pros; diag
 430157; BE348706; Hs.278543; ESTs; blad; diag
 430168; AW968343; Hs.145582; DKFZP434I1735 protein; blad; diag
 430223; NM_002514; Hs.235935; nephroblastoma overexpressed g; mela; diag
 430228; BE245562; Hs.2551; adrenergic, beta-2-, receptor; pros; mAb
 80 430228; AW950939; Hs.6382; ESTs, Highly similar to T00391; glio; diag
 430252; AI638774; Hs.105328; testes development-related NYD; test; CTL+s.m.
 430253; AK001514; Hs.236844; hypothetical protein FLJ10652; test; CTL+s.m.
 430255; AK000703; Hs.323822; Homo sapiens mRNA for KIAA1551; test; CTL+s.m.
 430259; BE550182; Hs.375142; RafGEF-like protein 3, mouse l; ovar; CTL+s.m.

- 430280; AA361258; Hs.237858; Interleukin 7 receptor; meta, lung, panc, stom, esoph, headnk, fibro; mAb+s.m.
 430287; AW182459; Hs.125759; ESTs, Weakly similar to LEU5_H; test; diag
 430294; A1538226; Hs.32976; guanine nucleotide binding pro; pros; diag
 430337; M36707; Hs.239500; calmodulin-like 3; lung; diag
 430354; AA954810; Hs.239784; human homolog of Drosophila Sc; ovar; diag
 430378; Z28572; Hs.2556; tumor necrosis factor receptor; lung, fibro, breast headnk, blad, breast, colon, stom; diag
 430393; BE185030; Hs.241305; estrogen-responsive B box prot; lung; diag
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; panc; diag
 430407; H23551; Hs.30974; ESTs; panc; diag
 430439; AL133561; Hs.380155; DKFZP434B061 protein; lung, test; diag
 430451; AA836472; Hs.297939; cathepsin B; ovar, lung, headnk, panc, stom; diag
 430454; AW469011; Hs.105635; ESTs; lung; diag
 430476; AA447465; Hs.2563; tachykinin, precursor 1 (subst; sarc; diag
 430487; D87742; Hs.241552; KIAA0268 protein; pros; diag
 430491; AL109791; Hs.241559; Homo sapiens mRNA full length; ovar; diag
 430498; X02910; Hs.241570; tumor necrosis factor (TNF sup; leuk; diag
 430508; A1015435; Hs.104637; ESTs; lung; mAb+s.m.
 430521; NM_016383; Hs.242183; HOM-TES-85 tumor antigen; test; CTL+s.m.
 430540; AW245422; Hs.106357; Homo sapiens cDNA: FLJ22105 f; meta; mAb
 430563; AA481269; Hs.348628; ATP-binding cassette, sub-fam; lung; diag
 430594; AK000790; Hs.246885; hypothetical protein FLJ20783; meta; diag
 430634; A1860651; Hs.26685; calcyphosine; ovar; diag
 430637; BE160081; Hs.256290; S100 calcium-binding protein A; meta; diag
 430647; AC003682; Hs.127988; ESTs, Weakly similar to Z211_H; test; diag
 430676; AF084866; Hs.372585; gb:Homo sapiens envelope prola; test; diag
 430677; Z26317; Hs.359784; desmoglein 2; lung, colon; mAb
 430678; A458174; Hs.192855; ESTs; lung; diag
 430686; NM_001942; Hs.2633; desmoglein 1; lung, headnk, meta; mAb
 430691; C14187; Hs.157208; aristless-related homeobox pr; EWS, ovar, panc; diag
 430704; AW813091; Hs.335799; ESTs; stom; diag
 430770; AA765694; Hs.123296; ESTs; meta; diag
 430832; A1073913; Hs.100686; ESTs, Weakly similar to JE0350; breast, colon, ovar, uter, lung, stom, fibro; diag
 430838; N46664; Hs.169395; hypothetical protein FLJ12015; meta; CTL+s.m.
 430890; X54232; Hs.2699; glypican 1; glio, lung, cerv, blad, esoph; mAb
 430985; AA490232; Hs.27323; ESTs, Weakly similar to I78885; lung; mAb
 431009; BE149762; Hs.48956; gap junction protein, beta 6 (; lung, blad, headnk, esoph; mAb
 431053; S40369; Hs.249141; Glutamate receptor subunit; glio; mAb
 431070; AW408164; Hs.249184; transcription factor 19 (SC1); blad; diag
 431089; BE041395; Hs.374629; ESTs, Weakly similar to unknown; blad, lung, pros, angio, fibro; diag
 431099; Y13367; Hs.249235; phosphoinositide-3-kinase, cla; pros; CTL+s.m.
 431103; M57399; Hs.44; pleiotrophin (heparin binding; sarc, meta; diag
 431124; AF284221; Hs.59506; doublesex and mab-3 related tr; lung; CTL+s.m.
 431151; BE207083; Hs.366053; gb:ba10d10.y1 NIH_MGC_7 Homo s; pros; mAb
 431164; AA493650; Hs.94367; thyroid transcription factor 1; fibro; CTL+s.m.
 431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Lau) endople; meta, pros, panc, colon, stom; mAb
 431211; M86849; Hs.323733; gap junction protein, beta 2; colon, blad, lung, panc, headnk, esoph; mAb
 431217; NM_013427; Hs.250830; Rho GTPase activating protein; pros; CTL+s.m.
 431221; AA449015; Hs.286145; SRB7 (suppressor of RNA polyme; lung; CTL+s.m.
 431222; X56777; Hs.273790; zona pellucida glycoprotein 3A; pros; diag
 431250; BE264649; Hs.251377; taxol resistance associated ge; esoph; diag
 431322; AW970622; Hs.376626; gb:EST382704 IMAGE resequences.; blad, ovar, uter; diag
 431347; A1133461; Hs.251664; insulin-like growth factor 2 (; blad; mAb+diag
 431354; BE046856; Hs.251673; DNA (cytosine-5)-methyltransf; test; CTL+s.m.
 431360; NM_000427; Hs.251680; lorlatin; meta, sarc; diag
 431362; A1874223; Hs.293560; ESTs; angio; diag
 431369; BE184455; Hs.251754; secretory leukocyte protease t; ovar, blad; diag
 431384; BE158000; Hs.334372; gb:MR2-HT0377-150200-202-e03 H; lung; diag
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, s; panc; diag
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gat; ovar, pros, blad; mAb
 431448; AL137517; Hs.306201; hypothetical protein DKFZp5640; blad; mAb
 431457; NM_012211; Hs.256297; Integrin, alpha 11; headnk; mAb
 431474; AL133990; Hs.180642; CEGP1 protein; breast, pros, blad; diag
 431494; AA991355; Hs.298312; hypothetical protein DKFZp434A; lung; diag
 431512; BE270734; Hs.2795; lactate dehydrogenase A; panc; s.m.
 431548; A1834273; Hs.9711; novel protein; lung, angio, pros; diag
 431553; X78075; Hs.2799; cartilage linking protein 1; sarc; diag
 431579; AW971082; Hs.222886; ESTs, Weakly similar to TRHY_H; pros; diag
 431616; AA508552; Hs.222874; ESTs, Weakly similar to I38022; pros, panc, colon; mAb
 431674; AA098901; Hs.301642; G-protein coupled receptor; ovar; mAb+s.m.
 431723; AW058350; Hs.278966; Homo sapiens mRNA; cDNA DKFZp5; fibro; diag
 431728; NM_007351; Hs.268107; multimerin; angio; diag
 431808; M30703; Hs.270833; amphiregulin (schwannoma-deriv; breast, headnk, panc, colon; diag
 431836; AF178532; Hs.271411; beta-site APP-cleaving enzyme; meta; mAb
 431870; AW449902; Hs.105500; ESTs; renal; diag
 431890; X17033; Hs.271988; integrin, alpha 2 (CD49B, alph; blad, headnk, lung, panc, cerv, stom; mAb
 431938; AA938471; Hs.54431; specific granule protein (28 k; panc; diag
 431939; AW008061; Hs.231994; ESTs; renal, colon; diag
 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 f; cerv, glio; diag
 431989; AW972870; Hs.291069; ESTs; ovar; diag
 431992; NM_002742; Hs.2891; protein kinase C, mu; pros, glio; s.m.
 432004; BE018302; Hs.2894; placental growth factor, vascu; renal; diag
 432015; AL157504; Hs.159115; Homo sapiens mRNA; cDNA DKFZp5; blad; diag
 432023; AW273128; Hs.300268; EST; lung; diag

- 432097; X51730; Hs.2905; progesterone receptor; blad; mAb+s.m.
 432117; AL036195; Hs.2909; protamine 1; test; CTL+s.m.
 432128; AA127221; Hs.66; ESTs; angio; diag
 432141; BE410964; Hs.272736; nuclear receptor binding prote; test; mAb+s.m.
 432189; AA527941; ; gb:nh30c04.s1 NCL_CGAP_Pr3 Hom; pros; diag
 432199; AI693815; Hs.127179; cryptic gene; panc; diag
 432210; AI567421; Hs.273330; Homo sapiens, clone IMAGE:3544; ovar, lung, blad; diag
 432222; AI204995; ; gb:an03c03.x1 Stratagene schtz; angio, blad, fibro; diag
 432231; AA339977; Hs.274127; CLST 11240 protein; fibro; diag
 432239; X81334; Hs.2938; matrix metalloproteinase 13 (c; blad, lung, headnk, esoph, sarc; s.m.
 432240; AI694767; Hs.129179; Homo sapiens cDNA FLJ13581 fis; pros; diag
 432305; M62402; Hs.274313; insulin-like growth factor bin; cerv; diag
 432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 fis; cerv, lung, fibro, pros; diag
 432407; AA221036; ; gb:zr03f12.r1 Stratagene NT2 r; lung, test,colon; diag
 432415; T16971; ; ESTs, Weakly similar to A43932; ovar, pros; diag
 432432; AA541323; Hs.115831; ESTs; uter, pros; diag
 432435; BE218886; Hs.282070; ESTs; pros, uter, colon, stom, fibro; diag
 432441; AW282425; Hs.163484; Intron of hepatocyte nuclear f; blad, fibro, pros; diag
 432473; AI202703; Hs.152414; ESTs; pros; diag
 432481; AW451645; Hs.151504; intron of collagen, type XI, a; sarc; diag
 432512; NM_003284; Hs.3017; transition protein 1 (during h; test; CTL+s.m.
 432519; AI221311; Hs.130704; ESTs, Weakly similar to BCHUIA; fibro, ovar, uter; CTL+s.m.
 432527; AW975028; Hs.102754; ESTs; pros, uter, ovar, cerv; diag
 432542; AW083920; Hs.16098; claudin 2; colon, panc; diag
 432583; AW023624; Hs.162282; potassium channel TASK-4; pota; lung; mAb
 432615; AA557191; Hs.55028; ESTs, Weakly similar to I54374; pros; diag
 432621; AI298501; Hs.21192; ESTs, Weakly similar to T48428; pros; mAb
 432629; AW860548; Hs.280658; ESTs; ovar; diag
 432653; N62096; Hs.293185; ESTs, Weakly similar to JC7328; pros, lung; mAb+s.m.
 432666; AW204069; Hs.351118; ESTs, Weakly similar to unname; test; diag
 432706; NM_013230; Hs.286124; CD24 antigen (small cell lung; colon, ovar, pros; mAb+CTL
 432730; AI066520; Hs.131358; ESTs; test; diag
 432731; F31178; Hs.287820; fibronectin 1; panc, fibro; diag
 432788; AA521091; Hs.178499; Homo sapiens cDNA: FLJ23117 fi; lung, ovar; CTL+s.m.
 432800; BE391048; Hs.278962; AIM-1 protein; mela, pros; mAb
 432842; AW674093; Hs.334822; hypothetical protein MGC4485; blad, lung, headnk; CTL+s.m.
 432850; X87723; Hs.3110; angiotensin receptor 2 (AT2); leio; mAb
 432855; AF017988; Hs.279565; secreted frizzled-related prot; panc; diag
 432867; AW016936; Hs.233364; ESTs; stom, colon; diag
 432878; BE386490; Hs.279663; Pirin; mela; CTL+s.m.
 432887; AI925047; Hs.162859; AK056805; Homo sapiens cDNA FL; pros; diag
 432938; T27013; Hs.3132; steroidogenic acute regulatory; ovar; diag
 432966; AA605114; Hs.325198; ESTs; pros; diag
 433012; NM_004045; Hs.279910; ATX1 (antioxidant protein 1, y; mela; diag
 433013; AI697890; Hs.127337; axin 2 (conductin, axd); colon; CTL+s.m.
 433043; W57554; Hs.125019; lymphoid nuclear protein (LAF-; pros, breast; diag
 433068; NM_006456; Hs.288215; sialyltransferase; breast, ovar, mela; s.m.
 433078; AW015188; Hs.121575; Homo sapiens cDNA FLJ12231 fis; blad; diag
 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, ; blad, lung, headnk, cerv; mAb
 433147; AF091434; Hs.43080; platelet derived growth factor, ovar, panc, fibro; diag
 433159; AB035898; Hs.150587; kinesin-like protein 2; ovar, uter, colon, blad; diag
 433170; AB037816; Hs.8982; KIAA1395; angio; diag
 433183; AF231338; Hs.222024; transcription factor BMAL2; lung; diag
 433228; F28212; Hs.14953; KIAA1491 protein; test; CTL+s.m.
 433258; AI806626; Hs.207300; ESTs, Weakly similar to ALUB_H; lung; diag
 433285; AW975944; Hs.237396; ESTs; breast, pros; diag
 433293; AF007835; Hs.32417; hypothetical protein MGC2742; fibro, pros, stom, panc; CTL+s.m.
 433323; AA805132; Hs.159142; ESTs; pros; diag
 433334; AI927208; Hs.231958; matrix metalloproteinase 28; panc; s.m.
 433336; AF017986; Hs.31386; secreted frizzled-related prot; ovar, fibro, headnk, lung, panc, blad; diag
 433364; AI075407; Hs.296083; ESTs, Moderately similar to I5; mela; diag
 433365; AF026944; Hs.293797; ESTs; blad; diag
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related c; angio; s.m.
 433388; AI432572; Hs.288539; hypothetical protein FLJ22191; ovar; CTL+s.m.
 433404; T32962; Hs.352670; Homo sapiens cDNA FLJ32064 fis; pros; diag
 433437; U20536; Hs.3280; caspase 6, apoptosis-related c; fibro, breast, cerv, lung, blad, panc, glio, colon; s.m.
 433444; AW975324; Hs.129816; ESTs; pros; diag
 433468; AA508353; Hs.105314; relaxin 1 (H1); pros; diag
 433485; AI493076; Hs.306098; aldo-keto reductase family 1, ; lung; s.m.
 433495; AW373784; Hs.71; alpha-2-glycoprotein 1, zinc; breast, pros; diag
 433576; BE080715; Hs.161091; ESTs; mela; diag
 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogs; colon; diag
 433671; AW138797; Hs.132906; 19A24 protein; fibro; mAb
 433701; AW445023; Hs.15155; ESTs; test; diag
 433724; AI827749; Hs.144924; serine/threonine protein kinase; test; CTL+s.m.
 433764; AW753676; Hs.39982; zinc finger protein RINZF (NM.; pros, ovar; diag
 433800; AI034361; Hs.135150; lung type-I cell membrane-asso; glio, lung, test; mAb
 433914; AF108138; Hs.112160; Homo sapiens DNA helicase homo; test; s.m.
 434011; AW953437; Hs.5486; clone FLB5214; pros; diag
 434105; AW952124; Hs.13094; presentilins associated rhombol; lung; diag
 434217; AW014795; Hs.23349; ESTs; angio; diag
 434262; AF121858; Hs.12169; sorting nexin 8; mela; CTL+s.m.
 434274; AA628539; Hs.57783; ESTs, Moderately similar to AL; test; diag

- 434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 f5; test; diag
 434340; AI193043; Hs.353146; ESTs, Weakly similar to T17226; lung; diag
 434360; AW015415; Hs.127780; ESTs; lung; diag
 5 434370; AF130988; Hs.58346; ectodysplasin 1, anhidrotic re; colon, stom; diag
 434377; AW137148; Hs.306593; Intron of perlestin (OSF-2os); headnk; diag
 434398; AA121098; Hs.3838; serum-inducible kinase (SNIK); angio, breast; CTL+s.m.
 434411; AA632649; Hs.201372; ESTs; stom, leuk; diag
 434414; AI798376; ; gbcr34b07.x1 NCL_CGAP_Ov23 Hs; lung, test, colon; diag
 10 434423; NM_006769; Hs.3844; LIM domain only 4; panc; diag
 434449; AW953484; Hs.3849; hypothetical protein FLJ22041; sarc; diag
 434487; AF143887; Hs.337588; ESTs, Moderately similar to S6; blad; mAb+s.m.
 434598; TS9538; ; gbyb65g12.s1 Stratagene ovary; angio; s.m.
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; test; CTL+s.m.
 434609; R76593; ; gbyl60c11.1 Soares placenta; pros; diag
 15 434636; AA083764; Hs.349208; hypothetical protein MGC3178; angio; diag
 434649; AA738254; Hs.165390; ESTs, Highly similar to A40350; test; diag
 434665; AA642125; Hs.74502; gbcr60c01.s1 NCL_CGAP_Lym3 Hs; panc; diag
 434666; AF151103; Hs.112259; T cell receptor gamma locus; pros; mAb+s.m.
 20 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 f5; panc; diag
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; melar; s.m.
 434846; AW295389; Hs.119768; ESTs; angio; diag
 434876; AF160477; Hs.61460; Ig superfamily receptor LNIR; lung, blad; mAb
 434927; H46612; Hs.293815; Homo sapiens HSPC285 mRNA, par; angio; diag
 25 434973; AW449285; Hs.313636; EST; pros; diag
 435045; BE297155; Hs.143698; ESTs; test; diag
 435047; AA454985; Hs.54973; cadherin-like protein VR20; pros; mAb
 435066; BE261750; Hs.4747; dyskeratosis congenita 1, dysk; colon; CTL+s.m.
 435080; AI831760; Hs.155111; hypothetical protein FLJ14428; renal; mAb
 30 435094; AI560129; Hs.289008; EST; ovar, cerv; diag
 435099; AC004770; Hs.4756; flap structure-specific endonu; blad, test, melar; CTL+s.m.
 435140; AA668123; Hs.134170; ESTs; fibro; diag
 435159; AA668879; Hs.116649; ESTs; lung; diag
 435206; AI432364; Hs.160594; ESTs; test; diag
 35 435243; AW292888; Hs.348932; hypothetical protein dJ434014; cerv, headnk; diag
 435292; N20514; Hs.172965; ESTs; melar; diag
 435299; AI745458; Hs.343026; ESTs, Weakly similar to T20593; fibro; diag
 435479; AF197137; Hs.155101; ATP synthase, H transporting, ; pros; s.m.
 435496; AW840171; Hs.265398; PAR-6 beta; breast, panc, ovar; diag
 435583; AF210317; Hs.95497; solute carrier family 2 (facil); blad; mAb+s.m.
 40 435575; AF213457; Hs.44234; triggering receptor expressed; fibro; mAb+s.m.
 435602; AF217518; Hs.283532; uncharacterized bone marrow pr; test; diag
 435615; Y15065; Hs.4975; potassium voltage-gated channel; glia; mAb
 435652; N32388; Hs.334370; uncharacterized hypothalamus p; panc; diag
 435793; AB037734; Hs.4993; KIAA1313 protein; ovar, lung, uter; diag
 45 435849; BE305242; Hs.16098; claudin 2; colon, panc; diag
 435876; AW612588; Hs.160271; G protein-coupled receptor 48; pros; mAb
 435897; AF269223; Hs.128322; l-complex 11 (a murine top hom; test; diag
 435904; AF261655; Hs.8910; 1,2-alpha-mannosidase IC; blad; s.m.
 50 435918; AF263538; Hs.86232; growth differentiation factor; test; diag
 435974; U29690; Hs.37744; Homo sapiens beta-1 adrenergic; pros, EWS; mAb+s.m.
 436032; AA150797; Hs.109276; latexin protein; panc, angio; diag
 436063; AK000028; Hs.356100; ribosomal protein S24; pros; diag
 436120; AI248193; Hs.119860; ESTs; fibro; diag
 55 436199; R38946; Hs.127951; hypothetical protein FLJ14503; renal; diag
 436246; AW450963; Hs.119991; ESTs; blad; diag
 436251; BE515065; Hs.296585; nucleolar protein (KKE/D repeat; colon, test, blad; CTL+s.m.
 436278; BE396290; Hs.5097; synaptogyrin 2; pros; mAb
 436291; BE568452; Hs.344037; protein regulator of cytokines; lung, blad, headnk; diag
 60 436293; AI601188; Hs.306201; ESTs; blad; diag
 436302; AL355841; Hs.99330; hypothetical protein FLJ23588; lung; diag
 436315; BE390513; Hs.27935; hypothetical protein MGC4837; melar; diag
 436396; AI683487; Hs.152213; wingless-type MMTV integration; lung, headnk, pros, panc; diag
 436420; AA443966; Hs.31595; ESTs; angio; mAb
 65 436476; AA326108; Hs.33829; bHLH protein DEC2; panc; diag
 436511; AA721252; Hs.291502; ESTs; lung; diag
 436553; AW407157; Hs.181125; immunoglobulin lambda locus; lung; diag
 436569; BE439539; Hs.301961; glutathione S-transferase M2 (c; blad; s.m.
 436614; AW104388; Hs.149091; ESTs; melar; CTL+s.m.
 70 436700; AI693690; Hs.301406; hypothetical protein PP3501; melar; mAb
 436729; BE621807; Hs.351316; transmembrane 4 superfamily me; panc, colon, stom, ovar, lung, blad; mAb
 436772; AW975688; Hs.348918; metallothionein 1E (functional; angio; diag
 436775; AA731111; Hs.372225; ESTs; uter, ovar; diag
 436839; AA767346; Hs.372277; ESTs; lung; diag
 75 436856; AI469355; Hs.127310; ESTs; melar; diag
 436954; AA740151; Hs.130425; ESTs; fibro, uter, ovar; diag
 436972; AA284679; Hs.25640; claudin 3; ovar, lung, pros; mAb
 437052; AA861697; Hs.120591; ESTs; pros; diag
 437099; N77793; Hs.48659; ESTs, Highly similar to S14458; test; diag
 80 437100; AI761073; Hs.14535; Homo sapiens cDNA: FLJ22314 f; panc, renal; diag
 437118; AI379921; Hs.177043; XP_171387 similar to rhotekin; fibro; diag
 437145; AF007216; Hs.5462; solute carrier family 4, sodium; panc, pros, stom; mAb
 437156; AI916600; Hs.121194; Homo sapiens cDNA: FLJ21569 f; stom, renal, colon; diag
 437181; AI306615; Hs.125343; ESTs, Weakly similar to KIAA07; blad; mAb+s.m.

- 5 437204; AL110216; Hs.355961; ESTs, Weakly similar to I55214; lung; CTL+s.m.
 437212; A1765021; Hs.210775; ESTs; renal, uter, ovar; diag
 437224; AL117628; Hs.97808; ESTs; test; diag
 10 437259; A1377755; Hs.120695; ESTs; lung; diag
 437267; AW511443; Hs.258110; ESTs; BPH; diag
 437269; AA334384; Hs.149420; ESTs; angio; diag
 437330; AL353944; Hs.50115; Homo sapiens mRNA; cDNA DKFZp7; sarc; diag
 437381; NM_003684; Hs.5591; MAP kinase-interacting serine; glio; CTL+s.m.
 437390; A1125859; Hs.112607; ESTs; lung; diag
 437412; BE089288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp5; lung; diag
 437435; AA249439; Hs.27027; hypothetical protein DKFZp762H; lung; diag
 437437; AA226869; Hs.351623; hypothetical protein DKFZp762L; test; CTL+s.m.
 15 437478; AL390172; Hs.317432; branched chain aminotransferase; angio; s.m.
 437553; A1829935; Hs.130497; ESTs, Weakly similar to MAT8_H; blad; mAb
 437571; AA760894; Hs.125350; ESTs; pros; diag
 437623; D63880; Hs.5719; chromosome condensation-relate; test; diag
 437740; AA810265; Hs.122915; ESTs; meta; diag
 437802; A1475995; Hs.122910; ESTs; panc; diag
 20 437862; AW978107; Hs.5884; Homo sapiens mRNA; cDNA DKFZp5; meta; CTL+s.m.
 437908; A1082424; Hs.351043; ESTs; test; diag
 437915; A1637993; Hs.202312; Homo sapiens clone N11 Ntera2D; lung, headnk, ovar, blad, uter; diag
 437931; A1249468; Hs.124434; ESTs; blad; diag
 437935; AW939591; Hs.5940; mucin 13, epithelial transmembr; colon, stom, uter, panc; mAb+s.m.
 25 437938; A1950087; Hs.369628; gbwwq05c02.x1 NCL_CGAP_J3d12 H; renal, ovar, uter, cerv, blad; diag
 437939; AW298600; Hs.64313; ESTs, Weakly similar to S59501; angio; mAb+s.m.
 437960; A1669586; Hs.369312; ESTs; uter, ovar; diag
 438167; R28363; Hs.24286; chemokine binding protein 2 (C; ovar, breast, uter; mAb
 438199; AW016531; Hs.122147; hypothetical protein FLJ13189; breast; diag
 30 438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nucl; meta; mAb+s.m.
 438233; W52448; Hs.56147; ESTs; pros, cerv; diag
 438274; A1918906; Hs.55080; ESTs; headnk; diag
 438403; AA806607; Hs.292205; ESTs; lung; mAb
 438438; AA257992; Hs.50651; Janus Kinase 1 (a protein tyro; EWS; s.m.
 35 438450; A1050866; Hs.65853; nodal, mouse, homolog; test; diag
 438456; AA913381; Hs.279763; ESTs; test; diag
 438552; AJ245820; Hs.6314; type I transmembrane receptor; pros, ovar; diag
 438670; A1275803; Hs.123428; ESTs; fibro; CTL+s.m.
 438702; A1879064; Hs.7164; ESTs; lung; diag
 40 438707; L08239; Hs.5326; amino acid system N transporte; ovar; mAb
 438746; A1885815; Hs.184727; Human melanoma-associated anti; panc, blad, meta, ovar; mAb+CTL
 438817; A1023799; Hs.163242; ESTs; ovar, uter, blad, renal; diag
 438859; A1559626; Hs.93522; Homo sapiens mRNA for KIAA1647; renal; diag
 438866; U44385; Hs.6441; tissue inhibitor of metallopro; meta; diag
 438873; A1302471; Hs.124292; Homo sapiens cDNA; FLJ23123 f; fibro; diag
 45 438898; A1819863; Hs.106243; ESTs; lung; diag
 438915; AA280174; Hs.355711; Williams-Beuren syndrome chrom; lung, test, meta; diag
 438929; AW195515; Hs.253177; ESTs; renal; diag
 438956; W00847; Hs.135058; Human DNA sequence from clone; lung; diag
 438968; AW979074; gb:EST391184 MAGE resequences.; renal; diag
 50 438983; AF085884; Hs.20029; proacrosin binding protein sp3; test; CTL+s.m.
 438993; AA828995; gb:rod77b08.s1 NCL_CGAP_Ov2 Hom; ovar; mAb+s.m.
 439053; BE244588; Hs.6456; chaperonin containing TCP1, su; test; diag
 439092; AA830149; gb:oc44f08.s1 NCL_CGAP_GCB1 Ho; pros; diag
 55 439176; A1446444; Hs.190394; ESTs, Weakly similar to B28096; pros; diag
 439180; A1393742; Hs.199067; v-erb-b2 avian erythroblastic; breast, ovar, uter, pros, blad, panc, colon, fibro, meta; mAb
 439221; AA737106; Hs.32250; ESTs, Moderately similar to I7; EWS; s.m.
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582; meta, fibro; diag
 439239; A1031540; Hs.235331; ESTs; blad; diag
 60 439285; AL133916; Hs.47860; hypothetical protein FLJ20093; lung, breast; diag
 439310; AF086120; Hs.102793; ESTs; meta; diag
 439318; AW837045; Hs.6527; G protein-coupled receptor 56; colon, breast, ovar, uter, cerv, pros, lung, headnk, blad, meta; mAb+s.m.
 439335; AA742697; Hs.62492; NM_052863; Homo sapiens secreto; fibro, uter; diag
 439366; AF100143; Hs.6540; fibroblast growth factor 13; pros; CTL+s.m.
 65 439382; BE247684; Hs.103070; ESTs; angio; diag
 439394; AA149250; Hs.56105; ESTs; lung; diag
 439410; AA632012; Hs.188746; ESTs; angio; diag
 439453; BE264974; Hs.6566; thyroid hormone receptor inter; lung, esoph, ovar; mAb+s.m.
 439496; BE616501; Hs.32343; Homo sapiens, Similar to RIKEN; meta, esoph; diag
 70 439559; AW970780; Hs.59483; leucine-rich repeat-containing; ovar, stom, meta, colon; mAb
 439668; A1091277; Hs.302634; frizzled (Drosophila) homolog; ovar, uter; mAb
 439670; AF088076; Hs.59507; ESTs, Weakly similar to AC0048; lung, headnk, cerv; diag
 439702; AW085525; Hs.55964; ESTs; meta; diag
 439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_H; ovar, lung, headnk; diag
 75 439735; A1635386; Hs.142846; hypothetical protein; pros; diag
 439737; A1751438; Hs.41271; Homo sapiens mRNA full length; panc; diag
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length; panc, fibro, breast; diag
 439755; AW748482; Hs.77873; B7 homolog 3; sarc; mAb
 439759; AL359055; Hs.67709; Homo sapiens mRNA full length; colon, stom, panc, leuk, lung; diag
 439778; AL109729; Hs.99364; putative transmembrane protein; pros; mAb+s.m.
 80 439780; AL109688; gb:Hom sapiens mRNA full length; blad, esoph; diag
 439820; AL360204; Hs.283853; Homo sapiens mRNA full length; ovar, uter, cerv, breast, pros; diag
 439864; A1720078; Hs.291997; ESTs, Weakly similar to A47582; test; diag
 439867; AA847510; Hs.161292; ESTs; panc; diag

- 439920; H05430; Hs.288433; neurotrophin; panc; mAb+diag
 439926; AW014875; Hs.137007; ESTs; blad, esoph, lung, cerv; diag
 439933; AW247529; Hs.6793; platelet-activating factor ace; breast, lung, blad; s.m.
 440042; A1073387; Hs.133898; ESTs; ovar; CTL+s.m.
 5 440086; NM_005402; Hs.6906; v-rat simian leukemia viral on; angio; diag
 440099; AL080058; Hs.6909; DKFZP564G202 protein; panc; diag
 440119; AA865455; Hs.125331; ESTs, Moderately similar to un; test; diag
 440138; AB033023; Hs.318127; hypothetical protein FLJ10201; lung; CTL+s.m.
 10 440151; AA868167; : gbcrak38e07.s1 Scores_testis_NH; sarc; diag
 440207; A1371978; Hs.128326; ESTs; test; diag
 440209; H05049; Hs.247837; neuronin 3; fibro; diag
 440210; AW674562; Hs.122128; ESTs; glio; diag
 440225; BE295782; Hs.159; tumor necrosis factor receptor; glio; mAb
 440238; AW451970; Hs.155644; paired box gene 2; ovar; diag
 15 440260; A1972867; Hs.7130; copine IV; pros; diag
 440273; A1805392; Hs.325335; Homo sapiens cDNA: FLJ23523 f; lung, fibro; diag
 440274; R24595; Hs.7122; scrapie responsive protein 1; sarc; diag
 440311; A1733079; Hs.125407; ESTs, Moderately similar to AL; renal; diag
 20 440325; NM_003812; Hs.7164; a disintegrin and metalloprote; lung; mAb
 440333; A1378424; Hs.288761; hypothetical protein FLJ21749; pros; CTL+s.m.
 440449; AA885430; Hs.201925; Homo sapiens cDNA FLJ13446 f; breast; diag
 440452; A1925136; Hs.55150; ESTs, Weakly similar to CAYP_H; fibro; diag
 440457; BE387593; Hs.21321; Homo sapiens clone FLB9213 PRO; mel; diag
 25 440484; BE328156; Hs.150358; ESTs; panc; diag
 440529; AW207640; Hs.16478; Homo sapiens cDNA: FLJ21718 f; pros; diag
 440659; AF134160; Hs.7327; claudin 1; lung; mAb
 440704; M69241; Hs.162; Insulin-like growth factor bin; lung, glio, ovar; diag
 440773; AA352702; Hs.37747; Homo sapiens, Similar to RIKEN; test; diag
 30 440801; AA906366; Hs.370038; ESTs; pros; diag
 440819; A1809444; Hs.202108; ESTs; pros; diag
 440901; AA909358; Hs.128612; ESTs; ovar, pros; diag
 440943; AW082298; Hs.146161; hypothetical protein MGC2408; lung; diag
 440983; M20681; Hs.7594; solute carrier family 2 (facil; test; mAb
 35 441020; W79283; Hs.35962; ESTs; lung, panc; diag
 441031; A1110684; Hs.7645; fibrinogen, B beta polypeptide; lung, panc, colon; CTL+s.m.
 441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 f; panc, ovar, stom, uter, lung; diag
 441134; W29092; Hs.346950; cellular retinoic acid-binding; sarc; diag
 441247; AW118681; Hs.128051; Homo sapiens thymic stromal ly; pros; diag
 40 441321; H17182; Hs.7771; B-cell associated protein; test; diag
 441345; AW068579; Hs.7780; Homo sapiens mRNA: cDNA DKFZp5; pros; diag
 441350; AB020690; Hs.7782; paraneoplastic antigen MA2; panc; mAb+CTL
 441377; BE218239; Hs.202656; ESTs; uter, endo, lung; diag
 441384; AA447849; Hs.288660; retinoic acid induced 3; ovar; mAb+s.m.
 45 441392; AW451831; Hs.222119; ESTs, Weakly similar to S30433; renal; diag
 441457; AW996651; Hs.43838; ESTs; angio; diag
 441495; AW294603; Hs.127039; ESTs; blad; diag
 441525; AW241867; Hs.127728; ESTs; lung; diag
 441553; AA281219; Hs.121296; ESTs; lung, test, ovar; CTL+s.m.
 50 441633; AW958544; Hs.112242; normal mucosa of esophagus spe; blad, lung, cerv, headnk, colon, panc; diag
 441780; AW294909; Hs.132208; ESTs; lung; diag
 441801; AW242799; Hs.86368; ESTs; blad; diag
 441835; AB036432; Hs.184; advanced glycosylation end pro; fibro; mAb
 441859; AW194384; Hs.380444; interleukin-4 induced gene-1 p; ovar, mel; fibro; mAb
 55 441878; A1801869; Hs.127982; ESTs; test; diag
 442006; AW975183; Hs.372210; ESTs, Weakly similar to S72482; fibro, angio; CTL+s.m.
 442082; R41823; Hs.7413; calyntenin-2; breast, pros, ovar; diag
 442104; L20971; Hs.188; phosphodiesterase 4B, cAMP-spe; angio; CTL+s.m.
 442108; AW452649; Hs.343259; ESTs; lung; diag
 60 442242; AV647908; Hs.90424; Homo sapiens cDNA: FLJ23285 f; BPH; diag
 442323; AW016669; Hs.29190; ESTs; breast; diag
 442333; A1650877; Hs.129302; ESTs; test; diag
 442432; BE093589; Hs.38178; hypothetical protein FLJ23468; blad, lung, panc, esoph, mel; CTL+s.m.
 442438; AA995998; Hs.370007; gbcrak26b03.s1 NCL_CGAP_Kid5 Ho; uter, ovar, renal; diag
 65 442441; A1820662; Hs.129598; ESTs; breast; diag
 442503; AF147078; Hs.375031; p53-responsive gene 5; mel; diag
 442506; BE568411; Hs.41726; ESTs; angio; diag
 442573; H93368; Hs.7567; branched chain aminotransferas; ovar, panc, angio, test; s.m.
 442577; AA292998; Hs.163900; ESTs; blad, panc, colon, stom, ovar; diag
 70 442580; A1733682; Hs.130239; ESTs; breast; diag
 442609; AL020996; Hs.8518; selenoprotein N; mel; diag
 442613; A1004002; Hs.130522; Kv channel-interacting protein; glio; diag
 442622; NM_000435; Hs.8548; Notch (Drosophila) homolog 3; ovar; mAb
 442711; AF151073; Hs.8645; hypothetical protein; angio, mel, sarc; diag
 75 442739; NM_007274; Hs.8679; cytosolic acyl coenzyme A thio; mel; s.m.
 442757; A1739528; Hs.28345; ESTs; mel; diag
 442818; AK001741; Hs.8739; hypothetical protein FLJ10879; breast; diag
 442821; BE391929; Hs.8752; transmembrane protein 4; ovar; diag
 442832; AW206560; Hs.253569; ESTs; pros, fibro; diag
 80 442896; R37725; Hs.283093; ESTs; panc; diag
 442994; A1026718; Hs.16954; ESTs; blad, fibro; diag
 443054; A1745185; Hs.84520; yes-associated protein 65 kDa; blad; diag
 443162; T49951; Hs.9029; DKFZP434G032 protein; blad, lung; CTL+s.m.
 443171; BE281128; Hs.9030; TONDU; blad, ovar; diag

- 443184; AI638728; Hs.135159; ESTs; sarc; diag
 443211; AI128388; Hs.143655; ESTs; blad, ovar, lung, headnk, stom, colon; diag
 443216; W80487; Hs.324521; hypothetical protein DC50; test; diag
 443257; AJ334040; Hs.11614; HSPC065 protein; fibro; CTL+s.m.
 443400; R28424; Hs.250648; ESTs; lung; diag
 443523; AK001575; Hs.9536; hypothetical protein FLJ10713; test; CTL+s.m.
 443537; D13305; Hs.203; cholecystokinin B receptor; test; mAb
 443648; AI085377; Hs.143610; ESTs; lung, headnk; diag
 443709; AI082692; Hs.134662; ESTs; fibro; diag
 443715; AI583187; Hs.9700; cyclin E1; lung, stom, ovar, colon; CTL+s.m.
 443785; AW449952; Hs.190125; basic-helix-loop-helix-PAS pro; glio, uter, ovar; CTL+s.m.
 443802; AW504924; Hs.9805; KIAA1291 protein; sarc; diag
 443883; AA114212; Hs.9930; serine (or cysteine) proteinase; sarc; s.m.
 443885; H91806; Hs.15284; ESTs; mela; diag
 443892; AI889572; Hs.246875; ESTs; lung; diag
 443950; NM_001425; Hs.9999; epithelial membrane protein 3; mela; mAb
 443968; AA287702; Hs.10031; KIAA0955 protein; angio; diag
 443983; H04482; Hs.163724; ESTs; mela; mAb
 443991; NM_002250; Hs.10082; potassium intermediate/small c; pros, colon, uter; mAb
 444009; AI380792; Hs.135104; ESTs; angio; diag
 444151; AW972917; Hs.128749; alpha-methylacyl-CoA racemase; pros; mAb
 444159; AF116846; Hs.10431; dead ringer (Drosophila)-like; test; CTL+s.m.
 444163; AI126099; FGENESH predicted RNaseH domain; blad; s.m.
 444301; AK000136; Hs.10760; asporin (LRR class 1); panc; diag
 444325; AW152618; Hs.16757; ESTs; esoph; diag
 444330; AI597655; Hs.49265; ESTs; angio; diag
 444342; NM_014398; Hs.10887; similar to lysosome-associated; hepC, lung, fibro, blad, esoph; diag
 444378; R41339; Hs.47860; neurotrophic tyrosine kinase; lung, glio; mAb+s.m.
 444409; AI792140; Hs.49265; ESTs; angio; diag
 444444; AI149332; Hs.14855; ESTs; blad; diag
 444471; AB020684; Hs.11217; KIAA0877 protein; glio, lung, colon; mAb
 444476; AF020038; Hs.11223; isocitrate dehydrogenase 1 (NA; blad; s.m.
 444484; AK002126; Hs.11260; hypothetical protein FLJ11254; pros; diag
 444633; AF111713; Hs.12284; junctional adhesion molecule 1; ovar, uter, breast, cerv, blad, headnk; mAb
 444649; AW207523; Hs.371001; ESTs; blad; diag
 444670; H58373; Hs.332938; hypothetical protein MGC5370; sarc; diag
 444754; T83911; Hs.11881; transmembrane 4 superfamily me; panc, omuc, stom, lung, colon; mAb+s.m.
 444809; BE207568; Hs.208219; oculospantin; mela; mAb
 444823; BE262989; Hs.12045; putative protein; test; diag
 444863; AW384082; Hs.104879; serine (or cysteine) proteinase; mela; s.m.
 444895; AI674383; Hs.22891; solute carrier family 7 (catio; ovar; mAb+s.m.
 444995; AJ272265; Hs.12230; secreted phosphoprotein 2, 24k; hepC, panc; diag
 445019; AI205540; Hs.281295; ESTs; headnk, lung, colon; diag
 445070; NM_000677; Hs.258; adenosine A3 receptor; glio, renal; mAb
 445076; AI206888; Hs.154131; ESTs; test; diag
 445084; H38914; Hs.250848; hypothetical protein FLJ14761; sarc; mAb
 445093; AI207197; Hs.158905; ESTs; test; diag
 445109; AF039916; Hs.12330; ectonucleoside triphosphate d; pros; s.m.
 445119; AF035121; Hs.12337; kinase insert domain receptor; angio; mAb
 445160; AI299144; Hs.101937; sine oculis homeobox (Drosophila); sarc; CTL+s.m.
 445182; AW189787; Hs.361778; ESTs; blad; diag
 445247; AW274290; Hs.153997; ESTs; mela; diag
 445279; R41900; Hs.22245; ESTs; angio; diag
 445363; NM_005993; Hs.12570; tubulin-specific chaperone d; test; diag
 445413; AA151342; Hs.12677; CGI-147 protein; pros, colon, uter, ovar, lung, panc; diag
 445418; AW139377; Hs.127179; cryptic gene; panc; diag
 445424; AB028945; Hs.12696; cortactin SH3 domain-binding p; pros; diag
 445443; AV653838; Hs.295131; ESTs; lung; diag
 445554; X91247; Hs.13046; thioredoxin reductase 1; lung; s.m.
 445684; AK001696; Hs.13109; Ran binding protein 11; angio; diag
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; angio; CTL+s.m.
 445784; AI253155; Hs.146065; ESTs; mela; CTL+s.m.
 445885; AI734009; Hs.127699; KIAA1603 protein; pros, fibro; diag
 445900; AF070526; Hs.125036; Homo sapiens clone 24787 mRNA; renal, leuk; mAb
 445911; AJ985987; Hs.145645; ESTs, Moderately similar to AL; blad; diag
 445982; BE410233; Hs.13501; pascadillo (zebrafish) homolog; mela; diag
 446057; AI420227; Hs.366053; Trp-p8 transient receptor pota; pros; mAb
 446082; AI274139; Hs.156452; ESTs; blad; diag
 446098; AW072215; Hs.208470; ESTs; angio; diag
 446100; AW967109; Hs.13804; hypothetical protein dJ462023; pros; diag
 446102; AW168067; Hs.317694; ESTs; lung; diag
 446113; AW967553; Hs.323518; Homo sapiens mRNA for FLJ00083; test; mAb
 446269; AW263155; Hs.14559; hypothetical protein FLJ10540; lung, headnk; CTL+s.m.
 446291; BE397753; Hs.14623; Interferon, gamma-inducible p; mela; diag
 446292; AF081497; Hs.279682; Rh type C glycoprotein; lung, cerv; mAb
 446293; AI420213; Hs.149722; LIM domain transcription factor; ovar, test; diag
 446320; AF126245; Hs.14791; acyl-Coenzyme A dehydrogenase; pros; s.m.
 446332; AK001635; Hs.14836; hypothetical protein FLJ10773; breast; diag
 446342; BE298665; Hs.14846; solute carrier family 7 (catio; uter, colon, pros, mela; mAb
 446428; AW082270; Hs.12496; ESTs, Weakly similar to ALU4_H; fibro; diag
 446528; AU076640; Hs.15243; nucleolar protein 1 (120kD); lung, test; diag
 446508; N75217; Hs.175622; ESTs; uter, fibro; diag
 446626; AW292180; Hs.156142; ESTs; pros; diag

- 446636; AC002563; Hs.15767; citron (rho-interacting, serin; lung; CTL+s.m.
 446644; NM_003272; Hs.21065; transmembrane 7 superfamily me; mela; mAb
 446673; NM_016361; Hs.15971; LPAP for lysophosphatidic acid; blad; diag
 446727; AB011095; Hs.16032; KIAA0523 protein; angio; CTL+s.m.
 446733; AA863360; Hs.26040; ESTs, Weakly similar to fatty; breast; s.m.
 446755; AW451473; Hs.16134; serine/threonine kinase 10; mela; CTL+s.m.
 446791; AI632278; Hs.185922; ESTs; test; diag
 446839; BE091926; Hs.16244; mitotic spindle coiled-coil re; test; diag
 446856; AI814373; Hs.164175; ESTs; lung; diag
 446868; AV660737; Hs.348297; ESTs; panc; diag
 446872; X97058; Hs.16362; pyrimidinergic receptor P2Y₁; G; lung; mAb
 446932; AA861459; Hs.125644; ESTs; fibro; diag
 446967; AI696629; Hs.156781; ESTs; fibro; diag
 446979; AI654443; Hs.197683; ESTs; test; diag
 446984; AB020722; Hs.16714; Rho guanine exchange factor (G; angio; CTL+s.m.
 446998; AK001898; Hs.16740; hypothetical protein FLJ11038; lung, headnk; diag
 446998; N99013; Hs.278966; Homo sapiens mRNA; cDNA DKFZp5; panc, fibro; diag
 446999; AA151520; Hs.351416; hypothetical protein MGC4485; headnk; diag
 447004; AW296968; Hs.157539; FGENESH predicted secreted pro; glio; diag
 447078; AW885727; Hs.9914; ESTs; lung; diag
 447126; AW150632; Hs.170307; Ral guanine nucleotide exchange; angio; diag
 447164; AF026941; Hs.17518; vipirin; similar to inflammat; colon, lung, breast, stom, hepC, esoph, mela; diag
 447178; AW594641; Hs.192417; ESTs; mela; diag
 447188; H65423; Hs.17631; hypothetical protein DKFZp434E; test; diag
 447210; AF035269; Hs.17752; phosphatidylserine-specific pt; pros, mela; s.m.
 447289; AW247017; Hs.36978; melanoma antigen, family A, 3; lung, mela; mAb+CTL
 447334; AA515032; Hs.91109; ESTs; blad; diag
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392; lung, blad, panc, headnk, mela; mAb+s.m.
 447350; AJ375572; Hs.172634; v-erb-a avian erythroblastic t; breast, ovar, uter; diag
 447377; X77343; Hs.334334; transcription factor AP-2 alpha; breast, lung, mela; CTL+s.m.
 447395; AI418412; Hs.184793; Homo sapiens cDNA: FLJ21880 f; panc; diag
 447437; U07225; Hs.339; purinergic receptor P2Y₁; G-pro; blad; mAb
 447499; AW262580; Hs.147674; protocadherin beta 16; pros, glio, ovar; mAb+s.m.
 447532; AK000614; Hs.18791; hypothetical protein FLJ20607; lung, blad; CTL+s.m.
 447534; AW953935; Hs.288655; ESTs; lung, test; diag
 447578; AA912347; Hs.136585; ESTs, Weakly similar to JCS314; ovar; s.m.
 447595; AW379130; Hs.18953; phosphodiesterase 9A; pros; CTL+s.m.
 447604; AW089933; Hs.301342; hypothetical protein MGC4342; mela; diag
 447636; Y10043; Hs.19114; high-mobility group (nonhiston; lung; CTL+s.m.
 447733; AF157482; Hs.19400; MAD2 (mitotic arrest deficient; test; diag
 447749; T53260; Hs.8297; ESTs; renal; diag
 447761; AF061573; Hs.19492; protocadherin 8; EWS, glio; mAb
 447768; X86400; Hs.19520; FXYD domain-containing ion tra; renal; mAb
 447818; W79940; Hs.355279; Homo sapiens clone 24670 mRNA; renal; diag
 447835; AW591623; Hs.164129; ESTs, Weakly similar to I38022; renal, ovar, uter; diag
 447881; BE620886; Hs.355279; GCN1 (general control of amino; renal; diag
 447937; AL109718; Hs.20034; Homo sapiens mRNA full length; mela; mAb
 447993; AW139525; Hs.170362; ESTs; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 448030; N30714; Hs.325960; membrane-spanning 4-domains, s; panc, leuk, renal, stom lung; mAb
 448045; AJ297436; Hs.20166; prostate stem cell antigen; blad, panc, pros; mAb
 448105; AW591433; Hs.298241; Transmembrane protease, serine; breast, panc, colon, lung, ovar, stom; mAb+diag+s.m.
 448133; AA723157; Hs.73769; folate receptor 1 (adult); ovar, fibro; mAb
 448140; AF146761; Hs.20450; BCM-like membrane protein prec; fibro, mela, leuk; mAb
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase; test; CTL+s.m.
 448181; AF272833; Hs.279763; hypothetical protein FLJ10504; test; diag
 448204; AI475124; Hs.170561; ESTs; sarc; diag
 448231; AI701916; Hs.202509; ESTs; angio; diag
 448258; BE386983; Hs.343214; hypothetical protein FLJ20396; mela, ovar; mAb
 448262; AW880830; Hs.186273; ESTs; blad; diag
 448275; BE514434; Hs.20830; kinesin-like 2; ovar, esoph, mela; diag
 448278; W07369; Hs.11782; ESTs; lung; diag
 448290; AK002107; Hs.20843; Homo sapiens cDNA FLJ11245 f; pros; diag
 448321; NM_005883; Hs.20912; adenomatous polyposis coli like; glio; CTL+s.m.
 448357; N20169; Hs.108923; RAB38, member RAS oncogene fam; lung, mela; diag
 448410; AK000227; Hs.21126; hypothetical protein FLJ20220; mela; diag
 448437; AW470125; Hs.220529; gbow60c04.x1 NCI_CGAP_Pan1 H; panc, color; diag
 448499; BE613260; Hs.77560; p53-regulated DDA3; glio; diag
 448569; BE382657; Hs.21486; signal transducer and activator; panc, headnk, fibro, cerv, mela, renal; CTL+s.m.
 448588; AI970276; Hs.156905; KIAA1676; test; CTL+s.m.
 448595; AB014544; Hs.21572; KIAA0644 gene product; breast, glio; mAb
 448664; AI879317; Hs.334691; splicing factor 3a, subunit 1; mela; CTL+s.m.
 448674; W311178; Hs.154140; ovary-specific acidic protein; angio; diag
 448692; AW013907; Hs.167531; methylcrotonoyl-Coenzyme A car; pros, pros; s.m.
 448706; AW291095; Hs.21814; Interleukin 20 receptor, alpha; pros, uter, blad, colon; mAb
 448719; AA033627; Hs.21858; trinucleotide repeat containin; mela, sarc; CTL+diag
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate; test; diag
 448811; AI590371; Hs.199460; ESTs; esoph, panc; mAb
 448939; BE267795; Hs.22595; hypothetical protein FLJ10637; test; CTL+s.m.
 448966; AW372914; Hs.86149; phosphoinositol 3-phosphate-4; mela; CTL+s.m.
 448981; AI968719; Hs.195387; ESTs; test; diag
 448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA); pros, cerv, colon, lung, stom, blad, headnk, ovar, breast; mAb
 448993; AI471630; Hs.355952; KIAA0144 gene product; lung, blad; diag
 448999; AF179274; Hs.22791; transmembrane protein with EGF; pros, glio; mAb

- 5 449003; X76342; Hs.389; alcohol dehydrogenase 7 (class); lung, headnk; s.m.
 449019; A1949095; Hs.67776; ESTs, Weakly similar to T22341; blad, lung; diag
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; blad, colon, ovar; s.m.
 449040; NM_012191; Hs.22919; putative tumor suppressor; lung; CTL+s.m.
 449078; AK001256; Hs.22975; KIAA1576 protein; mela; diag
 449101; AA205847; Hs.23016; G protein-coupled receptor; lung, headnk; mAb
 449109; AW270992; Hs.120949; ESTs, Weakly similar to ALU7_H; sarc; diag
 449156; AF103907; Hs.171353; prostate cancer antigen 3, non; pros; mAb+CTL
 10 449207; AL044222; Hs.23255; nucleoporin 155kD; lung; diag
 449228; AJ403107; Hs.148590; protein related with psoriasis; lung; diag
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; lung, cerv, headnk, blad, ovar, colon; mAb
 449317; AW293413; Hs.132906; 19A24 protein; mela; mAb
 449318; AW236021; Hs.78531; Homo sapiens, Similar to RIKEN; headnk, lung, angio; CTL+s.m.
 15 449322; A1638616; Hs.196566; ESTs; test; diag
 449338; H73444; Hs.394; adrenomedullin; renal; diag
 449394; AA004368; Hs.18160; Homo sapiens cDNA FLJ11550 fis; angio; mAb
 449437; A1702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fit; test; diag
 449448; D60730; Hs.57471; ESTs; blad, lung, headnk, breast; diag
 449467; AW205006; Hs.197042; ESTs; lung; diag
 20 449494; AW237014; Hs.315369; aquaporin 4; fibro; diag
 449569; A1656634; Hs.195389; ESTs; test; diag
 449592; A1655494; Hs.195718; ESTs; panc; diag
 449618; A1076459; Hs.15978; KIAA1272 protein; angio; diag
 449625; NM_014253; Hs.349094; odz (odd Oz/ten-m, Drosophila); pros; diag
 25 449650; AF055575; Hs.23838; calcium channel, voltage-depen; pros; mAb
 449680; A1033821; Hs.12160; ESTs; renal; diag
 449661; AW265634; Hs.133100; ESTs; glio, esoph, lung, blad ; diag
 449976; H06350; Hs.135056; Human DNA sequence from clone ; lung; diag
 450096; A1682088; Hs.79375; single-minded (Drosophila) hom; pros; CTL
 30 450098; W27249; Hs.8109; hypothetical protein FLJ21080; breast, lung, stom, uter; diag
 450149; AW969781; Hs.132853; Zic family member 2 (odd-paire; sarc; CTL+s.m.
 450152; A1138635; Hs.22968; intron of VEGFR; renal; diag
 450377; AB033091; Hs.355925; KIAA1265 protein; ovar, colon; diag
 35 450382; AA397658; Hs.60257; Homo sapiens cDNA FLJ13598 fis; pros; diag
 450400; A1694722; Hs.279744; ESTs; panc; diag
 450431; AW136797; Hs.266041; ESTs; test; diag
 450451; AW591528; Hs.202072; ESTs; uter, endo; diag
 450506; NM_004460; Hs.418; fibroblast activation protein; panc, esoph; diag
 40 450534; A1570189; Hs.25132; KIAA0470 gene product; angio; CTL+s.m.
 450581; AF081513; Hs.25195; TGF-beta 4; uter, cerv, test; diag
 450636; AW403954; Hs.25237; mesenchymal stem cell protein ; blad; mAb
 450642; R39773; Hs.7130; copine IV; pros; diag
 450656; AA010539; Hs.18912; unnamed protein product; fibro, uter; CTL+s.m.
 45 450663; H43540; Hs.25292; ribonuclease H1, large subunit; mela; s.m.
 450676; A1147155; Hs.279727; ESTs; sarc; diag
 450684; AA872605; Hs.25333; interleukin 1 receptor, type I; blad, lung, headnk; mAb
 450690; AA296696; Hs.333418; FXYD domain-containing ion tra; mela; diag
 450693; AW450461; Hs.203965; ESTs; pros, uter; diag
 50 450719; A1096837; Hs.21349; ESTs, Weakly similar to RB8B_H; test; diag
 450737; AW007152; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 450785; AA852713; Hs.108885; Homo sapiens, alpha-1 (VI) col; sarc; CTL+s.m.
 450832; AW970602; Hs.105421; ESTs; lung; diag
 451027; AW519204; Hs.40808; Homo sapiens, Similar to RIKEN; pros, uter, glio; diag
 55 451035; AU076785; Hs.430; plastin 1 (I isoform); panc; diag
 451050; AW937420; Hs.351869; ESTs; mela; diag
 451099; R52795; Hs.25954; interleukin 13 receptor, alpha; glio, fibro, mela; mAb
 451106; BE382701; Hs.25960; N-MYC oncogene; test, ovar; CTL+s.m.
 451110; A1955040; Hs.265398; PAR-6 beta (partitioning def; breast, ovar, lung, colon; CTL+s.m.
 60 451181; A1796330; Hs.207461; ESTs; panc; diag
 451253; H48299; Hs.26126; claudin 10; lung, ovar, panc; mAb
 451291; R39288; Hs.6702; ESTs; lung; diag
 451295; A1557212; Hs.17132; ESTs, Moderately similar to I5; panc; diag
 451320; AW118072; Hs.350251; diacylglycerol kinase, zeta (1; lung; s.m.
 65 451348; NM_006338; Hs.26312; glioma amplified on chromosome; ovar; mAb
 451388; AB029008; Hs.26334; spastic paraplegia 4 (autosomal; lung; diag
 451398; A1793124; Hs.144479; ESTs; breast, ovar; diag
 451411; AA017492; Hs.135655; EST; pros; diag
 451497; H83294; Hs.284122; Wnt inhibitory factor-1; uter, fibro, pros, colon, sarc; diag
 70 451541; BE279383; Hs.26557; plakophilin 3; lung, blad, ovar; diag
 451592; A1805416; Hs.213897; ESTs; lung, headnk; diag
 451635; AA018899; Hs.127178; cryptic gene; panc; diag
 451663; A1872360; Hs.209293; ESTs; pros; diag
 451720; AW970986; Hs.290853; ESTs; pros; diag
 451743; AW074266; Hs.336428; ESTs; lung; diag
 75 451820; AW058357; Hs.199248; ESTs; panc; mAb
 451844; T61430; ; gbyc06a03.s1 Stratagene lung ; blad; diag
 451982; F13036; Hs.27373; Homo sapiens mRNA; cDNA DKFZp5; pros, blad; mAb
 451999; AW176401; Hs.380623; DEAD/H (Asp-Glu-Ala-Asp/fis) b; test; CTL+s.m.
 80 452046; AB018345; Hs.27657; KIAA0802 protein; lung, uter; CTL+s.m.
 452208; AA024792; Hs.31895; hypothetical protein MGC4093; renal; diag
 452240; A1591147; Hs.61232; ESTs; blad, lung, headnk, panc, cerv; diag
 452243; AL355715; Hs.28555; programmed cell death 9 (PDCD9; breast; diag
 452244; N33530; Hs.176674; ESTs; mela; diag

- 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S; test; CTL+s.m.
 452295; BE379935; Hs.28866; programmed cell death 10; lung; diag
 452298; AI039243; Hs.278585; ESTs; angio; diag
 452304; AA025388; Hs.61311; ESTs, Weakly similar to S10590; lung, panc, blad, stom, esoph, fibro, colon; s.m.
 452316; AA298484; Hs.61265; ESTs, Moderately similar to G7; blad; diag
 452340; NM_002202; Hs.505; ISL1 transcription factor, LIM; panc, pros; CTL+s.m.
 452353; C18825; Hs.29191; epithelial membrane protein 2; pros, breast; mAb
 452355; N54926; Hs.29202; G protein-coupled receptor 34; glo, fibro, panc; mAb
 452367; U71207; Hs.29279; eyes absent (Drosophila) homolog; lung, pros, ovar, uter, CTL+s.m.
 452416; AA026115; Hs.114777; ESTs; fibro; diag
 452461; N78223; Hs.108106; transcription factor; blad, lung, headnk, ovar, glo, stom, colon, cerv; CTL+s.m.
 452571; W31518; Hs.34665; ESTs; stom, lung, panc, colon, fibro; diag
 452594; AU076405; Hs.29981; solute carrier family 26 (sulf); ovar; mAb
 452613; AA461599; Hs.23459; ESTs; lung; diag
 452679; Z42387; Hs.83883; transmembrane, prostate androg; pros, colon, panc, pros; mAb
 452705; H49605; Hs.246005; ESTs; panc; diag
 452717; AW160399; Hs.30376; hypothetical protein; pros; diag
 452721; AJ269529; Hs.301871; solute carrier family 37 (glyc); pros; mAb
 452732; BE300078; Hs.80449; Homo sapiens, clone IMAGE:3535; blad; diag
 452744; AI267652; Hs.246107; Homo sapiens mRNA; cDNA DKFZp4; melar; diag
 452792; AB037765; Hs.30652; KIAA1344 protein; pros, uter, breast; diag
 452795; AW392555; Hs.18878; hypothetical protein FLJ21620; renal, headnk, colon, lung, panc; CTL
 452796; AB011100; Hs.30656; KIAA0528 gene product; test; diag
 452833; BE559681; Hs.30736; KIAA0124 protein; lung, melar; CTL+s.m.
 452865; AI924046; Hs.119567; ESTs, Weakly similar to A47582; lung; diag
 452899; M96739; Hs.30956; nescient helix loop helix 1; sarc; CTL+s.m.
 452924; AW580939; Hs.97199; complement component C1q recep; angio; diag
 452933; AW391423; Hs.288555; Homo sapiens cDNA; FLJ22425 f; angio; CTL+s.m.
 452934; AA581322; Hs.4213; hypothetical protein MGC16207; lung, blad; diag
 452955; AW390282; Hs.31130; transmembrane 7 superfamily mem; pros; mAb+s.m.
 453006; AI362575; Hs.303171; ESTs; pros; diag
 453028; AB006532; Hs.31442; RacQ protein-like 4; blad, lung, test; CTL+s.m.
 453085; AW954243; Hs.351573; KIAA0251 protein; angio; diag
 453096; AW294631; Hs.351270; ESTs; pros; diag
 453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog; lung, headnk, colon; mAb
 453107; NM_016113; Hs.279746; vanilloid receptor-like prota; melar; mAb
 453134; AA032211; Hs.118493; ESTs; blad; diag
 453142; AA033648; Hs.7473; Homo sapiens gap junction prot; fibro; mAb
 453160; AJ263307; Hs.356901; H2B histone family, member L; lung, panc, pros; diag
 453210; AI133161; Hs.32360; hypothetical protein FLJ10667; lung; CTL+s.m.
 453216; AL137566; Hs.32405; progesterone receptor (PR); blad; mAb+s.m.
 453256; AI565587; Hs.32556; KIAA0379 protein; melar; diag
 453310; X70697; Hs.553; solute carrier family 6 (neuro; fibro; mAb
 453321; AI984381; Hs.232521; ESTs; blad; diag
 453323; AF034102; Hs.32951; solute carrier family 29 (nuc); ovar; CTL+s.m.
 453331; AJ240665; Hs.352537; ESTs; breast, lung, panc, esoph; mAb+diag+s.m.
 453344; BE349075; Hs.44571; ESTs; melar; diag
 453348; BE272318; Hs.8595; hypothetical protein FLJ12438; test; CTL+s.m.
 453365; AA035211; Hs.17404; SOX7 SRY (sex determining reg); angio, blad; CTL+s.m.
 453370; AI470523; Hs.139336; ATP-binding cassette, sub-fam; pros; mAb
 453389; BE273648; Hs.32963; cadherin 6, type 2, K-cadherin; renal, ovar, blad; mAb+s.m.
 453392; U23752; Hs.32964; SRY (sex determining region Y); ovar, lung, glo, sarc; CTL+s.m.
 453459; BE047032; Hs.257789; ESTs; ovar, cerv, blad, uter, panc, angio, lung; diag
 453464; AI884911; Hs.32989; receptor (calcitonin) activity; pros; mAb
 453633; AA357001; Hs.34045; hypothetical protein FLJ20764; lung, esoph, test; diag
 453637; NM_002589; Hs.34073; BH-protocadherin (brain-heart); headnk; mAb
 453642; AJ370936; Hs.34074; dipeptidylpeptidase VI; glo; mAb
 453779; N35187; Hs.43386; 28kD interferon responsive pro; melar; diag
 453789; AA628517; Hs.118502; ESTs; angio; diag
 453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1; glo, lung, uter, headnk, cerv, panc, pros, sarc; mAb
 453883; AI638516; Hs.347524; cofactor required for Sp1 tran; blad, lung; diag
 453884; AA355925; Hs.36232; KIAA0186 gene product; lung, ovar, test, esoph; diag
 453912; AL121031; Hs.356843; SWI/SNF related, matrix associ; melar; diag
 453922; AF053306; Hs.36708; budding uninhibited by benzimid; colon, stom, lung, test; CTL+s.m.
 453935; AI633770; Hs.42572; ESTs; panc; diag
 453941; U39817; Hs.36820; Bloom syndrome; lung, cerv, headnk; CTL+s.m.
 453984; AI961488; Hs.249196; ESTs; lung; diag
 453966; BE148734; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 453985; N44545; Hs.251865; ESTs; test; diag
 454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 fami; lung, headnk; s.m.
 454042; H22570; Hs.47860; hypothetical protein FLJ20093; lung; diag
 454066; X00356; Hs.37058; calcitonin/calcitonin-related; lung; diag
 454071; AI041793; Hs.42502; ESTs; breast; diag
 454077; AC005952; Hs.37062; Insulin-like 3 (Leydig cell); test; diag
 454098; W27953; Hs.217493; Plakophilin; lung; diag
 454117; BE410100; Hs.40368; adaptor-related protein comple; melar; CTL+s.m.
 454360; L78207; Hs.54470; ATP-binding cassette, sub-fam; glo; mAb
 454429; BE273437; Hs.301406; hypothetical protein PP3501; melar; mAb
 454439; AW819152; Hs.154320; DKFZP566O1846 protein; lung; diag
 454478; AW805749; Hs.372783; superoxide dismutase 2, mitocho; melar; s.m.
 455601; AI368680; Hs.816; SRY (sex determining region Y); lung, cerv, esoph; s.m.
 456034; AW450979; ; gb-UI-H-BI3-ata-a-12-0-UL1 N; blad, fibro; diag
 456062; AI866288; Hs.71962; ESTs, Weakly similar to B36298; fibro, ovar, uter; diag

5	456177; NM_012391; Hs.79414; prostate epithelium-specific E; breast, pros; diag		
10	456266; L29073; Hs.198726; cold shock domain protein A; panc; CTL+s.m.		
15	456321; NM_001327; Hs.87225; cancer/testis antigen; lung; CTL		
20	456553; AA721325; Hs.189058; ESTs, Highly similar to Simila; panc; diag		
25	456723; Z43902; Hs.4748; adenylate cyclase activating p; glio; mAb+s.m.		
30	456736; AW248217; Hs.1619; achaete-scute complex (Drosoph); lung; diag		
35	456759; BE259150; Hs.127792; delta (Drosophila)-like 3; glio; lung; mAb		
40	456847; A1360456; Hs.86088; ESTs; test; diag		
45	456938; X52509; Hs.161640; tyrosine aminotransferase; breast; s.m.		
50	456977; AK000252; Hs.169758; hypothetical protein FLJ20245; angio; diag		
55	457200; U33749; Hs.197764; thyroid transcription factor 1; fibro; CTL+s.m.		
60	457211; AW972565; Hs.32399; ESTs, Weakly similar to S51797; mela; pros; CTL+s.m.		
65	457292; A1921270; Hs.281462; hypothetical protein FLJ14251; blad; mAb		
70	457313; AF047002; Hs.241520; transcriptional coactivator; test; CTL+s.m.		
75	457411; AW085961; Hs.130093; iroquois-class homeobox protel; breast; fibro; diag		
80	457465; AW301344; Hs.122908; DNA replication factor; test, mela; diag		
	457498; A1732230; Hs.191737; ESTs; pros; diag		
	457561; AA331517; Hs.286055; chimerin (chimaerin) 2; glio; mAb		
	457590; A1612809; Hs.5378; hypothetical protein MGC10724; ovar; diag		
	457869; AU077186; Hs.108885; Homo sapiens, alpha-1 (VI) col; sarc; CTL+s.m.		
	458092; W67353; Hs.350558; KIAA0251 protein; lung; diag		
	458124; AW005548; Hs.124590; ESTs; fibro; diag		
	458435; A1418718; Hs.144121; ESTs, Weakly similar to T46916; glio; diag		
	458471; AV648609; Hs.194240; ESTs; renal, panc, hepC; diag		
	458933; A1638429; Hs.24763; RAN binding protein 1; lung, test; diag		
	459373; BE408266; Hs.301406; hypothetical protein PP3501; mela; mAb		
	459578; AW612538; Hs.304491; EST; mela; diag		
	459702; A1204995; ; gb:an03c03.x1 Stratagene schtz; blad, fibro; diag		
	459705; BE082764; Hs.270252; ESTs, Weakly similar to androg; fibro; mAb+s.m.		
	TABLE 3B		
35	Pkey: Unique Eos probeset identifier number		
	CAT number: Gene cluster number		
	Accession: Genbank accession numbers		
40	Pkey CAT Number Accession		
	103739 49403_2 AA115173 AA075709 AA076354 AA083101 AA076396 AA085391 AA070684 AA083368 AA075779 AA075221 AA076395 AA650486 AA083500		
	108282 108971_1 AA065143 AA065142		
	113230 2327174_1 A1820546 A1821336 T61430		
	118417 35983_1 AF080229 AF080232 U87593 U87592 U87591 U87590 A1636743 A1633818 AW206802 A1583718 AF080231 AF080234 AF080233 AL535594		
45			
	A1818326 AF080230 S46404 A1970376 AA463992 AW665466 BF512210 U87595 U87589 BE550633 A1672574 BE467547 A1680633 AW614951		
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	121335 1369289_1 AA404418 A1217248		
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50	322975 1784158_1 C16391 C16413		
	323332 245301_1 A1829520 A1791832 A1791823 AA229315 AA228414 AA229211		
	323817 887879_1 AA410943 BF366582 AA334202 AA332882 BF371899 AW948953		
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	406685 0_0 M18728		
55	409051 107934_1 AA075419 AA082953 AA080912 AA062835 AA071252 AA084926 AA078992 AA113913 AA081881 AA070343 AA083821 AA062836 AA113892		
	AA075318 AA076594 AA078900 AA134801 AA063293 AA083403 AW974305		
	409123 108378_1 AA070050 AA070823 AA063403		
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60			
	B1007625 B1027864 B1009100 B1006275 B1006270 B1031000 B1029864 B1006277 B1007627 B1006266 B1006991 B1006990 B1007763 B1007762		
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	411880 1139083_1 BE088101 T05990 AW872477		
	413804 1556661_1 BE168256 BE168190 T64682		
	414221 685586_1 AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945		
65	417886 1031334_1 AA210987 D57294 AA214584 AA207006 D56572		
	427260 11272_50 AA401424 AA400100 AA663848		
	427298 115241_1 AA933717 BF061897 AW628327 AA641788 AA400495		
	427521 513212_1 AW973352 BF222929 AW016853 BF059130 A1651829 BE551767 AA558414 A1339359 BF059601 A1961162 A1341422 A1206248 A1206165		
	AA548736 AA768578 A1539081 AW025957 AA736837 N79575 AW594357 AA480892		
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70	432169 112710_1 AA527941 AA635266 A1810608 A1620190		
	432282 539529_1 BG207209 BE166299 A1204995 BG199355 AW969908 AA528756 AW440776 B1044354		
	432407 MH1429_12 BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104		
75			
	AW847519 AA099426 AW817981 AW865396 BG961122 AA224498 AA308542 AW821833 BF902155 A1732411 BG778834 BG283641 BE748279		
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	AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 A1075321 L13823 AA216700 BF771864 AW861859		
	BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928		
	AW861687 AW821826 B1055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592		
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80			
	T23457 F04044 AA723859 AA977643 AA283764 A1123609 N21561 BF055052 BE856661 A1804220 AA843394 A1472045 A1740490 AA578830		
	H09495 A1283334 AA609495 A1122773 AW162643 AW161798 BF940077 A1808825 A1360866 A1123189 R40236 R20726 AW975899 BE764052		
	N31709 N31708 A031947 AW194138		
	434414 35978_1 AF134164 BF809407 AA218567 BF842863 A1267168 BF876178 BG999253 AW861851 AW858362 A1817548 BF771300 AA113928 AA223422		
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				AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175 BF854337
5	434596	14701_1		AF147374 T59538 T59589 T59598 T59542
	434609	14739_1		AF147390 R76593 R76594
	438966	1242593_1		AW979074 AA834841 AA828650
	438993	2580163_1		AI926361 AA834879 AA828995
	439092	919640_1		AW978407 AA830149 M85983 AW503637 BF352096
10	439780	49082_1		AL109688 R23665 R26578
	440151	1879911_1		AA868167 F21558 F31418 F35624
	444163	682245_1		BG403189 AI148521 AI184746 AI126098 R05933 BI057330
	451844	2327174_1		AI820546 AI821336 T61430
	456034	685586_1		AA136663 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	459702	539529_1		BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
15	TABLE 3C			
	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
20	Strand:	Indicates DNA strand from which exons were predicted.		
	NL_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	NL_position
25	325372	5866920	Minus	1117061-1117304
	325544	6682452	Plus	171228-171286
	327036	6531965	Plus	319951-320040
	327075	6531965	Plus	4041318-4041431
	327414	5867750	Plus	102481-102586
30	328700	5868264	Plus	764089-764203
	330211	6013592	Plus	59158-59215
	332798	Dunham, I. et al.	Minus	232147-231974
	333769	Dunham, I. et al.	Plus	7696625-7696707
	333904	Dunham, I. et al.	Minus	8217374-8217261
35	334223	Dunham, I. et al.	Minus	12734365-12734269
	334447	Dunham, I. et al.	Plus	14308764-14308824
	335115	Dunham, I. et al.	Minus	21388250-21388146
	335809	Dunham, I. et al.	Plus	26310772-26310909
	335824	Dunham, I. et al.	Plus	26376860-26376942
40	335825	Dunham, I. et al.	Plus	26378175-26378268
	335936	Dunham, I. et al.	Minus	27360474-27360400
	336034	Dunham, I. et al.	Plus	29014404-29014590
	336152	Dunham, I. et al.	Minus	30156053-30155870
	336636	Dunham, I. et al.	Plus	988418-989185
45	338008	Dunham, I. et al.	Plus	7697068-7697236
	338033	Dunham, I. et al.	Plus	8092128-8092271
	338158	Dunham, I. et al.	Minus	11794465-11794343
	338255	Dunham, I. et al.	Minus	15242294-15242231
	400494	9714719	Plus	169845-170272
50	400517	9795686	Minus	49996-50346
	400651	8117878	Minus	81488-81646
	400665	8118496	Plus	16879-17023
	400773	8131629	Minus	44116-44238,48208-48321
	400844	9188605	Plus	24746-24872,25035-25204
55	400846	9188605	Plus	39310-39474
	400881	2842777	Minus	91446-91603,92123-92265
	401093	8516137	Minus	22335-23166
	401234	9929642	Plus	120173-120337
	401424	8176894	Plus	24223-24428
60	401486	7341763	Plus	32585-32756,36281-36540,40791-40933,4401
	401704	3097841	Plus	24712-25374
	401732	1200312	Plus	19346-19525,19625-19708,19897-19973,2006
	401747	9789672	Minus	118596-118816,119119-119244,119609-11976
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287
65	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
	401785	7249190	Minus	165776-165998,166189-166314,166408-16656
	401797	6730720	Plus	6973-7118
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,4519
70	402145	8018280	Plus	113088-114800
	402199	8576116	Minus	84187-84744
	402230	9966312	Minus	29782-29932
	402239	7690131	Plus	38175-38304,42133-42266
	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
75	402265	3287673	Plus	21059-21168
	402305	7328724	Plus	40832-41362
	402420	9796339	Plus	129750-129919
	402424	9796344	Minus	64925-65073
	402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
80	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	402550	7652009	Minus	80413-80673
	402604	9909420	Plus	20393-20767
	402605	9909420	Minus	47680-47973

5	402606	9909429	Minus	81747-82094
	402680	8113438	Plus	137634-137768,139702-139893,140475-14059
	402777	9588235	Plus	126786-126948
	402860	9588237	Minus	76423-76560
	402888	9930892	Minus	54727-54901
	402992	7767907	Minus	42137-42515
	402994	2996643	Minus	4727-4969
	403046	3540153	Minus	55707-55859,56369-56511
10	403047	3540153	Minus	59793-59968
	403071	8954241	Plus	136688-137096
	403088	8954241	Plus	169894-170193,170504-170806
	403171	9838164	Minus	74502-74703
	403328	8469086	Minus	120428-120703
	403329	8516120	Plus	96450-96598
15	403381	9438267	Minus	26009-26178
	403409	9438598	Plus	6860-7054,12573-12771
	403433	9719611	Minus	72225-72437
	403478	9958258	Plus	116458-116564
	403715	7239669	Plus	85128-85292
20	403740	7630882	Plus	86504-87227
	403776	7770611	Minus	1414-1513,1624-1756
	403903	7710671	Minus	101165-102597
	404029	7671252	Plus	108716-111112
	404049	3688074	Minus	75765-78155
25	404210	5006246	Plus	169926-170121
	404240	5002624	Minus	116132-116407,116653-116922
	404253	9367202	Minus	55675-56055
	404286	2326514	Plus	51086-51301
	404298	9944263	Minus	73591-73723
30	404403	7272157	Minus	72053-72238
	404440	7528051	Plus	80430-81581
	404866	9366919	Minus	11743-11929
	404877	1519284	Plus	1095-2107
35	404927	7342002	Plus	68690-69563
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
	405001	6015406	Minus	104646-104819
	405025	7107727	Plus	105267-105343,106184-106294,106387-10653
	405121	8102330	Minus	35816-36004,36587-36684
40	405238	7249119	Minus	51728-51836
	405239	7249119	Plus	144345-144464,144690-144836,151750-15188
	405451	7622517	Minus	145949-146227
	405455	1054740	Plus	118677-118807,119091-119296,121626-12182
	405546	1054740	Plus	124010-124183
	405547	1054740	Plus	124361-124520,124914-125050
45	405646	4914350	Plus	741-969
	405704	4204244	Plus	138842-139051
	405770	2735037	Plus	61057-62075
	405849	7651817	Minus	17705-18287
50	405932	7767812	Minus	123525-123713
	406081	9123861	Minus	38115-38691
	406137	9166422	Minus	30487-31058
	406173	7230224	Plus	12925-13213
	406348	9255985	Minus	71754-71944
55	406360	9256107	Minus	7513-7673
	406399	9256288	Minus	63448-63554
	406434	9256651	Minus	17803-17931
	406467	9795551	Plus	182212-182958
	406506	7711374	Minus	6843-8077
60	406547	7711513	Minus	172780-174358

Table 4A lists about 425 genes up-regulated in breast cancer compared to normal adult tissues and to non-malignant breast tissues. These genes were selected from a starting collection of about 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array. The "average" breast cancer level was set to the 90th percentile value amongst breast cancer specimens. The "average" normal adult tissue level was set to the 75th percentile value amongst non-malignant adult tissues. Certain predicted protein domains are noted.

Table 5A lists about 231 genes up-regulated in breast cancer compared to normal adult tissues and to non-malignant breast tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected similarly as for Table 1. The "average" breast cancer level was set to the 90th percentile value amongst breast cancer specimens. The "average" normal adult tissue level was set to the 50th percentile value amongst non-malignant adult tissues. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

TABLE 4A: ABOUT 425 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES

75	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar accession number, GenBank accession number
	UniGeneID:	Unigene number
	Pred.ProtdDomains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; =N, less likely to contain. All other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
80	UniGene Title:	Unigene gene title
	R1:	Ratio of 90th percentile of tumor to 75th percentile of normal body tissue

Pkey	ExAccn	UniGeneID	Pred.ProtdDomains	UniGeneTitle	R1
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5	419551	AW582256	Hs.91011	TM=M;SS=M	anterior gradient 2 (Xenopus laevis)	9.7
	426174	AA547959	Hs.115838		Homo sapiens similar to Echinoidin	7.0
	409340	BE174629	Hs.321130	aa_permeases,pyridoxal_de	melanophilin (MLPH), mRNA	6.8
	428471	X57348	Hs.184510	14-3-3;TM=M;SS=N	stratfin	6.4
	417931	W95842	Hs.82961	trefoil;TM=N;SS=M	trefoil factor 3 (intestinal)	6.3
	447966	AA340605	Hs.105887	Jacalin;TM=N;SS=M	ESTs, Weakly similar to Homolog of	6.1
	406387				Target Exon	6.0
10	421814	L12350	Hs.108623	EGF,asp_1,vwc,TSPN,isp_3;	thrombospondin 2	5.8
	406867	AA157857	Hs.182265	filament,bZIP;TM=N;SS=M	keratin 19	5.8
	426104	A204418	Hs.190080		ESTs	5.8
	421481	AW391972	Hs.104636	TM=M;SS=M	KAA1324 protein	5.8
	422511	AU076442	Hs.117938	Collagen,none	collagen, type XVII, alpha 1	5.7
15	426539	AB011155	Hs.170290	SH3,PDZ,Guanylate_kin;TM=	discs, large (Drosophila) homolog 5	5.6
	419693	AA133749	Hs.301350	ATP1G1_PLM_MAT8;TM=Y;SS=M	FXD domain-containing ion transpor	5.5
	419329	AY007220	Hs.288998	S_100;TM=M;SS=N	S100-type calcium binding protein A	5.4
	418344	AA216387			glnz18b02.s1 NCL CGAP_Pr1 Homo sap	5.2
	407116	AA130986	Hs.271627		ESTs	5.1
20	417389	BE250964	Hs.82045	PTN_MK;TM=M;SS=Y	midkine (neurite growth-promoting f	5.1
	419452	U33635	Hs.90572	ig,pkinase;TM=Y;SS=M	PTK7 protein tyrosine kinase 7	5.1
	421552	AF026692	Hs.105700	Fz,NTR;TM=N;SS=M	secreted frizzled-related protein 4	5.1
	409453	A0885516	Hs.95612	cadherin,cadherin,Cadheri	ESTs	5.1
	409632	W74001	Hs.55279	serpin;TM=N;SS=N	serine (or cysteine) proteinase inh	5.1
25	417515	L24203	Hs.82237	zf-B_box,zf-UBR1;TM=M;SS=	ataxia-telangiectasia group D-assoc	5.0
	411573	AB029000	Hs.70823	Sulfatase;TM=M;SS=N	KAA1077 protein	5.0
	418751	BE389014	Hs.372548	SH2,none	phosphoinositide-3-kinase, regulato	5.0
	422087	X58968	Hs.111301	fn2,hemopexin,Peptidase_M	matrix metalloproteinase 2 (gelatin	5.0
	421143	AB024536	Hs.102171	ig,LRR,LRRNT,LRRCT;TM=M;S	immunoglobulin superfamily containi	4.9
30	408491	A088063	Hs.7882		ESTs	4.9
	417944	AU077196	Hs.82985	vwc,Collagen,COLFI;TM=N;S	collagen, type V, alpha 2	4.9
	409062	AL157488	Hs.50150		Homo sapiens mRNA; cDNA DKFZp564B18	4.9
	422281	M36803	Hs.346935	hemopexin;TM=N;SS=M	hemopexin	4.9
	425308	M97639	Hs.155585	ig,kringle,pkinase,Fz;TM=	receptor tyrosine kinase-like orpha	4.8
35	408349	BE546947	Hs.44276	homeobox;TM=M;SS=N	homeo box C10	4.8
	449019	AB949095	Hs.67776		ESTs, Weakly similar to T22341 hypo	4.8
	435561	AA351978	Hs.4943	MAGE,Cys_kno,EGF,laminin	hepatocellular carcinoma associated	4.8
	410687	U24389	Hs.65436	Lysyl oxidase;TM=N;SS=M	lysyl oxidase-like 1	4.8
	429455	AW72111	Hs.278694	lectin_c	CD209 antigen	4.8
40	414407	AA147026	Hs.76704		ESTs	4.8
	419390	A1701162	Hs.331904	PMP22_Claudin,PMP22_Claud	hypothetical protein MGC11138	4.7
	453902	BE502341	Hs.3402		ESTs	4.7
	411089	AA456454	Hs.355702		cell division cycle 2-like 1 (PITSL	4.7
	450172	NM_005864	Hs.24587	SH3,hormone3;TM=M;SS=N	signal transduction protein (SH3 co	4.7
45	449717	AB040935	Hs.23954	Glyco_transf_25;TM=N;SS=N	cerebral cell adhesion molecule	4.6
	451529	A0917901	Hs.208641	actin,none	ESTs	4.6
	435370	A1964074	Hs.225838	EGF,fn3,fibrinogen_C,toxi	ESTs	4.6
	411761	A1733848	Hs.71935	zf-C2H2;TM=M;SS=N	putative zinc finger protein from E	4.6
	424223	A1243706	Hs.143323	PHD,ARID,jmC,jmN,zf-C5H	putative DNA/chromatin binding moti	4.6
50	426935	NM_000088	Hs.172928	vwc,Collagen,COLFI;TM=M;S	collagen, type I, alpha 1	4.5
	408796	AA688292	Hs.170345	hormone_rec,zf-C4	ESTs	4.5
	407230	AA157857	Hs.182265	filament,bZIP;TM=N;SS=M	keratin 19	4.4
	422830	AC007954	Hs.121371		hypothetical protein DKFZp434P0111	4.4
	447528	AB112027	Hs.76277	TB2_DP1_HVA22;TM=Y;SS=M	Homo sapiens, clone MGC:9381, mRNA,	4.4
55	430168	AW968343	Hs.145582	efhand,efhand	DKFZP43411735 protein	4.4
	423225	AA852604	Hs.125359	ig,Ribosomal_S19;TM=M;SS=	Thy-1 cell surface antigen	4.4
	414822	AA156542	Hs.72127	homeobox_HLH	ESTs	4.4
	452683	A089575	Hs.374574	homeobox,none	progesterone membrane binding prote	4.4
	444784	D12485	Hs.11951	Somatomedin_B,Endonucleas	ectonucleotide pyrophosphatase/phos	4.4
60	453857	AL080235	Hs.35861	TM=Y;SS=M	Ras-Induced senescence 1 (RUS1)	4.4
	413859	AW992356	Hs.8364	SAM_PNT,none	Homo sapiens pyruvate dehydrogenase	4.3
	440369	AW176150	Hs.132449		downstream of breast cancer antigen	4.3
	418140	BE613836	Hs.83551	TM=M;SS=M	microfibrillar-associated protein 2	4.3
	441384	AA447849	Hs.288660	7tm_3,none	retinoic acid induced 3	4.3
65	424464	R68537	Hs.17962	homeobox,none	ESTs	4.3
	423582	BE000831	Hs.23837	TGFb_propeptide,TGF-beta,	Homo sapiens cDNA FLJ11812 fis, clo	4.3
	432562	BE531048	Hs.278422	zf-C2H2;TM=M;SS=N	DKFZP586G1122 protein	4.2
	433320	D60647	Hs.250879	rm	ESTs, Highly similar to CTXN RAT CO	4.2
	429165	AW009886	Hs.118258		prostate cancer associated protein	4.2
70	416984	H38765	Hs.80706	Flavodoxin_2;TM=M;SS=N	diaphorase (NADH/NADPH) (cytochrome	4.2
	448913	AA194422	Hs.22564	rm,zf-RanBP,pkinase,GST_-	myosin VI	4.2
	430154	AW583058	Hs.234726	serpin;TM=M;SS=M	serine (or cysteine) proteinase inh	4.2
	400496			TM=Y;SS=N	ENSP0000024716-GTP-binding protei	4.2
	442599	AF078037	Hs.324051	SH3,ank;TM=M;SS=N	RelA-associated inhibitor	4.2
75	448520	AB002367	Hs.21355	pkinase,DCX;TM=M;SS=N	doublecortin and CaM kinase-like 1	4.2
	431309	AW451711	Hs.313760	homeobox,none	ESTs, Weakly similar to I38022 hypo	4.2
	426485	NM_006207	Hs.170040	ig;TM=N;SS=M	platelet-derived growth factor rece	4.2
	435858	AF254260	Hs.283009	bZIP;TM=M;SS=N	tufalin 1	4.2
	446051	BE048061	Hs.37054	Ephrin_A_deamin,dsrm,z-el	ephrin-A3	4.2
80	451982	F13036	Hs.27373	NA;NA	Homo sapiens mRNA; cDNA DKFZp564O17	4.2
	450334	AF035959	Hs.24879	PAP2;TM=Y;SS=M	phosphatidic acid phosphatase type	4.1
	431890	X17033	Hs.271986	vwa,Integrin_A,FG-GAP;TM=	integrin, alpha 2 (CD49B, alpha 2 s	4.1
	434449	AW953484	Hs.3849	efhand,FKBP;TM=M;SS=N	hypothetical protein FLJ22041 simil	4.1
	422699	BE410590	Hs.119257	SH3,HS1_rep;TM=M;SS=N	ems1 sequence (mammary tumor and eq	4.1

5	423057	AW961597	Hs.130816		ESTs, Moderately similar to I38022	4.1
	452063	R53185	Hs.32366	HLH;TM=M;SS=N	ESTs, Weakly similar to TWST_HUMAN	4.1
	450680	AF131784	Hs.25318	ras,none	Homo sapiens clone 25194 mRNA seque	4.1
	418283	S79895	Hs.83942	Peptidase_C1;TM=N;SS=M	cathepsin K (pseudosclerosis)	4.1
	416361	AW204907	Hs.6872		ESTs, Weakly similar to CA13_HUMAN	4.1
	426255	BE262530	Hs.2006	GST_C,GST_N;TM=M;SS=N	glutathione S-transferase M3 (brain	4.1
	408113	T82427	Hs.194101	7tm_3,none	Homo sapiens cDNA: FLJ20869 fis, cl	4.1
	407792	AI077715	Hs.39384	TM=M;SS=Y	putative secreted ligand homologous	4.1
10	422765	AW409701	Hs.1578	BLR;TM=M;SS=N	baculoviral IAP repeat-containing 5	4.1
	429359	W00482	Hs.2399	hemopexin,Peptidase_M10;T	matrix metalloproteinase 14 (membra	4.1
	442572	AI001922	Hs.135121	HSP70	hypothetical protein FLJ22415	4.0
	448826	AI580252	Hs.255565		ESTs, Weakly similar to putative p1	4.0
	419648	T73661	Hs.91877	TM=N;SS=M	thyroid hormone responsive SPOT14 (4.0
	421485	AA243499	Hs.104800	TM=Y;SS=M	hypothetical protein FLJ10134	4.0
15	440273	AI805392	Hs.325335		Homo sapiens cDNA: FLJ23523 fis, cl	4.0
	417363	AW129357	Hs.329700		ESTs	4.0
	451277	AK001123	Hs.26176	TM=Y;SS=M	hypothetical protein FLJ10261	4.0
	421823	N40850	Hs.28625		ESTs	4.0
20	452239	AW379378	Hs.356289		protein tyrosine phosphatase, recep	4.0
	444286	AI625304	Hs.201008		ESTs	4.0
	451541	BE279383	Hs.26557	Armadillo_seg;TM=M;SS=N	plakophilin 3	4.0
	451304	M92642	Hs.26208	Collagen,TSPN;TM=M;SS=M	collagen, type XVI, alpha 1	4.0
	429556	AW139399	Hs.314807	TM=M;SS=N	ESTs	4.0
25	441094	U33819	Hs.7647	zf-C2H2,LIM,PHD,TFIIS;TM=	MYC-associated zinc finger protein	4.0
	407788	BE514982	Hs.38991	efhand,S_100,S_100,efhand	S100 calcium-binding protein A2	4.0
	451292	AB037716	Hs.26204	SH3;TM=M;SS=N	KIAA1295 protein	3.9
	437762	T78028	Hs.154679	C2,none	synaptotagmin I	3.9
	433399	N46406	Hs.84700	START;TM=M;SS=N	similar to phosphatidylcholine tran	3.9
30	408056	AA312329	Hs.42331	Ephrin;TM=M;SS=M	ephrin-A4	3.9
	404578	AF183810	Hs.26102	zf-C2H2,rubredoxin;TM=M;S	trichorhinophalangeal syndrome I gene	3.9
	443883	AA114212	Hs.9930	serpin;TM=M;SS=M	serine (or cysteine) proteinase inh	3.9
	445084	H38914	Hs.250848	TM=Y;SS=M	hypothetical protein FLJ14761	3.9
	453880	AI803166	Hs.135121	HSP70,none	ESTs, Weakly similar to I38022 hypo	3.9
35	424125	M31669	Hs.1735	TGF-beta,TGFb_propeptide;	inhibin, beta B (activin AB beta po	3.9
	437377	AL359573	Hs.124940	ras;TM=M;SS=N	GTP-binding protein	3.9
	422562	AI952060	Hs.118397	Zn_carbOpept,F5_F8_type_C	AE-binding protein 1	3.9
	422320	AI745249	Hs.23650	TM=Y;SS=N	ESTs, Weakly similar to AAB47496 NG	3.9
	433078	AW015188	Hs.121575	asp	Homo sapiens cDNA FLJ12231 fis, clo	3.9
40	411894	M57609	Hs.72916	zf-C2H2;TM=N;SS=M	GLI-Kruppel family member GLI3 (Gre	3.9
	425976	C75094	Hs.334514	voltage_CLC;TM=Y;SS=M	NG22 protein	3.9
	418113	AI272141	Hs.83484	HMG_box,homeobox;TM=M;SS=	SRY (sex determining region Y)-box	3.9
	418753	BE217818	Hs.87016		hypothetical protein FLJ22938	3.8
	452679	Z42387	Hs.83883	TM=Y;SS=M	transmembrane, prostate androgen in	3.8
45	421030	AW161357	Hs.101174	tubulin-binding;TM=N;SS=M	microtubule-associated protein tau	3.8
	431567	N51357	Hs.260855	TM=M;SS=N	Homo sapiens cDNA: FLJ21410 fis, cl	3.8
	426363	M58524	Hs.2025	TGF-beta,TGFb_propeptide;	transforming growth factor, beta 3	3.8
	447151	AI022813	Hs.92679	kinesin;TM=M;SS=M	Homo sapiens clone CDABP0014 mRNA s	3.8
	448717	R67419	Hs.21851	HLH,homeobox,none	Homo sapiens cDNA FLJ12900 fis, clo	3.8
50	425867	D60385	Hs.12079	cadherin;TM=Y;SS=M	calsyntenin-2	3.8
	423940	NM_012429	Hs.277728	CRAL_TRIC;TM=M;SS=N	SEC14 (S. cerevisiae)-like 2	3.8
	426742	AA383828	Hs.181131		ESTs	3.8
	435818	AA700553	Hs.368614	arf,ras,RecR,none	ESTs	3.8
55	420005	AW271106	Hs.133294		ESTs	3.8
	410867	X63556	Hs.750	EGF,TB,wnt,EB,TIL;TM=N;SS	fibrillin 1 (Marfan syndrome)	3.8
	402531	AB037745	Hs.104696	TM=M;SS=M	KIAA1324 protein	3.8
	449029	N28989	Hs.22891	aa_permeases;TM=Y;SS=M	solute carrier family 7 (cationic a	3.8
	424806	AA382523	Hs.105689	TM=Y;SS=N	MSTP031 protein	3.8
60	443933	AI091631	Hs.203845	lon_trans;TM=Y;SS=M	two pore potassium channel KT3.3	3.8
	432952	AA813887	Hs.188173		Homo sapiens cDNA FLJ12187 fis, clo	3.8
	424036	AA770688	Hs.348495	histone,CBFD_NFYB_HMF;TM=	H2A histone family, member L	3.7
	453828	AW970960	Hs.293821	Pep_M12B_propep.Reprolysi	ESTs	3.7
	407112	AA070801	Hs.51615	hormone_rec,zf-C4	ESTs, Weakly similar to ALU7_HUMAN	3.7
	445669	AI570830	Hs.174870		ESTs	3.7
65	446091	AW022192	Hs.200197	homeobox,none	ESTs	3.7
	424651	AI493206	Hs.120785		ESTs	3.7
	409178	BE393948	Hs.50915	trypsin;TM=M;SS=Y	kallikrein 5	3.7
	417059	AL037672	Hs.81071	TM=N;SS=Y	extracellular matrix protein 1	3.7
70	431194	D43704	Hs.250712	Ca_channel_LB,RepB_protein	calcium channel, voltage-dependent,	3.7
	430397	AI924533	Hs.105607	HCO3_cotransp;TM=Y;SS=N	bicarbonate transporter related pro	3.7
	418969	W33191	Hs.28907	SH3;TM=M;SS=N	hypothetical protein FLJ20258	3.7
	427378	BE515037	Hs.177556	MAGE;TM=M;SS=N	melanoma antigen, family D, 1	3.7
	424012	AW368377	Hs.137569	SAM,P53;TM=M;SS=N	tumor protein 63 kDa with strong ho	3.7
	418840	AI821614	Hs.185831		ESTs	3.7
75	433573	AF234887	Hs.57652	7tm_2,EGF,cadherin,lamini	cadherin, EGF LAG seven-pass G-type	3.7
	433430	AI863735	Hs.369982	thyroglobulin_1,GFDP,zf-	ESTs	3.7
	422491	AA338548	Hs.117546	TM=M;SS=Y	neuronatin	3.7
	435114	AA775483	Hs.288936	ODC_AZ,Ribosomal_L9_N;TM=	mitochondrial ribosomal protein L9	3.7
	416899	BE262645	Hs.80420	IL8;TM=M;SS=M	small inducible cytokine subfamily	3.7
	422110	AI376736	Hs.121555	kazal,none	secreted protein, acidic, cysteine-	3.7
80	448560	BE613183	Hs.23213	zf-RanBP,MDM2,Ndr	ESTs	3.6
	414945	BE076358	Hs.77667	UPAR_LY6;TM=M;SS=M	lymphocyte antigen 6 complex, locus	3.6
	422119	AI277829	Hs.111862	WD40;TM=M;SS=N	KIAA0590 gene product	3.6
	447335	BE617695	Hs.286192	TM=M;SS=N	hypothetical protein FLJ20940	3.6

5	450663	H43540	Hs.25292	RNase_HII;TM=N;SS=M	ribonuclease H1, large subunit	3.6
	417387	AW021102	Hs.21509	zf-C2H2:none	ESTs	3.6
	450825	AC005954	Hs.25527	POZ,Guanylate_kdn;TM=N;SS	light junction protein 3 (zona ocl	3.6
	439755	AW748482	Hs.77783	lg;TM=Y;SS=M	B7 homolog 3	3.6
	439873	BE159253	Hs.300638		ESTs	3.6
	439039	A1656707	Hs.48713	pklnase:none	ESTs	3.6
	419235	AW470411	Hs.288433		neurotmin	3.6
	445033	AV652402	Hs.72901	ank;TM=N;SS=N	cyclin-dependent kinase inhibitor 2	3.6
10	404394	AF332975	Hs.307004	EGF,fn1,vwc,vwd,MAM,Kerat	Zonadhesin	3.6
	452222	AW806287	Hs.21432	Sema,TIG,PSI,GDI	SEX gene	3.6
	422961	Y13620	Hs.122607	TM=M;SS=N	B-cell CLL/lymphoma 9	3.6
	420988	AW006352	Hs.159643		ESTs, Weakly similar to T32554 hypo	3.6
	439680	AW245741	Hs.58461	zf-C2H2,TFIIS,KRAB;TM=M;S	ESTs, Weakly similar to A35659 krue	3.6
15	426815	D59505	Hs.351344	lg,SET,PHD,zf-CXXC,Adap_c	ESTs, Weakly similar to K1C1_HUMAN	3.6
	437446	AA788946	Hs.101302	tn3,vwa,Collagen,TSPN;TM=	ESTs, Moderately similar to CA1C RA	3.6
	421690	AW162667	Hs.106857	ethand;TM=M;SS=N	calbindin 2, (29kD, calretinin)	3.5
	453939	AA418160	Hs.86043		Homo sapiens cDNA FLJ13558 fis, clo	3.5
20	426158	NM_001082	Hs.199057	Furin-like,ptknase,Recep_	v-erb-b2 avian erythroblastic leuko	3.5
	439246	AA98072	Hs.351474	ank,ptknase,UPF0073;TM=N;	membrane-associated tyrosine- and t	3.5
	410653	BE383768	Hs.65238	zf-C3HC4,Alp3;TM=M;SS=N	85 kDa retinoblastoma protein bindi	3.5
	412703	AW984744			gb:RC1-HN0015-040400-011-d03 HN0015	3.5
	427871	AW992405	Hs.352406	TM=M;SS=N	Homo sapiens, clone IMAGE:3507281,	3.5
	444273	AW93474	Hs.230	LRR,LRRNT;TM=M;SS=M	fibromodulin	3.5
25	434936	A1285970	Hs.183817	UCH-2	ESTs	3.5
	457869	AU077186	Hs.108885	vwa,Collagen;TM=M;SS=M	Homo sapiens, alpha-1 (VI) collagen	3.5
	422575	AK000546	Hs.118552	PTR2;TM=Y;SS=M	hypothetical protein FLJ20539	3.5
	428343	ALD43021	Hs.12705	WD40;TM=N;SS=M	ESTs	3.5
	426716	NM_006379	Hs.171921	lg,Sema,PSI;TM=N;SS=M	sema domain, immunoglobulin domain	3.5
30	423778	Y09267	Hs.132821	FMO-like,pyr_redox;TM=Y;S	flavin containing monooxygenase 2	3.5
	451558	NM_001089	Hs.26630	ABC_tran,SRP54;TM=Y;SS=M	ATP-binding cassette, sub-family A	3.5
	407926	AW956382	Hs.59771	TYA;TM=N;SS=M	ESTs	3.5
	447041	AL135480	Hs.250705		Homo sapiens cDNA FLJ11685 fis, clo	3.5
35	419073	AW372170	Hs.183918	death,ZU5;TM=N;SS=M	Homo sapiens cDNA FLJ12797 fis, clo	3.5
	446945	A1193115	Hs.16611	TM=M;SS=N	tumor protein D52-like 1	3.5
	416322	BE019494	Hs.79217	P5CR,NAD_Gly3P_dh,Octoplin	pyrroline-5-carboxylate reductase 1	3.5
	447347	AA570056	Hs.122730	NA;NA	ESTs, Moderately similar to KIAA121	3.5
	448984	AW751955	Hs.22753	TM=M;SS=N	hypothetical protein FLJ22318	3.5
40	421778	AA428000	Hs.283072	NA;NA	actin related protein 2/3 complex,	3.5
	423353	BE544348	Hs.127562	homeobox;TM=M;SS=N	homeo box C11	3.5
	432545	X52486	Hs.3041	cyclin:none	uracil-DNA glycosylase 2	3.5
	408495	W68796	Hs.237731		ESTs	3.5
	406851	AA609784	Hs.352392	lg,MHC_IL_beta;TM=M;SS=Y	major histocompatibility complex, c	3.5
45	418736	T18979	Hs.87908	helicase_C,AT_hook,SNF2_N	Snf2-related CBP activator protein	3.4
	410197	NM_005518	Hs.59889	HMG_CoA_synth;TM=N;SS=N	3-hydroxy-3-methylglutaryl-Coenzyme	3.4
	453597	BE281130	Hs.33713	KH-domain,Ribosomal_S3_C,	myo-inositol 1-phosphate synthase A	3.4
	417259	AW903838	Hs.81800	EGF,lg,lectin_c,sushi,Xli	chondroitin sulfate proteoglycan 2	3.4
	453985	N44545	Hs.251865	PH1:none	ESTs	3.4
	412634	U55984	Hs.356531		heat shock 90kD protein 1, alpha	3.4
50	407204	R41933	Hs.140237	histone,histone	ESTs, Weakly similar to ALU1_HUMAN	3.4
	444371	BE540274	Hs.239	Fork_head;TM=M;SS=N	forkhead box M1	3.4
	447334	AA515032	Hs.91109		ESTs	3.4
	426530	U24578	Hs.278625	A2M,NTR,ANATO,A2M_N,preny	complement component 4A	3.4
55	419749	X73608	Hs.93029	kazal,thyroglobulin_1;TM=	sparc/osteonectin, cwcr and kazal-I	3.4
	423595	R82826	Hs.220702	homeobox:none	ESTs	3.4
	406673	M34996	Hs.198253	lg,MHC_IL_alpha;TM=M;SS=M	major histocompatibility complex, c	3.4
	434241	AF119913		TM=N;SS=M	Homo sapiens PRO3077 mRNA, complete	3.4
60	412490	AW803564	Hs.288850		Homo sapiens cDNA: FLJ22528 fis, cl	3.4
	452277	AL049013	Hs.28783	ank;TM=M;SS=N	KIAA1223 protein	3.4
	431457	NM_012211	Hs.256297	FG-GAP,vwa;TM=Y;SS=M	Integrin, alpha 11	3.4
	421777	BE562088	Hs.108196	TM=M;SS=N	HSPC037 protein	3.4
	453082	H18835	Hs.31608	lon_trans;TM=Y;SS=M	hypothetical protein FLJ20041	3.4
	414085	AA114016	Hs.75746	aldehyd;TM=N;SS=M	aldehyde dehydrogenase 1 family, me	3.4
65	440300	N39760	Hs.8859	TM=M;SS=N	Homo sapiens, Similar to RIKEN cDNA	3.4
	400290	H18836	Hs.31608	Cys_knot	hypothetical protein FLJ20041	3.4
	433339	AF019226	Hs.8036	ras,ank;TM=M;SS=N	glioblastoma overexpressed	3.4
	419301	AA236166	Hs.132957	TM=Y;SS=M	tenomodulin protein	3.4
	414792	BE314949	Hs.87128	TM=Y;SS=M	hypothetical protein FLJ23309	3.4
70	451428	AW083384	Hs.11067		ESTs, Highly similar to T46395 hypo	3.4
	432210	A1667421	Hs.273330	EGF,kazal,laminin_EGF,lam	Homo sapiens, clone IMAGE:3544662,	3.4
	452242	R50956	Hs.159993		glycosyltransferase	3.4
	450676	A1147155	Hs.279727		ESTs	3.4
	413014	AW250533	Hs.75139	TM=M;SS=N	partner of RAC1 (arapain 2)	3.4
75	427919	AA173942	Hs.326416	CTF_NFL:none	Homo sapiens mRNA: cDNA DKFZp564H19	3.4
	424005	AB033041	Hs.137507	TM=Y;SS=N	vang (van gogh, Drosophila)-like 2	3.4
	422072	AB018255	Hs.111138	RhoGAP;TM=M;SS=N	KIAA0712 gene product	3.4
	440995	T57773	Hs.10263		ESTs	3.4
80	426150	NM_003658	Hs.167218	homeobox;TM=N;SS=M	BarH-like homeobox 2	3.3
	416877	BE386266	Hs.85658	zf-C2H2;TM=M;SS=N	hypothetical protein FLJ23436	3.3
	452191	AU076408	Hs.28309	UDPG_MGDP_dh,UDPG_MGDP_dh	UDP-glucose dehydrogenase	3.3
	450273	AW296454	Hs.24743	rtm:none	hypothetical protein FLJ20171	3.3
	456177	NM_012391	Hs.79414	Ets,SAM_PNT;TM=M;SS=N	prostate epithelium-specific Ets tr	3.3
	423062	NM_003655	Hs.5637	chromo;TM=N;SS=M	ESTs	3.3
	421848	X15880	Hs.108885	vwa,Collagen;TM=M;SS=M	collagen, type VI, alpha 1	3.3

5	433577	AW007080	Hs.284192		ESTs	3.3
	409636	AA305729	Hs.18272	Aa_trans;TM=Y;SS=N	amino acid transporter system A1	3.3
	404730	AA486704	Hs.33287	CTF_NFL:none	Nuclear factor I/B	3.3
	422940	BE077458		Sec7,PH,ANF_receptor,lig_	gb:RC1-BT0606-090500-015-b04 BT0606	3.3
	410001	AB041036	Hs.57771	trypsin;TM=M;SS=M	kalikrein 11	3.3
10	427461	AA531527	Hs.332040	TM=Y;SS=M	hypothetical protein MGC13010	3.3
	453468	W00712	Hs.32990	TM=M;SS=N	DKFZP566F084 protein	3.3
	443807	W52930	Hs.9822	HAT;TM=N;SS=M	HCNP protein; XPA-binding protein 2	3.3
	456034	AW450979			gb:UI-H-B13-ala-a-12-0-UI.s1 NCI_CG	3.3
	424307	AW293399	Hs.356377		nuclear receptor co-repressor 1	3.3
15	412755	BE144306	Hs.179891		ESTs, Weakly similar to P4HA_HUMAN	3.3
	429690	AW956329	Hs.23721	sugar_tr,Ribosomal_S25	ESTs	3.3
	423472	AF041260	Hs.129057	TM=M;SS=N	breast carcinoma amplified sequence	3.3
	424118	BE269041	Hs.140452	penilipin;TM=N;SS=M	cargo selection protein (mannose 6	3.3
	437275	AW976035	Hs.292396	Frizzled,Fz	ESTs, Weakly similar to A47582 B-ca	3.3
20	437464	AA323286	Hs.97837		Homo sapiens mRNA; cDNA DKFZp547J04	3.3
	433592	NM_004642	Hs.3436	TM=M;SS=N	deleted in oral cancer (mouse, homo	3.3
	434931	AW968941	Hs.166254		hypothetical protein DKFZp5661133	3.3
	451691	AI808278	Hs.208152	C2	ESTs	3.3
	430433	AA478883	Hs.273766	WW:none	ESTs	3.3
25	429343	AK000785	Hs.199480	VHS,ENTH,UIM;TM=N;SS=M	Homo sapiens, Similar to epsin 3, c	3.3
	450835	BE262773	Hs.25584	ArtGap;TM=N;SS=M	hypothetical protein FLJ10767	3.3
	414591	AI888490	Hs.248107		ESTs, Weakly similar to ALU8_HUMAN	3.3
	452579	AA131657	Hs.23830	CN_hydrolase	ESTs	3.3
	409960	BE261944	Hs.355264		hexokinase 1	3.3
30	406850	AI624300	Hs.172928	wvc,Collagen,COLFI;TM=M;S	collagen, type I, alpha 1	3.2
	453874	AW591783	Hs.36131	homeobox:none	collagen, type XIV, alpha 1 (unduli	3.2
	425964	AW889928	Hs.9071		progesterone membrane binding prote	3.2
	428412	AA428240	Hs.126083		ESTs	3.2
	430316	NM_000875	Hs.239176	fn3,Furin-like,pkinase,Re	Insulin-like growth factor 1 recept	3.2
35	440087	W28969	Hs.7718	KOW,Ribosomal_S4e,S4,rm;	hypothetical protein FLJ22678	3.2
	449933	AW157098	Hs.324104	DUF176;efhand;TM=M;SS=N	Human DNA sequence from clone RP1-6	3.2
	441128	AA570256	Hs.348504	TM=Y;SS=M	ESTs, Weakly similar to T23273 hypo	3.2
	434182	W20309	Hs.8107	G-gamma;TM=M;SS=N	G-protein gamma-12 subunit	3.2
	422737	M26939	Hs.119571	Collagen,COLFI;TM=N;SS=M	collagen, type III, alpha 1 (Ehlers	3.2
40	408202	AA227710	Hs.43658	OLF;TM=M;SS=N	DKFZP586L151 protein	3.2
	424971	AA479005	Hs.154036	PH;TM=M;SS=N	tumor suppressing subtransferable c	3.2
	407869	AI827976	Hs.24391	efhand;TM=M;SS=N	hypothetical protein FLJ13612	3.2
	444734	NM_001360	Hs.11806	ERG4_ERG24;TM=Y;SS=M	7-dehydrocholesterol reductase	3.2
	426991	AK001536	Hs.214410		Homo sapiens cDNA FLJ10674 fis, clo	3.2
45	414081	AW959976	Hs.365706	glr;TM=N;SS=Y	matrix Gla protein	3.2
	408795	AW749126	Hs.170345	hormone_rec,zf-C4	hypothetical protein FLJ13710	3.2
	452345	AA293279	Hs.29173	DSPc;TM=M;SS=N	hypothetical protein FLJ20515	3.2
	437879	BE262082	Hs.5894	TM=N;SS=N	hypothetical protein FLJ10305	3.2
	407872	AB039723	Hs.40735	Fz,Frizzled,7tm_2,DUF81;T	frizzled (Drosophila) homolog 3	3.2
50	427289	AI097346	Hs.323878	aminotran_5,SDF:none	phosphoserine aminotransferase	3.2
	432375	BE536069	Hs.2962	efhand,S_100;TM=N;SS=M	S100 calcium-binding protein P	3.2
	429415	NM_002593	Hs.202097	CUB,NTR;TM=N;SS=M	procollagen C-endopeptidase enhance	3.2
	412774	AA120865	Hs.380149	hormone_rec,zf-C4	ESTs	3.2
	445942	T80334	Hs.13479	TM=M;SS=N	hypothetical protein FLJ20847	3.2
55	439456	AI752409	Hs.109314	zf-C2H2;TM=N;SS=M	hypothetical protein FLJ20980	3.2
	414774	X02419	Hs.77274	kringle,trypsin,plant_thi	plasminogen activator, urokinase	3.2
	433336	AF017886	Hs.31386	Fz,NTR;TM=N;SS=M	secreted frizzled-related protein 2	3.2
	439505	AW799755	Hs.110953	HLH;TM=M;SS=N	retinoic acid induced 1	3.2
	420251	AW374968	Hs.379829		Human DNA sequence from clone RP5-1	3.2
60	413004	T35901	Hs.75117	TM=M;SS=N	Interleukin enhancer binding factor	3.2
	418686	Z36830	Hs.87268	annexin;TM=M;SS=N	annexin A8	3.2
	410279	BE271977	Hs.61809	ras;TM=M;SS=N	hypothetical protein FLJ14117	3.2
	424391	BE550112	Hs.158549		ESTs, Weakly similar to T2D3_HUMAN	3.2
	440409	AW294316	Hs.125608	thioered	ESTs	3.2
65	452689	F33868	Hs.284176	transferrin,KH-domain,rm	transferrin	3.2
	418154	BE165866	Hs.352403	hormone_rec,zf-C4:none	nuclear receptor subfamily 1, group	3.2
	434384	AA631910	Hs.370133		ESTs	3.2
	413436	AF238083	Hs.68061	DAGKc;TM=M;SS=N	sphingosine kinase 1	3.2
	431663	NM_016569	Hs.267182	T-box;TM=M;SS=N	TBX3-Iso protein	3.2
70	432874	W94322	Hs.279651	SH3;TM=M;SS=Y	melanoma inhibitory activity	3.2
	436252	AI539519	Hs.142827		Homo sapiens cDNA FLJ11562 fis, clo	3.2
	421044	AF061871	Hs.101302	fn3,vwa,Collagen,TSPN;TM=	Human DNA sequence from clone RP1-2	3.2
	419102	AA234098	Hs.42424		ESTs, Weakly similar to 2004399A ch	3.2
	419359	AL043202	Hs.90073	CAS_CSE1;TM=M;SS=N	chromosome segregation 1 (yeast hom	3.1
75	441859	AW194364	Hs.9877	Amino_oxidase,FAD_binding	interleukin-4 induced gene-1 protol	3.1
	426418	M90464	Hs.169825	Collagen,C4,VPR;TM=N;SS=M	collagen, type IV, alpha 5 (Alport	3.1
	413076	U10564	Hs.75188	pkinase;TM=M;SS=N	wee1 (S. pombe) homolog	3.1
	407874	AI766311	Hs.289047	COQ7	Homo sapiens cDNA FLJ14059 fis, clo	3.1
	448019	AW947164	Hs.195641		ESTs, Moderately similar to I38022	3.1
80	427024	AA397572	Hs.348902		chromosome 11 open reading frame 14	3.1
	410281	AF076612	Hs.166186	wvc,W2,MA3,MIF4G	Homo sapiens cDNA 23928 mRNA seque	3.1
	447205	BE617015	Hs.11006	LEA,penilipin;TM=M;SS=N	ESTs, Moderately similar to T17372	3.1
	434433	AW629759			gb:hh70e05.y1 NCI_CGAP_GUI Homo sap	3.1
	439737	AI751438	Hs.41271	C1q,Collagen:none	Homo sapiens mRNA full length inser	3.1
	450157	AW961576	Hs.60178	PH,Band_41,RhoGEF:none	ESTs	3.1
	445989	H97754	Hs.11108		ESTs	3.1
	442213	N36110	Hs.305971	sugar_tr;TM=Y;SS=M	solute carrier family 2 (facilitate	3.1

	402496			Target Exon	3.1
	438974	AF089816	Hs.6454	chromosome 19 open reading frame 3	3.1
	439335	AA742697	Hs.62492	NM_052863:Homo sapiens secretoglobi	3.1
5	412276	BE262621	Hs.73798	macrophage migration inhibitory fac	3.1
	416950	AL049798	Hs.80552	dermatopontin	3.1
	456157	AW979153	Hs.336881	ESTs	3.1
	452753	AA028049	Hs.277728	CRAL_TRIO,none	3.1
	414420	AA043424	Hs.76095	TM=M;SS=N	3.1
10	446229	A1744964	Hs.14449	TM=M;SS=N	3.1
	453143	AA382234	Hs.356289	serpin;TM=N;SS=M	3.1
	411441	AL042355	Hs.70202	WD40;TM=M;SS=N	3.1
	422921	BE082045	Hs.351625	AAA,hormone_rec,zf-C4	3.1
	444441	AW613841	Hs.301394	IRK;TM=Y;SS=N	3.1
15	436729	BE621807	Hs.351316	TM=Y;SS=M	3.1
	427890	AA435761	Hs.373623	RFX_DNA_binding,none	3.1
	444838	AV651680	Hs.208558	Integrin_A,FG-GAP,none	3.1
	427876	AI494291	Hs.369171	ESTs	3.1
	413040	AA193338	Hs.12321	Na,Ca_Ex;TM=Y;SS=M	3.1
20	427515	T79526	Hs.179516	EMP24_GP2SL;TM=Y;SS=M	3.1
	451092	AL207256	Hs.13766	filament;TM=N;SS=N	3.1
	442222	AI061301	Hs.164773	trypsin,kringle,UPAR_LY6	3.1
	452613	AA461599	Hs.23459	ESTs	3.1
	447191	NM_014521	Hs.17667	SH3;TM=M;SS=N	3.1
25	412890	T85247	Hs.351875	COX6C;TM=M;SS=M	3.1
	418313	BE244231	Hs.84038	TM=Y;SS=N	3.1
	440006	AK000517	Hs.6844	AAA,NB-ARC,PAAD_DAPIN;NA;	3.1
	434042	AI589941	Hs.8254		3.1
	420576	AA297634	Hs.54925		3.1
30	432269	NM_002447	Hs.2842	pkinase,Sema,PSI,TIG,A4_E	3.1
	424927	AW973666	Hs.153850		3.1
	440100	BE382685	Hs.158549		3.1
	452408	AA306477	Hs.29379	TM=M;SS=N	3.1
	441362	BE614410	Hs.23044	TM=N;SS=N	3.1
35	418444	AI902899	Hs.85155	zf-CCCH;TM=M;SS=N	3.1
	423464	NM_016240	Hs.128856	Collagen;TM=Y;SS=N	3.1
	424604	AW865388	Hs.151076	TM=M;SS=N	3.1
	420059	AF161486	Hs.94769	ras,none	3.1
	453271	AA903424	Hs.6786	LIM;TM=M;SS=N	3.1
40	411274	NM_002776	Hs.69423	trypsin;TM=M;SS=N	3.1
	434095	AA011117	Hs.3745	EGF,F5_F8_type_C;TM=N;SS=	3.1
	403439			ank;TM=M;SS=N	3.1
	413244	AW955951	Hs.159265	8TB,Pep_M12B_propep,Repro	3.1
45	411756	BE294350	Hs.71891	pkinase,F5_F8_type_C;TM=Y	3.1
	409007	AL122107	Hs.49599		3.1
	452547	AA335295	Hs.74120	LEA;TM=M;SS=N	3.1
	414359	M62194	Hs.75929	cadherin,Cadherin_C_term;	3.1
	433212	BE218049	Hs.121820		3.1
	449123	D50920	Hs.23106	TM=M;SS=N	3.1
50	431176	AI026984	Hs.293662	MCPsignal,laminin_B,lamin	3.0
	419245	AJ732742	Hs.87440	ESTs	3.0
	434493	AA635305	Hs.375591	ESTs	3.0
	449177	BE616694	Hs.288042	ESTs	3.0
	430449	AA352723	Hs.241471	hypothetical protein FLJ14299	3.0
55	452887	AI022223	Hs.107253	RNB6	3.0
	451678	AA374181	Hs.26799	hypothetical protein DKFZp761F241	3.0
	445457	AF168793	Hs.12743	DKFZP564D0764 protein	3.0
	407597	AA043925	Hs.339352	camitline O-octanoyltransferase	3.0
	431629	AJ077025	Hs.265827	Homo sapiens brother of CDO (BOC) m	3.0
60	432302	AA345857	Hs.274307	Interferon, alpha-inducible protein	3.0
	442549	AI751601	Hs.8375	KIAA1442 protein	3.0
	437959	AA472068	Hs.375604	TNF receptor-associated factor 4	3.0
	447400	AK000322	Hs.18457	KIAA1856 protein	3.0
	411734	AW374954	Hs.71779	hypothetical protein FLJ20315	3.0
65	443547	AW271273	Hs.356487	Homo sapiens DNA from chromosome 19	3.0
	417000	BE277919	Hs.306019	hypothetical protein FLJ12666	3.0
	416987	D86957	Hs.80712	ESTs, Weakly similar to ALU7_HUMAN	3.0
	424494	U78575	Hs.149255	KIAA0202 protein	3.0
	414496	W73853	Hs.355424	phosphatidylinositol-4-phosphate 5-	3.0
70	413336	AI569936	Hs.296178	ESTs	3.0
	434314	BE392921	Hs.3797	hypothetical protein FLJ22637	3.0
	401038			RAB26, member RAS oncogene family	3.0
	418245	AA088767	Hs.83883	C11000425:g14507721:ref NP_003310.	3.0
	407688	W25317	Hs.37616	transmembrane, prostate androgen in	3.0
75	456906	AF117646	Hs.156637	Human D9 splice variant 8 mRNA, com	3.0
	424744	AW175781	Hs.152720	Ces-Br-M (murine) ectropic retrovir	3.0
	452195	AA994712	Hs.116878	M-phase phosphoprotein 6	3.0
	415988	BE407713	Hs.78943	ESTs	3.0
	418399	AF131781	Hs.84753	bleomycin hydrolase	3.0
80	420568	F09247	Hs.247735	hypothetical protein FLJ12442	3.0
	404661			protocadherin alpha 10	3.0
	414152	NM_003248	Hs.75774	C9000306:xg112737260:ref XP_005682	3.0
	421307	BE539976	Hs.103305	thrombospondin 4	3.0
	444868	BE560471	Hs.12101	Homo sapiens mRNA; cDNA DKFZp434B04	3.0
				hypothetical protein	3.0

5	450214	BE439763	Hs.227571	RGS;TM=M;SS=N	regulator of G-protein signalling 4	3.0
	452664	AA398859	Hs.18397	TM=M;SS=M	hypothetical protein FLJ23221	3.0
	422105	AI929700	Hs.111680	TM=M;SS=N	endosulfine alpha	3.0
	422278	AF072873	Hs.114218	Fz,Frizzled,7tm_2;TM=Y;SS	frizzled (Drosophila) homolog 6	3.0
	434067	H18913	Hs.124023		Homo sapiens cDNA FLJ14218 fis, clo	3.0
10	412676	NM_000165	Hs.74471	connexin,Connexin43;TM=Y;	gap junction protein, alpha 1, 43kD	3.0
	426801	AA486846	Hs.271795		ESTs, Weakly similar to I38022 hypo	3.0
	421983	AI252640	Hs.110364	pro_isomerase:none	peptidylprolyl isomerase C (cycloph	3.0
	429299	AI620463	Hs.347408	TM=Y;SS=N	hypothetical protein MGC13102	3.0
	408912	AB011084	Hs.48924	Armadillo_seg;TM=M;SS=M	KIAA0512 gene product; ALEX2	3.0
	438746	AI885815	Hs.184727	transferrin,Guanylate_kin	Human melanoma-associated antigen p	3.0

TABLE 4B

15	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

20	Pkey	CAT Number	Accession
	418344	245371_1	AA216387 T63548 AA228676
	412703	1243670_1	AW984759 AW984744
	434241	63414_1	AF119913 AI207698 R57074
	422940	58443_1	BC012771 BG397153 BF366195 AA337277 AA319285 AW843252
25	456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	434433	111338_1	AA633408 AW749955 AW629759 AI651005

TABLE 4C

30	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
35	NL_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	NL_position
	406387	9256180	Plus	116229-116371,117512-117651
	400496	9743564	Plus	41515-41695
	402496	9797769	Minus	8615-9103
40	403439	9719679	Plus	91463-91632
	401038	7232177	Minus	4277-4469
	404661	9797073	Plus	33374-33675,33769-34008

TABLE 5A: ABOUT 231 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES THAT MAY ENCODE EITHER ENZYMES OR PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES, PEPTIDES, OR ANTIBODIES

	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar accession number, GenBank accession number				
50	UniGeneID:	UniGene number				
	Pred.Prot.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; =N, less likely to contain. All other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).				
	UniGene Title:	UniGene gene title				
55	R1:	Ratio of 90th percentile tumor to 50th percentile of normal body tissue				
	Pkey	ExAccn	UniGeneID	Pred.Prot.Domains	UniGeneTitle	R1
	409340	BE174629	Hs.321130	aa_permeases,pyridoxal_de	melanophilin (MLPH), mRNA	20.5
	421481	AW391972	Hs.104696	TM=M;SS=M	KIAA1324 protein	16.3
60	419693	AA133749	Hs.301350	ATP1G1_PLM_MAT8;TM=Y;SS=M	FXD domain-containing ion transpor	13.7
	417389	BE260964	Hs.82045	PTN_MK;TM=M;SS=Y	midkine (neurite growth-promoting f	13.7
	414521	D28124	Hs.76307	DAN;TM=M;SS=M	neuroblastoma, suppression of tumor (DAN)	13.7
	438091	AW373062	Hs.351546	hormone_rec,zf-C4:none	nuclear receptor subfamily 1, group	13.4
	413815	AL046341	Hs.75562	pklnase,F5_F8_type_C;TM=Y	discoilin domain receptor family, m	13.2
65	439180	AI393742	Hs.199067	Furin-like, pklnase, Recep_	v-erb-b2 avian erythroblastic leuke	13.2
	431441	U81961	Hs.2794	ASC;TM=Y;SS=N	sodium channel, nonvoltage-gated 1	12.5
	452547	AA335295	Hs.74120	LEA;TM=M;SS=N	adipose specific 2	12.4
	452239	AW379378	Hs.356289		protein tyrosine phosphatase, recep	12.1
	441384	AA447849	Hs.288660	7tm_3:none	retinoic acid induced 3	11.9
70	419223	X60111	Hs.1244	transmembrane4;TM=Y;SS=M	CD9 antigen (p24)	11.7
	413859	AW992356	Hs.8364	SAM_PNT:none	Homo sapiens pyruvate dehydrogenase	11.5
	410687	U24389	Hs.65436	Lysyl_Oxidase;TM=N;SS=M	lysyl oxidase-like 1	11.2
	422699	BE410590	Hs.119257	SH3,HS1_rep;TM=M;SS=N	ems1 sequence (mammary tumor and sq	10.1
	419452	U33635	Hs.90572	lg, pklnase;TM=Y;SS=M	PTK7 protein tyrosine kinase 7	9.9
75	427378	BE515037	Hs.177568	MAGE;TM=M;SS=N	melanoma antigen, family D, 1	9.9
	444784	D12485	Hs.11951	Somatostatin_B,Endonucleas	ectonucleotide pyrophosphatase/phos	9.9
	436972	AA284679	Hs.25640	PMP22_Claudin;TM=Y;SS=M	claudin 3	9.7
	412926	AI879076	Hs.75061	MARCKS;TM=N;SS=M	macrophage myristoylated alanine-ri	9.5
	425280	U31519	Hs.1872	PEPCK;TM=M;SS=N	phosphoenolpyruvate carboxykinase 1	9.5
80	426636	AA340864	Hs.278562	PMP22_Claudin;TM=Y;SS=M	claudin 7	9.4
	423778	Y09267	Hs.132821	FMO-like,pyr_redox;TM=Y;S	flavin containing monooxygenase 2	9.4
	424206	NM_003734	Hs.198241	Cu_amine_oxid,Cu_amine_ox	amine oxidase, copper containing 3	9.4
	444797	AB018333	Hs.12002	SH3,SAM;TM=M;SS=N	KIAA0790 protein	9.0

5	402559	AF043329	Hs.173717	PAP2;TM=Y;SS=M	PPAP2B Phosphatidic acid phosphatase type 2B	9.0
	443932	AW888222	Hs.9973	SH2,WW,PID,none	tensin	8.9
	421143	AB024536	Hs.102171	Ig.LRR,LRRT,LRRCT;TM=M;S	immunoglobulin superfamily containi	8.8
	433592	NM_004642	Hs.3436	TM=M;SS=N	deleted in oral cancer (mouse, homo	8.7
	410668	BE379794	Hs.159651	death,TNFR_c6;TM=Y;SS=M	hypothetical protein	8.7
	433662	W07162	Hs.150826	ras,ABC_tran,arf;TM=M;SS=	RAB25 RAB25, member RAS oncogene fa	8.6
	421653	AL117472	Hs.108924	SH3,Sorb;TM=M;SS=N	SH3-domain protein 5 (ponsin)	8.6
	425335	BE394327	Hs.296267	efhand,kazal,arf,ras,7tm_	folistatin-like 1	8.5
10	400290	H18836	Hs.31608	Cys_knot	hypothetical protein FLJ20041	8.5
	438089	W05391	Hs.351546	homona_rec,zf-C4,none	nuclear receptor subfamily 1, group	8.4
	426158	NM_001982	Hs.199067	Furin-like,pkinase,Recep_	v-erb-b2 avian erythroblastic leuke	8.3
	447191	NM_014521	Hs.17667	SH3;TM=M;SS=N	SH3-domain binding protein 4	8.2
	439941	AI392640	Hs.18272	Aa_trans;TM=Y;SS=N	amino acid transporter system A1	8.2
15	439318	AW837046	Hs.6527	7tm_2,CytC_asm,GPS;TM=Y;S	G protein-coupled receptor 56	8.1
	442213	N36110	Hs.305971	sugar_br;TM=Y;SS=M	solute carrier family 2 (facilitate	8.1
	412649	NM_002206	Hs.74369	Integrin_A,FG-GAP;TM=M;SS	Integrin, alpha 7	8.1
	448913	AA194422	Hs.22564	rm,zf-RanBP,pkinase,GST_	myosin VI	8.1
	420166	AW732276	Hs.95583	transmembrane4;TM=Y;SS=M	transmembrane 4 superfamily member	8.0
20	407102	AA007629	Hs.348601	transport_prot,SWIB,ASC	glycerol-3-phosphate dehydrogenase	7.9
	452516	AA058630	Hs.29759	TM=N;SS=M	RNA POLYMERASE I AND TRANSCRIPT REL	7.9
	413076	U10564	Hs.75188	pkinase;TM=M;SS=N	wee1 (S. pombe) homolog	7.9
	443604	C03577	Hs.9615	efhand;TM=M;SS=N	myosin regulatory light chain 2, sm	7.7
	429002	AW248439	Hs.2340	Armadillo_seg;TM=M;SS=N	junction plakoglobin	7.6
25	432562	BE531048	Hs.278422	zf-C2H2;TM=M;SS=N	DKFZP586G1122 protein	7.6
	426359	AA376409	Hs.10862	adenylatekinase,none	Homo sapiens cDNA: FLJ23313 fis, cl	7.5
	417733	AL048678	Hs.82503	NA;NA	H.sapiens mRNA for 3'UTR of unknown	7.5
	451541	BE279383	Hs.26557	Armadillo_seg;TM=M;SS=N	plakophilin 3	7.4
	443951	F13272	Hs.356835	PMP22_Claudin,none	feritin, light polypeptide	7.4
30	409660	BE261944	Hs.355264		hexokinase 1	7.3
	423184	NM_004428	Hs.1624	Ephrin;TM=M;SS=M	ephrin-A1	7.3
	405121	X04385	Hs.110802	Cys_knot,TGF-beta,vwa,vwc	von Willebrand factor (VWF), mRNA	7.1
	438974	AF089816	Hs.6454	PDZ;TM=N;SS=M	chromosome 19 open reading frame 3	7.1
	417771	AA804698	Hs.82547		retinoic acid receptor responder (l	7.0
35	424118	BE269041	Hs.140452	perilipin;TM=N;SS=M	cargo selection protein (mannose 6	7.0
	402705	X57951	Hs.180909	AhpC-TSA;TM=M;SS=M	peroxiredoxin 1 (PRDX1)	7.0
	417115	AW952792	Hs.334612	Sm,pkinase;TM=N;SS=N	small nuclear ribonucleoprotein pol	7.0
	442572	AD001922	Hs.135121	HSP70	hypothetical protein FLJ22415	6.9
	447216	R75812	Hs.169248	cytochrome_c;NA;NA	p75NTR-associated cell death execut	6.9
40	422278	AF072873	Hs.114218	Fz,Frizzled,7tm_2;TM=Y;SS	frizzled (Drosophila) homolog 6	6.9
	414657	AA424074	Hs.76780	TM=M;SS=N	protein phosphatase 1, regulatory (6.9
	447528	AI612027	Hs.76277	TB2_DP1_HVA22;TM=Y;SS=M	Homo sapiens, clone MGC:9381, mRNA,	6.9
	436729	BE621807	Hs.351316	TM=Y;SS=M	transmembrane 4 superfamily member	6.9
	428013	AF151020	Hs.181444	TM=Y;SS=M	hypothetical protein	6.9
45	444143	AW747996	Hs.160999	Bcl-2,none	ESTs, Moderately similar to A56194	6.8
	414443	AU077268	Hs.76144	Ig,pkinase;TM=Y;SS=N	platelet-derived growth factor rece	6.7
	418751	BE389014	Hs.372548	SH2,none	phosphoinositide-3-kinase, regula	6.7
	448479	H96115	Hs.21293	UDPGP;TM=M;SS=N	UDP-N-acetylglucosamine pyrophospho	6.6
	410552	X66945	Hs.748	Ig,pkinase,SH2,SH3,C2,PH,	fibroblast growth factor receptor 1	6.6
50	414883	AA926960	Hs.348669	CKS;TM=N;SS=N	CDC28 protein kinase 1	6.6
	417426	NM_002291	Hs.82124	laminin_EGF,laminin_Niem	laminin, beta 1	6.6
	428179	AI127772	Hs.279698	pkinase,PX,pkinase_C;TM=N	serum/glucocorticoid regulated kina	6.6
	443195	BE148235	Hs.193063	Aa_trans,none	Homo sapiens cDNA FLJ14201 fis, clo	6.5
55	424512	X53002	Hs.149846	Integrin_B,EGF;TM=Y;SS=M	Integrin, beta 6	6.5
	421733	AL119671	Hs.1420	Ig,pkinase;TM=Y;SS=M	fibroblast growth factor receptor 3	6.5
	428950	BE311879	Hs.194673	DED;TM=M;SS=N	phosphoprotein enriched in astrocyt	6.5
	450172	NM_005864	Hs.24587	SH3,hormone3;TM=M;SS=N	signal transduction protein (SH3 co	6.5
	416078	AL034349	Hs.79005		protein tyrosine phosphatase, recep	6.5
	408912	AB011084	Hs.48924	Armadillo_seg;TM=M;SS=M	KIAA0512 gene product; ALEX2	6.4
60	428373	AI751656	Hs.183986	Ig;TM=Y;SS=M	poliovirus receptor-related 2 (harp	6.4
	449029	N28989	Hs.22891	aa_permeases;TM=Y;SS=M	solute carrier family 7 (cationic a	6.4
	406621	X57809	Hs.181125	Ig,HSP70,Ppx-GppA;TM=M;SS	immunoglobulin lambda locus	6.4
	431629	AU077025	Hs.265827	TM=M;SS=Y	interferon, alpha-inducible protein	6.4
	428169	AI928984	Hs.182793	photoRC,UPF0118;TM=Y;SS=N	golgi phosphoprotein 2	6.4
65	443337	Y07604	Hs.9235	NDK;TM=N;SS=N	non-metastatic cells 4, protein exp	6.4
	451292	AB037716	Hs.26204	SH3;TM=M;SS=N	KIAA1295 protein	6.4
	425976	C75094	Hs.334514	voltage_CLC;TM=Y;SS=M	NG22 protein	6.4
	426539	AB011155	Hs.170280	SH3,PDZ,Guanylate_kin;TM=	discs, large (Drosophila) homolog 5	6.3
	417208	S67773	Hs.81665	Ig,pkinase;TM=Y;SS=M	v-kit Hardy-Zuckerman 4 feline sarc	6.3
70	438278	BE409248	Hs.57988	TFIIS,RNA_POL_M_15KD,UPF0	hypothetical protein FLJ22357 simil	6.3
	429455	AW72111	Hs.278694	lactin_c	CD209 antigen	6.3
	431685	AW296135	Hs.267659	CH,DAG_PE-bind,PH,RhoGEF,	vav 3 oncogene	6.3
	445033	AV652402	Hs.72901	ank;TM=N;SS=N	cyclin-dependent kinase inhibitor 2	6.3
	411756	BE294350	Hs.71891	pkinase,F5_F8_type_C;TM=Y	discolidin domain receptor family, m	6.3
75	453902	BE502341	Hs.3402		ESTs	6.3
	418005	AI185220	Hs.83164	Collagen,TSPN;TM=M;SS=M	collagen, type XV, alpha 1	6.2
	449924	W30681	Hs.146233	SH3,none	Homo sapiens cDNA: FLJ22130 fis, cl	6.2
	426520	BE545684	Hs.343566	aa_permeases,pyridoxal_de	KIAA0251 protein	6.2
	453064	R40334	Hs.89463		potassium large conductance calcium	6.2
80	448520	AB002367	Hs.21355	pkinase,DCX;TM=M;SS=N	doublecortin and CaM kinase-like 1	6.2
	452683	AI089575	Hs.374574	homeobox,none	progesterone membrane binding prote	6.2
	402575	AF043329	Hs.173717	PAP2;TM=Y;SS=M	PPAP2B Phosphatidic acid phosphatase type 2B	6.2
	444672	Z95636	Hs.11669	laminin_EGF,laminin_G,EGF	laminin, alpha 5	6.2
	450440	AB024334	Hs.25001	14-3-3;TM=M;SS=N	tyrosine 3-monooxygenase/tryptophan	6.2

5	432314	AA533447	Hs.285173	Xlnk,none	ESTs	6.1
	438564	AA381553	Hs.198253	Ig,MHC_II_alpha,none	major histocompatibility complex, c	6.1
	444252	R21135	Hs.54985		ESTs	6.1
	425184	BE278288	Hs.155048	Ig;TM=Y;SS=M	Lutheran blood group (Auberger b an	6.1
	431890	X17033	Hs.271986	vwa,Integrin_A,FG-GAP;TM=	Integrin, alpha 2 (CD49B, alpha 2 s	6.1
10	449475	AI348027	Hs.129826	transmembrane4;TM=Y;SS=M	hypothetical protein PP1057	6.0
	449538	AI559444	Hs.104679	TM=M;SS=M	ESTs	6.0
	414496	W73853	Hs.355424	pkinaase,F5_F8_type_C,adh_	ESTs	6.0
	414217	AI309298	Hs.279898	NA;NA	Homo sapiens cDNA: FLJ23165 fls, cl	5.9
	445333	BE537641	Hs.44278	ras,arf,TK;TM=N;SS=M	hypothetical protein FLJ12538 simil	5.9
15	431183	NM_006855	Hs.250686	ER_lumen_recept;TM=M;SS=M	KDEL (Lys-Asp-Glu-Leu) endoplasmic	5.9
	409645	AI142265	Hs.55498	polyprenyl_synth;TM=M;SS=N	geranylgeranyl diphosphate synthase	5.9
	412276	BE262621	Hs.73798	IMF,sugar_fr,none	macrophage migration inhibitory fac	5.9
	416137	BE279513	Hs.278607	pkinaase,UBA,ThiF;TM=M;SS=	ubiquitin activating enzyme E1-like	5.9
	412989	AI373162	Hs.75103	14-3-3;TM=N;SS=M	tyrosine 3-monooxygenase/tryptophan	5.9
20	414504	AW069181	Hs.115175	pkinaase,SAM;TM=M;SS=N	sterile-alpha motif and leucine zip	5.9
	433573	AF234887	Hs.57652	7tm_2,EGF,cadherin,lamini	cadherin, EGF LAG seven-pass G-type	5.9
	436415	BE265254	Hs.343258	Peptidase_M24,Furin-like,	proliferation-associated 2G4, 38kD	5.9
	413900	AW409747	Hs.75612	TPR,PDZ,WW,Guanylate_kin;	stress-induced-phosphoprotein 1 (Hs	5.9
	414155	AJ271671	Hs.7854	Zip;TM=Y;SS=M	zinc/fon regulated transporter-like	5.8
25	444006	BE395085	Hs.334762	Idl_recept_a,PKD,MHC_1;TM	type I transmembrane protein Fn14	5.8
	408269	AW888219	Hs.44077	CH;TM=M;SS=N	parvin, alpha	5.8
	411372	AI147861	Hs.213289	Glyco_transf_11,EGF,Idl_r	low density lipoprotein receptor (f	5.8
	450825	AC005954	Hs.25527	PDZ,Guanylate_kin;TM=N;SS	tight junction protein 3 (zona oocl	5.7
	456534	X91195	Hs.100623	LIM,PDZ,pkinaase;TM=N;SS=M	phospholipase C, beta 3, neighbor p	5.7
30	451558	NM_001089	Hs.26630	ABC_tran,SRP54;TM=Y;SS=M	ATP-binding cassette, sub-family A	5.7
	446812	AL042279	Hs.16206	pkinaase	uncharacterized hypothalamus protei	5.7
	424307	AW293399	Hs.356377		nuclear receptor co-repressor 1	5.7
	405484	XM_093451		TM=N;SS=M	C3002124*:g 12737280 ref XP_006682	5.7
	425367	BE271188	Hs.155975	TM=M;SS=Y	protein tyrosine phosphatase, recep	5.7
35	444607	AW405635	Hs.293687	PI-PLC-X,PH,PI-PLC-Y	ESTs	5.6
	412150	M21574	Hs.74615	zf-C2H2,DUF18,elfhand,C2,P	hypothetical protein FLJ10697	5.6
	450334	AF035959	Hs.24879	Ig,pkinaase,DUF11;TM=M;SS=	platelet-derived growth factor rece	5.6
	453880	AI803166	Hs.135121	PAP2;TM=Y;SS=M	phosphatidic acid phosphatase type	5.6
	439578	AW263124	Hs.350547	HSP70,none	ESTs, Weakly similar to I38022 hypo	5.6
40	450954	AI904740	Hs.25691	WD40;TM=M;SS=N	nuclear receptor co-repressor/HDAC3	5.6
	414555	N98569	Hs.76422	TM=Y;SS=M	receptor (calcitonin) activity modi	5.6
	409963	AA133590	Hs.377830	phoslip;TM=M;SS=Y	phospholipase A2, group IIA (plate	5.6
	450463	AW952018	Hs.201398	MBOAT,none	calcium/calmodulin-dependent protei	5.6
	425177	AF127577	Hs.155017	C1q,Collagen;TM=M;SS=Y	G protein coupled receptor interact	5.5
45	445496	AB007860	Hs.12802	TM=N;SS=M	nuclear receptor interacting protei	5.5
	428981	BE313077	Hs.93135	SH3,ank,PH,ArfGAP;TM=M;SS	development and differentiation enh	5.5
	424441	X14850	Hs.147097	rm	ESTs, Weakly similar to ALU2_HUMAN	5.5
	415662	AW972481	Hs.170810	histone,CBFD_NFYB_HMF;TM=	H2A histone family, member X	5.5
	422105	AI929700	Hs.111680	pkinaase,none	ESTs, Highly similar to G01887 MEK	5.5
50	429556	AW139399	Hs.314807	TM=M;SS=N	endosulfine alpha	5.5
	408056	AA312329	Hs.42331	TM=M;SS=N	ESTs	5.5
	425205	NM_005854	Hs.155106	Ephrin;TM=M;SS=M	ephrin-A4	5.5
	444633	AF111713	Hs.12284	TM=Y;SS=N	receptor (calcitonin) activity modi	5.5
	431585	AF161470	Hs.260622	Ig;TM=Y;SS=M	junctional adhesion molecule 1	5.5
55	429555	U48959	Hs.211582	TM=Y;SS=N	butyrate-induced transcript 1	5.5
	431886	L77964	Hs.271980	pkinaase,fn3,Ig,none	myosin, light polypeptide kinase	5.5
	453143	AA382234	Hs.356289	pkinaase;TM=M;SS=N	mitogen-activated protein kinase 6	5.4
	451863	AL120634	Hs.331803	serpin;TM=N;SS=M	protein tyrosine phosphatase, recep	5.4
	422293	X94453	Hs.114366	cpn60_TCP1,E1-E2_ATPase,C	ATPase, Ca transporting, plasma mem	5.4
60	432179	X75208	Hs.2913	aldehyd,aakinaase;TM=M;SS=N	pyrroline-5-carboxylate synthetase	5.4
	408048	NM_007203	Hs.42322	EPH_lbd,fn3,pkinaase,SAM;T	EphB3	5.4
	448153	Y10805	Hs.20521	Paralemmin;TM=M;SS=N	A kinase (PRKA) anchor protein 2	5.4
	421251	Z28913	Hs.102948	NusG;TM=N;SS=M	HMT1 (hnRNP methyltransferase, S. c	5.4
	439039	AI656707	Hs.48713	LIM,PDZ;TM=N;SS=M	enigma (LIM domain protein)	5.4
65	409882	AJ243191	Hs.56874	pkinaase,none	ESTs	5.4
	451295	AI557212	Hs.17132	HSP20;TM=N;SS=M	heat shock 27kD protein family, mem	5.4
	442549	AI751601	Hs.8375	pkinaase,DAG_PE-blind,pkina	ESTs, Moderately similar to I54374	5.4
	445930	AF055009	Hs.13456	MATH,zf-TRAF,zf-C3HC4;TM=	TNF receptor-associated factor 4	5.4
	453082	H18835	Hs.31608	DAGKc,DAGKa,ank,WD40,bZIP	Homo sapiens clone 24747 mRNA seque	5.4
70	426432	AF001601	Hs.169857	ion_trans;TM=Y;SS=M	hypothetical protein FLJ20041	5.4
	415753	U52819	Hs.78781	Arylessterase;TM=M;SS=N	paraoxonase 2	5.4
	450778	U81375	Hs.25450	PDGF;TM=M;SS=M	vascular endothelial growth factor	5.4
	414739	U83867	Hs.77196	Nucleoside_tran;TM=Y;SS=M	solute carrier family 29 (nucleosid	5.3
	421233	AA209534	Hs.284243	elfhand,SH3,spectrin;TM=N;	spectrin, alpha, non-erythrocytic 1	5.3
75	414774	X02419	Hs.77274	transmembrane4;TM=Y;SS=M	tetraspan NET-6 protein	5.3
	414368	W70171	Hs.75939	kringle,trypsin,plant_thi	plasminogen activator, urokinase	5.3
	446051	BE048061	Hs.37054	PRK,CoaE;TM=N;SS=N	uridine monophosphate kinase	5.3
	423619	T48691	Hs.249159	Ephrin_A_deamin,dsm,z-al	ephrin-A3	5.3
	440188	AK001812	Hs.7036	7tm_1,7tm_2;TM=Y;SS=M	adrenergic, alpha-2A-, receptor	5.3
80	414135	NM_004419	Hs.2128	ROK;TM=M;SS=N	N-Acetylglucosamine kinase	5.3
	444838	AV651680	Hs.208558	Rhodanese,DSPE_Y_phosphat	dual specificity phosphatase 5	5.3
	447918	AI129320	Hs.115175	Integrin_A,FG-GAP,none	ESTs	5.3
	405517	AF000974	Hs.119498	pkinaase,SAM,none	ESTs, Highly similar to JC5818 gamm	5.3
	413588	AA971014	Hs.75432	LIM;TM=M;SS=N	thyroid hormone receptor interactor 6	5.2
	411089	AA456454	Hs.355702	IMPDH_C,CBS,IMPDH_N;TM=M;	IMP (inosine monophosphate) dehydro	5.2
	416157	NM_003243	Hs.342874	zona_pellucida;TM=Y;SS=M	cell division cycle 2-like 1 (PITSL	5.2
					transforming growth factor, beta re	5.2

5	407744	AB020629	Hs.38095	ABC_tran,PRK;TM=Y;SS=M	ATP-binding cassette, sub-family A	5.2
	446108	AL036596	Hs.42322	Paralemmin;TM=M;SS=N	A kinase (PRKA) anchor protein 2	5.2
	422034	AC006486	Hs.333059	Ets;TM=M;SS=N	Ets2 repressor factor	5.2
	417098	AB017365	Hs.173859	Frtzied,Fz,7tm_2,loxin_2	frizzled (Drosophila) homolog 7	5.2
	430526	AF181862	Hs.242407	7tm_3;TM=Y;SS=M	G protein-coupled receptor, family	5.2
	414176	BE140638	Hs.75794	7tm_1,CRCB;TM=Y;SS=N	EDG-2 (endothelial differentiation	5.2
	416710	AI268325	Hs.54890	Peptidase_M49,EGF,Ig,Neur	hypothetical protein FLJ23590	5.2
	417896	AA379770	Hs.82890	DAD;TM=Y;SS=M	defender against cell death 1	5.2
10	413244	AW955951	Hs.159265	BTB,Pep_M12B_propep,Repro	kruppel-related zinc finger protein	5.2
	421837	AF135168	Hs.108802	AAA,cdc48_N,cdc48_2,NB-AR	N-ethylmaleimide-sensitive factor	5.2
	429379	NM_014840	Hs.200598	pkinase,RIO1;TM=M;SS=N	KIAA0537 gene product	5.2
	429619	AL120751	Hs.211568		eukaryotic translation initiation f	5.2
	437275	AW976035	Hs.292396	Frtzied,Fz	ESTs, Weakly similar to A47582 B-cc	5.1
15	421071	AI311238	Hs.104476	TM=Y;SS=M	ESTs, Weakly similar to CGHU1E coli	5.1
	448581	NM_002709	Hs.21537		protein phosphatase 1, catalytic su	5.1
	452568	AA805634	Hs.300870	P13_P14_kinase;TM=M;SS=M	Homo sapiens mRNA; cDNA DKFZp547M07	5.1
	452069	AB028949	Hs.183994	Metallophos;TM=M;SS=N	KIAA1026 protein	5.1
	437175	AW968078	Hs.87773	pkinase,pkinase_C,none	protein kinase, cAMP-dependent, cat	5.1
20	437056	AI147061		spectrin,SH3,PH,CH	gbzok33a11.1.s1 Soares_NSF_F8_9W_OT_P	5.1
	450998	BE387614	Hs.25797	rm;TM=M;SS=N	splicing factor 3b, subunit 4, 49kd	5.1
	444441	AW613841	Hs.301394	IRK;TM=Y;SS=N	hypothetical protein MGC3101	5.1
	446528	BE613248	Hs.172084	PHD;TM=M;SS=N	Homo sapiens, clone IMAGE:3627860,	5.1
	452345	AA293279	Hs.29173	DSPC;TM=M;SS=N	hypothetical protein FLJ20515	5.1
25	443412	W84893	Hs.9305		angiotensin receptor-like 1	5.1
	412853	M34176	Hs.74626	Adaptin_N,Alpha_adaptinC2	adaptor-related protein complex 2,	5.1
	439866	AA280717	Hs.6727	rm,NTF2;TM=M;SS=N	Ras-GTPase activating protein SH3 d	5.1
	439975	AW328081	Hs.6817	Ham1p_lik;TM=M;SS=N	inosine triphosphatase (nucleoside	5.1
	435523	T62849	Hs.11090	TM=Y;SS=M	membrane-spanning 4-domains, subfam	5.1
30	433423	BE407127	Hs.8997	HSP70,Ig,Ppx-GppA;TM=M;SS	heat shock 70kd protein 1A	5.1
	412641	M16660	Hs.74335	HSP90,HATPase_c;TM=M;SS=N	heat shock 90kd protein 1, beta	5.1
	431236	AV656840	Hs.285115	fn3;TM=Y;SS=M	interleukin 13 receptor, alpha 1	5.1
	438552	AJ245820	Hs.6314		type 1 transmembrane receptor (seiz	5.0
35	422765	AW409701	Hs.1578	BIIR;TM=M;SS=N	baculoviral IAP repeat-containing 5	5.0
	427502	AB11865	Hs.7133	TM=M;SS=N	Homo sapiens, clone IMAGE:3161564,	5.0
	414166	AW888941	Hs.75789	DEAD,hallcase_C,rm,Ndr,C	N-myc downstream regulated	5.0
	424954	NM_000546	Hs.1846	P53,WD40,IRK;TM=M;SS=N	tumor protein p53 (Li-Fraumeni) synd	5.0
	422089	AA523172	Hs.103135	REJ,PLAT,PKD,WSC,LRR	ESTs, Weakly similar to SFR4_HUMAN	5.0
	426636	BE242634	Hs.2055	ThiF,UBACT;TM=M;SS=N	ubiquitin-activating enzyme E1 (A1S	5.0
40	410793	AW581906	Hs.66392	SH3,efhand,C2,PH,RhoGEF,M	intersectin 1 (SH3 domain protein)	5.0

TABLE 5B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
437056	428504_3	AW976398 AI147061 AA765223 AA743380 AI803927

TABLE 5C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
405464	5922025	Plus	199214-199579,199672-199920,200262-20049

TABLE 6A: 777 GENES UP-REGULATED IN COLON CANCER COMPARED TO NORMAL ADULT TISSUES

Table 6A lists 777 genes up-regulated in colon cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" colon cancer level was set to the 90th percentile amongst 85 colon cancers. The "average" normal adult tissue level was set to the 90th percentile amongst 209 non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the 209 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
5	447033	AI357412	Hs.157601	ESTs	31.35
	409041	AB033025	Hs.50081	KIAA1199 protein	29.00
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	26.41
	422330	D30783	Hs.115263	epiregulin	24.38
	428187	AI887303	Hs.285529	G protein-coupled receptor 49	24.00
10	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	23.55
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	22.70
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	21.60
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	21.15
	415989	AI267700	Hs.317584	ESTs	20.95
15	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	19.35
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	18.68
	421470	R27496	Hs.1378	annexin A3	18.05
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	17.30
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	17.15
20	450531	AW301032	Hs.203800	ESTs	16.60
	432867	AW016936	Hs.233364	ESTs	16.35
	443211	AI128388	Hs.143655	ESTs	15.80
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	15.10
	405964	M21305		gb:Human alpha satellite and satellite 3	15.00
25	410355	S58544	Hs.153057	sperm associated antigen 1	14.70
	441377	BE218239	Hs.202656	ESTs	14.45
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	14.35
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	14.35
	440304	BE159984	Hs.125395	ESTs	14.25
30	426427	M86689	Hs.169840	TTK protein kinase	13.60
	451561	N52812	Hs.177403	ESTs	12.80
	434032	AW009951	Hs.206892	ESTs	12.75
	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone CO	12.65
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfam	12.55
35	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	12.40
	446232	AI281848	Hs.194691	retinoic acid induced 3	12.25
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	12.18
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	11.85
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	11.80
40	422011	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	11.65
	452461	N78223	Hs.108106	transcription factor	11.42
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	11.35
	400534				11.00
	448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	10.75
45	453688	AW381270	Hs.194110	hypothetical protein PRO2730	10.75
	426890	AA393167	Hs.41294	ESTs	10.60
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	10.55
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	10.50
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	10.50
50	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp584F093 (fr	10.40
	425761	AW654214	Hs.196729	ESTs	10.25
	404567				10.15
	428536	AI143139	Hs.2288	visinin-like 1	10.10
	414972	BE263782	Hs.77695	KIAA0008 gene product	10.05
55	459504	BE514127		gb:601315974F1 NIH_MGC_8 Homo sapiens cD	9.95
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	9.90
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	9.85
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	9.85
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	9.78
60	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	9.73
	420900	AL045633	Hs.44269	ESTs	9.68
	438639	AI278360	Hs.31409	ESTs	9.55
	439521	AI808955	Hs.58248	ESTs	9.55
	445676	AI247763	Hs.16928	ESTs	9.50
65	408489	AI082437	Hs.26690	ESTs	9.50
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	9.37
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	9.00
	423349	AF010258	Hs.127428	homeo box A9	8.96
	400195	NA			8.90
70	411765	H43346		gb:yp09a04.r1 Soares breast 3NbHBst Homo	8.90
	418895	AA894638	Hs.14600	ESTs	8.85
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	8.80
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	8.75
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	8.65
75	414559	AV656184	Hs.76452	C-reactive protein, pentraxin-related	8.64
	445436	AI224105	Hs.151408	ESTs	8.50
	403776				8.50
	433447	U29195	Hs.3281	neuronal pentraxin II	8.50
	407168	R45175	Hs.117183	ESTs	8.31
80	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	8.30
	422505	AL120862	Hs.124165	ESTs	8.25
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	8.20
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	8.15
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	8.10
	409687	T51125	Hs.8493	ESTs	8.05

	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	8.00
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	7.93
	406360	NA		NA	7.80
5	443450	N66045	Hs.133529	ESTs	7.75
	414422	AA147224	Hs.337232	ESTs	7.75
	442611	BE077155	Hs.177537	hypothetical protein DKFZp61B1514	7.70
	438604	AA811896	Hs.44604	ESTs	7.60
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	7.55
	400250	NA		NA	7.53
10	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	7.50
	404996				7.50
	450459	AI697193	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	7.45
	445019	AI205540	Hs.281295	ESTs	7.30
15	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	7.25
	448816	AB033052	Hs.22151	KAA1226 protein	7.25
	444361	W76027	Hs.23920	hypothetical protein FLJ11105	7.25
	449370	AK002114	Hs.23495	hypothetical protein FLJ11252	7.20
	433859	AW696758	Hs.273789	ESTs	7.20
20	416143	AI955650	Hs.79033	glutaminyl-peptide cyclotransferase (glu	7.20
	456120	AA535244	Hs.78305	RAB2, member RAS oncogene family	7.20
	419751	AW195581	Hs.93121	KAA0761 protein	7.16
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	7.15
	456553	AA721325	Hs.189058	ESTs, Highly similar to Similar to a C.e	7.15
25	421373	AA808229	Hs.167771	ESTs	7.10
	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	7.00
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	6.96
	444798	BE242144	Hs.12013	ATP-binding cassette, sub-family E (QABP	6.95
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	6.95
30	413573	AI733859	Hs.149089	ESTs	6.95
	442660	AW138174	Hs.130651	ESTs	6.93
	427878	C05766	Hs.181022	CGI-07 protein	6.90
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	6.85
	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp58611518 (f	6.82
35	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.80
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp5861121 (f	6.80
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	6.80
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	6.75
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	6.75
40	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp58611922 (f	6.71
	401644				6.70
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	6.70
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	6.69
	406747	AI925153	Hs.217493	annexin A2	6.65
45	445191	AF048686	Hs.12393	dTDP-D-glucose 4,6-dehydratase	6.60
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	6.60
	428392	H10233	Hs.2265	secretory granule, neuroendocrine prota	6.55
	427072	H38046	Hs.303193	ESTs	6.55
	452588	AA889120	Hs.110637	homeo box A10	6.53
50	439809	R41396	Hs.101774	hypothetical protein FLJ23045	6.50
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selen	6.50
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	6.50
	423685	BE350494	Hs.49753	ovine autoantigen with coiled coil domai	6.50
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	6.50
55	410908	AA121686	Hs.10592	ESTs	6.47
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	6.47
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.45
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	6.42
	451389	N73222	Hs.279009	matrix Gla protein	6.40
60	438202	AW169287	Hs.22588	ESTs	6.40
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	6.40
	425860	L29339	Hs.1964	solute carrier family 5 (sodium/glucose	6.37
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.36
	436539	AI005457	Hs.275048	ESTs	6.35
65	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	6.34
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	6.32
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger)	6.31
	407237	AA169872	Hs.6216	Homo sapiens hepatocellular carcinoma-as	6.30
	413597	AW302885	Hs.117183	ESTs	6.30
70	429529	AA454190	Hs.24283	ESTs, Moderately similar to reduced expr	6.30
	409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled	6.25
	407746	AK001862	Hs.38114	hypothetical protein FLJ11100	6.20
	426921	AA037145	Hs.172855	cleavage stimulation factor, 3' pre-RNA,	6.20
	438050	BE262816	Hs.6061	protein kinase, AMP-activated, beta 1 no	6.20
75	416857	AA188775	Hs.292453	ESTs	6.20
	409683	U33317	Hs.711	defensin, alpha 6, Paneth cell-specific	6.18
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	6.15
	420098	AA775910	Hs.95011	syntrophin, beta 1 (dystrophin-associate	6.15
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.15
80	433393	AF038564	Hs.98074	litchy (mouse homolog) E3 ubiquitin prote	6.11
	424745	AA214618	Hs.152759	activator of S phase kinase	6.10
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	6.10
	454438	AA224053	Hs.172405	cell division cycle 27	6.08
	407771	AL138272	Hs.62713	ESTs	6.08

	416057	AI927382	Hs.29857	ESTs	6.05
	442917	AA314907	Hs.85950	ESTs	6.00
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	6.00
5	453700	AB009426	Hs.560	apolipoprotein B mRNA editing enzyme, ca	5.96
	412246	AI160873	Hs.69233	zinc finger protein	5.96
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	5.95
	418668	AW407987	Hs.173518	M-phase phosphoprotein homolog	5.95
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	5.95
10	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	5.90
	409913	BE243842	Hs.283077	centrosomal P4.1-associated protein; unc	5.90
	429201	X03178	Hs.198246	group-specific component (vitamin D bind	5.87
	408908	BE296227	Hs.250822	serine/threonine kinase 15	5.86
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	5.86
15	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	5.85
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.85
	441645	AI222279	Hs.201555	ESTs, Weakly similar to T23406 hypotheti	5.85
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	5.85
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	5.85
20	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.82
	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	5.80
	459309	AA040620	Hs.5672	hypothetical protein AF140225	5.80
	410060	NM_001448	Hs.58367	glypican 4	5.79
	423806	AA331247	Hs.86617	ESTs	5.77
25	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	5.75
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	5.75
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.75
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	5.75
	442957	AI949952	Hs.49397	ESTs	5.75
30	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	5.70
	426518	Z43039	Hs.170198	KIAA0009 gene product	5.70
	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE3685398, mRNA,	5.70
	415385	R17798	Hs.7535	COBW-like protein	5.70
	409757	NM_001898	Hs.123114	cystatin SN	5.69
35	433687	AA743991		gb:ny57g01.s1 NCL CGAP_Pr18 Homo sapiens	5.68
	424492	AI133482		gb:HA2093 Human fetal liver cDNA library	5.60
	452606	N45202	Hs.90012	hypothetical protein FLJ23441	5.60
	438777	AA825487	Hs.142179	ESTs	5.60
40	417235	AA810278	Hs.24250	ESTs	5.60
	451177	AI969716	Hs.13034	ESTs	5.60
	415227	AW821113	Hs.72402	ESTs	5.58
	436217	T53925	Hs.107	fibrinogen-like 1	5.56
	452881	AW135220	Hs.241921	ESTs	5.55
45	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	5.55
	426235	AI631964	Hs.34447	ESTs	5.55
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	5.53
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	5.52
	442980	AA857025	Hs.8878	kinesin-like 1	5.50
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.50
50	453884	AA355925	Hs.36232	KIAA0186 gene product	5.47
	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.47
	419502	AU076704	Hs.90765	fibrinogen, A alpha polypeptide	5.47
	420218	AW958037	Hs.286	ribosomal protein L4	5.45
	421155	H87879	Hs.102267	lysyl oxidase	5.45
55	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	5.45
	456435	AI880384	Hs.270747	ESTs, Weakly similar to ALU2_HUMAN ALU S	5.45
	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	5.44
	446372	AB020844	Hs.14945	long fatty acyl-CoA synthetase 2 gene	5.42
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	5.41
60	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	5.41
	453080	AI423056	Hs.23921	hypothetical protein DKFZp547A023	5.35
	430217	N47863	Hs.336901	ribosomal protein S24	5.33
	417372	T99755	Hs.334728	ESTs	5.30
	415139	AW975942	Hs.48524	ESTs	6.30
65	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	5.29
	424086	AI351010	Hs.102267	lysyl oxidase	5.27
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	5.27
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	5.26
	452131	AI860677	Hs.72325	Human DNA sequence from clone RP1-187J11	5.25
70	436016	AA806465	Hs.121536	Human DNA sequence from clone RP11-472E5	5.25
	449347	AV649748	Hs.295901	KIAA0493 protein	5.25
	445038	AI635444	Hs.143917	dJ467N11.1 protein	5.25
	453921	AI824009	Hs.44577	ESTs	5.25
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	5.25
75	421076	AW007988	Hs.233299	ESTs, Weakly similar to I38022 hypotheti	5.25
	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	5.24
	433384	AI021992	Hs.124244	ESTs	5.23
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	5.21
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	5.20
80	441795	N58115	Hs.21137	AD024 protein	5.20
	449416	AI651016	Hs.246311	ESTs	5.20
	418379	AA218940	Hs.137516	fidgetin-like 1	5.20
	426753	T89832	Hs.170278	ESTs	5.18
	422109	S73265	Hs.1473	gastrin-releasing peptide	5.17

	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	5.17
	416806	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	5.17
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	5.15
5	427728	AJ245600	Hs.180545	Homo sapiens mRNA for hypothetical prote	5.15
	447713	AI420733	Hs.207063	ESTs	5.15
	425739	T19016	Hs.159410	molybdopterin synthase sulfurylase	5.15
	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	5.15
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	5.13
10	441139	AW449009	Hs.126647	ESTs	5.13
	451121	AW973795	Hs.128927	Homo sapiens cDNA FLJ13903 fis, clone TH	5.10
	435202	AI971313	Hs.170204	KIAA0551 protein	5.10
	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	5.10
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	5.09
	422805	AA436989	Hs.121017	H2A histone family, member A	5.07
15	411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	5.06
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	5.06
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	5.05
	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	5.05
	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	5.05
20	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.05
	441675	AI914329	Hs.5461	ESTs	5.00
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	5.00
	401480	NA		NA	5.00
25	408562	AA363323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	4.96
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	4.92
	414718	H96348	Hs.107987	ESTs	4.91
	419139	AI123517	Hs.269940	ESTs	4.90
	430789	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	4.90
30	425420	BE536911	Hs.234545	hypothetical protein NUF2R	4.90
	408758	NM_003686	Hs.47504	exonuclease 1	4.90
	439741	BE379646	Hs.6904	Homo sapiens mRNA full length insert cDN	4.90
	418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	4.90
	433927	AI557019	Hs.116467	small nuclear protein PRAC	4.89
35	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	4.88
	455777	AA524285	Hs.154172	ESTs, Moderately similar to BCGF_HUMAN B	4.87
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (tr	4.87
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	4.86
	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (R	4.85
40	418396	AI765805	Hs.26691	ESTs	4.85
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	4.84
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	4.80
	406414				4.75
	430178	AW449612	Hs.152475	ESTs	4.71
45	411901	AA166730	Hs.6966	Human DNA sequence from clone RP1-187J11	4.70
	404025	NA		NA	4.70
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	4.68
	436662	AI582393	Hs.126695	ESTs	4.68
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	4.68
50	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	4.65
	431041	AA490967	Hs.197955	KIAA0704 protein	4.65
	417860	AW408557	Hs.235498	hypothetical protein FLJ14075	4.65
	410658	AW105231	Hs.192035	ESTs	4.65
	425895	AI269484	Hs.161427	zinc finger protein 215	4.65
	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	4.65
55	436397	AA715013	Hs.169835	ESTs	4.60
	439225	AA192669	Hs.45032	ESTs	4.60
	423197	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	4.60
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	4.60
60	412723	AA648459	Hs.335951	hypothetical protein AF301222	4.59
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	4.59
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	4.58
	430704	AW813091	Hs.335799	ESTs	4.56
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	4.55
65	433326	AI379486	Hs.159430	ESTs	4.55
	437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 ferri	4.55
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	4.55
	423343	AA324643	Hs.246106	ESTs	4.55
	418467	H57585	Hs.37467	ESTs	4.55
70	408887	AA437199	Hs.6556	cell division cycle 25C	4.54
	419423	D26488	Hs.90315	KIAA0007 protein	4.54
	414132	AI801235	Hs.48480	ESTs	4.53
	423948	AW392342	Hs.283077	centrosomal P4.1-associated protein; unc	4.53
	425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acylt	4.50
75	451009	AA013140	Hs.115707	ESTs	4.50
	431064	AI903735		gb:MR-BT035-200199-031 BT035 Homo sapien	4.50
	432725	AL137496	Hs.9001	ESTs	4.50
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	4.50
	410486	AW235094	Hs.69233	zinc finger protein	4.50
80	428532	AF157326	Hs.184788	TBP-interacting protein	4.50
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	4.50
	408380	AF123050	Hs.44532	diubiquitin	4.49
	423936	U77629	Hs.135639	ectoderm-ectoderm complex (Drosophila) homol	4.47
	434294	AJ271379	Hs.76194	ribosomal protein S5	4.47

	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	4.46
	447102	BE167434	Hs.98471	ESTs, Weakly similar to T18712 hypotheti	4.45
	410142	AA081924	Hs.124918	KIAA1795 protein	4.45
	434894	AW977850	Hs.23856	hypothetical protein MGC5297	4.45
5	420092	AA814043	Hs.88045	ESTs	4.45
	400115	NA		NA	4.45
	430967	H16791	Hs.31445	ESTs	4.41
	438078	AI016377	Hs.131693	ESTs	4.41
10	412359	AW837985		gb:QV3-LT0048-140200-083-e05 LT0048 Homo	4.40
	429774	AI522215	Hs.50883	KIAA1804 protein	4.40
	426214	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	4.40
	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	4.40
	450480	X82125	Hs.25040	zinc finger protein 239	4.40
15	421211	AA284966	Hs.266308	mosaic serine protease	4.40
	419261	X07876	Hs.89791	wingless-type MMTV Integration site fami	4.40
	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	4.37
	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT	4.35
	410568	AW162948	Hs.64542	cleavage and polyadenylation specific fa	4.35
20	459574	AI741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	4.35
	448243	AW369771	Hs.52620	Integrin, beta 8	4.35
	438069	N80701	Hs.33790	ESTs	4.35
	446152	AI292036	Hs.150028	ESTs	4.34
25	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	4.32
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	4.30
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	4.30
	422835	BE218705	Hs.121378	metallothionein-like 5, testis-specific	4.30
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.30
	439619	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypotheti	4.30
30	458076	R80061	Hs.164478	hypothetical protein FLJ21939 similar to	4.30
	450192	AA263143	Hs.24596	RAD51-interacting protein	4.29
	443232	AF161521	Hs.9081	phenylalanyl-tRNA synthetase beta-subuni	4.28
	413881	L00190	Hs.75599	serine (or cysteine) proteinase inhibito	4.26
	434217	AW014795	Hs.23349	ESTs	4.26
35	409723	AW885757	Hs.257862	ESTs	4.25
	417956	AA210704	Hs.190465	ESTs	4.25
	458433	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	4.25
	409928	AL137163	Hs.57549	hypothetical protein dJ47384	4.24
40	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	4.22
	424583	AF017445	Hs.150526	fucose-1-phosphate guanylyltransferase	4.20
	429436	AA452934	Hs.279813	hypothetical protein	4.20
	424625	AW904466	Hs.321197	PDZ domain protein (Drosophila InaD-like	4.20
	448912	D83781	Hs.22559	KIAA0197 protein	4.20
	442671	AI005668	Hs.134779	EST	4.20
45	411893	R82845	Hs.273789	ESTs	4.20
	456281	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	4.20
	421106	AA877124	Hs.172844	ESTs	4.20
	451401	AI793163		gb:cn52g03.y5 NCI_CGAP_Co8 Homo sapiens	4.20
	404516	NA		NA	4.20
50	414968	C16096	Hs.22826	tropomodulin 3 (ubiquitous)	4.20
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	4.20
	419229	AI827237	Hs.282884	ESTs	4.18
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	4.16
	453911	AW503857	Hs.4007	Sarcolemmal-associated protein	4.16
55	433159	AB035898	Hs.150587	kinesin-like protein 2	4.15
	419247	S65791	Hs.89764	fragile X mental retardation 1	4.15
	432491	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	4.15
	422093	AF151852	Hs.111449	CGI-94 protein	4.15
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	4.15
60	446999	AA151520	Hs.334822	hypothetical protein MGC4485	4.15
	414538	AW612228	Hs.107987	ESTs	4.14
	453931	AL121278	Hs.25144	ESTs	4.12
	427718	AI798680	Hs.25933	ESTs	4.11
	453863	X02544	Hs.572	orosomucoid 1	4.10
65	440209	H05049	Hs.22269	neurexin 3	4.10
	435148	AI918049	Hs.124961	ESTs	4.10
	409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.10
	448692	AW013907	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	4.10
	426301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	4.10
70	444188	AI393165	Hs.699	peptidylprolyl isomerase B (cyclophilin	4.10
	457059	BE561665	Hs.177677	exosome component Rrp40	4.10
	407162	N63855	Hs.142634	zinc finger protein	4.10
	406117				4.10
	434370	AF130988	Hs.58346	ectodysplasin 1, anhidrotic receptor	4.09
75	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MA	4.08
	448666	NM_014953	Hs.323346	KIAA1008 protein	4.07
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	4.07
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	4.07
	456030	AA136106	Hs.184852	KIAA1553 protein	4.05
80	434082	AI373481	Hs.131715	hypothetical protein PRO1777	4.05
	443646	AI085198	Hs.164226	ESTs	4.05
	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	4.05
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	4.05
	432619	AW291722	Hs.278526	related to the N terminus of tre	4.05

	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	4.05
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	4.04
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	4.04
5	424176	AL137273	Hs.142307	hypothetical protein	4.04
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.04
	418203	X54942	Hs.83758	CDC28 protein kinase 2	4.03
	435420	AI928513	Hs.59203	ESTs	4.03
	406666	V00495	Hs.184411	albumin	4.02
10	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	4.00
	449448	D60730	Hs.57471	ESTs	4.00
	421037	AI684808	Hs.197653	ESTs	4.00
	448310	AI480316		gb:tm28n09.x1 Scores_NFL_T_GBC_S1 Homo s	4.00
	408155	AB014528	Hs.43133	KIAA0628 gene product	4.00
15	413841	M34276	Hs.75576	plasminogen	3.98
	400110	NA		NA	3.98
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.97
	443715	AI583187	Hs.9700	cyclin E1	3.97
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.97
20	450164	AI239923	Hs.30098	ESTs	3.97
	451592	AI805416	Hs.213897	ESTs	3.95
	402373	AL135225	Hs.301865	dopachrome tautomerase (dopachrome delta	3.95
	426199	AA371865	Hs.97090	ESTs	3.95
	414148	BE084049		gb:PM0-BT0651-270400-003-02 BT0651 Homo	3.95
25	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	3.94
	449532	W74653	Hs.271593	ESTs, Moderately similar to A47582 B-cel	3.93
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	3.93
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	3.92
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.91
30	416185	AW975861	Hs.47367	KIAA1785 protein	3.91
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	3.90
	432596	AJ224741	Hs.278461	matrilin 3	3.90
	451229	AW967707	Hs.48473	ESTs	3.90
	413583	AL120806	Hs.5888	ESTs	3.90
35	432702	AW973953	Hs.293744	ESTs	3.90
	437207	T27503	Hs.15929	hypothetical protein FLJ12910	3.90
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	3.90
	423697	BE088697	Hs.131834	Homo sapiens mRNA; cDNA DKFZp43480328 (f	3.90
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	3.90
40	432289	AI860145	Hs.55118	ESTs	3.89
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	3.88
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.88
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	3.88
	410094	BE147897	Hs.58593	general transcription factor IIF, polype	3.88
45	441826	AW503603	Hs.129915	phosphotriesterase related	3.87
	444059	R69743	Hs.116774	integrin, alpha 1	3.86
	426262	AI782141	Hs.196270	folate transporter/carrier	3.85
	452641	AW952893	Hs.237825	signal recognition particle 72kD	3.85
50	454403	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	3.85
	448315	AW290912	Hs.20797	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.85
	411343	U77949	Hs.69563	CDC6 (cell division cycle 6, S. cerevisi)	3.85
	409734	BE161664	Hs.56155	hypothetical protein	3.85
	454014	AW016670	Hs.233275	ESTs	3.84
	453116	AI276680	Hs.146088	ESTs	3.83
55	449508	AK001566	Hs.23618	hypothetical protein FLJ10704	3.82
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	3.82
	435040	AI932350	Hs.152825	ESTs	3.81
	426249	F05422	Hs.168352	nucleoporin-like protein 1	3.81
	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	3.81
60	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.81
	437631	AA764749	Hs.267245	hypothetical protein FLJ14803	3.80
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	3.80
	405769				3.80
	438295	AI394151	Hs.37932	ESTs	3.80
65	453628	AW243307	Hs.83937	hypothetical protein	3.80
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	3.80
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 6730	3.76
	423881	AK001720	Hs.134403	hypothetical protein FLJ10858	3.75
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	3.75
70	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.75
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.74
	420726	K02402	Hs.1330	coagulation factor IX (plasma thrombopla	3.74
	418413	R95735	Hs.117763	ESTs, Weakly similar to A48666 cell prol	3.73
	443354	AW970672	Hs.9247	protein kinase, AMP-activated, alpha 1 c	3.73
75	406667	M12523	Hs.184411	albumin	3.72
	436411	AW674352		gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD	3.72
	417246	AI760098	Hs.21411	ESTs	3.72
	410664	NM_006033	Hs.65370	lipase, endothelial	3.71
	432686	BE223007	Hs.152460	Homo sapiens cDNA FLJ12909 fis, clone NT	3.70
	442881	AI023175	Hs.167022	ESTs	3.70
80	432356	AA831032	Hs.111670	ESTs, Highly similar to J12257 proyl ol	3.70
	450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	3.70
	405460	NA		NA	3.70
	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.70

	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-4	3.70
	425282	AW163518	Hs.155485	huntingtin interacting protein 2	3.69
	439857	AA847194	Hs.232002	ESTs	3.69
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfamily	3.69
5	444471	AB020684	Hs.11217	KIAA0877 protein	3.69
	419559	Y07828	Hs.91096	ring finger protein	3.68
	437641	AA811452	Hs.291911	ESTs	3.67
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	3.66
10	417791	AW965339	Hs.111471	ESTs	3.66
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	3.66
	432023	AW273128	Hs.330144	EST	3.65
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.65
	450600	BE079478	Hs.24880	ESTs	3.65
	420595	AA278865	Hs.88523	ESTs	3.65
15	404477	NA	NA	NA	3.65
	457003	S78234	Hs.172405	cell division cycle 27	3.65
	443055	AV653742	Hs.15536	hypothetical protein DKFZp761J139	3.65
	452220	BE158006	Hs.212296	ESTs	3.65
20	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	3.64
	457465	AW301344	Hs.122908	DNA replication factor	3.63
	436149	AI754308	Hs.159452	ESTs	3.63
	433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	3.63
	427920	Z11502	Hs.181107	annexin A13	3.63
	424841	AB001106	Hs.151413	glia maturation factor, beta	3.62
25	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.61
	411975	AI916058	Hs.144583	ESTs	3.61
	409239	AA740875	Hs.44307	ESTs, Moderately similar to I38022 hypot	3.61
	429628	H09604	Hs.13268	ESTs	3.60
	449722	BE280074	Hs.23960	cyclin B1	3.60
30	428389	AW135714	Hs.283127	ESTs, Weakly similar to T19201 hypotheti	3.60
	419945	AW290975	Hs.118923	ESTs	3.60
	410365	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	3.60
	420585	AW505139	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	3.60
35	407809	AW082279	Hs.244106	ESTs	3.60
	457708	AA805443	Hs.179909	hypothetical protein FLJ22995	3.60
	427943	AW959075	Hs.238797	ESTs, Moderately similar to I38022 hypot	3.60
	428771	AB028992	Hs.193143	KIAA1069 protein	3.59
	446638	AL133063	Hs.15783	Homo sapiens mRNA; cDNA DKFZp434P1115 (f	3.59
	418688	T85017	Hs.1192	KIAA0074 protein	3.58
40	436981	AW375974	Hs.156704	ESTs	3.58
	430514	AA318501	Hs.241587	megakaryocyte-enhanced gene transcript 1	3.57
	415245	N59650	Hs.27252	ESTs	3.55
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	3.55
	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	3.55
45	401165	NA	NA	NA	3.55
	415382	AI743539	Hs.72465	ESTs, Weakly similar to non-lens beta ga	3.55
	433968	AL157518	Hs.90421	PRO2463 protein	3.55
	421528	AB037837	Hs.105461	hypothetical protein FLJ20357	3.55
50	443325	BE398006	Hs.90462	Homo sapiens, clone IMAGE:4132043, mRNA,	3.55
	444355	BE383686	Hs.191621	ESTs, Moderately similar to ALU6_HUMAN A	3.55
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.55
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	3.55
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	3.54
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.54
55	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	3.53
	446619	AJ076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.53
	432542	AW083920	Hs.16098	claudin 2	3.52
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	3.51
60	423441	R68649	Hs.278359	absent in melanoma 1 like	3.51
	452940	AA029722	Hs.2173	fucosyltransferase 4 (alpha (1,3) fucosy	3.50
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	3.48
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.48
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.47
65	449915	NM_004529	Hs.404	myeloid/lymphoid or mixed-lineage leukem	3.46
	427975	AI536065	Hs.122460	ESTs	3.45
	400297	AI127076	Hs.334473	hypothetical protein DKFZp554O1278	3.45
	404253				3.45
	435567	AW504944	Hs.162990	Homo sapiens cDNA FLJ14193 fis, clone NT	3.45
70	432158	W33165	Hs.22983	UDP-glucose:glycoprotein glucosyltransfe	3.45
	417315	AI080042	Hs.336901	ribosomal protein S24	3.44
	419140	AI982647	Hs.215725	ESTs	3.43
	446901	AI347274		gbtc05d02.x1 NCI_CGAP_Co16 Homo sapiens	3.42
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.42
75	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	3.41
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	3.41
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.41
	419131	AA406293	Hs.411167	ESTs	3.40
	430264	AA470519		gbnc71f10.s1 NCI_CGAP_Pr1 Homo sapiens	3.40
80	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	3.40
	453531	AA417940	Hs.271400	ESTs, Weakly similar to JC5795 CDEP prot	3.40
	444826	AI674482	Hs.148441	ESTs	3.40
	445354	AV653485	Hs.6390	Homo sapiens clone FLB3344 PRO0845 mRNA,	3.40
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	3.40

	418939	AW630803	Hs.89497	lamin B1	3.40
	418134	AA397769	Hs.88617	ESTs	3.40
	430544	AA481066	Hs.105153	Homo sapiens, clone IMAGE:3461987, mRNA,	3.39
5	427927	AJ879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	3.39
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.39
	410406	AJ969703	Hs.1466	glycerol kinase	3.38
	408494	AA554714	Hs.187578	Homo sapiens cDNA FLJ11639 fis, clone HE	3.38
	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypothe	3.38
10	446432	AJ377320	Hs.150058	ESTs	3.36
	456653	AJ807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	3.35
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.35
	428261	AW006855	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	3.35
	421039	NM_003478	Hs.101299	cutlin 5	3.35
15	407819	R42185	Hs.274803	ESTs	3.35
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	3.35
	433361	AW469373	Hs.300141	ribosomal protein L39	3.35
	435022	AW183385	Hs.54627	ESTs, Weakly similar to FTDH_HUMAN 10-FO	3.35
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	3.35
20	454018	AW016892	Hs.100855	ESTs	3.35
	439871	R88518	Hs.46736	hypothetical protein FLJ23476	3.35
	453941	U39817	Hs.36820	Bloom syndrome	3.34
	411560	AW851186	Hs.179909	hypothetical protein FLJ22995	3.33
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	3.33
25	438008	AA775026	Hs.203802	ESTs	3.33
	421246	AW582962	Hs.102897	CGI-47 protein	3.33
	451707	AW051061	Hs.60973	ESTs	3.33
	457574	H88717	Hs.27774	ESTs, Highly similar to AF161349 1 HSPC0	3.31
	443613	AJ079356		gb:acc39b09.s1 Soares_NhHMPu_S1 Homo sapi	3.31
30	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	3.31
	438746	AJ885815	Hs.184727	ESTs	3.30
	408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferri	3.30
	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Ze	3.30
	458855	AW361299	Hs.107000	hypothetical protein FLJ11294	3.30
35	417221	AW379029	Hs.118338	ESTs, Weakly similar to unnamed protein	3.30
	424770	AA425562	Hs.11065	Homo sapiens HDCME13P mRNA, partial cds	3.30
	417720	AA205625	Hs.208067	ESTs	3.29
	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease,	3.29
	452862	AW378065	Hs.8687	ESTs	3.28
40	414343	AL036166	Hs.323378	coated vesicle membrane protein	3.28
	437222	AL117588	Hs.12778	ESTs	3.28
	422665	AJ011812	Hs.119018	transcription factor NRF	3.28
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.28
	448565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	3.27
45	447829	AJ433029	Hs.164104	ESTs	3.27
	427576	BE242611	Hs.2173	fucosyltransferase 4 (alpha (1,3) fucosy	3.27
	456132	BE219771	Hs.237146	hypothetical protein FLJ12752	3.26
	407305	AA715284		gb:mv35f03.r1 NCL_CGAP_Br5 Homo sapiens	3.26
50	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.26
	424581	M62062	Hs.150917	catenin (cadherin-associated protein), a	3.25
	445592	AV654382	Hs.17947	ESTs, Weakly similar to T16534 hypothe	3.25
	453320	AW450240	Hs.257274	ESTs	3.25
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.25
55	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	3.25
	410659	AJ080175	Hs.68826	ESTs	3.25
	446202	AJ279706	Hs.149474	ESTs	3.25
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	3.25
	439282	AA832333	Hs.333045	ESTs	3.25
	401823	NA		NA	3.25
60	441264	AA927170	Hs.23290	ESTs	3.25
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	3.24
	408321	AW405882	Hs.44205	coristatin	3.24
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked mol	3.24
	404519				3.24
65	443268	AJ800271	Hs.129446	hypothetical protein FLJ12496	3.23
	422660	AW297582	Hs.103267	hypothetical protein FLJ22548 similar to	3.23
	427961	AW293165	Hs.143134	ESTs	3.22
	427660	AJ741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	3.22
	411643	AJ924519	Hs.192570	hypothetical protein FLJ22028	3.21
70	458652	AW375610	Hs.117102	hypothetical protein FLJ13046 similar to	3.21
	426472	BE246138	Hs.308853	ESTs	3.21
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.21
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.21
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.20
75	443162	T49951	Hs.9028	DKFZP434G032 protein	3.20
	431678	AW072372	Hs.267446	hypothetical protein FLJ11184	3.20
	430439	AL133561	Hs.241426	DKFZP434B061 protein	3.20
	407201	N31998	Hs.164256	hypothetical protein FLJ20657	3.20
	437905	AW363121	Hs.175598	ESTs, Weakly similar to T26935 hypothe	3.20
80	434160	BE551196	Hs.114275	ESTs	3.20
	407995	AJ094748	Hs.100134	hypothetical protein FLJ12787	3.20
	412956	BE243311	Hs.8024	IK cytokine, down-regulator of HLA II	3.19
	414386	X00442	Hs.75990	haptoglobin	3.19
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	3.18

	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.18
	433764	AW753676	Hs.39982	ESTs	3.17
	459370	AA889982	Hs.271826	ESTs, Weakly similar to I38022 hypotheti	3.17
	429616	AI982722	Hs.120845	ESTs	3.17
5	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	3.16
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.16
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.16
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.15
10	443830	AI142095	Hs.143273	ESTs	3.15
	413516	BE145907		gb:MR0-HT0208-221299-204-e12 HT0208 Homo	3.15
	433527	AW235613	Hs.133020	ESTs	3.15
	427986	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone H	3.15
	457453	Z70695	Hs.272240	Homo sapiens cDNA FLJ11086 fis, clone PL	3.15
15	427687	AW003867	Hs.1570	histamine receptor H1	3.15
	455068	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	3.15
	441720	AI346487	Hs.28739	ESTs	3.15
	419569	AI971651	Hs.91143	Jagged 1 (Alagille syndrome)	3.15
	445921	AW015211	Hs.146181	ESTs	3.15
20	429957	AW204530	Hs.99500	ESTs	3.15
	403137				3.14
	425268	AI807883	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	3.14
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	3.14
	439635	AA477288	Hs.94891	hypothetical protein FLJ22729	3.14
25	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	3.14
	439277	R80061	Hs.164478	hypothetical protein FLJ21939 similar to	3.13
	443584	AI807036	Hs.267245	hypothetical protein FLJ14803	3.13
	406668	T62745	Hs.184411	albumin	3.13
	452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	3.13
30	437594	AA761431	Hs.74335	heat shock 90kD protein 1, beta	3.13
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	3.13
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	3.13
	414080	AA135257	Hs.47783	B aggressive lymphoma gene	3.11
	450209	AW008921	Hs.13138	Homo sapiens, clone IMAGE:3448343, mRNA,	3.11
35	441790	AW294909	Hs.132208	ESTs	3.11
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	3.10
	449664	R06212	Hs.127733	ESTs	3.10
	435979	W03698	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.10
	424602	AK002055	Hs.161046	hypothetical protein FLJ11193	3.10
40	402963				3.10
	428967	AW978441	Hs.296100	ESTs	3.10
	455838	BE145808		gb:MR0-HT0208-101299-103-f11 HT0208 Homo	3.10
	407502	U52096		gb:Human zinc finger protein (kr-znf1) m	3.10
	426853	U32974	Hs.172777	baculoviral IAP repeat-containing 4	3.10
45	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	3.10
	421056	AI076890	Hs.146847	TRAF family member-associated NFKB activ	3.10
	420617	AK001652	Hs.99423	ATP-dependent RNA helicase	3.10
	421841	AA908197	Hs.108850	MAK-related kinase	3.10
	429534	AW976987	Hs.163327	ESTs, Weakly similar to 2109260A B cell	3.10
50	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	3.09
	433037	NM_014158	Hs.279938	HSPC067 protein	3.09
	443183	R16258	Hs.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	3.09
	457726	AI217477	Hs.194591	ESTs	3.08
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	3.08
55	433013	AI697890	Hs.127337	axin 2 (conductin, axil)	3.08
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.07
	420276	AA290938	Hs.190561	ESTs, Highly similar to SORL1_HUMAN SORT1	3.07
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.07
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	3.07
60	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, c	3.07
	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	3.07
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	3.06
	436554	AI985810	Hs.301173	ESTs	3.06
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	3.06
65	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	3.06
	445413	AA151342	Hs.12677	CGI-147 protein	3.06
	452909	NM_015368	Hs.30985	pannexin 1	3.05
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	3.05
	425942	AU077195	Hs.164036	glucosamine (N-acetyl)-6-sulfatase (Sanf	3.05
70	406333				3.05
	428454	U55936	Hs.184376	synaptosomal-associated protein, 23kD	3.05
	411864	AW948147		gb:RC0-MT0013-280300-031-e03 MT0013 Homo	3.05
	458632	AI744445	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	3.05
	448292	BE281316	Hs.47334	hypothetical protein FLJ14495	3.05
75	459055	N23235	Hs.30567	ESTs, Weakly similar to B34087 hypotheti	3.05
	402167				3.05
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	3.05
	437828	AW976806	Hs.73149	paired box gene 8	3.05
	404232				3.05
80	418164	AI761820	Hs.41074	ESTs, Weakly similar to I39294 McLeod sy	3.05
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.05
	452787	AW294022	Hs.222707	KIAA1718 protein	3.05
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.05
	410718	AI920783	Hs.191435	ESTs	3.04

5	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	3.04
	446861	AI696518	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	3.03
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	3.02
	452834	AI638627	Hs.105685	KIAA1688 protein	3.02
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	3.02
	416568	H64844	Hs.138558	ESTs	3.02
	425834	NM_001639	Hs.1957	amyloid P component, serum	3.02
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	3.01
10	412719	AW016610	Hs.129911	ESTs	3.01
	439586	AA922936	Hs.110039	ESTs	3.01
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	3.01
	429703	T93154	Hs.28705	ESTs	3.00
	400286	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.00
	415261	T40928	Hs.8346	ESTs	3.00
15	419435	AI200540	Hs.14877	ESTs, Weakly similar to (define not ava	3.00
	429985	NM_015836	Hs.227274	tryptophanyl tRNA synthetase 2 (mitochon	3.00
	423038	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.00
	407182	AA312551	Hs.230157	ESTs	3.00
	424202	BE350295	Hs.15032	RAN binding protein 17	3.00
20	444585	AW170015	Hs.6594	ESTs	3.00
	420552	AK000492	Hs.98806	hypothetical protein	3.00
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	3.00
	441928	AI370188	Hs.211454	ESTs	3.00
25	430888	BE155293	Hs.76064	ribosomal protein L27a	3.00
	417805	AI867277	Hs.183733	ESTs	3.00
	447175	AI365208	Hs.293606	ESTs	3.00
	417177	NM_004458	Hs.81452	fatty acid-Coenzyme A ligase, long-chain	3.00
	435447	AI872932		gb:wm72e03.x1 NCICGAP_U12 Homo sapiens	3.00
30	405394				3.00
	454975	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.00
	441535	AL135735	Hs.7885	phosphatidylinositol binding clathrin as	3.00
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.00

35

TABLE 6B

Pkey:	Unique Eos probeset identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

40

Pkey	CAT number	Accession
45	411765	125700_1 H43346 AA248302 AA095182
	411864	1262055_1 AW948147 BE092318 AW948138 AW948130 AW948148 AW948129 AW948136 AW948152 AW948144 AW948137 AW948160
	412359	128085_1 AW837985 AW837938 AA101955 AW837913 AW837935
	413516	1374595_1 BE145907 BE145796 BE145803 BE145851 BE145923 BE145812 BE145809 BE145852 BE145856
	414148	142133_1 BE084049 AW292907 AA135984
50	424492	240008_1 AI133482 AI207619 AA341626
	430264	315008_1 AA470519 BE303010 BE302954 BE384120
	431064	327472_1 AI903735 AA491283 AI694953 AW976903 AA761362
	433687	373061_1 AA743991 AA604852 AW272737
	434414	38585_1 AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
55		AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139
		AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730
		AA157715 AA053524 AW849581 AW854568 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AJ829309 AW991957
		N66951 AA527374 H66215 AA045584 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659
		BE081531 H59570
60	435447	406400_1 AI872832 AA682306 BE220163 W88695 T81307 H91447
	436411	419334_1 AW674352 AA715374 Z25205
	443613	575391_1 AI079358 W23287
	446901	697809_1 AI347274 AW844024
	448310	757918_1 AI480316 AW847535
65	451401	868474_1 AI793163 AW875182 AW875178 AW875176
	454403	1170435_1 BE065985 BE065944 BE066008 BE066083 BE066093
	454975	1247077_1 AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905
		AW848214
70	455838	1374605_1 BE145808 BE145807 BE181883

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TABLE 6C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NI_position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
5	400534	6981826	Minus	278637-279292
	401165	9438376	Minus	168244-168423
	401480	7321503	Plus	166120-166347,166451-166557,169651-169832
	401644	8576138	Plus	82655-83959
	401823	2262095	Minus	42576-42697,43189-43287,45830-45974
10	402167	8571795	Plus	109122-110357
	402963	5419653	Minus	12950-15959
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403776	7770611	Minus	1414-1513,1624-1756
	404025	7341444	Plus	131740-131905
15	404232	8218045	Minus	71800-71956
	404253	9367202	Minus	55675-56055
	404477	8080699	Plus	113390-113577
	404516	8151967	Plus	114153-114322
	404519	8152000	Plus	12817-13000
20	404567	7249169	Minus	101320-101501
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405394	6624123	Minus	31900-32373
	405460	7684569	Minus	52223-52389
	405769	3046270	Minus	76844-77193
25	406117	9142932	Plus	54304-54584
	406333	9213235	Plus	64689-64798
	406360	9256107	Minus	7513-7673
	406414	9256407	Plus	49593-49850

30 TABLE 7A: 516 GENES UP-REGULATED IN COLON CANCER COMPARED TO NORMAL COLON

Table 7A lists 516 genes up-regulated in colon cancer compared to normal colon. These were selected as for Table 6A except for using all CEP and colon sample in the normal body tissue list as the normal samples in determining the denominator value and the ratio was equal to or greater than 5.0.

35	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigene number
	Unigene Title:	Unigene gene title
	R1:	Ratio of tumor to normal colon

40

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
45	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	57.52
	406667	M12523	Hs.184411	albumin	49.94
	409041	AB033025	Hs.50081	KIAA1199 protein	49.18
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	42.22
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	34.64
50	429201	X03178	Hs.198246	group-specific component (vitamin D bind	33.38
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	33.10
	447033	AI357412	Hs.157601	ESTs	31.24
	428839	AF767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	26.84
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	25.40
55	413841	M34276	Hs.75576	plasminogen	24.68
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	24.00
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	23.18
	452862	AW378065	Hs.8687	ESTs	21.34
	415989	AI267700	Hs.317584	ESTs	20.92
60	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	19.22
	421470	R27496	Hs.1378	annexin A3	17.92
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	17.36
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	17.28
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	17.08
65	421462	AF016495	Hs.104624	aquaporin 9	17.02
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	16.98
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	16.70
	432340	AA534222		gbx121d02.s1 NCI_CGAP_AA1 Homo sapiens	16.64
	433447	U29195	Hs.3281	neuronal pentraxin II	16.59
70	414386	X00442	Hs.75990	haptoglobin	16.19
	425260	L47726	Hs.1870	phenylalanine hydroxylase	16.08
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	15.82
	439518	W76326		gbcd60d04.r1 Soares_fetal_heart_NbHH19W	15.80
	443211	AI128388	Hs.143655	ESTs	15.78
75	439608	AW864696	Hs.301732	hypothetical protein MGC5306	15.52
	414559	AV656184	Hs.76452	C-reactive protein, pentraxin-related	15.42
	412719	AW016610	Hs.129911	ESTs	15.24
	439451	AF066270	Hs.278554	heterochromatin-like protein 1	15.18
	448974	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	15.03

	416402	NM_000715	Hs.1012	complement component 4-binding protein,	14.60
	453863	X02544	Hs.572	orosomucoid 1	14.35
	441243	AJ767056	Hs.193002	ESTs	14.30
5	413318	AJ076607	Hs.75285	Inter-alpha (globulin) inhibitor, H2 pol	14.30
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	13.91
	433213	AW665130	Hs.137190	ESTs	13.80
	428261	AW006855	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	13.52
	438578	AA811244	Hs.164168	ESTs	13.40
10	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	13.36
	417006	AW673606	Hs.80758	aspartyl-HRNA synthetase	13.00
	449199	AJ990122	Hs.196988	ESTs	12.98
	436393	AW022213	Hs.143617	ESTs	12.90
	413585	AJ133452	Hs.75431	fibrinogen, gamma polypeptide	12.83
15	451561	N52812	Hs.177403	ESTs	12.72
	420734	AW972872	Hs.293738	ESTs	12.70
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily	12.50
	441377	BE218239	Hs.202656	ESTs	12.45
	435981	H74319	Hs.188620	ESTs	12.38
20	417296	L36156	Hs.81884	sulfotransferase family, cytosolic, 2A,	12.38
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	12.38
	459370	AA889982	Hs.271826	ESTs, Weakly similar to I38022 hypothe	12.34
	430290	AJ734110	Hs.136355	ESTs	12.30
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	12.26
25	450628	AW382884	Hs.204715	ESTs	12.24
	446232	AJ281848	Hs.194691	retinoic acid induced 3	12.16
	428223	AA424313	Hs.98402	ESTs	12.08
	432582	AJ623817	Hs.168457	ESTs	12.08
	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	12.02
30	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	12.01
	407202	N58172	Hs.109370	ESTs	11.84
	422109	S73265	Hs.1473	gastrin-releasing peptide	11.68
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ111980 fis, clone HE	11.68
	447532	AK000814	Hs.18791	hypothetical protein FLJ20607	11.67
35	443162	T49951	Hs.9029	DKFZP434G032 protein	11.67
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	11.62
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	11.46
	453909	AW004045	Hs.203365	ESTs	11.42
40	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	11.34
	452903	AJ953425	Hs.246911	ESTs, Weakly similar to I38022 hypothe	11.32
	433011	H07860	Hs.306044	CGI-05 protein	11.30
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	11.22
	455777	AA524285	Hs.154172	ESTs, Moderately similar to BCGF_HUMAN B	11.20
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	11.08
45	407168	R45175	Hs.117183	ESTs	10.91
	407633	NM_007069	Hs.37189	similar to rat HREV107	10.90
	400534				10.88
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	10.76
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	10.68
50	440626	AJ832243	Hs.211471	ESTs	10.63
	427544	AJ767152	Hs.181400	ESTs, Weakly similar to I78885 serratia	10.62
	447974	R76886		gb:Y164b03.s1 Soares placenta Nb2HP Homo	10.52
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	10.52
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	10.50
55	457065	AJ476318	Hs.192480	ESTs	10.40
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	10.38
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	10.34
	414718	H95348	Hs.107987	ESTs	10.29
	447506	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (tr	10.28
60	404567				10.14
	428536	AJ143139	Hs.2288	visinin-like 1	10.06
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	10.05
	437267	AW511443	Hs.258110	ESTs	10.00
	420583	H77859	Hs.65450	reticulin 4	10.00
65	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	9.99
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	9.97
	449555	AJ021987	Hs.59970	ESTs	9.91
	459504	BE514127		gb:601315974F1 NIH_MGC_8 Homo sapiens cD	9.90
	434609	R76593		gb:Y160c11.r1 Soares placenta Nb2HP Homo	9.90
70	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	9.88
	447853	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	9.84
	448106	AJ800470	Hs.171941	ESTs	9.64
	439192	AW970536	Hs.105413	ESTs	9.64
	446619	AJ076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	9.61
75	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	9.50
	440691	AA431599	Hs.132799	hypothetical protein FLJ23451	9.44
	440404	AJ015881	Hs.324527	mitochondrial ribosomal protein S5	9.40
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	9.36
	401742	NA		NA	9.30
80	416393	N54037	Hs.262869	plasminogen-like	9.28
	413339	AJ818080	Hs.194290	ESTs	9.28
	437641	AA811452	Hs.291911	ESTs	9.28
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (tr	9.22
	431319	AA873350	Hs.302232	ESTs	9.21

	434008	AA740878	Hs.112982	ESTs	9.20
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	9.16
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	9.16
5	413697	AW302885	Hs.117183	ESTs	9.15
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	9.14
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	9.14
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	9.05
	456653	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	8.98
10	450164	AI239923	Hs.30098	ESTs	8.95
	432867	AW016936	Hs.233364	ESTs	8.93
	437396	BE140398	Hs.21621	hypothetical protein DKFZp762O076	8.92
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	8.92
	452712	AW838616		gb:RC5-LT0054-140200-013-D01 LT0054 Homo	8.90
15	419131	AA406293	Hs.41167	ESTs	8.86
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	8.82
	418895	AA894638	Hs.14600	ESTs	8.82
	422665	AJ011812	Hs.119018	transcription factor NRF	8.82
	409757	NM_001898	Hs.123114	cystatin SN	8.78
20	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	8.74
	412446	AJ768015	Hs.92127	ESTs	8.71
	433285	AW975944	Hs.237396	ESTs	8.68
	414538	AW612228	Hs.107987	ESTs	8.64
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	8.62
25	430835	AI240006	Hs.192326	ESTs	8.60
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	8.59
	445537	AJ245871	Hs.12844	EGF-like-domain, multiple 6	8.52
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	8.52
	428355	BE256452	Hs.2257	vitronectin (serum spreading factor, som	8.50
30	444478	W07318	Hs.240	M-phase phosphoprotein 1	8.47
	439398	AA284267	Hs.221504	ESTs	8.44
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	8.43
	403776				8.42
	418973	AA233056	Hs.191518	ESTs	8.42
35	445436	AI224105	Hs.151408	ESTs	8.38
	417958	AA767382	Hs.193417	ESTs	8.34
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	8.34
	425761	AW664214	Hs.196729	ESTs	8.33
	449419	R34910	Hs.119172	ESTs	8.29
40	407007	U22961		gb:Human mRNA clone with similarity to L	8.28
	420900	AL045633	Hs.44269	ESTs	8.25
	452503	AB000509	Hs.29736	TNF receptor-associated factor 5	8.23
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	8.18
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	8.16
45	432363	AA534489		gb:ncf76g11.s1 NCI_CGAP_Co3 Homo sapiens	8.16
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	8.12
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	8.10
	418379	AA218940	Hs.137516	fidgetin-like 1	8.07
	424560	AA158727	Hs.150555	protein predicted by clone 23733	8.06
50	453116	AI276680	Hs.146086	ESTs	8.04
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	8.04
	409687	T51125	Hs.8493	ESTs	8.00
	407790	AI027274	Hs.288941	Homo sapiens cDNA FLJ14866 fis, clone PL	8.00
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	8.00
55	418036	Z37976	Hs.83337	latent transforming growth factor beta b	7.99
	422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	7.96
	421633	AF121860	Hs.106260	sorting nexin 10	7.92
	432542	AW083920	Hs.16098	claudin 2	7.86
	414869	AA157291	Hs.21479	ubiquitin 1	7.84
60	419502	AJ076704	Hs.90765	fibrinogen, A alpha polypeptide	7.80
	406666	V00495	Hs.184411	albumin	7.78
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.78
	439616	BE018635	Hs.58582	Homo sapiens cDNA FLJ12789 fis, clone NT	7.77
	406360	NA		NA	7.76
65	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	7.76
	431510	AA580082	Hs.112264	ESTs	7.76
	414312	AA155694	Hs.191060	ESTs	7.71
	443450	N66045	Hs.133529	ESTs	7.70
	449870	AI672487	Hs.15423	hypothetical protein HDCMC04P	7.64
70	425681	AB018297	Hs.159183	KIAA0754 protein	7.63
	408897	N50204	Hs.283709	lipopolysaccharide specific response-7 p	7.62
	443285	AI301918	Hs.334264	ESTs	7.60
	420807	AA280627	Hs.57846	ESTs	7.60
	424650	AW576156	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	7.60
75	410718	AJ920783	Hs.191435	ESTs	7.60
	430848	AW021726		gb:dZ7e02.y1 Morton Fetal Cochlea Homo	7.60
	434294	AJ271379	Hs.76194	ribosomal protein S5	7.60
	445808	AV655234	Hs.298083	ESTs, Moderately similar to PCA259 ferri	7.56
	438604	AA811896	Hs.44604	ESTs	7.54
80	458997	AW937420	Hs.69662	ESTs	7.54
	400289	X07620	Hs.2258	matrix metalloproteinase 10 (stromelysin	7.54
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	7.52
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 (Hsapi	7.49
	404996				7.48

	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	7.48
	433859	AW896758	Hs.273789	ESTs	7.44
	423952	AW877787	Hs.136102	KIAA0853 protein	7.44
5	431193	AW749505	Hs.296770	KIAA1719 protein	7.43
	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	7.40
	417479	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC	7.40
	424613	AL079850	Hs.151236	highly charged protein	7.37
	417720	AA205625	Hs.208067	ESTs	7.35
10	449347	AV649748	Hs.295901	KIAA0493 protein	7.34
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	7.34
	447499	AW262580	Hs.147674	protocadherin beta 16	7.32
	426890	AA393167	Hs.41294	ESTs	7.31
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	7.28
	445019	AI205540	Hs.281295	ESTs	7.28
15	419474	AW868619	Hs.155849	ESTs	7.24
	417015	M83772	Hs.80876	flavin containing monooxygenase 3	7.24
	411765	H43346		gb:yp09a04.r1 Soares breast 3NbhBst Homo	7.24
	448816	AB033052	Hs.22151	KIAA1226 protein	7.18
20	416143	AI955650	Hs.79033	glutaminyl-peptide cyclotransferase (glu	7.18
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	7.18
	420777	AA280223	Hs.130865	ESTs	7.16
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	7.14
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	7.14
25	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	7.14
	448706	AW291085	Hs.21814	interleukin 20 receptor, alpha	7.13
	441124	T97717	Hs.119563	ESTs	7.12
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	7.10
	446432	AI377320	Hs.150058	ESTs	7.10
30	439295	AW206091	Hs.253536	ESTs	7.08
	436902	AW247145	Hs.192729	ESTs	7.08
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	7.08
	414865	AA157155	Hs.274414	hypothetical protein FLJ14457	7.08
	421373	AA808229	Hs.167771	ESTs	7.06
35	432435	BE218866	Hs.282070	ESTs	7.05
	427933	AW974643	Hs.190571	ESTs	7.04
	436330	NM_004413	Hs.109	dipeptidase 1 (renal)	7.04
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	7.01
	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	6.98
40	446322	N23033	Hs.155814	ESTs	6.98
	442577	AA292998	Hs.163900	ESTs	6.96
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	6.94
	412280	AW205116	Hs.272814	hypothetical protein DKFZp434E1723	6.92
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	6.90
45	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	6.90
	453204	R10799	Hs.191890	ESTs	6.90
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.88
	427878	C05768	Hs.181022	CGI-07 protein	6.88
	454438	AA224053	Hs.172405	cell division cycle 27	6.86
50	424402	M63108	Hs.1769	luteinizing hormone/choriogonadotropin r	6.86
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	6.84
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	6.80
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	6.80
	419629	AB020695	Hs.91662	KIAA0888 protein	6.80
55	451686	AA059246	Hs.110293	ESTs	6.80
	430829	AW451999	Hs.194024	ESTs	6.78
	446501	AI302616	Hs.150819	ESTs	6.78
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	6.78
60	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.76
	437773	U24186	Hs.283018	replication protein A complex 34 kd subu	6.73
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	6.72
	425478	AB007953	Hs.268840	ESTs	6.70
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	6.70
	418555	AA17215	Hs.87159	hypothetical protein FLJ12577	6.67
65	453102	NM_007197	Hs.31664	trizzled (Drosophila) homolog 10	6.62
	433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.62
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.60
	450480	X82125	Hs.25040	zinc finger protein 239	6.58
	445191	AF048686	Hs.12393	dTDP-D-glucose 4,6-dehydratase	6.56
70	414575	H11257	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	6.54
	432639	AW973785		gb:EST385886 MAGE resequences, MAGM Homo	6.54
	410116	AW630671	Hs.58836	squamous cell carcinoma antigen recogniz	6.54
	449894	AK001578	Hs.24129	CLLL7 protein	6.53
	442914	AW188551	Hs.89519	hypothetical protein FLJ14007	6.53
75	424745	AA214618	Hs.152759	activator of S phase kinase	6.52
	441801	AW242799	Hs.86366	ESTs	6.52
	435542	AA687376	Hs.269533	ESTs	6.51
	427072	H38046	Hs.303193	ESTs	6.50
	418051	AW192535	Hs.19479	ESTs	6.46
80	436217	T53925	Hs.107	fibrinogen-like 1	6.46
	439809	R41396	Hs.101774	hypothetical protein FLJ23045	6.48
	430704	AW813091	Hs.335799	ESTs	6.44
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.43
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	6.41

	428392	H10233	Hs.2265	secretory granule, neuroendocrine protel	6.40
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	6.40
	438202	AW169287	Hs.22588	ESTs	6.38
	458311	AF069478		gb:AF069478 Homo sapiens astrocytoma fib	6.36
5	451389	N73222	Hs.279009	matrix Gla protein	6.36
	427899	AA829286	Hs.332053	serum amyloid A1	6.35
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.34
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	6.34
10	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	6.32
	433908	AW298141	Hs.157975	ESTs	6.32
	430114	AA847744	Hs.99640	ESTs	6.32
	434032	AW009951	Hs.206892	ESTs	6.31
	444656	AI277924	Hs.145199	ESTs	6.30
	433607	AA602004	Hs.23260	ESTs	6.26
15	440659	AF134160	Hs.7327	claudin 1	6.25
	435663	AI023707	Hs.134273	ESTs	6.24
	409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled	6.24
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like	6.24
	447500	AI381900	Hs.159212	ESTs	6.24
20	407237	AA169872	Hs.6216	Homo sapiens hepatocellular carcinoma-as	6.22
	417715	AW969587	Hs.86366	ESTs	6.22
	423276	AC003034	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	6.20
	438138	R98299	Hs.177502	ESTs	6.20
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	6.20
25	416857	AA188775	Hs.292453	ESTs	6.20
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	6.18
	429598	AA811257	Hs.269710	ESTs	6.18
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.18
	438940	AF075045	Hs.271609	ESTs	6.18
30	400195	NA	NA	NA	6.15
	430473	AW130690	Hs.59962	ESTs	6.12
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	6.10
	420096	AA775910	Hs.95011	syntrophin, beta 1 (dystrophin-associate	6.10
	427513	AI476318	Hs.192480	ESTs	6.10
35	448934	AI598134	Hs.225592	ESTs, Highly similar to T51146 ring-box	6.10
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	6.08
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	6.08
	424856	AA347746	Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	6.08
	409048	H59990	Hs.37699	ESTs	6.08
40	427674	NM_003528	Hs.2178	H2B histone family, member Q	6.08
	452689	F33868	Hs.284176	transferrin	6.06
	453804	AA300204	Hs.35276	KIAA0852 protein	6.06
	442875	BE623003	Hs.23625	Homo sapiens clone TCCTA00142 mRNA sequ	6.05
	408243	Y00787	Hs.624	interleukin 8	6.04
45	420721	AA927802	Hs.159471	ZAP3 protein	6.04
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	6.04
	435420	AI928513	Hs.59203	ESTs	6.04
	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	6.02
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	6.00
50	442116	AI884570	Hs.128813	ESTs	6.00
	423668	NM_005256	Hs.129818	growth arrest-specific 2	6.00
	422011	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	5.99
	441794	AW197794	Hs.253338	ESTs	5.99
	434739	AA804487	Hs.144130	ESTs	5.98
55	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	5.96
	420218	AW958037	Hs.286	ribosomal protein L4	5.96
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	5.94
	445548	AW468821	Hs.156054	ESTs	5.94
	439096	AA830185	Hs.269680	ESTs	5.94
60	452606	N45202	Hs.90012	hypothetical protein FLJ23441	5.94
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	5.94
	417246	AI760098	Hs.21411	ESTs	5.94
	433190	M26901	Hs.3210	renin	5.92
	418744	AI887288	Hs.196379	ESTs, Weakly similar to putative p150 [H	5.92
65	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	5.92
	434342	AI791138	Hs.116768	ESTs	5.92
	406688	T62745	Hs.184411	albumin	5.92
	418668	AW407987	Hs.173518	M-phase phosphoprotein homolog	5.90
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	5.90
70	408867	AA437199	Hs.656	cell division cycle 25C	5.90
	409913	BE243842	Hs.283077	centrosomal P4.1-associated protein; unc	5.88
	450380	AI863675	Hs.114017	ESTs	5.88
	413026	AA809485	Hs.124219	hypothetical protein FLJ12934	5.88
	454653	AW812227		gb:RC2-ST0173-201099-011-g09 ST0173 Homo	5.87
75	457876	AI821940	Hs.264622	ESTs, Moderately similar to ALLU8_HUMAN A	5.86
	437222	AL117588	Hs.12778	ESTs	5.86
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	5.86
	426269	HI5302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp556A1046 (f	5.84
	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434D0515 (f	5.84
80	441645	AI222279	Hs.201555	ESTs, Weakly similar to T23406 hypotheti	5.84
	401352				5.84
	419088	AI538323	Hs.52620	Integrin, beta 8	5.84
	431379	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	5.83

	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	5.82
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fs, clone NT	5.82
	419220	AA811938	Hs.291759	ESTs	5.82
	439303	W00605	Hs.102784	ESTs	5.80
5	415954	AA171850	Hs.42251	ESTs	5.80
	418849	AW474547	Hs.53555	Homo sapiens PIG-M mRNA for mannosyltran	5.80
	429945	NM_005729	Hs.226483	diaphanous (Drosophila, homolog) 2	5.80
	439527	AW298119	Hs.202536	ESTs	5.78
	435380	AA679001	Hs.192221	ESTs	5.78
10	424086	AI351010	Hs.102257	lysyl oxidase	5.76
	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	5.76
	428460	AA428865	Hs.98563	ESTs	5.74
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fs, clone C	5.74
	413982	BE503035	Hs.279193	ESTs	5.74
15	453240	AI969564	Hs.166254	hypothetical protein DKFZp5661133	5.74
	410505	AW752139	Hs.314323	ESTs	5.72
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.72
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	5.72
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	5.71
20	433384	AI021992	Hs.124244	ESTs	5.70
	415385	R17798	Hs.7535	COBW-like protein	5.70
	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	5.70
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	5.68
	448666	NM_014953	Hs.323346	KIAA1008 protein	5.68
25	412246	AI160873	Hs.69233	zinc finger protein	5.68
	426518	Z43039	Hs.170198	KIAA0009 gene product	5.66
	418269	AA806113	Hs.189025	ESTs	5.64
	443316	AI478463	Hs.18443	aldehyde dehydrogenase 8 family, member	5.64
	422805	AA436989	Hs.121017	H2A histone family, member A	5.62
30	442252	AI733395	Hs.129124	ESTs	5.60
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	5.60
	435040	AI932350	Hs.152825	ESTs	5.59
	438777	AA825487	Hs.142179	ESTs	5.58
	433849	BE465884	Hs.280728	ESTs	5.58
35	438639	AI278360	Hs.31409	ESTs	5.58
	411274	NM_002776	Hs.69423	kalikrein 10	5.55
	435008	AF150262	Hs.162898	ESTs	5.55
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	5.54
40	452881	AW135220	Hs.241921	ESTs	5.54
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	5.54
	424492	AI133482		gb:HA2093 Human fetal liver cDNA library	5.54
	418971	AA360392	Hs.87113	ESTs	5.52
	453716	AA037675	Hs.152675	ESTs	5.52
	406972	M32053		gb:Human H19 RNA gene, complete cds.	5.51
45	417543	AA203620	Hs.110153	ESTs	5.51
	419423	D26488	Hs.90315	KIAA0007 protein	5.51
	434674	AA831879	Hs.136985	ESTs	5.50
	442980	AA857025	Hs.8878	kinesin-like 1	5.50
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.50
50	404227	NA		NA	5.49
	412766	BE544475	Hs.54347	ESTs	5.49
	441708	AA69911	Hs.26498	hypothetical protein FLJ21657	5.49
	408432	AW195262		gb:cn67b05.x1 NCI_CGAP_CML1 Homo sapiens	5.48
55	437440	AA846804	Hs.123694	ESTs	5.48
	410486	AW235094	Hs.69233	zinc finger protein	5.46
	456435	AI880384	Hs.270747	ESTs, Weakly similar to ALU2_HUMAN ALU S	5.44
	437378	AI198823	Hs.160473	ESTs	5.44
	436907	AA737171	Hs.131809	ESTs	5.44
	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	5.44
60	413582	AW295647	Hs.71331	hypothetical protein MGC5350	5.42
	441795	NS8115	Hs.21137	AD024 protein	5.42
	452443	AW068658	Hs.20943	ESTs	5.42
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	5.40
65	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fs, clone CO	5.40
	441217	AI922183	Hs.213246	ESTs	5.40
	432383	AK000144	Hs.274449	Homo sapiens cDNA FLJ20137 fs, clone CO	5.40
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length Insert cDN	5.40
	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo	5.40
70	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fs, clone L	5.39
	446142	AI754693	Hs.145968	ESTs	5.38
	408562	AA436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	5.36
	433929	AI375499	Hs.27379	ESTs	5.36
	421155	H87879	Hs.102267	lysyl oxidase	5.34
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	5.34
75	453931	AL121278	Hs.25144	ESTs	5.34
	409091	AW970386	Hs.269423	ESTs	5.33
	416057	AI927382	Hs.29857	ESTs	5.33
	438647	AA813118	Hs.163230	ESTs	5.32
80	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.32
	445038	AI535444	Hs.143917	dJ467N11.1 protein	5.30
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fs, clone MA	5.30
	403432				5.29
	435820	AA700580	Hs.189000	ESTs	5.28

	401714	NA	NA	5.28
	449508	AK001566	Hs.23618 hypothetical protein FLJ10704	5.28
	413151	H47969	Hs.141971 ESTs, Weakly similar to ALU1_HUMAN ALU S	5.28
	414853	U31116	Hs.77501 sarcoglycan, beta (43kD dystrophin-assoc	5.28
5	417372	T99755	Hs.334728 ESTs	5.28
	443613	AI079356	gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapi	5.28
	412610	X90908	Hs.74126 fatty acid binding protein 6, ileal (gas	5.27
	408943	NM_007070	Hs.49105 FKBP-associated protein	5.26
10	415139	AW975942	Hs.48524 ESTs	5.26
	447982	H22953	Hs.137551 ESTs	5.26
	430789	AA632577	Hs.310235 ESTs, Weakly similar to I78885 serine/th	5.24
	453921	AI824009	Hs.44577 ESTs	5.24
	409582	R27430	Hs.271565 ESTs	5.24
15	420911	U77413	Hs.100293 O-linked N-acetylglucosamine (GlcNAc) tr	5.23
	422956	BE545072	Hs.122579 hypothetical protein FLJ10461	5.23
	418661	NM_001949	Hs.1189 E2F transcription factor 3	5.22
	446271	D82484	Hs.330994 ESTs	5.22
	435905	AW997484	Hs.5003 KIAA0456 protein	5.21
20	434551	BE387162	Hs.280858 ESTs, Highly similar to A35661 DNA excis	5.21
	415245	N59650	Hs.27252 ESTs	5.20
	436016	AA806465	Hs.121536 Human DNA sequence from clone RP11-472E5	5.20
	431242	AA987742	Hs.251278 KIAA1201 protein	5.20
	439818	AL360137	Hs.19934 Homo sapiens mRNA full length insert cDN	5.20
25	424281	AA766243	gb:aa13b11.s1 NCL_CGAP_GCB1 Homo sapiens	5.20
	449138	AW294215	Hs.195631 ESTs	5.20
	449416	AI651016	Hs.246311 ESTs	5.20
	430092	AI821399	Hs.16514 ESTs	5.20
	436574	AW293527	Hs.126465 ESTs	5.18
30	433377	AI752713	Hs.43845 ESTs	5.18
	440987	AA911705	Hs.130229 ESTs	5.18
	426116	AA868729	Hs.144694 ESTs	5.18
	441928	AI370188	Hs.211454 ESTs	5.17
35	432657	AA831815	Hs.270940 ESTs, Weakly similar to I78885 serine/th	5.17
	438011	BE466173	Hs.145696 splicing factor (CC1.3)	5.16
	437257	AI283085	Hs.290931 ESTs, Weakly similar to YFJ7_YEAST HYPOT	5.16
	423926	X03833	Hs.1722 interleukin 1, alpha	5.16
	433393	AF038564	Hs.98074 itchy (mouse homolog) E3 ubiquitin prote	5.15
	415757	AA830854	Hs.187810 ESTs	5.14
40	420170	U43374	Hs.95631 Human normal keratinocyte mRNA	5.14
	420493	AI635113	Hs.270366 ESTs, Weakly similar to I78885 serine/th	5.12
	425739	T19016	Hs.159410 molybdopterin synthase sulfurylase	5.12
	440652	AI216751	Hs.143977 ESTs	5.12
	419706	C04649	Hs.77899 tropomyosin 1 (alpha)	5.12
45	427728	AJ245600	Hs.180545 Homo sapiens mRNA for hypothetical prote	5.12
	416113	AA173525	Hs.118758 ESTs, Weakly similar to RLF [H.sapiens]	5.12
	446223	BE300091	Hs.119699 hypothetical protein FLJ12969	5.11
	407624	AW157431	Hs.248941 ESTs	5.11
50	447197	R36075	gb:zh88b01.s1 Soares placenta Nb2HP Homo	5.11
	452465	AA610211	Hs.34244 ESTs	5.10
	442833	AA328153	Hs.88201 ESTs, Weakly similar to A Chain A, Cryst	5.10
	448952	AI609595	Hs.208038 ESTs	5.10
	408170	AW204516	Hs.31835 ESTs	5.08
	424238	AA337401	Hs.137635 ESTs	5.07
55	421072	AI216069	Hs.89113 ESTs	5.06
	424717	H03754	Hs.152213 wingless-type MMTV integration site fami	5.06
	423654	AI674253	Hs.35828 ESTs	5.06
	436862	AI821940	Hs.264622 ESTs, Moderately similar to ALU8_HUMAN A	5.05
	436554	AI985810	Hs.301173 ESTs	5.05
60	433264	D85782	Hs.3229 cysteine dioxygenase, type I	5.04
	452387	AI680772	Hs.306094 trinucleotide repeat containing 12	5.04
	412666	AL080116	Hs.74420 origin recognition complex, subunit 3 (y	5.03
	430287	AW182459	Hs.125759 ESTs, Weakly similar to LEU5_HUMAN LEUKE	5.03
	413293	AL047483	Hs.302498 GTP-binding protein homologous to Saccha	5.00
65	418217	AI910647	Hs.13442 ESTs	5.00
	401480	NA	NA	5.00
	456179	H75490	Hs.271930 ESTs	5.00

TABLE 7B

70	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
<hr/>			
75	Pkey	CAT number	Accession
	408432	1058667_1	AW195262 R27868 AW811262
	408690	107490_1	AW864542 AA056567 AW882724
	411765	125700_1	H43346 AA248302 AA095182
	414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
80	424281	237742_1	AA766243 AA338252 AA338213

5	424492	240008_1	AI133482 AI207619 AA341626
	428679	294049_1	AA431765 AA432015
	430848	324621_1	AW021726 AA487752 AA488085
	432340	345248_1	AA534222 AA632632 T81234
	432363	345469_1	AA534489 AW970240 AW970323
	432639	351744_1	AW973785 H60163 AA557608
	434609	38950_1	R76593 AF147390 R76594
	439518	47334_1	W76326 AF086341 W72300
10	443613	575391_1	AI078356 W23287
	447197	711623_1	R36075 AI366546 R36167
	447974	745643_1	R76886 AI453674 R77049
	452712	828309_1	AW838616 AW838660 BE144343 AI914520 AW888910 BE184854 BE184784
	454653	1228081_1	AW812227 AW812294 AW812092
15	458311	543550_1	AF069478 AF069479 AF069480

TABLE 7C

20	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	NI_position:	Indicates nucleotide positions of predicted exons.

25	Pkey	Ref	Strand	NI_position
	400534	6981826	Minus	278637-279292
	401352	9931258	Minus	26064-26208
30	401480	7321503	Plus	166120-166347,166451-166557,169651-169832
	401714	6715702	Plus	96484-96681
	401742	2911728	Plus	64003-64147
	403432	9719611	Minus	68204-68392
	403776	7770611	Minus	1414-1513,1624-1756
	404227	7838233	Minus	93110-93259
35	404567	7249169	Minus	101320-101501
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	406360	9256107	Minus	7513-7673

40 Table 8A shows 538 genes significantly down-regulated in colon cancer compared to normal colon. These were selected as for Table 7A and the ratio was equal to or less than than 0.33.

TABLE 8A: 538 GENES SIGNIFICANTLY DOWN-REGULATED IN COLON CANCER COMPARED TO NORMAL COLON

45	Pkey:	Unique Eos probeset identifier number
	ExAccon:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
50	R1:	Ratio of tumor to normal colon

	Pkey	ExAccon	UnigeneID	Unigene Title	R1
55	421996	AW583807	Hs.1460	glucagon	0.0233
	429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	0.0307
	457407	AA505035	Hs.195651	ESTs	0.0416
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PNM099 son3 prot	0.0564
	426651	AU076646	Hs.171683	nuclear receptor subfamily 1, group H, m	0.0567
60	425920	AL049977	Hs.162209	claudin 8	0.0601
	431436	AA505035	Hs.195651	ESTs	0.0607
	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	0.0629
	442009	AJ733281	Hs.128320	ESTs	0.0634
	416889	AW250318	Hs.80395	mat, T-cell differentiation protein	0.0707
65	429050	X81333	Hs.194777	meprin A, beta	0.0714
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	0.0735
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	0.0739
	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protein	0.0769
	443506	H10661	Hs.192124	ESTs, Weakly similar to I38022 hypotheti	0.0838
70	415314	N88802	Hs.5422	glycoprotein M6B	0.0853
	451181	AJ798330	Hs.207461	ESTs	0.0873
	429001	AF098961	Hs.194720	ATP-binding cassette, sub-family G (WHIT	0.0888
	426635	BE395109	Hs.129327	hypothetical protein MGC13057	0.0900
	429350	AJ754634	Hs.131987	ESTs	0.0927
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	0.0931

5	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	0.0951
	441066	AW205427	Hs.190726	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.0957
	431252	NM_005478	Hs.251380	insulin-like 5	0.0985
	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	0.0987
	433546	AI075877	Hs.125461	hypothetical protein FLJ11539	0.1007
10	415154	D63175		gb:HUMS01809B Clontech human placenta po	0.1032
	409921	AW600239		gb:EST00009 pGEM-T library Homo sapiens	0.1067
	432440	X63597	Hs.2996	sucrase-isomaltase	0.1107
	430468	NM_004673	Hs.241519	angiotensin-like 1	0.1114
	427167	AI239607	Hs.99196	hypothetical protein MGC11324	0.1147
15	441212	AW242447	Hs.146182	cytosolic beta-glucosidase	0.1167
	423605	AF047826	Hs.129887	cadherin 19, type 2	0.1190
	411381	AW841862	Hs.306831	Homo sapiens cDNA: FLJ22549 fis, clone H	0.1211
	412639	AW961284	Hs.296235	ESTs	0.1239
	453399	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	0.1240
20	403548				0.1248
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	0.1274
	457982	AW856093	Hs.183617	ESTs	0.1277
	448835	BE277929	Hs.11081	UBX domain-containing 2	0.1277
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	0.1291
25	441805	AA285136	Hs.301914	neuronal specific transcription factor D	0.1309
	407639	AW205369	Hs.312830	ESTs	0.1315
	421741	AK001879	Hs.107527	hypothetical protein FLJ11017	0.1325
	454790	AW820852		gb:RC2-ST0301-120200-011-412 ST0301 Homo	0.1328
	451742	T77690	Hs.117970	ankyrin 2, neuronal	0.1335
30	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	0.1379
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	0.1393
	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	0.1396
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	0.1456
	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	0.1459
35	404767				0.1460
	407265	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	0.1462
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	0.1463
	452768	AW069459	Hs.61539	ESTs	0.1466
	418692	AK000268	Hs.87383	hypothetical protein	0.1471
40	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	0.1471
	407551	Y10516		gb:H.sapiens mRNA for CD58 T3 protein.	0.1486
	402076				0.1487
	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	0.1500
	442080	AW444761	Hs.44565	ESTs	0.1500
45	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	0.1513
	429545	AI824164	Hs.77667	lymphocyte antigen 6 complex, locus E	0.1523
	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myo	0.1529
	435056	AW023337	Hs.5422	glycoprotein M6B	0.1532
	426034	AI276899	Hs.56123	Homo sapiens cDNA FLJ13443 fis, clone PL	0.1538
50	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	0.1542
	408221	AA912183	Hs.47447	ESTs	0.1552
	425220	AW975317	Hs.162987	ESTs	0.1558
	445200	AA084460	Hs.12409	somatostatin	0.1558
	443238	T78886	Hs.284450	ESTs	0.1563
55	456064	AA256213	Hs.72010	ESTs	0.1582
	428133	AW167727	Hs.11873	ESTs	0.1605
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	0.1615
	437734	AA693951	Hs.180284	ESTs	0.1637
	414290	AI568801	Hs.71721	ESTs	0.1638
60	418935	T28499	Hs.89485	carbonic anhydrase IV	0.1656
	411939	AI365585	Hs.146246	ESTs	0.1660
	442496	R55073	Hs.124130	ESTs	0.1676
	450693	AW450461	Hs.203965	ESTs	0.1698
	420736	AI263022	Hs.82204	ESTs	0.1718
65	405385				0.1745
	404638				0.1751
	427333	AF067797	Hs.176658	aquaporin 8	0.1757
	404246				0.1763
	433785	BE044593	Hs.112704	ESTs	0.1767
70	412056	T28160	Hs.778	guanylate cyclase activator 1B (retina)	0.1769
	406980	S69265		(NONE)	0.1781
	421686	AL035250	Hs.1408	endothelin 3	0.1784
	452854	AA437061	Hs.14060	prokineticin 1 precursor	0.1795
	400514				0.1805
75	454186	BE141030		gb:MRD-HT0067-201099-002-h11 HT0067 Homo	0.1808
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	0.1812
	413724	AA131466	Hs.23757	hypothetical protein FLJ12666	0.1812
	412474	AI791451		gb:n50c09.y5 NCI_CGAP_Ov2 Homo sapiens	0.1812
	436008	AI078428	Hs.58785	ESTs	0.1820
80	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	0.1828
	431728	NM_007351	Hs.268107	multimerin	0.1832
	419746	AW857943	Hs.127216	hypothetical protein FLJ13465	0.1835
	410677	NM_003278	Hs.65424	telranectin (plasminogen-binding protein	0.1838
	415672	N53097	Hs.193579	ESTs	0.1838
	419050	NM_000036	Hs.89570	adenosine monophosphate deaminase 1 (iso	0.1838
	417342	W40277	Hs.81994	glycophorin C (Gerbich blood group)	0.1842
	413714	AI560944	Hs.71428	ESTs	0.1845

	427061	AB032971	Hs.173392	KIAA1145 protein	0.1847
	405282				0.1848
	400163				0.1855
5	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.1863
	447414	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	0.1876
	407891	AA486620	Hs.41135	endomucin-2	0.1895
	437140	AA312799	Hs.283689	activator of CREM in testis	0.1901
	431544	AK000770	Hs.299329	Homo sapiens cDNA FLJ20763 fis, clone CO	0.1904
10	436659	AI217900	Hs.144464	ESTs	0.1905
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	0.1926
	453698	AA037615	Hs.42746	ESTs	0.1928
	423743	AB023148	Hs.173373	KIAA0931 protein	0.1941
	428412	AA428240	Hs.126083	ESTs	0.1942
15	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	0.1944
	434683	AW298724	Hs.202639	ESTs	0.1957
	421885	AA609911	Hs.109012	MAX dimerization protein	0.1957
	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	0.1969
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	0.1881
20	419758	U31973	Hs.93173	phosphodiesterase 6C, cGMP-specific, con	0.2004
	437740	AA810265	Hs.122915	ESTs	0.2016
	405610				0.2017
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	0.2025
	416961	BE391478	Hs.80617	ribosomal protein S16	0.2041
25	401465				0.2045
	437425	AW183714	Hs.20981	hypothetical protein DKFZp547M238	0.2049
	416231	H30333	Hs.165062	ESTs	0.2049
	401753				0.2050
	433430	AI863735	Hs.186755	ESTs	0.2051
30	432150	AK000224	Hs.272789	hypothetical protein FLJ20217	0.2052
	411644	H92064	Hs.278626	Arg/Abi-interacting protein ArgBP2	0.2059
	403957				0.2063
	435900	AI243036	Hs.16094	ESTs	0.2070
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	0.2075
35	445500	AW451938	Hs.257512	ESTs	0.2075
	419956	AL137939	Hs.40096	ESTs	0.2090
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	0.2093
	423655	AA722425	Hs.182785	ESTs, Moderately similar to 1207289A rev	0.2118
	401381				0.2120
40	426452	AW614271	Hs.121647	ESTs, Highly similar to AC006014.8 simil	0.2122
	433476	AA594394	Hs.152616	ESTs	0.2125
	423405	NM_014151	Hs.128155	HSPC053 protein	0.2130
	442826	AI018777	Hs.131241	ESTs	0.2132
	427060	AW378993	Hs.90286	ESTs	0.2137
45	437354	AA749215	Hs.291886	ESTs	0.2137
	447734	AI421412	Hs.163659	ESTs	0.2144
	424585	AA464840	Hs.131987	ESTs	0.2146
	458016	AW188039	Hs.131813	ESTs	0.2151
	423893	AL031709	Hs.134846	Human DNA sequence from clone 316G12 on	0.2151
	401521				0.2157
50	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (0.2165
	401024				0.2171
	414802	AI793107	Hs.27018	Rts	0.2179
	441083	BE562611		gb:601336446F1 NIH_MGC_44 Homo sapiens c	0.2185
55	417355	D13168	Hs.82002	endothelin receptor type B	0.2186
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	0.2188
	442930	AW881975	Hs.213923	ESTs	0.2193
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	0.2209
	444567	AV654020	Hs.184261	ESTs, Weakly similar to T26686 hypotheti	0.2212
	405854				0.2217
60	415471	F09747	Hs.268707	ESTs	0.2222
	449243	AW295031	Hs.198671	ESTs	0.2229
	436088	AA704687	Hs.191294	ESTs	0.2232
	434098	AA625499		gb:af69g08.r1 Soares_NihHMPu_S1 Homo sapi	0.2242
	427552	NM_005771	Hs.179508	retinol dehydrogenase homolog	0.2243
65	416439	AA180363	Hs.118769	ESTs	0.2244
	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	0.2254
	459395	Z30300	Hs.281935	ESTs	0.2257
	439039	AI658707	Hs.48713	ESTs	0.2268
70	433576	AA600175	Hs.39720	ESTs	0.2268
	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	0.2273
	428415	AA337211	Hs.184222	Down syndrome critical region gene 1	0.2283
	441899	AI372588	Hs.8022	TU3A protein	0.2283
	437191	NM_005846	Hs.331555	serine protease inhibitor, Kazal type, 5	0.2290
75	434839	AI743069	Hs.134736	ESTs	0.2294
	435731	AA699581	Hs.186811	ESTs	0.2299
	400865				0.2304
	446294	AI284935		gb:qk55g09.x1 NCL_CGAP_Co8 Homo sapiens	0.2305
80	414193	BE260069		gb:601150964F1 NIH_MGC_19 Homo sapiens c	0.2309
	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	0.2315
	453098	Z25935	Hs.86379	ESTs	0.2315
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	0.2319
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	0.2320
	443482	AW188093	Hs.250385	ESTs	0.2326

5	432134	AI816782	Hs.122583	hypothetical protein FLJ21934	0.2329
	421539	AA292747	Hs.97296	ESTs	0.2330
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	0.2344
	408001	AA046458	Hs.95285	ESTs	0.2347
	409331	M36634	Hs.53973	vasoactive intestinal peptide	0.2351
10	431094	AW972276	Hs.116195	ESTs	0.2354
	429575	AA706003	Hs.99387	ESTs	0.2358
	404958				0.2361
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	0.2364
	452742	AW589945	Hs.97876	hypothetical protein DKFZp564K0322	0.2380
15	417511	AL049176	Hs.82223	chordin-like	0.2381
	404927				0.2387
	430297	AW243166	Hs.129806	ESTs	0.2412
	447482	AB033059	Hs.18705	KIAA1233 protein	0.2415
	418332	R34976	Hs.78293	ESTs	0.2416
20	454145	AA046872	Hs.62798	ESTs	0.2421
	422472	R59096	Hs.279939	mitochondrial carrier homolog 1	0.2424
	404070				0.2427
	421232	AA989220	Hs.292100	ESTs	0.2427
	414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens c	0.2432
25	412622	AW664708	Hs.171959	ESTs	0.2433
	454430	AI082777	Hs.61384	sema domain, seven thrombospondin repeat	0.2437
	416894	AW161284	Hs.79564	neuronal PAS domain protein 1	0.2443
	426724	AA383623	Hs.293616	ESTs	0.2444
	405073				0.2445
30	401236	H24185	Hs.92918	hypothetical protein	0.2451
	414203	BE262170	Hs.78629	ATPase, Na ⁺ /K ⁺ transporting, beta 1 poly	0.2452
	401776				0.2462
	404696				0.2471
	426666	AW500131	Hs.171763	CD22 antigen	0.2474
35	427078	AI676082	Hs.111902	ESTs	0.2478
	424682	AW604804	Hs.151717	KIAA0437 protein	0.2481
	440383	AA884208	Hs.30484	ESTs	0.2494
	419118	AA234223	Hs.139204	ESTs	0.2495
	443515	AV657547	Hs.288014	Homo sapiens, clone IMAGE:3867243, mRNA	0.2499
40	424648	AA344576		gb:EST50478 Gall bladder I Homo sapiens	0.2500
	404805				0.2505
	446066	AI343931	Hs.149383	ESTs	0.2506
	408345	R93851	Hs.63063	ESTs	0.2508
	418358	L02840	Hs.84244	potassium voltage-gated channel, Shab-re	0.2510
45	416950	AL049798	Hs.80552	dermatopontin	0.2513
	423555	AW958201	Hs.178589	hepatocellular carcinoma antigen gene 52	0.2515
	449833	R82252	Hs.106106	protein kinase (cAMP-dependent, catalytic)	0.2519
	459275	AI808913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	0.2523
	405897	M57417		gb:Homo sapiens mucin (mucin) mRNA, part	0.2526
50	422743	BE304678	Hs.119598	ribosomal protein L3	0.2532
	459688	U72671	Hs.151250	intercellular adhesion molecule 5, telom	0.2536
	450880	AK002183	Hs.285885	Homo sapiens cDNA FLJ11321 fis, clone PL	0.2536
	457330	AB013818	Hs.247220	peroxisome biogenesis factor 10	0.2536
	451979	F06972	Hs.27372	BMX non-receptor tyrosine kinase	0.2549
55	440274	R24595	Hs.7122	scrapie responsive protein 1	0.2553
	430097	AI523245	Hs.127638	ESTs	0.2558
	410626	BE407727		gb:601299771F1 NIH_MGC_21 Homo sapiens c	0.2564
	402695				0.2565
	453992	AW014995	Hs.281080	ESTs	0.2569
60	453888	AW450670	Hs.252819	ESTs	0.2569
	401371				0.2574
	456145	BE299427	Hs.21446	KIAA1716 protein	0.2579
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiester	0.2580
	422591	L07648	Hs.118630	MAX-interacting protein 1	0.2582
65	452359	BE167229	Hs.29206	hypothetical protein MGC14376	0.2584
	447569	AI393202	Hs.147554	hypothetical protein FLJ23392	0.2586
	405880				0.2588
	420321	D78761	Hs.96857	hypothetical protein	0.2595
	454415	AK000846	Hs.58679	solute carrier family 7, (cationic amino	0.2602
70	437032	AW867372	Hs.302063	Immunoglobulin heavy constant mu	0.2604
	448025	BE502965	Hs.170426	ESTs	0.2605
	444304	AW828433	Hs.271296	ESTs, Weakly similar to I54374 gene NF2	0.2605
	424885	AI333771	Hs.82204	ESTs	0.2608
	425381	D84371	Hs.1898	paraoxonase 1	0.2611
75	457413	AA743462	Hs.165337	ESTs	0.2618
	452078	AA022620	Hs.52170	ESTs	0.2624
	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	0.2628
	401974				0.2639
	411319	BE537094		gb:601063333F1 NIH_MGC_10 Homo sapiens c	0.2646
80	417761	R13727	Hs.21435	ESTs	0.2648
	426132	AA370501		gb:EST82261 Prostate gland I Homo sapien	0.2653
	455771	BE084820	Hs.186711	hypothetical protein FLJ20070	0.2653
	414349	BE512968		gb:601172296F1 NIH_MGC_15 Homo sapiens c	0.2660
	402182				0.2660
	402610				0.2661
	444814	BE010749	Hs.255097	ESTs	0.2663
	450017	W56434	Hs.201608	ESTs	0.2663

5	408684	R61377	Hs.12727	hypothetical protein FLJ21610	0.2667
	444209	A1753134	Hs.146494	ESTs	0.2668
	415022	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid	0.2677
	416184	R48481	Hs.269177	ESTs, Weakly similar to ALU6_HUMAN ALU S	0.2681
	422909	AA533356		gb:ng67110.s1 NCI_CGAP_Pr10 Homo sapiens	0.2681
10	412047	AA934589	Hs.49696	ESTs	0.2693
	426356	BE536836	Hs.98682	hypothetical protein FKSG32	0.2703
	442238	AW135374	Hs.270949	ESTs, Moderately similar to F41925 hypot	0.2709
	402425				0.2710
	450545	AW135582	Hs.201767	ESTs	0.2710
15	417118	U38654	Hs.50477	RAB27A, member RAS oncogene family	0.2725
	419850	F06844		gb:HSC1ME091 normalized infant brain cDN	0.2727
	428020	L19058	Hs.181581	glutamate receptor, ionotropic, kainate	0.2730
	441493	AW070446	Hs.127037	ESTs	0.2733
	413541	BE147036		gb:QV4-HT0222-091199-024-e10 HT0222 Homo	0.2733
20	428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	0.2734
	455597	BE008545	Hs.156110	immunoglobulin kappa constant	0.2740
	447809	AW207605	Hs.164230	ESTs, Highly similar to JC7266 3',5'-cyc	0.2740
	444195	A9002351	Hs.10587	KIAA0353 protein	0.2743
	415160	T82802		gb:yd38a04.r1 Soares fetal liver spleen	0.2747
25	421823	N40850	Hs.28625	ESTs	0.2755
	434464	BE063921	Hs.295971	ESTs	0.2755
	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [0.2756
	430073	U86136	Hs.232070	telomerase-associated protein 1	0.2762
	432018	AA524447	Hs.152377	ESTs	0.2763
30	422954	AW998605		gb:PM0-BN0065-100300-001-b10 BN0065 Homo	0.2768
	416397	H53035	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	0.2775
	442420	A1024834	Hs.131729	ESTs	0.2775
	410950	AW811633		gb:RC2-ST0158-091099-011-d05 ST0158 Homo	0.2778
	427114	A1219896	Hs.97592	ESTs	0.2778
35	448466	A1522109	Hs.171066	ESTs	0.2778
	434445	A1349306	Hs.11782	ESTs	0.2784
	457115	AA420712		gb:nc63c07.s1 NCI_CGAP_Pr1 Homo sapiens	0.2785
	459511	A1142379		gb:ng64c01.r1 Soares testis_NHT Homo sap	0.2786
	421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase (alanine	0.2794
40	433633	A1880516	Hs.84630	ESTs, Weakly similar to 2004399A chromos	0.2799
	440236	AW996722	Hs.125297	ESTs	0.2799
	405691				0.2804
	405334				0.2804
	403047				0.2809
45	412506	AW957159		gb:EST369229 MAGE resequences, MAGD Homo	0.2809
	441042	AA077736		gb:7B48A07 Chromosome 7 Fetal Brain cDNA	0.2815
	434660	AA764768	Hs.121158	hypothetical protein DKFZp434J0113	0.2816
	444453	AW379394	Hs.145126	ESTs	0.2817
	457736	AK000390	Hs.4206	hypothetical protein FLJ20124	0.2820
50	454012	M76424	Hs.37014	carbonic anhydrase VII	0.2821
	427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombo	0.2822
	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epithe	0.2827
	435021	AA922192	Hs.54709	ESTs	0.2828
	413344	U46024	Hs.75302	myotubular myopathy 1	0.2837
55	447787	BE620108		gb:601483015F1 NIH_MGC_69 Homo sapiens c	0.2840
	457290	AA465293	Hs.105069	ESTs	0.2841
	468244	A1929453	Hs.122489	Homo sapiens cDNA FLJ13289 fs, clone OV	0.2841
	437483	AL390174		gb:Homo sapiens mRNA; cDNA DKFZp547J184	0.2842
	407938	AA905097	Hs.85050	phospholamban	0.2845
60	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	0.2846
	428212	AW444451	Hs.134812	ESTs	0.2853
	424433	H04607	Hs.9218	ESTs	0.2857
	425195	AA352026	Hs.94319	VPS10 domain receptor protein	0.2857
	404769				0.2863
65	411620	AW854536		gb:RC3-CT0255-200100-024-e08 CT0255 Homo	0.2868
	428746	AW503820	Hs.192861	Spl-B transcription factor (Spl-1/PU.1 r	0.2870
	431822	AA516049		gb:ng65d01.s1 NCI_CGAP_Uip2 Homo sapiens	0.2872
	441290	W27501	Hs.89605	cholinergic receptor, nicotinic, alpha p	0.2874
	422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	0.2877
70	421935	AA131632	Hs.109672	CMP-NeuAC;(beta)-N-acetylglucosaminide	0.2878
	447955	BE544271	Hs.288390	hypothetical protein FLJ22795	0.2880
	405364				0.2881
	422165	AL041199	Hs.1481	histidine decarboxylase	0.2882
	431087	H12723	Hs.290791	ESTs	0.2882
75	450610	AA010370	Hs.60386	nuclear RNA export factor 3	0.2882
	445627	AW818475	Hs.7363	ESTs	0.2883
	436144	AW881250	Hs.148367	ESTs	0.2886
	445152	A1214667	Hs.283597	ESTs	0.2891
	430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	0.2891
80	455614	A1693369	Hs.202274	ESTs	0.2899
	419683	AA248897	Hs.48784	ESTs	0.2900
	411886	AL046810	Hs.20021	vesicle-associated membrane protein 1 (s	0.2904
	430770	AA765694	Hs.123296	ESTs	0.2913
	444459	A1680624	Hs.148676	ESTs	0.2913
	444918	A1202282	Hs.283362	ESTs	0.2915
	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	0.2915
	435598	AA689470	Hs.163026	ESTs	0.2921

5	413056	BE063031		gb:MR0-BT0265-231199-002-e09 BT0265 Homo	0.2922
	443998	AI620661	Hs.296276	ESTs	0.2924
	424412	H15512	Hs.10043	hypothetical protein FLJ13074	0.2925
	421204	AW081587	Hs.165051	ESTs	0.2928
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	0.2938
10	440507	H06994		gb:yl81b07.r1 Soares infant brain INIS H	0.2943
	445555	AW974013	Hs.260809	ESTs	0.2945
	438570	AW888554	Hs.84298	CD74 antigen (invariant polypeptide of m	0.2948
	447195	T73745	Hs.279870	ESTs, Weakly similar to A46010 X-linked	0.2950
	423267	AL137416	Hs.126177	Homo sapiens mRNA; cDNA DKFZp434O192 (fr	0.2956
15	421920	BE551245	Hs.1438	gamma-aminobutyric acid (GABA) receptor,	0.2956
	412177	Z23091	Hs.73734	glycoprotein V (platelet)	0.2959
	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	0.2959
	433745	AF075320	Hs.28880	hypothetical protein FLJ14540	0.2969
	417935	R53697	Hs.170044	ESTs	0.2970
20	420674	NM_000055	Hs.1327	butyrylcholinesterase	0.2973
	413537	BE146866		gb:QV4-HT0222-211099-014-r06 HT0222 Homo	0.2973
	445194	AI215667	Hs.175044	ESTs	0.2974
	454135	AW135965	Hs.246783	ESTs	0.2976
	403418				0.2988
25	457605	AV657778	Hs.3314	setenoprotein P, plasma, 1	0.2989
	408896	AI610447	Hs.48778	niban protein	0.2993
	448542	BE256176	Hs.278712	eukaryotic translation initiation factor	0.2994
	417945	R29072		gb:F1-101D 22 week old human fetal liver	0.2994
	412518	BE047637	Hs.173739	hypothetical protein FLJ10297	0.2996
30	424566	M16801	Hs.1790	nuclear receptor subfamily 3, group C, m	0.2997
	430778	D80337	Hs.247916	natriuretic peptide precursor C	0.3000
	451531	AA018311	Hs.114762	ESTs	0.3003
	444926	AI202492	Hs.212933	ESTs, Weakly similar to CLD4_HUMAN CLAUD	0.3003
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	0.3012
35	459456	AA486036	Hs.190124	ESTs	0.3012
	417111	AW016321	Hs.82306	desitin (actin depolymerizing factor)	0.3012
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	0.3012
	451959	AA056203	Hs.27337	hypothetical protein FLJ20623	0.3012
	410482	AW772187	Hs.191859	ESTs	0.3013
40	417700	M36542	Hs.1101	POU domain, class 2, transcription facto	0.3018
	404414				0.3019
	432247	AA531287	Hs.105805	ESTs	0.3023
	453471	AL037887	Hs.208179	ESTs	0.3028
	417481	AA203281	Hs.21798	ESTs	0.3029
45	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	0.3032
	448744	AL135424	Hs.9469	pleckstrin homology domain-containing, f	0.3033
	429223	BE284152	Hs.221994	ESTs	0.3034
	404501	AW247252	Hs.75514	nucleoside phosphorylase	0.3037
	406829	AW419128	Hs.84298	CD74 antigen (invariant polypeptide of m	0.3039
50	438839	AW297945	Hs.128490	ESTs	0.3039
	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	0.3042
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	0.3045
	458789	AL157468	Hs.325825	Homo sapiens cDNA FLJ20848 fs, clone AD	0.3048
	443294	AI733625	Hs.133053	ESTs	0.3050
55	447023	AA356764	Hs.17109	integral membrane protein 2A	0.3052
	458583	AI479348	Hs.157081	hypothetical protein MGC4170	0.3058
	414567	BE281057	Hs.184519	hypothetical protein FLJ12849	0.3057
	445123	AI762911	Hs.145369	ESTs	0.3064
	412682	AW983772		gb:RC3-HN0002-060400-012-h09 HN0002 Homo	0.3065
60	434361	AF129755	Hs.117772	ESTs	0.3071
	414026	BE241713		gb:TCAAP1ED472 Pediatric acute myelogeno	0.3072
	432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	0.3073
	408350	AW183350	Hs.250127	ESTs	0.3074
	401042				0.3077
65	422586	AA312704	Hs.59457	hypothetical protein FLJ22127	0.3077
	438692	AB007950	Hs.6360	KIAA0481 gene product	0.3077
	447452	BE618258	Hs.102480	Homo sapiens, clone IMAGE:3869590, mRNA,	0.3083
	444414	AW293214	Hs.8752	transmembrane protein 4	0.3085
	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fs, clone L	0.3088
70	430410	AF099144	Hs.250700	trypsin beta 1	0.3090
	419299	AI311085	Hs.62406	hypothetical protein FLJ22573	0.3091
	400572				0.3094
	444010	AW976457	Hs.282887	ESTs	0.3096
	451699	AL118571	Hs.121657	ESTs, Weakly similar to DP1_HUMAN POLYPO	0.3096
75	432471	BE244667	Hs.296155	CGI-100 protein	0.3105
	405277				0.3106
	455765	AM97900	Hs.33067	ESTs	0.3106
	452090	AA022684	Hs.124673	Homo sapiens cDNA FLJ11477 fs, clone HE	0.3106
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	0.3106
80	405592				0.3106
	423621	BE002904		gb:QV4-BN0090-070400-163-c07 BN0090 Homo	0.3107
	417919	AI928203	Hs.86379	ESTs	0.3110
	414484	BE314385		gb:601154649F1 NIH_MGC_19 Homo sapiens c	0.3110
	457433	AW410408	Hs.271167	L-pipecolic acid oxidase	0.3116
	426449	AL134009	Hs.169936	Homo sapiens mRNA; cDNA DKFZp586N1918 (f	0.3116
	419942	U25138	Hs.93841	potassium large conductance calcium-acti	0.3119
	458544	AI631036	Hs.196843	ESTs	0.3119

5	447778	BE620592	Hs.71190	ESTs, Weakly similar to S16506 hypotheti	0.3121
	449097	BE271708	Hs.95110	ESTs, Weakly similar to A55943 1-phospha	0.3125
	429338	AW170591	Hs.13967	ESTs, Weakly similar to PSM_HUMAN PROSTA	0.3125
	451385	AA017656	Hs.26216	gb:ze39h01.r1 Soares retina N2b4HR Homo	0.3125
	446404	AA019961	Hs.241569	LOC50627	0.3130
	446616	R65964	Hs.129056	ESTs, Weakly similar to ALU8_HUMAN ALU S	0.3132
	409404	BE220053	Hs.12891	ESTs	0.3135
	417318	AW953937	Hs.299087	ESTs	0.3139
10	443980	AI459140	Hs.77348	ESTs	0.3140
	459138	AI903291	Hs.192311	gb:RC-BT029-080199-047 BT029 Homo sapien	0.3142
	414807	AI738616	Hs.75819	hydroxyprostaglandin dehydrogenase 15-(N	0.3143
	434704	AW135276	Hs.239760	ESTs	0.3143
	414214	D49958	Hs.7934	glycoprotein M6A	0.3145
15	446378	AI905699	Hs.231444	citrate synthase	0.3145
	459233	AI939966	Hs.145601	gb:MR0-CT0015-160799-002-b06 CT0015 Homo	0.3146
	428193	NM_004235	Hs.289848	Kruppel-like factor 4 (gut)	0.3148
	426515	BE394222	Hs.145601	Homo sapiens, Similar to hypothetical pr	0.3150
	426597	AA382250	Hs.289848	ESTs	0.3153
20	459729	AL037285	Hs.289848	EST, Weakly similar to ALU4_HUMAN ALU SU	0.3157
	405071				0.3160
	407457	AJ242724	Hs.130732	gb:Homo sapiens mRNA for partial putativ	0.3162
	409922	AW505582	Hs.257194	KIAA1575 protein	0.3172
	438219	AI916151	Hs.197143	ESTs	0.3173
25	412944	AA384110	Hs.44	ESTs	0.3175
	431103	M57399	Hs.122710	pleiotrophin (heparin binding growth fac	0.3178
	426662	AA879474	Hs.11114	ESTs	0.3178
	444391	AL137597	Hs.272805	hypothetical protein dJ1181N3.1	0.3179
	432168	AK000563	Hs.125472	hypothetical protein FLJ20556	0.3181
30	411084	T18987	Hs.155975	ESTs, Moderately similar to KIAA0877 pro	0.3183
	425367	BE271188	Hs.22140	protein tyrosine phosphatase, receptor t	0.3185
	448812	H30775	Hs.13256	BM88 antigen	0.3188
	411288	AW835511	Hs.280776	gb:QV0-LT0015-180200-127-d02 LT0015 Homo	0.3189
	422884	AW860975	Hs.156607	ESTs	0.3190
35	405535		Hs.152531		0.3195
	458663	AV658444	Hs.152531	tankyrase, TRF1-interacting ankryrin-rela	0.3195
	455353	W26786	Hs.306969	gb:15d7 Human retina cDNA randomly prime	0.3195
	414540	BE379050	Hs.184922	Homo sapiens, clone MGC:10782, mRNA, com	0.3195
	428568	AC004755	Hs.182470	Homo sapiens chromosome 19, fosmid 37602	0.3195
40	428106	BE620016	Hs.4190	PTD010 protein	0.3198
	411856	H67899	Hs.156135	Homo sapiens cDNA: FLJ23269 fis, clone C	0.3202
	445682	AW378397	Hs.193288	gb:RC3-HT0220-031299-012-g06 HT0220 Homo	0.3205
	437568	AI954795	Hs.272312	ESTs	0.3205
	448943	AI608810	Hs.87500	ESTs	0.3205
45	431999	AL133573	Hs.229535	Homo sapiens mRNA; cDNA DKFZp434J2235 (f	0.3207
	419279	AA235900	Hs.156607	ESTs	0.3208
	405913		Hs.152531		0.3209
	426383	D83407	Hs.152531	Down syndrome critical region gene 1-lik	0.3212
	424729	AF063012	Hs.177131	heart and neural crest derivatives expro	0.3212
50	440020	AI480204	Hs.22452	ESTs	0.3213
	429082	AL135682	Hs.229535	Homo sapiens mRNA for KIAA1737 protein,	0.3215
	433663	AF083131	Hs.229535	CATX-15 protein	0.3215
	400641				0.3216
	406140				0.3216
55	415280	R56473	Hs.268715	ESTs	0.3217
	447635	AI669669	Hs.195362	ESTs	0.3217
	401887				0.3217
	400767				0.3221
	457713	H47495	Hs.13810	hypothetical protein MGC15504	0.3221
60	448758	AB018311	Hs.21917	KIAA0768 protein	0.3222
	444750	AW242684	Hs.243623	ESTs	0.3223
	411466	AW847669	Hs.278909	gb:IL3-CT0213-280100-056-G10 CT0213 Homo	0.3226
	432749	NM_014438	Hs.248613	interleukin 1, eta	0.3231
	408112	AW451982	Hs.65366	ESTs	0.3231
65	433234	AB040928	Hs.332943	KIAA1495 protein	0.3231
	422831	R02504	Hs.221926	ESTs	0.3234
	403215				0.3236
	451868	R85962	Hs.221926	ESTs, Weakly similar to I38022 hypotheti	0.3236
	446901	AI347274	Hs.13377	gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	0.3242
70	430553	AW392821	Hs.159650	gb:CM4-ST0275-021299-053-h09 ST0275 Homo	0.3254
	445848	AA774824	Hs.159650	Homo sapiens clone 23649 and 23755 unkno	0.3257
	441143	AI027604		ESTs	0.3257
	405138				0.3262
	412888	M86151		gb:EST02679 Hippocampus, Stratagene (cat	0.3262
75	409662	AW452320	Hs.279726	ESTs	0.3262
	425438	T62216	Hs.210473	ESTs	0.3263
	416428	AA180256	Hs.306752	Homo sapiens cDNA FLJ14872 fis, clone PL	0.3263
	423512	AW844694	Hs.293130	Homo sapiens cDNA: FLJ21391 fis, clone C	0.3264
	436777	AA731199	Hs.266914	ESTs	0.3267
80	431651	BE250915	Hs.40368	hypothetical protein FLJ10355	0.3267
	454117	BE410100	Hs.134478	adaptor-related protein complex 1, sigma	0.3268
	426048	AI768853	Hs.25925	ESTs	0.3269
	451096	BE383234	Hs.97450	Homo sapiens, clone MGC:15393, mRNA, com	0.3270
	426942	AA393551		ESTs	0.3271

5	454947	AW846590	gb:QV0-CT0180-011099-025-d07 CT0180 Homo	0.3275
	413814	BE169692	gb:PM1-HT0527-290200-006-a05 HT0527 Homo	0.3275
	422818	AA040290	Hs.97848 ESTs	0.3277
	423634	AW959908	Hs.1690 heparin-binding growth factor binding pr	0.3278
	414002	NM_006732	Hs.75678 FBJ murine osteosarcoma viral oncogene h	0.3278
10	452164	AI863171	gb:tz44b02.x1 NCL_CGAP_Bm52 Homo sapien	0.3279
	458477	NM_000314	Hs.10712 phosphatase and tensin homolog (mutated	0.3279
	433197	AB040889	Hs.281022 KIAA1456 protein	0.3280
	405701			0.3282
	437782	AI370876	Hs.79090 exportin 1 (CRM1, yeast, homolog)	0.3284
15	459001	AI761313	Hs.204605 ESTs	0.3286
	422783	AA598956	Hs.120439 ethanolamine kinase	0.3289
	417036	AF039918	Hs.80975 ectonucleoside triphosphate diphosphohyd	0.3290
	456041	BE270795	Hs.268864 ESTs	0.3295
	423310	AA325225	Hs.124023 Homo sapiens cDNA FLJ14218 fis, clone NT	0.3296
20	427530	AA405093	Hs.126519 ESTs	0.3296
	420172	AA601122	Hs.95655 secreted and transmembrane 1	0.3297
	445610	AI831648	Hs.143993 ESTs	0.3297
	411328	AW837063	gb:QV1-LT0037-150200-069-g08 LT0037 Homo	0.3300

Table 8B

25	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
30	Accession:	Genbank accession numbers		
35	Pkey	CAT number	Accession	
40	409921	1159516_1	AW600239 AW600255 AW505332	
	410626	1212621_1	BE407727	
45	410845	1223881_1	AW807182 AW807328 AW807063 AW807183 AW807192 AW807033 AW807061 AW807286 AW807097 AW807270 AW807372 AW807280 AW807283	
	410950	1227728_1	AW811633 AW811652 AW811898	
50	411288	1237709_1	AW835511 AW835517 AW835513	
	411319	1238595_1	BE537094 AW836542	
55	411328	1238987_1	AW837063 AW935682 AW935957	
	411466	1246771_1	AW847669 AW847667 BE145799	
60	411514	1246638_1	AW850178 AW850233 AW850445 AW850446	
	411620	1252014_1	AW854536 AW854417 AW854495 AW854355	
65	411880	1263110_1	AW872477 BE088101 T05990	
	412474	129869_1	AI791451 AI791288 BE019234 BE296601 AA111939	
70	412506	1301336_1	AW957159 H09937 T75143	
	412682	1321672_1	AW983772 AW983730 AW983769 AW983836 AW983835 AW983837	
75	412888	1334784_1	M86151 BE061884 BE061883 BE061898 BE061882 BE061887 BE061891 BE061890 BE061896 BE061893 BE061895 BE061894 BE061885 BE007474	
			BE007481 BE007553	
80	413056	1347545_1	BE063031 BE063002 BE063008 BE063024 BE063040 BE063006 BE063072	
	413537	1375441_1	BE146866 BE146865 BE146867	
85	413541	1375499_1	BE147036 BE146951 BE146958 BE146966 BE146976 BE146955	
	413814	1391574_1	BE169692 BE169421	
90	414026	1411109_1	BE241713 BE241912	
	414193	1424706_2	BE260069	
95	414349	1437515_1	BE512968	
	414484	1452830_1	BE314385	
100	414539	1460320_1	BE379046 BE395459	
	415154	1525577_1	D63175 D78984 D63269	
105	415160	1525766_1	T82802 D78670 R08505	
	416035	1567254_1	H42314 H43080 H45217 H15384	
110	417945	1711126_1	R29072 R29717 R29699 R29709 R29751 R29609 R29060 R29718 R29057 R29591 R29683 R29575 R28913 R28910	
	419850	188485_1	F06844 F06845 Z45488 AW748501 AW748591 AW752021 AW748545 AW853362 AW853363 AW853427 AA251253	
115	422909	222858_1	AA533356 AW468427 R67736 AA779031 AA614088 AI823404 AA318991 AA720986	
	422954	223239_1	AW998605 AW993131 BE514709 AA319445	
120	423621	230314_1	BE002904 H64880 AA328679	
	424648	241947_1	AA344576 AA732430 AA344601	
125	426132	261431_1	AA370501 AW962784 AA370727	
	426497	268121_1	AA379913 AA379981 AW983523	
130	430553	319868_1	AW392821 AW392809 AW843258 AW843049 AW603156 BE165656 AW821728	
	431822	338082_1	AA516049 AW004922	
135	434098	380006_1	AA625499 AA625269 AA625184	
	437483	43756_1	AL390174 AW898817	
140	440507	495677_1	H06994 BE147898	
	441042	50823_1	AA077738 AA078505 BE562497 Z17859	
145	441083	50904_1	BE562611 AA436054	
	445682	647580_1	AW378397 AW378390 AW378358 AI247957	
150	446294	670076_1	AI284935 AW409822 BE408182	
	446901	697809_1	AI347274 AW844024	
155	447787	73719_1	BE620108 BE312062 AW896316 BE262546	
	451385	86787_1	AA017656 AA017374 AA019761	
160	452164	902091_1	AI863171 BE047919	
	454186	1049791_1	BE141030 BE141474 BE141467 BE141753 BE141024 BE141761 AW177593 AW177579 AW177582 AW177585 AW177587 AW807582 AW177581	
165			BE141477 BE141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460	
			BE141749 AW177598	

454790 1234752_1 AW820852 AW820773 AW821088
 454947 1245953_1 AW846590 AW846615 AW846584 AW846592 AW846621 AW846610
 455353 1284289_1 W26786 AW938612 AW902272
 457115 286601_1 AA420712 AA469165 AA420737
 459138 918860_1 AI903291 AI903455 AI903367 AI903403 AI903447 AI903405 AI903364 AI903229 AI903240 AI903346
 459233 944881_1 AI939966 AI939988 AI939951 AI939981 AI939976 AI939959

Table 8C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400514	9796594	Minus	78844-79025,80850-80991,89754-89941,93750-93891
400641	8117693	Plus	4785-4992
400672	8118724	Minus	148067-148503
400767	8131627	Minus	80531-80629,82169-82278
400865	1945037	Minus	44482-45526
401024	8117489	Plus	60551-60802
401042	8117611	Plus	151364-151606
401371	9650602	Plus	80901-81283
401381	8570226	Minus	118629-119146,119392-119657
401465	6682292	Plus	25676-25800
401521	7705251	Plus	9127-9234
401753	9838183	Minus	155287-155529,159719-159997
401776	9966323	Plus	115535-115743,117746-117839,120290-120455
401887	7229981	Plus	93973-94120
401974	3126777	Plus	85330-85683
402076	8117410	Plus	128316-128627
402182	8575917	Minus	98298-98439
402425	9796347	Minus	50224-50395
402610	9926549	Minus	22955-23124
402695	8569871	Minus	159927-160055
403047	3540153	Minus	59793-59968
403215	7630945	Minus	177270-177971
403418	6862692	Minus	176202-176395
403548	8081591	Minus	38760-39352
403957	8076835	Minus	81649-81754
404070	2996642	Plus	7210-7414,10043-10195
404246	7406725	Plus	82477-82628,82721-82817,82910-83071,83149-83387
404414	7382165	Plus	143127-143398
404605	9212566	Plus	125032-125291
404638	9796751	Minus	99433-99528,100035-100161
404696	9800109	Minus	60037-60144,62675-63081
404767	7882827	Minus	23244-23759
404769	8089713	Minus	175801-176823
404927	7342002	Plus	68690-69563
404958	7407941	Minus	2731-4531
405071	7708797	Minus	11115-11552
405073	7769921	Plus	31419-31774
405138	8576241	Plus	90303-90516
405277	3980473	Plus	23471-23572
405282	3810573	Minus	10482-10689
405334	3135285	Plus	139386-139856
405364	2281075	Minus	48325-48491,49136-49252
405385	6552772	Plus	48332-48454
405535	9795658	Plus	63384-63545
405610	5757553	Minus	71907-72080
405654	4895155	Minus	53624-53759
405691	4508112	Plus	171350-171739
405701	4263751	Plus	93243-93364
405880	6758747	Minus	55673-56287
405913	7712139	Minus	7484-7678
406140	9168231	Minus	49887-50219
406592	4567182	Plus	352560-352963

Table 9A lists about 1,234 genes up-regulated in colon cancer compared to normal adult tissues and to non-malignant colon tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 2.5, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 70th percentile value amongst non-malignant tissues, the "average" colon value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of having an oncogenic function or of transducing an intracellular signal, or of being modifiable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion transporter). In order to remove gene-specific

background levels of non-specific hybridization, the 15th percentile value amongst the over non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 9A: 1,234 genes up-regulated in colon cancer compared to normal adult tissues and to non-malignant colon tissues

TABLE 9A: 1,234 genes up-regulated in colon cancer compared to normal colon tissues and to normal colon tissues					
	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigenID:	Unigene number			
	Unigene Title:	Unigene gene title			
10	R1:	90 th percentile of tumor samples divided by the 70 th percentile of normal body tissue samples, where the 15 th percentile of normal body tissues was subtracted from the numerator and denominator			
	Pkey	ExAccn	UnigenID	Unigene Title	R1
15	436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosyl	29.34
	406690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carc	25.56
	406667	M12523			20.28
20	414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),	18.84
	428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	17.38
	416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating isle	16.99
	446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intestin	16.61
	431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S3B4_H	16.42
25	437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel	15.92
	407242	M18728		(locuslink)NM_002483:Homo sapiens carc	15.84
	423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease I	15.59
	441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	15.02
	406685	M18728		(locuslink)NM_002483:Homo sapiens carc	14.54
30	422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo	13.68
	432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	13.23
	421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	13.21
	453863	X02544	Hs.572	Hs.572:orosomucoid 1	13.06
	421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefol factor 1	12.35
35	436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	12.11
	422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	11.99
	418888	AJ076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, Li c	11.87
	407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carc	11.81
	424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	11.27
40	414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	11.18
	407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	10.82
	413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	10.73
	450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	10.57
	418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.39
45	423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	10.10
	423371	AJ076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	9.91
	421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog	9.68
	447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	9.44
	421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	9.38
50	406741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carc	9.34
	427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (9.18
	422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX),	9.06
	406687	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	9.02
	409153	W03754	Hs.50813	NM_017625:Homo sapiens intelectin (ITLN)	8.89
55	424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	8.53
	422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	8.23
	452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590	8.10
	430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	8.05
	413881	L00190	Hs.76599	(locuslink)NM_000488:Homo sapiens serine	7.96
60	406399				7.73
	422424	AI186431	Hs.296638	Hs.296638:prostate differentiation facto	7.71
	428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homol	7.43
	417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:22588 1	7.40
	435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	7.29
65	430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	7.25
	451917	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	7.21
	421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	7.19
	452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	7.18
	452594	AJ076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfa	7.03
70	424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysl	7.00
	443426	AF098158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	6.92
	452194	AI694413	Hs.373599	Hs.373599:EST	6.88
	411975	AI916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	6.76
	408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	6.59
75	422310	AA316622	Hs.98370	(locuslink)NM_030522:Homo sapiens cytoch	6.55
	431330	X69532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	6.53
	420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protei	6.49
	422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	6.33
	412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	6.31
80	451035	AJ076785	Hs.430	NM_002670:Homo sapiens plastin 1 (I iso)	6.30
	428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	6.29
	430577	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	6.28
	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	6.27
	444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	6.26
	409632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cyste)	6.23

5	417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	6.23
	413938	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cysteine) 118787:transforming growth factor, beta	6.23
	422627	BE336857	Hs.118787	NM_017767:Homo sapiens solute carrier family 12 member 1	6.19
	411825	AK000334	Hs.352415	NM_002888:Homo sapiens small inducible cytokine A1	6.17
	446921	AB012113	Hs.16530	NM_004442:Homo sapiens EphB2 (EPHB2), tyrosine kinase	6.17
	415214	AI445236	Hs.125124	NM_001265:Homo sapiens caudal type homeobox 1	6.17
	414816	Y13709	Hs.77399	NM_003890:Homo sapiens IgG Fc binding protein	6.16
	422106	D84239	Hs.111732	(locuslink)NM_005709:Homo sapiens PDZ-73	6.14
10	423803	NM_005709	Hs.132945	Hs.28792:Homo sapiens cDNA FLJ11041, f1	6.13
	452281	T93500	Hs.28792	Hs.19322:Homo sapiens, similar to RIKEN	6.09
	447342	AI199268	Hs.19322	Hs.353013:chromosome 20 open reading frame	6.02
	443957	AA521049	Hs.353013	(locuslink)NM_003158:Homo sapiens serine	5.95
	403220			Hs.23960:cyclin B1	5.90
15	408908	BE296227	Hs.250822	NM_025257:Homo sapiens chromosome 6 open	5.88
	449722	BE280074	Hs.23960	(locuslink)NM_025130:Homo sapiens hypoth	5.87
	425976	C75094	Hs.334514	NM_000492:Homo sapiens cystic fibrosis transmembrane	5.79
	414617	AI395520	Hs.288817	NM_014324:Homo sapiens alpha-methylacyl-CoA	5.79
	408983	NM_000492	Hs.663	NM_005409:Homo sapiens small inducible cytokine A1	5.77
20	423445	NM_014324	Hs.128749	Hs.151529:ESTs	5.77
	421379	Y15221	Hs.103982	NM_004616:Homo sapiens transmembrane 4 subunit	5.76
	431301	AA502384	Hs.151529	Hs.145807:hypothetical protein FLJ13593	5.71
	418318	U47732	Hs.84072	Hs.25640:claudin 3	5.71
	415992	C05837	Hs.145807	NM_032865:Homo sapiens hypothetical protein	5.68
25	436972	AA284679	Hs.25640	Hs.105448:protein kinase, lysine deficient	5.66
	414987	AA524394	Hs.294022	NM_003561:Homo sapiens lysophospholipase A2	5.61
	431657	AI345227	Hs.105448	NM_000483:Homo sapiens apolipoprotein C-III	5.57
	424273	W40460	Hs.144442	NM_001898:Homo sapiens cystatin SN (CST1)	5.55
	413916	N49813	Hs.75615	Hs.356664:hypothetical protein FLJ32334	5.54
30	409757	NM_001898	Hs.123114	(locuslink)NM_005242:Homo sapiens coagulation factor	5.53
	430204	AA618335	Hs.356664	NM_000505:Homo sapiens coagulation factor	5.50
	426227	U67058	Hs.154299	Hs.77356:transferrin receptor (p90, CD71)	5.38
	420542	NM_000505	Hs.1321	NM_002217:Homo sapiens pre-alpha (globulin)	5.33
	414809	AI434699	Hs.77356	NM_019894:Homo sapiens transmembrane protein	5.32
35	414639	X67055	Hs.76716	NM_000506:Homo sapiens coagulation factor	5.32
	410418	D31382	Hs.63325	(locuslink)NM_014324:Homo sapiens alpha-1	5.28
	414590	NM_000506	Hs.76530	Hs.184727:ESTs, weakly similar to T45738	5.28
	444151	AW972917	Hs.128749	NM_139053:Homo sapiens epidermal growth factor	5.27
40	438746	AI885815	Hs.184727	Hs.97411:hypothetical protein MGC12335	5.26
	408704	AA056635	Hs.5366	(locuslink)NM_005392:Homo sapiens nucleoside	5.25
	414798	AI286323	Hs.97411	NM_006437:Homo sapiens ADP-ribosyltransferase	5.25
	436251	BE515065	Hs.296585	NM_003979:Homo sapiens retinoic acid inducible	5.23
	414753	AF158255	Hs.77225	NM_002250:Homo sapiens potassium channel	5.23
45	428970	BE276891	Hs.194691	NM_013238:Homo sapiens DNAJ domain-containing	5.22
	443991	NM_002250	Hs.10082	Hs.1957:amyloid P component, serum	5.20
	432978	AF126743	Hs.279884	NM_004443:Homo sapiens EphB3 (EPHB3), mRNA	5.18
	425834	NM_001639	Hs.1957	NM_000676:Homo sapiens adenosine A2b receptor	5.13
	432179	X75208	Hs.2913	NM_000035:Homo sapiens aldolase B, fructose	5.12
	408482	NM_000676	Hs.45743	Hs.115833:ESTs	5.11
50	430135	NM_000035	Hs.234234	NM_014256:Homo sapiens UDP-GlcNAc:betaGalNAc	5.08
	426174	AA547959	Hs.115833	NM_005700:Homo sapiens dipeptidylpeptidase	5.07
	403218			Hs.191762:hypothetical protein MGC20258	5.00
55	411142	NM_014256	Hs.69009	(locuslink)NM_001645:Homo sapiens apolipoprotein	4.98
	449027	AJ271216	Hs.22880	NM_052816:Homo sapiens tripartite motif	4.96
	433083	AL042759	Hs.191762	Hs.247280:chromosome 20 open reading frame	4.92
	431779	AW971178	Hs.268571	Hs.1584:cartilage oligomeric matrix protein	4.91
	421408	AI688223	Hs.91096	NM_033013:Homo sapiens nuclear receptor	4.91
	430603	AA148164	Hs.247280	NM_033100:Homo sapiens MT-protocadherin	4.90
60	422867	L32137	Hs.1584	NM_003823:Homo sapiens tumor necrosis factor	4.89
	422539	AJ009936	Hs.118138	Hs.2062:vitamin D (1,25-dihydroxy) vitamin D	4.86
	424010	AL080188	Hs.137556	NM_031265:Homo sapiens mucin and cadherin	4.83
	428953	AA306610	Hs.348183	Hs.2253:complement component 2	4.81
65	457001	J03258	Hs.2082	NM_005192:Homo sapiens cyclin-dependent kinase	4.79
	425983	AK000226	Hs.165619	NM_021978:Homo sapiens suppression of tumorigenesis	4.77
	428269	M26301	Hs.2253	Hs.211101:ESTs	4.74
	418322	AA284166	Hs.84113	NM_019062:Homo sapiens hypothetical protein	4.72
	409889	AW630041	Hs.56937	Hs.199695:hypothetical protein MAC30	4.72
	447472	AW207347	Hs.211101	Hs.168974:ESTs	4.69
70	423164	AK000232	Hs.124835	NM_002543:Homo sapiens oxidized low density lipoprotein	4.69
	428345	R11141	Hs.199695	Hs.302738:Homo sapiens cDNA: FLJ21425, f1	4.67
	430680	AW138724	Hs.168974	Hs.239812:serologically defined breast cancer	4.65
	414998	NM_002543	Hs.77729	NM_001226:Homo sapiens caspase 6, apoptosis	4.64
	417165	R80137	Hs.302738	Hs.283552:hypothetical protein BC016153	4.64
75	403221			Hs.198253:major histocompatibility complex class II	4.64
	415000	AW025529	Hs.239812	NM_001827:Homo sapiens CDC28 protein kinase	4.60
	433437	U20536	Hs.3280	NM_014698:Homo sapiens KIAA0792 gene product	4.60
	414052	AW578849	Hs.283552	(locuslink)NM_017895:Homo sapiens DEAD-box	4.59
80	406673	M34965	Hs.198253	NM_001710:Homo sapiens B-factor, properdin	4.57
	418203	X54942	Hs.83758	Hs.296770:KIAA1719 protein	4.57
	422714	AB018335	Hs.119387	NM_014791:Homo sapiens maternal embryonic	4.56
	410639	BE269047	Hs.65234		
	411393	AW797437	Hs.69771		
	431193	AW749505	Hs.296770		
	428450	NM_014791	Hs.184339		

5	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	4.56
	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	4.55
	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	4.55
	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00255	4.55
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens sialidase 1 (lyso	4.54
	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	4.53
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	4.53
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	4.52
10	408194	AA601038	Hs.191797	Hs.191797:ESTs	4.50
	439580	AF086401	Hs.293847	Hs.293847:ESTs	4.49
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	4.48
	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome profif	4.48
	432378	AI93046	Hs.146133	Hs.146133:ESTs	4.47
	431958	X63629	Hs.2877	NM_001793:Homo sapiens cadherin 3, type	4.47
15	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	4.47
	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	4.46
	422511	AU076442	Hs.117938	NM_000494:Homo sapiens collagen, type XV	4.46
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	4.44
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis,	4.44
20	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	4.43
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	4.43
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	4.40
	426479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	4.38
	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	4.37
25	414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	4.36
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23656	4.36
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	4.35
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	4.33
	409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	4.33
30	432575	AA553722	Hs.194346	Hs.194346:Spir-2 protein	4.33
	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	4.32
	439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	4.32
	418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	4.30
35	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	4.30
	424825	AF207069	Hs.163357	NM_001084:Homo sapiens procollagen-lysin	4.30
	429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	4.30
	411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	4.29
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	4.29
40	408847	AW290597	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	4.28
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	4.28
	425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	4.27
	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	4.27
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	4.26
45	414361	AI086138	Hs.204044	Hs.204044:ESTs	4.26
	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	4.24
	415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	4.22
	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	4.20
	420039	NM_004605	Hs.376147	Hs.376147:Homo sapiens cDNA FLJ39099 fis	4.19
50	446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	4.18
	421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	4.18
	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	4.18
	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-like	4.18
	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	4.17
55	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	4.17
	426761	AI015709	Hs.172089	Hs.172089:pro-oncotic receptor inducing	4.16
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	4.15
	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	4.15
	453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	4.14
60	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3)-glycoprote	4.14
	403219				4.14
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	4.14
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	4.13
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	4.12
65	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (4.12
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	4.12
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	4.11
	413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (4.10
	428698	AA852773	Hs.334838	Hs.334838:KIAA1866 protein	4.09
70	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	4.07
	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	4.07
	417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	4.06
	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	4.06
	425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	4.05
75	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	4.04
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (4.03
	425280	U31519	Hs.1872	NM_002591:Homo sapiens phosphoenolpyruva	4.03
	411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 6 (m	4.03
	452017	AF109302	Hs.27495	Hs.27495:prostate cancer associated prot	4.02
80	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	4.01
	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	4.01
	456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	4.01
	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	4.01
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	4.01

	416065	BE267931	Hs.78998	NM_002592:Homo sapiens proliferating cell	3.99
	403739				3.99
	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	3.98
5	405484				3.98
	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	3.98
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antigen	3.97
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	3.97
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	3.97
10	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	3.96
	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	3.96
	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	3.96
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	3.95
	413278	BE563085	Hs.833	Hs.833:interferon-stimulated protein, 15	3.95
15	400130		Hs.155560	NM_001746:Homo sapiens catenin (CANX),	3.93
	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	3.93
	443802	AW504924	Hs.9805	Hs.9805:exportin 5	3.93
	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	3.92
	456829	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	3.92
20	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	3.91
	422293	X94453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synthet	3.90
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/muc	3.89
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomutas	3.89
	447343	AA256841	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	3.88
	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	3.88
25	413950	AA249096	Hs.32793	Hs.32793:Homo sapiens cDNA FLJ31108 fis,	3.88
	409453	AI885516	Hs.95612	Hs.95612:ESTs	3.87
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	3.86
	421910	NM_014586	Hs.109437	NM_014586:Homo sapiens hormonally upregu	3.86
	434263	N34895	Hs.79187	Hs.79187:coxsackie virus and adenovirus	3.85
30	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	3.85
	433682	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	3.84
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	3.84
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	3.84
	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.83
35	408056	AA312329	Hs.42331	Hs.42331:ephrin-A4	3.83
	407233	X16354	Hs.50984	(locuslink)NM_001712:Homo sapiens carcin	3.83
	426514	BE616633	Hs.170195	Hs.170195:bone morphogenetic protein 7 (3.82
	451541	BE279383	Hs.26557	NM_007183:Homo sapiens plakophilin 3 (PK	3.82
	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	3.81
40	426378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	3.81
	409636	AA305729	Hs.18272	(locuslink)NM_030674:Homo sapiens solute	3.81
	407786	AA687538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	3.80
	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	3.79
45	414561	AI064813	Hs.195155	Hs.195155:solute carrier family 38, memb	3.79
	405556				3.79
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	3.79
	400529				3.79
50	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.78
	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	3.78
	429638	AI916662	Hs.211577	(locuslink)NM_004986:Homo sapiens kinect	3.77
	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	3.77
	415003	M11437	Hs.77741	Hs.77741:kininogen	3.77
	443639	BE269042	Hs.9661	Hs.9661:proteasome (prosome, macropain)	3.76
55	400290	H18836	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	3.76
	431350	AI192528	Hs.164537	Hs.164537:ESTs	3.76
	430154	AW583058	Hs.234726	NM_001085:Homo sapiens serine (or cystei	3.75
	435099	AC004770	Hs.4756	NM_004111:Homo sapiens flap structure-sp	3.75
	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	3.74
60	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	3.74
	413063	AL035737	Hs.75184	Hs.75184:chitinase 3-like 1 (cartilage g	3.73
	420665	AW469240	Hs.371581	Hs.371581:ESTs	3.73
	452299	AW206330	Hs.355663	Hs.355663:ESTs	3.72
	444664	N26362	Hs.11616	NM_016086:Homo sapiens map kinase phosph	3.72
65	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase 1	3.72
	444006	BE395085	Hs.334762	(locuslink)NM_032832:Homo sapiens hypoth	3.72
	449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	3.71
	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	3.71
	427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated	3.71
70	427333	AF067797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	3.70
	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	3.70
	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	3.70
	456362	AW973003	Hs.179909	(locuslink)NM_024831:Homo sapiens nuclea	3.69
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.69
	437018	AU076916	Hs.5398	Hs.5398:guanine monophosphate synthetase	3.69
75	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	3.69
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fi	3.69
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	3.68
	413813	M96956	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	3.68
	428376	AF118665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	3.67
80	431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	3.67
	446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	3.67
	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	3.67
	448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte acti	3.67

5	452679	Z42387	Hs.83883	(locustlink)NM_020182:Homo sapiens transmembrane protein 7 (CLDN7)	3.66
	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	3.66
	433020	AJ375726	Hs.227152	NM_016391:Homo sapiens hypothetical protein	3.66
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (apex)	3.66
	413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	3.66
10	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec51 alpha form	3.65
	409152	AA176585	Hs.194346	Hs.194346:Spir-2 protein	3.64
	404826				3.63
	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	3.63
	409964	AW368226	Hs.67928	Hs.67928:ESTs	3.63
15	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA: cDNA DKFZp56	3.63
	452098	AI858183		BF755039:QV0-CT0583-181000-428-107 CT058	3.62
	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protein	3.61
	439223	AW238299	Hs.250618	NM_025217:Homo sapiens UL16 binding protein	3.60
	408137	AI694131	Hs.29002	Hs.29002:KIAA1706 protein	3.59
20	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	3.59
	436856	AI469355	Hs.127310	(locustlink)NM_144624:Homo sapiens kinase	3.59
	449667	AB023227	Hs.23860	Hs.23860:KIAA1010 protein	3.59
	406684	X16354	Hs.50964	(locustlink)NM_001712:Homo sapiens cardiolipin	3.58
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	3.58
25	426031	AA295251	Hs.166066	(locustlink)NM_006697:Homo sapiens cisplatin	3.58
	417526	AA568906	Hs.82240	Hs.82240:syntaxin 3A	3.57
	443044	N28522	Hs.8935	NM_014298:Homo sapiens quinolinate phosphatase	3.57
	424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	3.57
	432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility complex	3.56
30	413880	AI660842	Hs.110915	NM_021258:Homo sapiens interleukin 22 receptor	3.55
	421357	AK000609	Hs.103808	NM_017896:Homo sapiens chromosome 20 open reading frame	3.55
	436827	H72187	Hs.356668	(locustlink)NM_005274:Homo sapiens guanine nucleotide-binding protein	3.55
	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate dehydrogenase	3.55
	420162	BE378432	Hs.95577	NM_052884:Homo sapiens cyclin-dependent kinase	3.55
35	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	3.55
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	3.55
	413588	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine monophosphate)	3.54
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	3.54
	435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphatase	3.54
40	431211	M86849	Hs.323733	Hs.323733:gap junction protein, beta 2	3.54
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger protein	3.53
	414812	X72755	Hs.77387	NM_002416:Homo sapiens monokine induced by interferon	3.53
	423068	M25629	Hs.123107	NM_002257:Homo sapiens kallikrein 1, renal	3.53
	443180	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN12)	3.53
45	425047	U34038	Hs.154299	NM_005242:Homo sapiens coagulation factor	3.53
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	3.52
	444184	T87841	Hs.282990	(locustlink)NM_033550:Homo sapiens chromatin	3.52
	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	3.51
	413781	J05272	Hs.850	(locustlink)NM_000883:Homo sapiens IMP (inosine monophosphate)	3.51
50	409213	U61412	Hs.51133	NM_005975:Homo sapiens PTK6 protein tyrosine kinase	3.51
	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell death	3.51
	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373	3.51
	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF receptor	3.51
	413842	NM_005764	Hs.271473	Hs.271473:epithelial protein up-regulate	3.51
55	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisiae	3.51
	411678	AI907114	Hs.71465	NM_003129:Homo sapiens squalene epoxidase	3.51
	437704	AA766142	Hs.131810	Hs.131810:Homo sapiens cDNA FLJ35976	3.51
	419693	AA133749	Hs.301350	Hs.301350:FXD domain-containing ion transport	3.51
	407971	AI489117	Hs.62918	Hs.62918:CDK91 cell division cycle 91-1	3.50
60	424865	AF011333	Hs.153563	NM_002349:Homo sapiens lymphocyte antigen	3.50
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	3.50
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	3.50
	436278	BE396290	Hs.5097	Hs.5097:synaptogyrin 2	3.50
	440334	BE276112	Hs.7165	NM_003804:Homo sapiens zinc finger protein	3.50
65	428788	AF082283	Hs.193516	NM_003921:Homo sapiens B-cell CLL/lymphoma	3.50
	424909	S78187	Hs.153752	(locustlink)NM_004358:Homo sapiens cell death	3.49
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyridoxal)	3.49
	417129	AI381800	Hs.300684	Hs.300684:calcitonin gene-related peptide	3.48
	409463	AI458165	Hs.17296	NM_023930:Homo sapiens hypothetical protein	3.48
70	407137	T97307			3.48
	454380	AB020713	Hs.56966	(locustlink)NM_024923:Homo sapiens hypothetical	3.48
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433	3.48
	423750	AF165083	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PF2D)	3.47
	446946	AI878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DNA)	3.47
75	413380	AI904232	Hs.75323	Hs.75323:prohibitin	3.46
	430237	AI272144	Hs.236522	Hs.236522:DKFZP434P106 protein	3.46
	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 open reading frame	3.45
	407770	AW607831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN15)	3.45
	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	3.44
80	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	3.44
	420319	AW406289	Hs.96593	NM_019034:Homo sapiens ras homolog gene	3.44
	425209	AL049761	Hs.155140	NM_001895:Homo sapiens casein kinase 2	3.44
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	3.43
	429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inactivated)	3.43
	426459	AF151812	Hs.169992	NM_015966:Homo sapiens serologically defined	3.43
	437987	BE277414	Hs.5947	NM_005370:Homo sapiens melanoma transforming	3.43
	428093	AW594506	Hs.104830	Hs.104830:ESTs	3.43

	414862	BE621310	Hs.923	Hs.923: single-stranded DNA binding prote	3.43
	400750				3.42
	413186	AU077141	Hs.374548	Hs.374548: solute carrier family 16 (mono	3.41
5	425263	NM_001197	Hs.155419	NM_001197: Homo sapiens BCL2-interacting	3.40
	453857	AL080235	Hs.35861	Hs.35861: Ras-induced senescence 1	3.40
	428474	AB023182	Hs.184523	Hs.184523: serine/threonine kinase 38 lik	3.39
	410315	AI638871	Hs.378965	Hs.378965: Homo sapiens cDNA FLJ37658 fis	3.39
	428205	AB020643	Hs.183006	Hs.183006: likely homolog of mouse hepari	3.39
10	450506	NM_004460	Hs.418	(locuslink)NM_004460: Homo sapiens fibrob	3.39
	413179	N99692	Hs.75227	NM_005002: Homo sapiens NADH dehydrogenas	3.38
	440676	NM_004987	Hs.112378	(locuslink)NM_004987: Homo sapiens LIM an	3.38
	400847				3.37
	431585	AW296135	Hs.267659	NM_006113: Homo sapiens vav 3 oncogene (V	3.37
15	410199	AW377424	Hs.205126	Hs.205126: Homo sapiens cDNA: FLJ22667 fi	3.37
	432633	AI796390	Hs.210667	Hs.210667: ESTs	3.36
	429344	R94038	Hs.374664	NM_005538: Homo sapiens inhibin, beta C (3.36
	424685	W21223	Hs.151734	Hs.151734: nuclear transport factor 2	3.36
	458950	AF111170	Hs.306165	Hs.306165: ESTs, Highly similar to unknow	3.35
	418313	BE244231	Hs.84038	NM_015937: Homo sapiens CGI-06 protein (L	3.35
20	453454	AW052006	Hs.374973	NM_004697: Homo sapiens PRP4 pre-mRNA pro	3.35
	400448				3.35
	424142	AI678727	Hs.378970	Hs.378970: Homo sapiens cDNA FLJ35102 fis	3.35
	430720	U85768	Hs.247838	NM_002991: Homo sapiens small inducible c	3.35
25	416412	NM_014742	Hs.79305	Hs.79305: KIAA0255 gene product	3.35
	429824	AA266363	Hs.121520	Hs.121520: Homo sapiens cDNA FLJ35792 fis	3.35
	412948	BE243313	Hs.334851	Hs.334851: LIM and SH3 protein 1	3.34
	451129	BE072881		BE072881: RC2-BT0548-200300-012-e09 BT054	3.34
	425322	U63630	Hs.155637	NM_006904: Homo sapiens protein kinase, D	3.34
30	446291	BE397753	Hs.14623	Hs.14623: Interferon, gamma-inducible pro	3.34
	431731	BE266322	Hs.211374	(locuslink)NM_145051: Homo sapiens hypoth	3.34
	423198	M81933	Hs.1634	Hs.1634: cell division cycle 25A	3.34
	448053	AW977382	Hs.15898	Hs.15898: 2,4-dienoyl CoA reductase 2, pe	3.34
	414045	NM_002951	Hs.75722	NM_002951: Homo sapiens ribophorin II (RP	3.34
35	421190	U95031	Hs.102482	Hs.102482: mucin 5, subtype B, tracheobro	3.34
	419607	R52557	Hs.91579	NM_033416: Homo sapiens similar to HYPOTH	3.33
	435975	AL118990	Hs.373554	(locuslink)NM_130786: Homo sapiens alpha-	3.33
	418416	U11700	Hs.84999	NM_000053: Homo sapiens ATPase, Cu++ tran	3.33
	433570	AI580053	Hs.109007	Hs.109007: Homo sapiens, Similar to LOC16	3.33
40	441128	AA570256	Hs.348504	Hs.348504: hypothetical protein BC014072	3.33
	432320	AW411066	Hs.274351	NM_016032: Homo sapiens zinc finger, DHHC	3.33
	444019	BE173977	Hs.10098	NM_019082: Homo sapiens putative nucleola	3.32
	432680	T47364	Hs.278613	(locuslink)NM_005532: Homo sapiens Interf	3.32
	410219	T98226	Hs.171952	Hs.171952: occludin	3.32
45	410663	AA194952	Hs.36093	Hs.36093: Homo sapiens cDNA FLJ12885 fis,	3.32
	402829				3.32
	445921	AW015211	Hs.153799	Hs.153799: Homo sapiens cDNA FLJ38333 fis	3.32
	414198	AW505308	Hs.75812	NM_004563: Homo sapiens phosphoenolpyruva	3.32
	443425	AI056776	Hs.133397	Hs.133397: ESTs	3.32
50	436485	X59135	Hs.156110	Hs.156110: immunoglobulin kappa constant	3.31
	410268	AA316181	Hs.61635	NM_012449: Homo sapiens six transmembrane	3.30
	425159	NM_004341	Hs.154868	NM_004341: Homo sapiens carbamoyl-phospha	3.30
	420614	AL110291	Hs.99384	Hs.99384: abhydrolase domain containing 1	3.30
	421814	L12350	Hs.108623	NM_003247: Homo sapiens thrombospondin 2	3.30
55	432215	AU076609	Hs.2934	NM_001033: Homo sapiens ribonucleotide re	3.30
	409402	AF208234	Hs.695	Hs.695: cystatin B (statin B)	3.30
	421038	AL080192	Hs.101282	Hs.101282: Homo sapiens mRNA; cDNA DKFZp4	3.29
	424408	AI754813	Hs.146428	Hs.146428: collagen, type V, alpha 1	3.29
	448775	AB025237	Hs.388	NM_002452: Homo sapiens nudix (nucleoside	3.29
60	442821	BE391929	Hs.8752	Hs.8752: transmembrane protein 4	3.29
	459306	AW578452		AW578452: RC1-CT0252-030100-023-b07 CT025	3.28
	400846				3.28
	422256	M64673	Hs.1499	NM_005526: Homo sapiens heat shock transc	3.28
	408089	H59799	Hs.42644	Hs.42644: thioredoxin-like 2	3.28
65	432078	BE314877	Hs.24553	(locuslink)NM_022369: Homo sapiens hypoth	3.27
	435575	AF213457	Hs.44234	NM_018965: Homo sapiens triggering recept	3.27
	456534	X91195	Hs.100623	NM_138689: Homo sapiens protein phosphata	3.27
	447335	BE617695	Hs.286192	NM_032192: Homo sapiens protein phosphata	3.27
	414368	W70171	Hs.75939	NM_012474: Homo sapiens uridine monophosp	3.27
70	422599	BE387202	Hs.118638	Hs.118638: non-metastatic cells 1, protei	3.26
	437897	AA770561	Hs.146170	Hs.146170: hypothetical protein FLJ22959	3.26
	431183	NM_006855	Hs.250696	NM_006855: Homo sapiens KDE1 (Lys-Asp-Glu	3.26
	457635	AV660978	Hs.3569	Hs.3569: chromosome 20 open reading frame	3.26
	432391	AI732374	Hs.339827	Hs.339827: ESTs, Weakly similar to protea	3.25
75	417640	D30857	Hs.82353	NM_006404: Homo sapiens protein C recepto	3.25
	440086	NM_005402	Hs.6906	NM_005402: Homo sapiens v-ral simian leuk	3.25
	401179				3.25
	411125	AA151647	Hs.68877	Hs.68877: cytochrome b-245, alpha polypep	3.25
80	453323	AF034102	Hs.32951	NM_001532: Homo sapiens solute carrier fa	3.25
	407236	W79485	Hs.173980	Hs.173980: nuclear matrix protein NMP200	3.25
	447250	AI878909	Hs.17883	NM_002707: Homo sapiens protein phosphata	3.25
	452875	BE275760	Hs.30928	NM_005114: Homo sapiens translocase of ou	3.24
	428390	AI640377	Hs.350077	NM_000582: Homo sapiens ribosomal protein	3.24
	425811	AL039104	Hs.159557	NM_002266: Homo sapiens karyopherin alpha	3.24

5	446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	3.24
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens integral membrane	3.24
	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	3.23
	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	3.23
	444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	3.23
	444734	NM_001360	Hs.11806	NM_001360:Homo sapiens 7-dehydrocholeste	3.23
	424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens vltag	3.23
	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-li	3.23
10	409686	AK000002	Hs.55879	(locuslink)NM_033450:Homo sapiens multidi	3.23
	418681	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	3.23
	419705	AW368634	Hs.154331	Hs.154331:ESTs	3.22
	420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	3.22
	413835	AI272727	Hs.249163	NM_024308:Homo sapiens fatty acid hydrox	3.22
	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	3.22
15	425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenanc	3.21
	435472	AW972330	Hs.283022	NM_018643:Homo sapiens triggering recept	3.21
	451932	AA360954	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.21
	420085	AI741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	3.21
	412006	AW451618	Hs.290216	Hs.290216:ESTs	3.21
20	424954	NM_000546	Hs.1846	NM_000546:Homo sapiens tumor protein p53	3.21
	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	3.21
	414602	AW630088	Hs.76550	NM_052886:Homo sapiens mal, T-cell diffe	3.20
	400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.20
25	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	3.20
	452203	X57522	Hs.352018	NM_000593:Homo sapiens transporter 1, AT	3.20
	413431	AW246428	Hs.75355	NM_003348:Homo sapiens ubiquitin-conjuga	3.19
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	3.19
	408716	AI567839	Hs.151714	(locuslink)NM_033405:Homo sapiens peroxi	3.19
30	433627	AF078866	Hs.284296	NM_033161:Homo sapiens surfactant 4 (SURF4)	3.19
	430393	BE185030	Hs.241305	(locuslink)NM_006470:Homo sapiens tripar	3.19
	417286	AA122237	Hs.81874	NM_002413:Homo sapiens microsomal glutat	3.18
	434224	AA380731	Hs.84	NM_000206:Homo sapiens interleukin 2 rec	3.18
	428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associat	3.18
35	445680	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	3.18
	420531	AI652069	Hs.98614	NM_004587:Homo sapiens ribosome binding	3.18
	417389	BE260964	Hs.82045	Hs.82045:midkine (neurite growth-promoti	3.18
	412276	BE262621	Hs.73798	Hs.73798:macrophage migration inhibitory	3.18
	452700	AI859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	3.18
40	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB27)-like 2	3.18
	414883	AA926960	Hs.348669	Hs.348669:CDC28 protein kinase 1	3.18
	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	3.18
	447698	AI420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	3.17
	424089	AL036662	Hs.144949	Hs.144949:ESTs	3.17
45	414788	X78342	Hs.77313	Hs.77313:cyclin-dependent kinase (CDC2)	3.17
	442315	AA173992	Hs.7956	Hs.7956:ESTs	3.17
	449944	AF290512	Hs.58215	(locuslink)NM_033046:Homo sapiens rhotek	3.17
	425244	AK002127	Hs.155313	NM_022105:Homo sapiens death associated	3.16
	428484	AF104032	Hs.184601	(locuslink)NM_003486:Homo sapiens solute	3.16
50	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	3.16
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	3.15
	447151	AI022813	Hs.92679	(locuslink)NM_145754:Homo sapiens kinesin	3.15
	418662	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	3.15
	410636	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.15
55	423599	AI805664	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	3.15
	435886	BE265839	Hs.12126	NM_018487:Homo sapiens hepatocellular ca	3.15
	458778	AW451034	Hs.326525	NM_001669:Homo sapiens arylsulfatase D (3.14
	420190	AI816209	Hs.95867	(locuslink)NM_024112:Homo sapiens chromo	3.14
	428371	AB012193	Hs.183874	NM_003589:Homo sapiens cutlin 4A (CUL4A)	3.14
60	450690	AA296696	Hs.333418	(locuslink)NM_014164:Homo sapiens FXD d	3.14
	413900	AW409747	Hs.75612	NM_006819:Homo sapiens stress-induced-ph	3.13
	406598	X03068	Hs.73931	Hs.73931:major histocompatibility comple	3.13
	407797	AK000524	Hs.39850	Hs.39850:uridine kinase-like 1	3.13
	447321	AW271217	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.13
65	426841	AI052358	Hs.131741	Hs.131741:ESTs	3.13
	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	3.12
	420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mRNA, comple	3.12
	438444	AI064707	Hs.301226	Hs.301226:Homo sapiens, clone IMAGE:3456	3.12
	439778	AL109729	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.12
70	412326	R07566	Hs.73817	NM_002983:Homo sapiens small inducible c	3.12
	447656	NM_003726	Hs.19126	NM_003726:Homo sapiens src family associ	3.12
	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	3.11
	421779	AI879159	Hs.108219	NM_004626:Homo sapiens wingless-type MMT	3.11
	400262		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.11
75	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	3.11
	449230	BE613348	Hs.356392	Hs.356392:ESTs, Highly similar to S-phas	3.11
	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	3.11
	432026	AA524545	Hs.224630	Hs.224630:Homo sapiens cDNA FLJ33318 fis	3.11
	433179	AW362945	Hs.162459	Hs.162459:ESTs	3.11
80	452264	AJ077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	3.11
	418641	BE243136	Hs.86947	NM_001109:Homo sapiens a disintegrin and	3.10
	421612	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens 8D6 an	3.10
	427349	AA360154	Hs.177415	(locuslink)NM_001997:Homo sapiens Finkel	3.10
	457670	AF119686	Hs.23449	NM_018842:Homo sapiens insulin receptor	3.10

5	438407	AI457122	Hs.129673	Hs.129673:eukaryotic translation initiat	3.10
	428293	BE250944	Hs.183556	Hs.183556:solute carrier family 1 (neur	3.10
	435823	AW749865	Hs.117077	Hs.117077:zinc finger protein 264	3.10
	418181	U37012	Hs.83727	NM_013291:Homo sapiens cleavage and poly	3.10
	434826	AF155661	Hs.22265	Hs.22265:pyruvate dehydrogenase phosphat	3.09
10	428734	BE303044	Hs.192023	NM_003757:Homo sapiens eukaryotic transl	3.09
	423022	AA320525	Hs.201076	Hs.201076:ESTs	3.08
	427648	AI376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	3.08
	404240				3.08
	408989	AW361666	Hs.49500	Hs.49500:KIAA0746 protein	3.08
15	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	3.08
	446506	AI123118	Hs.15159	(locustink)NM_016326:Homo sapiens chemok	3.08
	402260				3.08
	429671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	3.08
	409267	NM_012453	Hs.52515	NM_012453:Homo sapiens transducin (beta)	3.08
20	445937	AI452943	Hs.321231	(locustink)NM_003779:Homo sapiens UDP-Ga	3.07
	431243	U46455	Hs.252189	NM_002999:Homo sapiens syndecan 4 (amphi	3.07
	422611	AA158177	Hs.118722	(locustink)NM_004480:Homo sapiens fucosyl	3.07
	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ131360 fis	3.07
	449644	AW960707	Hs.148324	Hs.148324:ESTs	3.07
25	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) proteinase	3.07
	417457	AA378907	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30577 fis	3.07
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	3.07
	424927	AW973666	Hs.153850	Hs.153850:hypothetical protein C321D2.4	3.07
	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	3.07
30	426440	BE382756	Hs.169902	NM_006516:Homo sapiens solute carrier fa	3.06
	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	3.06
	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	3.06
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	3.06
	421802	BE261458	Hs.108408	(locustink)NM_016022:Homo sapiens CGI-78	3.06
35	421905	AI660247	Hs.32699	Hs.32699:Homo sapiens, Similar to RIKEN	3.06
	430542	AI557486	Hs.119122	Hs.119122:ribosomal protein L13a	3.06
	427268	X78520	Hs.174139	NM_001829:Homo sapiens chloride channel	3.06
	412525	AA581439	Hs.152328	Hs.152328:ESTs	3.06
	422813	AV656571	Hs.121068	(locustink)NM_003270:Homo sapiens transm	3.05
40	441406	Z45957	Hs.7837	Hs.7837:phosphoprotein regulated by mito	3.05
	408806	AW847814	Hs.75608	Hs.75608:tight junction protein 2 (zona	3.05
	435730	AB020635	Hs.4984	Hs.4984:KIAA0828 protein	3.05
	432871	NM_016142	Hs.279617	Hs.279617:hydroxysteroid (17-beta) dehyd	3.05
	447783	AF054178	Hs.19561	NM_005001:Homo sapiens NADH dehydrogenas	3.05
45	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	3.05
	450447	AF212223	Hs.25010	NM_018698:Homo sapiens hypothetical prot	3.05
	427337	Z46223	Hs.176663	NM_000569:Homo sapiens Fc fragment of Ig	3.05
	406363				3.05
	439841	AF038961	Hs.6710	NM_004870:Homo sapiens mannose-6-phospho	3.05
50	431738	AW237726	Hs.288549	NM_032826:Homo sapiens ubiquitin UBF-1	3.04
	447966	AA340605	Hs.105887	(locustink)NM_145252:Homo sapiens simila	3.04
	439246	AI498072	Hs.351474	Hs.351474:Homo sapiens cDNA FLJ30002 fis	3.04
	419493	AF001212	Hs.90744	Hs.90744:proteasome (prosome, macropain)	3.04
	427597	D15049	Hs.179770	NM_002842:Homo sapiens protein tyrosine	3.04
55	430281	AI878842	Hs.237924	NM_016016:Homo sapiens CGI-69 protein (L	3.04
	446620	AA128808	Hs.179902	(locustink)NM_022109:Homo sapiens CDw92	3.04
	452865	AI924046	Hs.119567	Hs.119567:ESTs, Weakly similar to ALU1_H	3.04
	422164	NM_014312	Hs.112377	Hs.112377:cortical thymocyte receptor (X	3.04
	444301	AK000136	Hs.10760	NM_017680:Homo sapiens asporin (LRR clas	3.04
60	451455	AI937227	Hs.8821	NM_021175:Homo sapiens hepcidin antimicr	3.03
	417777	AI823763	Hs.7055	Hs.7055:Homo sapiens cDNA FLJ33420 fis	3.03
	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	3.03
	450825	AC005954	Hs.25527	(locustink)NM_014428:Homo sapiens tight	3.03
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	3.03
65	409430	R21945	Hs.346735	Hs.346735:Homo sapiens, clone IMAGE:3881	3.03
	440659	AF134160	Hs.7327	NM_021101:Homo sapiens claudin 1 (CLDN1)	3.03
	432268	BE311856	Hs.274230	Hs.274230:3'-phosphoadenosine 5'-phospho	3.03
	438930	AW843633	Hs.343261	Hs.343261:histocompatibility (minor) 13	3.02
	412599	AU076782	Hs.248267	(locustink)NM_021126:Homo sapiens mercap	3.02
70	426788	U66615	Hs.172280	NM_003074:Homo sapiens SWI/SNF related,	3.02
	426966	NM_001761	Hs.1973	NM_001761:Homo sapiens cyclin F (CCNF),	3.02
	448847	AI587180	Hs.110906	Hs.110906:hypothetical protein BC004501	3.02
	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	3.02
	414702	L22005	Hs.76932	NM_004359:Homo sapiens cell division cyc	3.02
75	430024	AI808780	Hs.227730	NM_000210:Homo sapiens Integrin, alpha 6	3.02
	424394	BE277024	Hs.146381	Hs.146381:RNA binding motif protein, X c	3.01
	442993	BE018682	Hs.166196	Hs.166196:ATPase, Class I, type 8B, memb	3.01
	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	3.01
	410293	AK000047	Hs.61950	NM_018992:Homo sapiens hypothetical prot	3.01
80	454358	AW792876	Hs.288936	NM_031420:Homo sapiens mitochondrial rib	3.01
	411531	AB014511	Hs.70604	Hs.70604:ATPase, Class II, type 9A	3.00
	447032	AK000310	Hs.17138	(locustink)NM_017755:Homo sapiens hypoth	3.00
	414249	AI797994	Hs.279929	(locustink)NM_017510:Homo sapiens gp25L2	3.00
	448440	AA173467	Hs.62402	Hs.62402:p21/Cdc42/Rac1-activated kinase	3.00
	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EFNA1)	3.00
	419452	U33635	Hs.90572	Hs.90572:PTK7 protein tyrosine kinase 7	3.00
	417878	U90916	Hs.82845	Hs.82845:Homo sapiens cDNA: FLJ21930 fis	3.00

5	431884	AA521246	Hs.210792	Hs.210792:Homo sapiens cDNA FLJ36691 fis	3.00
	425261	BE385099	Hs.355814	Hs.355814:Homo sapiens clone IMAGE:29333	3.00
	445229	BE276013	Hs.343828	Hs.343828:Homo sapiens mRNA; cDNA DKFZp7	3.00
	412146	M92444	Hs.73722	Hs.73722:APEX nuclease (multifunctional	2.99
	437763	AA469369	Hs.5831	Hs.5831:tissue inhibitor of metalloprote	2.99
	406865	AI025931	Hs.181357	Hs.181357:laminin receptor 1 (67kD, ribo	2.99
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	2.99
	417259	AW903838	Hs.81800	Hs.81800:chondroitin sulfate proteoglyca	2.98
10	453902	BE502341	Hs.3402	NM_139177:Homo sapiens chromosome 17 ope	2.98
	432396	AW295956	Hs.11900	(locuslink)NM_032527:Homo sapiens hypoth	2.98
	411358	R47479	Hs.94761	Hs.94761:KIAA1691 protein	2.98
	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	2.98
	448913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6),	2.98
15	440943	AW082298	Hs.146161	NM_032331:Homo sapiens hypothetical prot	2.98
	414013	AA766605	Hs.47099	NM_024642:Homo sapiens hypothetical prot	2.98
	452124	AA454220	Hs.61170	Hs.61170:ESTs	2.98
	416391	AI878927	Hs.79284	NM_002402:Homo sapiens mesoderm specific	2.97
	418092	J05581	Hs.89603	NM_002456:Homo sapiens mucin 1, transmem	2.97
20	426375	AK000597	Hs.169549	NM_017893:Homo sapiens sema domain, immu	2.97
	437296	AA350994	Hs.20281	Hs.20281:MAPK phosphatase-7	2.97
	407736	N41744	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	2.97
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	2.97
	424756	AW504657	Hs.152931	(locuslink)NM_002296:Homo sapiens lamin	2.97
25	430354	AA954810	Hs.239784	Hs.239784:scribble	2.97
	417079	U65590	Hs.81134	(locuslink)NM_000577:Homo sapiens interl	2.97
	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	2.97
	414186	U33446	Hs.75799	Hs.75799:protease, serine, 8 (prolactin)	2.97
	432065	AA401039	Hs.2903	Hs.2903:protein phosphatase 4 (formerly	2.96
30	452012	AA307703	Hs.279766	(locuslink)NM_012310:Homo sapiens knesi	2.96
	412429	AV650262	Hs.75765	NM_002089:Homo sapiens GRO2 oncogene (GR	2.96
	452714	AW770994	Hs.30340	Hs.30340:hypothetical protein KIAA1165	2.96
	429922	Z97630	Hs.226117	NM_005318:Homo sapiens H1 histone family	2.96
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	2.96
35	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	2.96
	428781	AF164799	Hs.193384	Hs.193384:putative 28 kDa protein	2.96
	445350	AF052112	Hs.12540	NM_006330:Homo sapiens lysophospholipase	2.96
	422396	W21872	Hs.7907	(locuslink)NM_145059:Homo sapiens L-fuco	2.96
	429597	NM_003816	Hs.2442	Hs.2442:a disintegrin and metalloprotein	2.95
40	421179	U72684	Hs.148495	NM_002810:Homo sapiens proteasome (proso	2.95
	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of oig	2.95
	427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	2.95
	430589	AJ002744	Hs.246315	NM_017423:Homo sapiens UDP-N-acetyl-alpha	2.95
	409220	BE243323	Hs.51233	(locuslink)NM_003842:Homo sapiens tumor	2.95
45	443883	AA114212	Hs.9930	Hs.9930:serine (or cysteine) proteinase	2.95
	445720	AL040482	Hs.286173	Hs.286173:KIAA1595 protein	2.95
	429583	NM_008412	Hs.209119	NM_006412:Homo sapiens 1-acylglycerol-3-	2.95
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif	2.94
50	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	2.94
	419152	L12711	Hs.89643	(locuslink)NM_001064:Homo sapiens transk	2.94
	444824	AA843575	Hs.12056	NM_001677:Homo sapiens asialoglycoprotei	2.94
	413629	AU077025	Hs.265827	NM_022873:Homo sapiens interferon, alpha	2.94
	425118	AU076611	Hs.154672	Hs.154672:methylene tetrahydrofolate deh	2.94
55	422010	AA302049	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	2.93
	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	2.93
	412338	AA151527	Hs.69485	(locuslink)NM_024661:Homo sapiens hypoth	2.93
	413073	AL038165	Hs.75187	NM_014765:Homo sapiens translocase of ou	2.93
	412088	AI689496	Hs.108932	Hs.108932:ESTs	2.93
60	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	2.92
	426746	J03626	Hs.2057	NM_000373:Homo sapiens uridine monophosp	2.92
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	2.92
	417944	AU077196	Hs.82985	NM_000393:Homo sapiens collagen, type V,	2.92
	428343	AL043021	Hs.12705	(locuslink)NM_145294:Homo sapiens simila	2.92
65	435940	AF220053	Hs.54960	NM_018468:Homo sapiens uncharacterized h	2.92
	451608	AA384525	Hs.26745	NM_016499:Homo sapiens HSPC244 (MGC:1337	2.92
	434608	AA805443	Hs.179909	NM_024831:Homo sapiens nuclear receptor	2.92
	437186	AA338305	Hs.377816	Hs.377816:Homo sapiens cDNA FLJ36808 fis	2.91
	429574	BE268321	Hs.208912	Hs.208912:hypothetical protein MGC861	2.91
70	438549	BE386801	Hs.21858	Hs.21858:serine (or cysteine) proteinase	2.91
	440246	W52010	Hs.191379	Hs.191379:ESTs	2.91
	426924	BE222542	Hs.128782	Hs.128782:Homo sapiens cDNA FLJ31512 fis	2.91
	444193	Y17801	Hs.10574	Hs.10574:solute carrier family 2, (facil	2.91
	422030	X51416	Hs.110849	(locuslink)NM_004451:Homo sapiens estrog	2.91
75	415938	BE383507	Hs.78921	NM_003488:Homo sapiens A kinase (PRKA) a	2.91
	450167	AA446404	Hs.24563	NM_013248:Homo sapiens NTF2-like export	2.91
	408815	AW957974	Hs.25485	(locuslink)NM_024559:Homo sapiens hypoth	2.91
	414820	AA371931	Hs.77422	Hs.77422:protocadherin protein 2 (colonic	2.91
	410013	AF067173	Hs.57904	Hs.57904:mago-nashi homolog, proliferati	2.91
	444823	BE262989	Hs.12045	Hs.12045:C2f protein	2.91
80	422197	AW974265	Hs.111632	Hs.111632:Lsm3 protein	2.90
	432710	AA609685	Hs.278672	NM_005898:Homo sapiens membrane componen	2.90
	405203				2.90
	432465	D56165	Hs.275163	NM_002512:Homo sapiens non-metastatic ca	2.90
	412926	AI879076	Hs.75061	Hs.75061:macrophage myristoylated alanin	2.90

	455967	L12535	Hs.75551	(locuslink)NM_012425:Homo sapiens Ras su	2.90
	402104				2.90
	414814	D14697	Hs.77393	(locuslink)NM_002004:Homo sapiens farnes	2.90
	442739	NM_007274	Hs.8679	(locuslink)NM_007274:Homo sapiens cyto	2.90
5	456157	AW579153	Hs.336881	Hs.336881:ESTs	2.90
	429505	AW820035	Hs.278679	NM_033274:Homo sapiens a disintegrin and	2.89
	430567	NM_003028	Hs.244542	Hs.244542:Homo sapiens cDNA FLJ38908 fis	2.89
	437822	AW450485	Hs.4437	NM_000991:Homo sapiens ribosomal protein	2.89
	438543	AA810141	Hs.192182	Hs.192182:ESTs	2.89
10	426168	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythro	2.89
	441455	AJ271671	Hs.7854	NM_014437:Homo sapiens solute carrier fa	2.89
	420166	AW732276	Hs.95583	NM_012339:Homo sapiens transmembrane 4 s	2.89
	415674	BE394784	Hs.78596	NM_002797:Homo sapiens proteasome (proso	2.89
	409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	2.89
15	418062	AW630656	Hs.83383	NM_006406:Homo sapiens peroxiredoxin 4 (2.89
	436540	BE397032	Hs.14468	NM_020230:Homo sapiens peter pan homolog	2.89
	426675	AW084791	Hs.133122	Hs.133122:hypothetical protein FLJ14524	2.89
	417018	M16038	Hs.80887	Hs.80887:v-yes-1 Yamaguchi sarcoma viral	2.89
	421684	BE281591	Hs.106768	NM_018120:Homo sapiens hypothetical prot	2.88
20	429404	NM_005738	Hs.10706	NM_005738:Homo sapiens ADP-ribosylatio	2.88
	411030	BE387193	Hs.67896	(locuslink)NM_007346:Homo sapiens oploid	2.88
	413822	R08950	Hs.272044	Hs.272044:ESTs, Weakly similar to hypoth	2.88
	438085	R52518	Hs.7967	Hs.7967:ESTs, Weakly similar to extensin	2.88
	409132	AJ224538	Hs.50732	NM_005399:Homo sapiens protein kinase, A	2.88
25	440490	AW513684	Hs.7218	Hs.7218:acetyl-Coenzyme A synthetase 2 (2.87
	431498	AK001777	Hs.258551	NM_012100:Homo sapiens aspartyl aminopep	2.87
	423570	AW838306	Hs.129819	NM_018344:Homo sapiens hypothetical prot	2.87
	448569	BE382657	Hs.21486	Hs.21486:signal transducer and activator	2.87
	451711	AK000461	Hs.26890	NM_017829:Homo sapiens cat eye syndrome	2.87
30	442643	U82756	Hs.374973	(locuslink)NM_004697:Homo sapiens PRP4 p	2.87
	447887	AA114050	Hs.211610	NM_001228:Homo sapiens caspase 8, apopto	2.87
	421178	BE267994	Hs.102419	Hs.102419:zinc finger protein	2.87
	443329	BE262943	Hs.9234	NM_032635:Homo sapiens seven transmembra	2.87
	416448	L13210	Hs.79339	NM_005567:Homo sapiens lactin, galactosi	2.87
35	453145	R63438	Hs.183454	Hs.183454:Homo sapiens cDNA FLJ14883 fis	2.86
	427775	R26944	Hs.180777	Hs.180777:Homo sapiens mRNA; cDNA DKFZp5	2.86
	424732	D60001	Hs.152629	Hs.152629:KIAA0179 protein	2.86
	426125	X87241	Hs.166994	Hs.166994:FAT tumor suppressor homolog 1	2.86
	450273	AW296454	Hs.24743	Hs.24743:hypothetical protein FLJ20171	2.86
40	407082	Z47055			2.86
	450038	AA005159	Hs.188489	Hs.188489:ESTs	2.86
	457274	AW674193	Hs.227152	NM_016391:Homo sapiens hypothetical prot	2.85
	417831	H18423	Hs.82685	Hs.82685:CD47 antigen (Rb-related antige	2.85
45	417824	AA084788	Hs.82646	NM_006145:Homo sapiens DnaJ (Hsp40) homo	2.85
	426989	A1815208	Hs.100293	Hs.100293:O-linked N-acetylglucosamine (2.85
	434916	AF161383	Hs.284207	Hs.284207:hypothetical protein BC003615	2.85
	412664	AA421404	Hs.346868	NM_006824:Homo sapiens EBNA1 binding pro	2.85
	414172	AW954324	Hs.75790	(locuslink)NM_002642:Homo sapiens phosph	2.85
50	409504	AA304961	Hs.699	Hs.699:peptidylprolyl isomerase B (cyclo	2.84
	439820	H05430	Hs.288433	NM_016522:Homo sapiens neurotrophin (HNT)	2.84
	418462	BE001596	Hs.85266	Hs.85266:integrin, beta 4	2.84
	442199	BE277633	Hs.372542	NM_004879:Homo sapiens etoposide-induced	2.84
	406710	A1708347	Hs.184014	Hs.184014:ribosomal protein L31	2.84
55	433435	BE545277	Hs.340969	NM_005726:Homo sapiens Ts translation el	2.84
	415402	AA164687	Hs.177576	Hs.177576:mannosyl (alpha-1,3)-glycopro	2.84
	448730	AB032983	Hs.21894	Hs.21894:KIAA1157 protein	2.84
	433027	AF191018	Hs.279923	(locuslink)NM_014366:Homo sapiens putati	2.84
	449090	AK001735	Hs.22983	NM_020121:Homo sapiens UDP-glucose ceram	2.84
60	439737	A1751438	Hs.41271	Hs.41271:Homo sapiens mRNA full length l	2.84
	403912				2.84
	423225	AA852604	Hs.125359	NM_005288:Homo sapiens Thy-1 cell surfac	2.84
	458376	AB023179	Hs.9059	Hs.9059:KIAA0962 protein	2.84
	429211	AF052693	Hs.198249	NM_005268:Homo sapiens gap junction prot	2.84
65	452518	AA280722	Hs.24758	Hs.24758:Homo sapiens cDNA FLJ32068 fis	2.84
	418127	BE243982	Hs.83532	(locuslink)NM_002389:Homo sapiens membra	2.83
	448489	A1523875		R45782:Ha616-f Adult heart, Clontech Hom	2.83
	426194	T50872	Hs.2001	NM_001061:Homo sapiens thromboxane A syn	2.83
	422129	AJ076635	Hs.1478	NM_000185:Homo sapiens serine (or cystal	2.83
70	437651	BE560672	Hs.13543	(locuslink)NM_145214:Homo sapiens tripar	2.83
	415173	AW501735	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	2.83
	408201	AK000568	Hs.43654	NM_017882:Homo sapiens ceroid-lipofuscin	2.83
	444758	AL044878	Hs.11899	NM_000859:Homo sapiens 3-hydroxy-3-methy	2.83
	423323	A1951628	Hs.127007	NM_003740:Homo sapiens potassium channel	2.83
75	439720	A1935202	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	2.83
	435550	A1224456	Hs.324507	Hs.324507:hypothetical protein FLJ20986	2.83
	425907	AA365762	Hs.155965	Hs.155965:ESTs	2.83
	426234	BE314534	Hs.168159	Hs.168159:bifunctional apoptosis regulat	2.82
	427640	AF058293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	2.82
80	433233	AB040927	Hs.301804	Hs.301804:KIAA1494 protein	2.82
	415697	A1365603	Hs.279696	Hs.279696:DKFZP5661024 protein	2.82
	441321	H17182	Hs.7771	NM_007273:Homo sapiens repressor of estr	2.82
	430040	AW503115	Hs.227823	NM_014287:Homo sapiens pM5 protein (PM5)	2.82
	449954	AA841636	Hs.37477	Hs.37477:ESTs, Weakly similar to T46220	2.82

	427022	AW245839	Hs.173255	NM_004596:Homo sapiens small nuclear rib	2.82
	410047	AI167810	Hs.379753	Hs.379753:Homo sapiens cDNA FLJ33176 fis	2.82
	400845				2.81
5	419501	AW843822	Hs.199961	Hs.199961:ESTs, Weakly similar to hypoth	2.81
	418140	BE613836	Hs.83551	(locuslink)NM_002403:Homo sapiens microf	2.81
	422032	AA476966	Hs.110857	NM_016310:Homo sapiens polymerase (RNA)	2.81
	419768	T72104	Hs.93194	Hs.93194:apolipoprotein A-I	2.81
	436673	AF201931	Hs.5268	Hs.5268:zinc finger, DHHC domain contain	2.81
10	421140	AA298741	Hs.102135	NM_006280:Homo sapiens signal sequence r	2.81
	450126	BE018138	Hs.24447	(locuslink)NM_005866:Homo sapiens type I	2.81
	439018	AW300887	Hs.26638	NM_031457:Homo sapiens membrane-spanning	2.81
	433061	AW068033	Hs.296422	(locuslink)NM_025233:Homo sapiens nucleo	2.81
	400278		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	2.81
15	407338	AA773213	Hs.91202	Hs.91202:Homo sapiens cDNA FLJ25946 fis,	2.81
	410240	AL157424	Hs.61289	Hs.61289:synaptotagmin 2	2.80
	423880	BE278111	Hs.134200	Hs.134200:KFPZP564C186 protein	2.80
	422098	H03117	Hs.111497	Hs.111497:neuronal protein 17.3	2.80
	426680	AA320160	Hs.171811	NM_001625:Homo sapiens adenylate kinase	2.80
20	437672	AW748265	Hs.5741	NM_016230:Homo sapiens flavohemoprotein	2.80
	456602	AA411607	Hs.118964	NM_017660:Homo sapiens hypothetical prot	2.80
	457329	AI634860	Hs.359682	(locuslink)NM_016442:Homo sapiens type 1	2.80
	426437	BE076537	Hs.169895	Hs.169895:ubiquitin-conjugating enzyme E	2.79
	412627	BE391959	Hs.74278	Hs.74278:chloride intracellular channel	2.79
25	452695	AW780199	Hs.30327	NM_003688:Homo sapiens mitogen-activated	2.79
	409531	BE384319	Hs.54702	(locuslink)NM_007255:Homo sapiens xylosy	2.79
	448988	Y09763	Hs.22785	NM_021987:Homo sapiens gamma-aminobutyri	2.79
	447627	AF090922	Hs.152738	NM_016050:Homo sapiens mitochondrial rib	2.79
	419846	NM_015977	Hs.285681	NM_032951:Homo sapiens Williams Beuren s	2.79
30	412969	AI373162	Hs.75103	NM_003406:Homo sapiens tyrosine 3-monoox	2.79
	424867	AI024860	Hs.153591	NM_005787:Homo sapiens Not56 (D. melanog	2.79
	410600	AW575742	Hs.351676	Hs.351676:Homo sapiens cDNA FLJ25921 fis	2.79
	451452	BE560065	Hs.26433	NM_001382:Homo sapiens dolichyl-phosphat	2.79
	407844	AW073716	Hs.8037	(locuslink)NM_005723:Homo sapiens tetras	2.79
35	448752	AA593867	Hs.300842	NM_024820:Homo sapiens KIAA1608 protein	2.79
	419235	AW470411	Hs.288433	NM_016522:Homo sapiens neurotrophin (HNT)	2.78
	407754	AA527348	Hs.288967	Hs.288967:Homo sapiens, similar to RIKEN	2.78
	422282	AF019225	Hs.114309	(locuslink)NM_003661:Homo sapiens apolip	2.78
	414181	AK000476	Hs.75798	NM_016470:Homo sapiens chromosome 20 ope	2.78
40	418869	AW516565		AA229762:nc49f01.r1 NCI_CGAP_P3 Homo sa	2.78
	419444	NM_002496	Hs.90443	NM_002496:Homo sapiens NADH dehydrogenas	2.78
	430250	NM_016929	Hs.283021	NM_016929:Homo sapiens chloride intracel	2.78
	412760	AW379030	Hs.41324	Hs.41324:ESTs	2.78
	423013	AW875443	Hs.22209	Hs.22209:secreted modular calcium-bindin	2.78
45	449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	2.78
	447402	H54520	Hs.351327	(locuslink)NM_017828:Homo sapiens hypoth	2.78
	417896	AA379770	Hs.82890	Hs.82890:defender against cell death 1	2.78
	422051	AW327546	Hs.111024	(locuslink)NM_005984:Homo sapiens solute	2.78
	450607	AL050373	Hs.25213	NM_015677:Homo sapiens hypothetical prot	2.78
50	419757	AA773820	Hs.63970	Hs.63970:ESTs	2.77
	409932	AI376750	Hs.57600	NM_001283:Homo sapiens adaptor-related p	2.77
	408044	BE206839	Hs.42287	NM_001952:Homo sapiens E2F transcription	2.77
	430014	H59354	Hs.374303	(locuslink)NM_144691:Homo sapiens hypoth	2.77
	451690	AW451469	Hs.209990	Hs.209990:ESTs	2.77
55	446950	AA305800	Hs.5672	(locuslink)NM_030799:Homo sapiens golgi	2.77
	444207	AI565004	Hs.374415	Hs.374415:ESTs	2.77
	417089	H52280	Hs.18612	Hs.18612:Homo sapiens cDNA: FLJ21909 fis	2.77
	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	2.77
	425978	BE253927	Hs.24983	Hs.24983:hypothetical protein from EUROI	2.77
60	422753	AI928995	Hs.1575	Hs.1575:small nuclear ribonucleoprotein	2.77
	449051	AW961400	Hs.333526	NM_032339:Homo sapiens hypothetical prot	2.77
	450701	H39960	Hs.288467	Hs.288467:Homo sapiens cDNA FLJ12280 fis	2.77
	412890	T85247	Hs.351875	NM_004374:Homo sapiens cytochrome c oxid	2.77
	415752	BE314524	Hs.78776	NM_012342:Homo sapiens putative transmem	2.76
65	427609	AK000436	Hs.179791	NM_017817:Homo sapiens RAB20, member RAS	2.76
	450770	AA019924	Hs.28803	Hs.28803:ESTs	2.76
	419594	AA013051	Hs.91417	(locuslink)NM_007027:Homo sapiens topois	2.76
	450876	AF189062	Hs.285976	(locuslink)NM_013384:Homo sapiens LAG1 I	2.76
	417767	BE242241	Hs.82542	NM_001637:Homo sapiens acyl-oxacyl hydro	2.76
70	439968	AA224760	Hs.153	NM_000971:Homo sapiens ribosomal protein	2.76
	426520	BE545684	Hs.343566	Hs.343566:KIAA0251 protein	2.75
	441028	AI333660	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	2.75
	445033	AV652402	Hs.72901	NM_078487:Homo sapiens cyclin-dependent	2.75
	418478	U38945	Hs.1174	NM_000077:Homo sapiens cyclin-dependent	2.75
75	428157	AI738719	Hs.198427	NM_000189:Homo sapiens hexokinase 2 (HK2	2.75
	416178	AI808527	Hs.192822	NM_030949:Homo sapiens protein phosphata	2.75
	435025	T08990	Hs.4742	Hs.4742:GPAA1P anchor attachment protein	2.75
	421917	AB028943	Hs.109445	Hs.109445:hypermethylated in cancer 2	2.75
	406621	X57809	Hs.181125	Hs.181125:immunoglobulin lambda locus	2.75
80	408195	AL034548	Hs.43627	NM_006943:Homo sapiens SRY (sex determin	2.75
	412600	L28824	Hs.74101	Hs.74101:spleen tyrosine kinase	2.75
	452806	AW014549	Hs.58373	Hs.58373:ESTs	2.75
	451356	AA748418	Hs.33368	Hs.33368:hypothetical protein FLJ11175	2.75
	421643	BE281170	Hs.106357	NM_007126:Homo sapiens valosin-containing	2.74

5	423527	AI206955	Hs.105861	(locustlink)NM_024712:Homo sapiens engulf	2.74
	428000	R35145	Hs.291904	Hs.291904:accessory protein BAP31	2.74
	441555	AW953575	Hs.303125	Hs.303125:p53-induced protein PIGPC1	2.74
	450247	AF123303	Hs.24713	NM_013386:Homo sapiens hypothetical prot	2.74
	422691	NM_003365	Hs.119251	NM_003365:Homo sapiens ubiquinol-cytochr	2.74
10	440457	BE387593	Hs.21321	(locustlink)NM_145808:Homo sapiens granul	2.74
	422675	BE018517	Hs.119140	NM_001970:Homo sapiens eukaryotic transl	2.74
	428428	AL037544	Hs.184298	NM_001799:Homo sapiens cyclin-dependent	2.73
	423598	BE247600	Hs.377968	NM_020400:Homo sapiens G protein-coupled	2.73
	428297	AA236291	Hs.183583	NM_030666:Homo sapiens serine (or cystei	2.73
15	421921	H83363	Hs.355993	NM_012456:Homo sapiens translocase of in	2.73
	403217				2.73
	423671	AW860155	Hs.234101	Hs.234101:Homo sapiens, similar to chol	2.73
	418733	AA227714	Hs.374897	Hs.374897:Homo sapiens cDNA FLJ36874 fis	2.73
	400275		Hs.4888	NM_006513:Homo sapiens seryl-tRNA synthe	2.73
20	445084	H38914	Hs.250848	Hs.250848:Homo sapiens cDNA FLJ14761 fis	2.73
	411872	AW327356	Hs.90918	Hs.90918:chromosome 11 open reading fram	2.73
	403483				2.73
	438119	AW963217	Hs.203961	Hs.203961:ESTs, Weakly similar to hypoth	2.73
	422009	AI742845	Hs.110713	NM_003472:Homo sapiens DEK oncogene (DNA	2.73
25	436995	AI160015	Hs.125489	Hs.125489:KIAA1951 protein	2.73
	400509				2.73
	429305	AF095727	Hs.287832	Hs.287832:myelin protein zero-like 1	2.73
	445899	AI263736	Hs.145626	Hs.145626:Homo sapiens, Similar to hypot	2.72
	453557	AA522464	Hs.285996	NM_024955:Homo sapiens hypothetical prot	2.72
30	446859	AI494299	Hs.16297	NM_005694:Homo sapiens COX17 homolog, cy	2.72
	424439	AA579635	Hs.1770	Hs.1770:ligase I, DNA, ATP-dependent	2.72
	437809	AL137723	Hs.5855	Hs.5855:Homo sapiens mRNA; cDNA DKFZp434	2.72
	428466	AF151063	Hs.184456	NM_016486:Homo sapiens hypothetical prot	2.71
	445176	AI878907	Hs.12379	NM_001419:Homo sapiens ELAV (embryonic l	2.71
35	438000	AI825880	Hs.5985	Hs.5985:non-kinase Cdc42 effector protei	2.71
	429359	W00482	Hs.2399	NM_004995:Homo sapiens matrix metallopro	2.71
	427782	AI956052	Hs.115960	NM_024036:Homo sapiens hypothetical prot	2.71
	415169	W42913	Hs.78089	NM_004231:Homo sapiens ATPase, H+ transp	2.71
	400277		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	2.71
40	426263	AI908774	Hs.259785	Hs.259785:camitine palmitoyltransferase	2.71
	445515	BE388665	Hs.179999	Hs.179999:Homo sapiens, clone IMAGE:3457	2.71
	416976	BE243985	Hs.80680	Hs.80680:major vault protein	2.71
	441238	AI372555	Hs.322456	NM_032039:Homo sapiens hypothetical prot	2.71
	420511	AF052692	Hs.98485	NM_024009:Homo sapiens gap junction prot	2.71
45	424965	AW956282	Hs.144609	NM_080652:Homo sapiens similar to RIKEN	2.71
	421808	AK000157	Hs.108502	NM_017688:Homo sapiens hypothetical prot	2.71
	412973	L37368	Hs.75104	Hs.75104:RNA binding protein S1, serine-	2.70
	410113	AW995564	Hs.250824	Hs.250824:Homo sapiens cDNA: FLJ23435 fi	2.70
	413092	AA126856	Hs.118665	Hs.118665:ESTs	2.70
50	447096	BE539199	Hs.62112	(locustlink)NM_003457:Homo sapiens zinc f	2.70
	450493	M93718	Hs.166373	Hs.166373:nitric oxide synthase 3 (endot	2.70
	413745	AW247252	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	2.70
	450747	AI064821	Hs.129953	Hs.129953:Ewing sarcoma breakpoint regio	2.70
	436042	AF284422	Hs.119178	(locustlink)NM_020248:Homo sapiens cation	2.70
55	432981	NM_002733	Hs.3136	Hs.3136:protein kinase, AMP-activated, g	2.70
	431341	AA307211	Hs.251531	NM_002789:Homo sapiens proteasome (proso	2.70
	408204	AA454501	Hs.43666	NM_007079:Homo sapiens protein tyrosine	2.70
	416770	AW163570	Hs.79768	NM_014740:Homo sapiens KIAA0111 gene pro	2.70
	447507	H59686	Hs.18747	NM_005837:Homo sapiens POP7 (processing	2.70
60	424500	AF040704	Hs.149443	(locustlink)NM_007022:Homo sapiens putati	2.69
	414237	BE536554	Hs.278270	Hs.278270:inactive progesterone receptor	2.69
	400231		Hs.169476	NM_002046:Homo sapiens glyceraldehyde-3-	2.69
	431209	NM_001533	Hs.2730	Hs.2730:heterogeneous nuclear ribonucleo	2.69
	444118	AA458542	Hs.10326	NM_007263:Homo sapiens coatomer protein	2.69
65	424608	X80695	Hs.151134	Hs.151134:oxidase (cytochrome c) assembl	2.69
	418546	AA224827		AA224827:nc32g04.s1 NCL CGAP_Pr2 Homo sa	2.69
	440002	AW769844	Hs.111222	Hs.111222:hypothetical protein FLJ22875	2.69
	449957	D31365	Hs.24220	(locustlink)NM_016479:Homo sapiens scotin	2.69
	432920	U37689	Hs.3128	NM_006232:Homo sapiens polymerase (RNA)	2.69
70	450306	AL080080	Hs.24766	NM_030755:Homo sapiens thioredoxin domai	2.69
	429544	BE299343	Hs.2430	NM_005997:Homo sapiens transcription fac	2.68
	428582	BE336699	Hs.185055	Hs.185055:BENE protein	2.68
	445139	AB037848	Hs.12365	Hs.12365:synaptotagmin XIII	2.68
	453905	NM_002314	Hs.36566	NM_016735:Homo sapiens LIM domain kinase	2.68
75	418883	BE387036	Hs.1211	NM_001611:Homo sapiens acid phosphatase	2.68
	420957	X98743	Hs.100555	Hs.100555:DEAD/H (Asp-Glu-Ala-Asp/His) b	2.68
	418187	NM_004604	Hs.83734	NM_004604:Homo sapiens syntactin 4A (plac	2.68
	408533	AW969543	Hs.144609	NM_080652:Homo sapiens similar to RIKEN	2.68
	433184	AA147979	Hs.285005	NM_020243:Homo sapiens translocase of ou	2.68
80	455303	AW892049		BE066891:PM3-BT0338-211299-002-e12 BT033	2.68
	452600	AI910842	Hs.103381	Hs.103381:ESTs, Weakly similar to hypoth	2.67
	415410	AF037332	Hs.278569	NM_014748:Homo sapiens KIAA0064 gene pro	2.67
	426432	AF001601	Hs.169857	NM_000305:Homo sapiens paraoxonase 2 (PO	2.67
	435049	AL122067	Hs.4746	NM_021941:Homo sapiens hypothetical prot	2.67
	450528	NM_014072	Hs.25063	NM_031268:Homo sapiens PRO461 protein (2.67
	433339	AF019226	Hs.80036	NM_004283:Homo sapiens RAB3D, member RAS	2.67
	408783	AF192522	Hs.47701	NM_013389:Homo sapiens NPC1 (Niemann-Pic	2.67

	451798	BE297567	Hs.27047	Hs.27047:hypothetical protein FLJ20392	2.67
	427716	L38951	Hs.180446	Hs.180446:karyopherin (importin) beta 1	2.67
	436319	H90727	Hs.5123	Hs.5123:hypothetical protein BC008246	2.67
	415116	AA160363	Hs.269956	Hs.269956:ESTs	2.67
5	425838	NM_014071	Hs.159613	NM_014071:Homo sapiens nuclear receptor	2.66
	418706	U73524	Hs.87465	NM_006831:Homo sapiens ATP/GTP-binding p	2.66
	410165	BE560228	Hs.71869	NM_013258:Homo sapiens apoptosis-associa	2.66
	410134	U68140	Hs.58927	(locuslink)NM_002533:Homo sapiens nuclea	2.66
10	430066	AJ929659	Hs.237825	Hs.237825:signal recognition particle 72	2.66
	425910	AA830797	Hs.184760	NM_005760:Homo sapiens CCAAT-box-binding	2.66
	427954	J03060	Hs.247551	NM_002455:Homo sapiens metaxin 1 (MTX1),	2.66
	439971	W32474	Hs.301746	Hs.301746:Homo sapiens cDNA FLJ37267 fis	2.66
	438449	AK001333	Hs.6216	Hs.6216:DnaJ (Hsp40) homolog, subfamily	2.66
15	435906	AJ686379	Hs.110796	(locuslink)NM_020150:Homo sapiens SAR1 p	2.66
	433387	L76528	Hs.3260	NM_000021:Homo sapiens presenilin 1 (Alz	2.66
	447191	NM_014521	Hs.17667	(locuslink)NM_014521:Homo sapiens SH3-do	2.66
	444099	D87432	Hs.10315	NM_003983:Homo sapiens solute carrier fa	2.66
	417821	BE245149	Hs.82643	NM_002822:Homo sapiens protein tyrosine	2.66
20	418529	AW005695	Hs.250897	Hs.250897:TRK-fused gene	2.65
	426025	AW138330	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	2.65
	420187	AK001714	Hs.95744	NM_019028:Homo sapiens hypothetical prot	2.65
	408150	BE620274	Hs.43112	Hs.43112:Homo sapiens mRNA; cDNA DKFZp43	2.65
	444395	N66148	Hs.11125	(locuslink)NM_014041:Homo sapiens signal	2.65
25	431222	X56777	Hs.273790	NM_007155:Homo sapiens zona pellucida gl	2.65
	406790	AA293303	Hs.356342	Hs.356342:ESTs, Highly similar to 211320	2.65
	440708	AF038962	Hs.7381	Hs.7381:voltage-dependent anion channel	2.65
	416526	H61082	Hs.14743	Hs.14743:ESTs	2.65
	413995	BE048146	Hs.75671	NM_004603:Homo sapiens syntaxin 1A (bral	2.65
30	424908	AW513963	Hs.39143	Hs.39143:hypothetical protein MGC13125	2.65
	442110	AF113008	Hs.8102	NM_001023:Homo sapiens ribosomal protein	2.65
	452882	AW972990	Hs.196270	NM_030780:Homo sapiens folate transporte	2.65
	406862	AW150807	Hs.356262	Hs.356262:ESTs, Highly similar to A31233	2.64
	451295	AI557212	Hs.17132	Hs.17132:ESTs	2.64
35	448428	AF282874	Hs.21201	NM_015480:Homo sapiens necln 3 (DKFZP56	2.64
	426611	BE178050	Hs.171271	NM_001904:Homo sapiens catenin (cadherin	2.64
	426216	N77630	Hs.13895	Hs.13895:Homo sapiens cDNA FLJ11654 fis,	2.64
	407223	H96850		H96850:yyw03b12.s1 Soares melanocyte 2NbH	2.64
40	427725	U66839	Hs.180533	NM_002756:Homo sapiens mitogen-activated	2.64
	420157	AA857991	Hs.123106	Hs.123106:ESTs	2.64
	428471	X57348	Hs.184510	Hs.184510:statifin	2.64
	451544	AK000429	Hs.26570	NM_017814:Homo sapiens hypothetical prot	2.64
	413245	BE244334	Hs.75249	Hs.75249:ADP-ribosylation factor-like 6	2.64
45	415020	BE249915	Hs.293533	Hs.293533:Homo sapiens cDNA FLJ37093 fis	2.64
	437193	BE259190	Hs.289721	Hs.289721:growth arrest-specific 5	2.64
	418684	U82987	Hs.87246	NM_014417:Homo sapiens BCL2 binding comp	2.64
	410668	BE379794	Hs.159651	NM_014452:Homo sapiens tumor necrosis fa	2.64
	436183	AI146327	Hs.334802	(locuslink)NM_024718:Homo sapiens hypoth	2.64
	441226	BE563042	Hs.118820	Hs.118820:hypothetical protein BC007882	2.64
50	432788	AA521091	Hs.178499	Hs.178499:HSPC063 protein	2.64
	432746	AA564512	Hs.372775	Hs.372775:Homo sapiens, clone IMAGE:3946	2.64
	450377	AB033091	Hs.355925	Hs.355925:KIAA1265 protein	2.64
	434633	AI189587	Hs.120915	Hs.120915:ESTs	2.64
55	424707	BE061914	Hs.10844	Hs.10844:leucine-rich alpha-2-glycoprote	2.64
	427600	AW630918	Hs.179774	Hs.179774:proteasome (prosome, macropain	2.63
	446522	NM_003876	Hs.15196	NM_003876:Homo sapiens putative receptor	2.63
	436906	H95990	Hs.181244	Hs.181244:major histocompatibility compl	2.63
	410701	AF198620	Hs.10283	NM_005105:Homo sapiens RNA binding motif	2.63
60	410182	NM_001983	Hs.59544	NM_001983:Homo sapiens excision repair c	2.63
	406716	AW148546	Hs.169476	Hs.169476:glyceraldehyde-3-phosphate deh	2.63
	430308	BE540865	Hs.238990	NM_004064:Homo sapiens cyclin-dependent	2.63
	431074	BE072772	Hs.8997	Hs.8997:Sad1 unc-84 domain protein 1	2.63
	412867	AU076861	Hs.74637	Hs.74637:testis enhanced gene transcript	2.63
65	440524	R71264	Hs.16798	Hs.16798:Homo sapiens mRNA; cDNA DKFZp56	2.63
	435968	AW161481	Hs.111577	(locuslink)NM_030926:Homo sapiens integr	2.63
	422572	X12784	Hs.119129	NM_001845:Homo sapiens collagen, type IV	2.63
	447528	AI612027	Hs.76277	NM_138393:Homo sapiens hypothetical prot	2.63
	406774	AW518383	Hs.177592	Hs.177592:ribosomal protein, large, P1	2.63
70	439755	AW748482	Hs.77873	Hs.77873:B7 homolog 3	2.63
	435311	W86610	Hs.185736	Hs.185736:ESTs	2.63
	428699	AW578252	Hs.190161	Hs.190161:LR8 protein	2.62
	410678	BE540516	Hs.378825	Hs.378825:Homo sapiens cDNA FLJ37850 fis	2.62
	414839	X63692	Hs.77462	(locuslink)NM_001379:Homo sapiens DNA (c	2.62
	443217	NM_001545	Hs.9078	Hs.9078:immature colon carcinoma transcr	2.62
75	448749	AW859679	Hs.21902	Hs.21902:Homo sapiens clone 25237 mRNA s	2.62
	450009	AI399947	Hs.166486	Hs.166486:Homo sapiens cDNA FLJ11432 fis	2.62
	407687	AK002011	Hs.37558	NM_018339:Homo sapiens hypothetical prot	2.62
	442232	AI357813	Hs.337460	Hs.337460:ESTs, Highly similar to HYEP_H	2.62
80	419625	U91616	Hs.182885	NM_004556:Homo sapiens nuclear factor of	2.62
	416114	AI695549	Hs.183868	Hs.183868:glucuronidase, beta	2.62
	439437	AI207788	Hs.343628	Hs.343628:sialyltransferase 4B (beta-gal	2.61
	408452	AA054683	Hs.222728	Hs.222728:Homo sapiens cDNA FLJ39004 fis	2.61
	443142	AI696513	Hs.108705	Hs.108705:protein phosphatase 2 (formerl	2.61
	426152	BE299190	Hs.167246	Hs.167246:P450 (cytochrome) oxidoreducta	2.61

	419667	AU077005	Hs.92208	NM_003815:Homo sapiens a disintegrin and	2.61
	415072	BE253687	Hs.77876	Hs.77876:hypothetical gene MGC19595	2.61
	406670	W79632	Hs.256301	Hs.256301:hypothetical protein MGC13170	2.61
	403399				2.61
5	419579	W49529	Hs.296200	NM_023948:Homo sapiens hypothetical prot	2.61
	437202	AA326110	Hs.374481	Hs.374481:ESTs, Weakly similar to T34549	2.61
	414020	NM_002984	Hs.75703	NM_002984:Homo sapiens small inducible c	2.61
	421295	AW081061	Hs.103180	Hs.103180:DC2 protein	2.61
	446488	AB037782	Hs.15119	Hs.15119:KAA1361 protein	2.61
10	442504	BE503373	Hs.334335	NM_022484:Homo sapiens hypothetical prot	2.60
	448204	AW75124	Hs.170561	Hs.170561:ESTs	2.60
	449175	AJ005892	Hs.23170	(locuslink)NM_012280:Homo sapiens FtsJ h	2.60
	411201	T74588	Hs.8509	Hs.8509:ESTs, Weakly similar to C3HU com	2.60
	424805	AF230904	Hs.153260	NM_031892:Homo sapiens SH3-domain kinase	2.60
15	425421	L11669	Hs.157145	Hs.157145:tetracycline transporter-like	2.60
	422739	H20106	Hs.119591	(locuslink)NM_004069:Homo sapiens adapto	2.60
	450858	C18459	Hs.25597	Hs.25597:elongation of very long chain f	2.59
	443195	BE148235	Hs.193063	Hs.193063:Homo sapiens cDNA FLJ14201 fis	2.59
	430504	H52761	Hs.44095	Hs.44095:cyclin M3	2.59
20	439578	AW263124	Hs.350547	NM_024665:Homo sapiens nuclear receptor	2.59
	416041	AA345547	Hs.53263	(locuslink)NM_024647:Homo sapiens nucleo	2.59
	451920	AA224483	Hs.27239	Hs.27239:zinc finger, DHHC domain contai	2.59
	414163	BE262310	Hs.75782	NM_001521:Homo sapiens general transcrip	2.59
	422140	BE295918	Hs.112193	(locuslink)NM_025259:Homo sapiens chromo	2.59
25	452817	AA322859	Hs.284275	Hs.284275:p21 (CDKN1A)-activated kinase	2.59
	413353	AW283542	Hs.75309	Hs.75309:eukaryotic translation elongati	2.59
	421700	BE515018	Hs.107014	NM_016641:Homo sapiens membrane interact	2.59
	410801	BE275469	Hs.66493	NM_016430:Homo sapiens Down syndrome cri	2.59
	440511	AF132959	Hs.7236	NM_015953:Homo sapiens eNOS interacting	2.59
30	407887	AA579668	Hs.41072	(locuslink)NM_004568:Homo sapiens serine	2.59
	425356	BE244879	Hs.155939	NM_005541:Homo sapiens inositol polyphos	2.59
	408102	U46351	Hs.621	Hs.621:lectin, galactoside-binding, solu	2.59
	417952	AI192838	Hs.173135	Hs.173135:dual-specificity tyrosine-(Y)-	2.59
	433053	BE301809	Hs.279952	NM_015917:Homo sapiens glutathione S-tra	2.59
35	450935	BE514743	Hs.379039	NM_005851:Homo sapiens tumor suppressor	2.59
	417891	W79410	Hs.82887	(locuslink)NM_021959:Homo sapiens protel	2.59
	438364	AK000860	Hs.6191	NM_020441:Homo sapiens coronin, actin-bi	2.59
	430976	AA505112	Hs.282990	NM_033550:Homo sapiens chromosome 20 ope	2.58
	444838	AV651680	Hs.208558	Hs.208558:ESTs	2.58
40	416435	AI431301	Hs.374897	Hs.374897:Homo sapiens cDNA FLJ36874 fis	2.58
	415444	BE247295	Hs.78452	Hs.78452:solute carrier family 20 (phosp	2.58
	452222	AW806287	Hs.21432	Hs.21432:SEX gene	2.58
	400541				2.58
45	444309	U83236	Hs.10803	Hs.10803:calcium and Integrin binding 1	2.58
	416116	H51847	Hs.99858	Hs.99858:ribosomal protein L7a	2.58
	418629	BE247550	Hs.86859	(locuslink)NM_005310:Homo sapiens growth	2.58
	432996	AF105025	Hs.279901	Hs.279901:PTD009 protein	2.57
	426781	AL048967	Hs.172207	(locuslink)NM_007363:Homo sapiens non-PO	2.57
50	452636	BE515074	Hs.145279	Hs.145279:SET translocation (myeloid leu	2.57
	406851	AA609784	Hs.352392	Hs.352392:major histocompatibility compl	2.57
	447674	BE270540	Hs.19192	NM_001798:Homo sapiens cyclin-dependent	2.57
	445647	AV654627	Hs.271808	Hs.271808:Homo sapiens cDNA FLJ38018 fis	2.57
	444736	AA533491	Hs.23317	NM_032824:Homo sapiens hypothetical prot	2.57
	402861				2.57
55	450069	AI698139	Hs.202093	Hs.202093:ESTs	2.57
	414029	BE297731	Hs.75709	NM_002355:Homo sapiens mannose-6-phospha	2.57
	427700	AA262294	Hs.180383	NM_001946:Homo sapiens dual specificity	2.57
	449961	AW265634	Hs.133100	Hs.133100:ESTs	2.56
60	449378	AW684026	Hs.59892	Hs.59892:ESTs, Weakly similar to alpha 5	2.56
	442599	AF078037	Hs.324051	(locuslink)NM_006663:Homo sapiens RelA-a	2.56
	448633	AA311426	Hs.21635	NM_001070:Homo sapiens tubulin, gamma 1	2.56
	416078	AL034349	Hs.79005	NM_002844:Homo sapiens protein tyrosine	2.56
	428044	AA093322	Hs.301404	NM_006743:Homo sapiens RNA binding motif	2.56
65	451564	AJ076698	Hs.132760	(locuslink)NM_001467:Homo sapiens glucos	2.56
	457601	AF041429	Hs.284265	(locuslink)NM_145169:Homo sapiens simila	2.56
	439630	AA313607	Hs.58633	Hs.58633:Homo sapiens cDNA: FLJ22145 fis	2.55
	419587	S62907	Hs.91343	NM_000807:Homo sapiens gamma-aminobutyrl	2.55
	448279	BE250564	Hs.283655	Hs.283655:lysophospholipase II	2.55
70	453350	AI917771	Hs.61780	(locuslink)NM_024658:Homo sapiens import	2.55
	423720	AL044191	Hs.23388	NM_030817:Homo sapiens hypothetical prot	2.55
	400237		Hs.83347	NM_001087:Homo sapiens angio-ssociated,	2.55
	420856	BE513294	Hs.205736	Hs.205736:KAA1978 protein	2.55
	421541	NM_003942	Hs.105584	Hs.105584:ribosomal protein S6 kinase, 9	2.55
75	434848	BE256304	Hs.32148	NM_018445:Homo sapiens AD-015 protein (L	2.55
	424488	AK000413	Hs.149227	(locuslink)NM_017806:Homo sapiens hypoth	2.55
	449089	U78850	Hs.250465	Hs.250465:Homo sapiens mRNA: cDNA DKFZp4	2.55
	430053	AF052155	Hs.227949	NM_030673:Homo sapiens SEC13-like 1 (S	2.55
	437469	AW753112	Hs.15514	Hs.15514:hypothetical protein MGC3260	2.55
80	407755	AI151353	Hs.29742	Hs.29742:Homo sapiens cDNA FLJ32147 fis	2.55
	446673	NM_016361	Hs.15871	NM_016361:Homo sapiens LPAP for lysophos	2.55
	411766	AA399671	Hs.71969	Hs.71969:Homo sapiens mRNA: cDNA DKFZp66	2.55
	415198	AW009480	Hs.943	Hs.943:natural killer cell transcript 4	2.55
	436495	BE258948	Hs.290874	Hs.290874:Homo sapiens, clone MGC31984	2.55

5	417785	X59812	Hs.82568	NM_000784:Homo sapiens cytochrome P450,	2.55
	443358	H65417	Hs.17757	(locuslink)NM_021622:Homo sapiens plecks	2.55
	452349	AB028944	Hs.29189	Hs.29189:ATPase, Class VI, type 11A	2.55
	427721	AI582843	Hs.180455	NM_005053:Homo sapiens RAD23 homolog A (2.54
	407559	AA313352	Hs.280858	Hs.280858:Homo sapiens cDNA FLJ32370 fis	2.54
10	413426	U88837	Hs.75354	Hs.75354:GCN1 general control of amino-a	2.54
	425465	L18964	Hs.1904	Hs.1904:protein kinase C, iota	2.54
	444152	AI125694	Hs.149305	Hs.149305:hypothetical protein MGC2603	2.54
	451820	AW058357	Hs.199248	NM_000958:Homo sapiens prostaglandin E r	2.54
	414356	BE384361	Hs.182885	(locuslink)NM_004556:Homo sapiens nuclea	2.54
15	444410	BE387360	Hs.33719	Hs.33719:Homo sapiens, similar to data s	2.54
	415200	AL040328	Hs.78202	NM_003072:Homo sapiens SWI/SNF related,	2.54
	403955				2.54
	430361	AI033955	Hs.239926	Hs.239926:sterol-C4-methyl oxidase-like	2.54
	432401	NM_013330	Hs.274479	NM_013330:Homo sapiens NME7 (NME7), mRNA	2.54
20	446719	W39500	Hs.301872	Hs.301872:hypothetical protein MGC4840	2.54
	439941	AI392640	Hs.18272	NM_030674:Homo sapiens solute carrier fa	2.54
	436685	W28661	Hs.5288	Hs.5288:Homo sapiens mRNA; cDNA DKFZp434	2.54
	424522	AL134847	Hs.149957	Hs.149957:ribosomal protein S6 kinase, 9	2.54
	442904	AW575008	Hs.11355	Hs.11355:thymopolein	2.54
25	422605	H16646	Hs.118666	Hs.118666:hypothetical protein PP591	2.54
	442069	AW664144	Hs.297007	Hs.297007:Homo sapiens cDNA FLJ32174 fis	2.53
	447362	AW176120	Hs.9061	NM_024099:Homo sapiens hypothetical prot	2.53
	416305	AU076628	Hs.79187	NM_001338:Homo sapiens coxsackie virus a	2.53
	422624	BE616678	Hs.76152	NM_006854:Homo sapiens KDEL (Lys-Asp-Glu	2.53
30	447298	BE617527	Hs.239818	NM_006219:Homo sapiens phosphoinositida-	2.53
	412833	AW960547	Hs.298262	Hs.298262:ribosomal protein S19	2.53
	404854				2.53
	415761	AA132666	Hs.78802	(locuslink)NM_002093:Homo sapiens glyco	2.53
	431104	AW970859	Hs.313503	Hs.313503:ESTs	2.53
35	439180	AI393742	Hs.199067	Hs.199067:v-erb-b2 erythroblastic leukem	2.53
	424250	AF073310	Hs.143648	NM_003749:Homo sapiens insulin receptor	2.53
	452878	AW081128	Hs.246374	Hs.246374:Homo sapiens cDNA FLJ31250 fis	2.53
	415742	BE410243	Hs.78769	NM_003249:Homo sapiens thimet oligopepti	2.53
	404140				2.53
40	407255	AA012992	Hs.256301	Hs.256301:hypothetical protein MGC13170	2.53
	422509	AA258513	Hs.117865	Hs.117865:solute carrier family 17 (anto	2.53
	434866	AW002565	Hs.355460	Hs.355460:Homo sapiens cDNA: FLJ21763 fi	2.53
	429743	AA804398	Hs.288995	(locuslink)NM_017961:Homo sapiens hypoth	2.53
	433047	M86135	Hs.279946	NM_004990:Homo sapiens methionine-tRNA s	2.52
45	418945	BE246762	Hs.89499	Hs.89499:arachidonate 5-lipoxygenase	2.52
	445926	AF054284	Hs.334826	NM_012433:Homo sapiens splicing factor 3	2.52
	411353	BE383533	Hs.279784	Hs.279784:prolactin regulatory element b	2.52
	448252	BE622791	Hs.12199	NM_030577:Homo sapiens hypothetical prot	2.52
	447365	BE383676	Hs.334	(locuslink)NM_005435:Homo sapiens Rho gu	2.52
50	414844	AA296874	Hs.77494	NM_080916:Homo sapiens deoxyguanosine ki	2.52
	444025	AA578364	Hs.349093	NM_015945:Homo sapiens ovarian cancer ov	2.52
	416149	AA311965	Hs.79058	NM_003168:Homo sapiens suppressor of Ty	2.52
	418741	H83265	Hs.8881	Hs.8881:Homo sapiens cDNA FLJ32163 fis,	2.52
	437952	D63209	Hs.5944	NM_014585:Homo sapiens solute carrier fa	2.52
55	445625	BE246743	Hs.353181	(locuslink)NM_025092:Homo sapiens hypoth	2.52
	431565	AF161470	Hs.260622	Hs.260622:butyrate-induced transcript 1	2.52
	410179	W27723	Hs.59498	(locuslink)NM_003718:Homo sapiens cell d	2.52
	431476	BE612705	Hs.256697	(locuslink)NM_005340:Homo sapiens histid	2.52
	405672	M26041	Hs.198253	(locuslink)NM_002122:Homo sapiens major	2.52
60	418180	BE618087	Hs.83724	Hs.83724:hypothetical protein MGC5466	2.52
	428248	AI126772	Hs.40479	Hs.40479:Homo sapiens cDNA FLJ25802 fis,	2.52
	419935	AB020980	Hs.93832	Hs.93832:putative membrane protein	2.52
	446143	BE245342	Hs.306079	NM_013336:Homo sapiens protein transport	2.51
	426691	NM_006201	Hs.171834	(locuslink)NM_006201:Homo sapiens PCTAIR	2.51
65	408124	U89337	Hs.42853	NM_004381:Homo sapiens cAMP responsive e	2.51
	456266	L29073	Hs.198726	NM_003651:Homo sapiens cold shock domain	2.51
	428921	Z43809	Hs.194638	Hs.194638:polymerase (RNA) II (DNA direc	2.51
	414721	X90392	Hs.77091	NM_006730:Homo sapiens deoxyribonuclease	2.51
	422807	Z45471	Hs.118684	NM_006923:Homo sapiens stromal cell-deri	2.51
70	421846	AA017707	Hs.1432	NM_002743:Homo sapiens protein kinase C	2.51
	414874	D26351	Hs.77515	NM_002224:Homo sapiens inositol 1,4,5-tr	2.51
	432956	AL037895	Hs.279861	NM_015959:Homo sapiens CGI-31 protein (L	2.51
	438393	AA351815	Hs.50740	Hs.50740:Homo sapiens mRNA; cDNA DKFZp76	2.51
	418360	AW296974	Hs.84264	NM_006401:Homo sapiens acidic (leucine-r	2.50
75	401061				2.50
	426559	AB001914	Hs.170414	Hs.170414:paired basic amino acid cleavi	2.50
	412204	AI125507	Hs.24937	Hs.24937:transformer-2 alpha (htra-2 alp	2.50
	448950	AF286887	Hs.9275	NM_020410:Homo sapiens CGI-152 protein (2.50
	409936	AK001691	Hs.57655	(locuslink)NM_018234:Homo sapiens dudufi	2.50
80	414675	R79015	Hs.288958	Hs.288958:RAB22A, member RAS oncogene fa	2.50
	409983	D50922	Hs.57729	(locuslink)NM_012289:Homo sapiens Ketch-	2.50
	450914	AI743761	Hs.142528	Hs.142528:ESTs	2.50
	444630	AI753230	Hs.323562	(locuslink)NM_032121:Homo sapiens hypoth	2.50
	401353				2.50
	441680	AW444598	Hs.7940	(locuslink)NM_021159:Homo sapiens RAP1,	2.50
	406860	AA876469		AA876469:oe48b04.s1 NCI_CGAP_P25 Homo s	2.50
	449163	AW161356	Hs.23119	NM_003492:Homo sapiens chromosome X open	2.50

432975	AA331517	Hs.286055	Hs.286055:chimerin (chimaerin) 2	2.50
430600	AW950967	Hs.274348	NM_004639:Homo sapiens HLA-B associated	2.50
407584	W25945	Hs.8173	Hs.8173:hypothetical protein FLJ10803	2.50

5 TABLE 9B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

10	Pkey	CAT Number	Accession
	406685	0_0	M18728
	452098	161393_1	BG028348 BF772844 H83066 AW817969 H90985 BF755039 AJ858183
	451129	1495511_1	BE072881 A1762181 BE072946
15	459306	223120_4	AW578452
	448489	2189115_1	R45782 R45781
	418869	12789_14	AA229762 AA230035
	418546	242836_1	T59708 AA224827 T59843 BE156903
20	455303	1152492_1	BE066891 BE066895 AW892049 BE066897 BE803884
	406860	0_0	AA876469

TABLE 9C

25 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

30	Pkey	Ref	Strand	NL_position
	406399	9256288	Minus	63448-63554
	403220	7630969	Plus	64338-64517
	403218	7630969	Plus	58039-58149
35	403221	7630969	Plus	66294-66438,66936-67124
	403219	7630969	Plus	61858-61995
	403739	7630882	Plus	44563-44766,48209-49483,52255-52495
	405484	5922025	Plus	199214-199579,199672-199920,200262-20049
40	405556	1552511	Plus	163497-163623,164715-164968,165369-16550
	400529	9796988	Plus	138232-138423
	404826	6572184	Plus	47726-48046
	400750	8119087	Plus	198991-199168,199316-199548
	400847	9188605	Plus	44643-44835
45	400448	9887687	Minus	177372-177674
	402829	8918414	Plus	101532-101852,102006-102263
	400846	9188605	Plus	39310-39474
	401179	9438647	Plus	113477-113893
	404240	5002624	Minus	116132-116407,116653-116922
50	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
	406363	9256114	Plus	14403-14802,17000-17147,17241-17368
	405203	7230116	Plus	125295-125463
	402104	8119072	Plus	122409-122600
	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
	400845	9188605	Plus	34428-34612
55	403217	7630969	Plus	54089-54163,55427-55623
	403483	9966188	Minus	144546-144854
	400509	9796539	Minus	157909-158430
	403399	6684178	Plus	61841-62145,62367-62756
	400541	7574902	Plus	126235-126380,126478-126597
60	402861	2814366	Minus	14933-15231,15387-15627
	403955	7770475	Minus	54527-54740
	404854	7143420	Plus	14260-14537
	404140	9843520	Plus	37761-38147
	401061	3242744	Minus	99468-99549,100707-100848,100918-101107,
65	401353	9931296	Minus	50831-51352

70 Table 10A lists about 1,103 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium). These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 2.5, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 85th percentile value amongst non-malignant tissues minus the colonic derived samples, the "average" colon value was greater than or equal to 50 units. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the over non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

75 TABLE 10A: 1,103 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium)

80 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenesID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
5	436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosi	15.54
	428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	14.52
	446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intestin	14.04
	431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S3B4_H	14.02
	423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease 1	13.72
10	406690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carcin	13.44
	418406	X73501	Hs.84905	Hs.84905:cytokeratin 20	12.70
	406667	M12523			12.42
	416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating isle	11.98
	437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel	11.58
15	422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo	11.50
	418888	AJ076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, LI c	10.16
	418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.11
	422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	10.01
	421582	AJ910275	Hs.350470	NM_003225:Homo sapiens trefoil factor 1	9.77
20	441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	9.69
	424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	9.48
	453863	X02544	Hs.572	Hs.572:corosomucoid 1	9.20
	407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	9.18
	436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	9.04
25	423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	8.69
	430178	AW449612	Hs.152475	Hs.152475:ESTs	8.51
	423673	BE003054	Hs.1696	NM_002426:Homo sapiens matrix metallopro	8.43
	447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	8.17
	409683	U33317	Hs.711	NM_001926:Homo sapiens defensin, alpha 6	8.12
30	431777	AA570296	Hs.307047	NM_032579:Homo sapiens colon and small I	8.08
	450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	8.06
	427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (7.95
	436624	T64297	Hs.351719	NM_001443:Homo sapiens fatty acid bindin	7.74
	410407	X66839	Hs.63287	NM_001216:Homo sapiens carbonic anhydras	7.46
35	413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	7.41
	407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	7.40
	412374	X01388	Hs.73849	NM_000040:Homo sapiens apolipoprotein C-	7.34
	407244	M10014			7.31
	419741	NM_007019	Hs.93002	Hs.93002:ubiquitin-conjugating enzyme E2	7.31
40	406741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	7.26
	414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),	7.21
	404519				7.18
	413585	AI133452	Hs.75431	NM_000509:Homo sapiens fibrinogen, gamma	7.13
	422281	M36803	Hs.346935	NM_000813:Homo sapiens hemopexin (HPX),	7.10
45	414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	7.02
	430828	AI763257	Hs.86327	Hs.86327:homeo box B9	6.83
	433927	AI557019	Hs.116467	NM_032391:Homo sapiens small nuclear pro	6.81
	406687	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	6.78
	423538	AW603823	Hs.146268	Hs.146268:ESTs, Weakly similar to C71400	6.53
50	434206	AW136973	Hs.362915	Hs.362915:Homo sapiens cDNA FLJ34876 fis	6.37
	409041	AB033025	Hs.50081	Hs.50081:KIAA1199 protein	6.33
	432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	6.19
	422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	6.19
	436330	NM_004413	Hs.109	NM_004413:Homo sapiens dipeptidase 1 (re	6.01
55	421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog	6.00
	430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	5.97
	413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	5.94
	420923	AF097021	Hs.273321	NM_006418:Homo sapiens differentially ex	5.94
	428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homol	5.90
60	428082	U22376	Hs.1334	NM_005375:Homo sapiens v-myb myeloblasto	5.89
	452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590	5.89
	431727	AW293464	Hs.162031	Hs.162031:ESTs	5.85
	421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	5.84
	432023	AW273128	Hs.300268	Hs.300268:EST	5.75
65	447033	AI357412	Hs.157601	Hs.157601:ESTs	5.69
	411734	AW374954	Hs.71779	Hs.71779:ESTs, Weakly similar to S24C_AR	5.69
	406685	M18728		(locuslink)NM_002483:Homo sapiens carcin	5.55
	428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	5.48
	443247	BE614387	Hs.333893	Hs.333893:cell division cycle associated	5.45
70	409153	W03754	Hs.50813	NM_017825:Homo sapiens intelectin (ITLN)	5.44
	449388	H53191	Hs.36723	Hs.36723:ESTs, Weakly similar to C05G5.5	5.38
	428046	AW812795	Hs.337534	Hs.337534:Homo sapiens cDNA FLJ25241 fi	5.38
	433013	AI697890	Hs.127337	(locuslink)NM_004655:Homo sapiens actin 2	5.38
	419079	AW014836	Hs.18844	Hs.18844:ESTs	5.37
75	428355	BE256452	Hs.2257	NM_000638:Homo sapiens vitronectin (seru	5.35
	422956	BE545072	Hs.122579	(locuslink)NM_018058:Homo sapiens epithe	5.34
	424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysl	5.30
	450543	AI394037	Hs.170296	Hs.170296:Homo sapiens cDNA: FLJ22090 fi	5.30
	428187	AI687303	Hs.285529	Hs.285529:G protein-coupled receptor 49	5.30
80	435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	5.28
	411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier fa	5.28
	427722	AK000123	Hs.180479	NM_017671:Homo sapiens chromosome 20 ope	5.26
	430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	5.26
	414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	5.21
	430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	5.16

5	447208	BE315291	Hs.237971	NM_024096:Homo sapiens hypothetical prot	5.14
	430207	AW079559	Hs.152258	Hs.152258:ESTs	5.12
	417491	AW376842	Hs.1085	NM_004863:Homo sapiens guanylate cyclase	5.12
	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.07
	447342	AI199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	5.06
	452194	AI694413	Hs.373599	Hs.373599:EST	5.01
	421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	4.99
	406399				4.98
	403220				4.94
10	408380	AF123050	Hs.44532	NM_006398:Homo sapiens ubiquitin D (UBD)	4.92
	415214	AI445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tr	4.92
	431330	X69532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	4.85
	420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protel	4.84
	452594	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfa	4.81
15	441377	BE218239	Hs.202656	Hs.202656:ESTs	4.81
	444666	BE293347	Hs.11638	(locuslink)NM_016234:Homo sapiens fatty-	4.80
	415701	NM_003878	Hs.78619	(locuslink)NM_003878:Homo sapiens gamma-	4.80
	419354	M82839	Hs.1252	NM_000042:Homo sapiens apolipoprotein H	4.80
	455630	AV655701	Hs.75183	NM_000773:Homo sapiens cytochrome P450,	4.78
20	422310	AA316622	Hs.98370	(locuslink)NM_030622:Homo sapiens cytoch	4.78
	423337	NM_004655	Hs.127337	NM_004655:Homo sapiens adn 2 (conductin	4.75
	422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	4.73
	408908	BE296227	Hs.250822	(locuslink)NM_003158:Homo sapiens serine	4.70
	423936	U77629	Hs.135639	NM_005170:Homo sapiens achaete-scute com	4.70
25	404661				4.68
	408704	AA056635	Hs.5366	NM_139053:Homo sapiens epidermal growth	4.67
	420005	AW271106	Hs.133294	Hs.133294:ESTs	4.66
	451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (I iso)	4.61
30	427506	AK000134	Hs.179100	NM_017678:Homo sapiens hypothetical prot	4.60
	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	4.59
	453884	AA355925	Hs.36232	NM_021067:Homo sapiens KIAA0186 gene pro	4.55
	431301	AA502384	Hs.151529	Hs.151529:ESTs	4.54
	408983	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis t	4.54
35	449032	AA045573	Hs.22900	NM_004289:Homo sapiens nuclear factor (e	4.54
	434540	NM_016045	Hs.3945	NM_016045:Homo sapiens chromosome 20 ope	4.54
	407242	M18728		(locuslink)NM_002483:Homo sapiens carc	4.53
	458748	AI381530	Hs.371132	Hs.371132:ESTs	4.53
	408298	AI745325	Hs.271923	Hs.271923:Homo sapiens cDNA: FLJ22785 fi	4.51
40	424273	W40460	Hs.144442	NM_003581:Homo sapiens phospholipase A2,	4.50
	411975	AI916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	4.49
	425371	D49441	Hs.155981	NM_005823:Homo sapiens mesothelin (MSLN)	4.49
	451917	AW391351	Hs.50820	Hs.50820:hypothetical cardiac skeletal m	4.46
	432867	AW016936	Hs.233364	Hs.233364:ESTs	4.44
45	419559	Y07828	Hs.91096	NM_007028:Homo sapiens tripartite motif-	4.44
	430294	AI538226	Hs.32976	(locuslink)NM_004485:Homo sapiens guanin	4.42
	411248	AA551538	Hs.69321	Hs.69321:KIAA1359 protein	4.39
	402496				4.38
	430937	X53463	Hs.2704	NM_002083:Homo sapiens glutathione perox	4.37
50	434414	AI798376		AF134163:Homo sapiens Human endogenous r	4.36
	443426	AF098158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	4.35
	422539	AJ009938	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.33
	436972	AA284679	Hs.25640	Hs.25640:claudin 3	4.33
	450531	AW301032	Hs.203800	Hs.203800:ESTs	4.33
	403055				4.31
55	414809	AI434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71	4.31
	400965				4.30
	430204	AA618335	Hs.356664	Hs.356664:hypothetical protein FLJ32334	4.29
	432978	AF126743	Hs.279884	NM_013238:Homo sapiens DNAJ domain-conta	4.29
60	417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:225881	4.28
	430832	AI073913	Hs.100686	Hs.100686:anterior gradient protein 3	4.28
	408482	NM_000676	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	4.28
	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	4.27
	414617	AI339520	Hs.288817	(locuslink)NM_025130:Homo sapiens hypoth	4.27
	452940	AA029722	Hs.2173	NM_002033:Homo sapiens fucosyltransferas	4.27
65	439211	AI890347	Hs.271923	Hs.271923:Homo sapiens cDNA: FLJ22785 fi	4.27
	459299	BE094291	Hs.155651	NM_021784:Homo sapiens hepatocyte nuclea	4.25
	449720	AA311152	Hs.288708	(locuslink)NM_025113:Homo sapiens hypoth	4.24
	411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc:betaGa	4.24
	421777	BE562088	Hs.108196	NM_016095:Homo sapiens HSPC037 protein (4.21
70	419395	BE268326	Hs.90280	Hs.90280:5-aminimidazole-4-carboxamide	4.20
	443211	AI128388	Hs.143655	Hs.143655:ESTs	4.20
	403218				4.20
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	4.19
75	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	4.19
	426227	U67056	Hs.154299	(locuslink)NM_005242:Homo sapiens coagul	4.19
	421408	AI688223	Hs.91096	NM_052816:Homo sapiens tripartite motif-	4.18
	421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	4.18
	440869	NM_014297	Hs.7486	NM_014297:Homo sapiens protein expressed	4.17
80	414075	U11862	Hs.75741	NM_001091:Homo sapiens amiloride binding	4.17
	444151	AW972917	Hs.128749	(locuslink)NM_014324:Homo sapiens alpha-	4.16
	440409	AW294316	Hs.125608	Hs.125608:ESTs	4.16
	445564	AB028957	Hs.12896	Hs.12896:KIAA1034 protein	4.16
	424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	4.12

	401866				4.11
	431611	U58766	Hs.264428	Hs.264428:tissue specific translatatio	4.10
	430187	A1799909	Hs.158989	Hs.158989:Homo sapiens cDNA FLJ37936 fis	4.10
	414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation facto	4.08
5	449281	A1808699	Hs.162717	NM_032756:Homo sapiens hypothetical prot	4.08
	449722	BE280074	Hs.23960	Hs.23960:cyclin B1	4.08
	418318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 s	4.06
	435066	BE261750	Hs.4747	NM_001363:Homo sapiens dyskeratosis cong	4.05
	414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	4.04
10	403221				4.04
	409889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	4.03
	449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidyl/peptida	4.03
	431657	A1345227	Hs.105448	Hs.105448:protein kinase, lysine deficie	4.01
	439759	AL359055	Hs.67709	Hs.67709:Homo sapiens mRNA full length i	4.00
15	441362	BE614410	Hs.23044	NM_080668:Homo sapiens similar to RIKEN	3.99
	417900	BE250127	Hs.82906	Hs.82906:CDK20 cell division cycle 20 ho	3.99
	428987	NM_004751	Hs.194710	NM_004751:Homo sapiens glucosaminyl (N-a	3.99
	456977	AK000252	Hs.169758	NM_017723:Homo sapiens hypothetical prot	3.99
	445919	T53519	Hs.334692	Hs.334692:hypothetical protein MGC14141	3.98
20	423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical prot	3.98
	422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	3.97
	422363	T55979	Hs.115474	NM_002915:Homo sapiens replication facto	3.97
	433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apopto	3.97
	415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	3.96
25	425934	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	3.96
	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	3.95
	432407	AA221036		AF134164:Homo sapiens Human endogenous r	3.95
	408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	3.94
30	408494	AA554714	Hs.187578	Hs.187578:Homo sapiens cDNA FLJ11639 fis	3.94
	412610	X90908	Hs.74126	NM_001445:Homo sapiens fatty acid bindin	3.94
	433323	AA805132	Hs.159142	Hs.159142:lunatic fringe homolog (Drosop	3.94
	422515	AW500470	Hs.117950	Hs.117950:phosphoribosylaminimidazole c	3.92
	436543	NM_002212	Hs.5215	Hs.5215:integrin beta 4 binding protein	3.91
	418113	A1272141	Hs.83484	Hs.83484:SRF (sex determining region Y)-	3.91
35	433083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20268	3.90
	431939	AW008061	Hs.231994	Hs.231994:Homo sapiens, clone IMAGE:4341	3.90
	453439	A1572438	Hs.32976	NM_004485:Homo sapiens guanine nucleotid	3.89
	441888	A1733306	Hs.128071	NM_022901:Homo sapiens hypothetical prot	3.89
	432150	AK000224	Hs.272789	NM_017716:Homo sapiens membrane-spanning	3.89
40	425234	AW152225	Hs.165909	Hs.165909:ESTs, Weakly similar to hypoth	3.89
	423803	NM_005709	Hs.132945	(locustink)NM_005709:Homo sapiens PDZ-73	3.87
	410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	3.85
	436251	BE515065	Hs.296585	(locustink)NM_006392:Homo sapiens nucleo	3.85
	422424	A186431	Hs.296638	Hs.296638:prostate differentiation facto	3.84
45	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	3.84
	424905	NM_002497	Hs.153704	NM_002497:Homo sapiens NIMA (never in mi	3.84
	416209	AA236776	Hs.79078	NM_002358:Homo sapiens MAD2 mitotic arre	3.83
	430680	AW138724	Hs.168974	Hs.168974:ESTs	3.83
50	434370	AF130988	Hs.58346	NM_022336:Homo sapiens ectodysplasin 1,	3.82
	436481	AA379597	Hs.5199	NM_014176:Homo sapiens HSPC150 protein s	3.82
	453700	AB009428	Hs.560	NM_001644:Homo sapiens apolipoprotein B	3.81
	410619	BE512730	Hs.65114	Hs.65114:keratin 18	3.81
	409420	Z15008	Hs.54451	NM_005562:Homo sapiens laminin, gamma 2	3.79
55	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	3.79
	432179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPH3), mR	3.78
	453967	AW009077	Hs.232947	Hs.232947:ESTs	3.78
	426106	A1678765	Hs.21812	Hs.21812:ESTs	3.78
	434170	AA626509	Hs.159642	(locustink)NM_001490:Homo sapiens glucos	3.78
60	418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	3.78
	444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	3.74
	419229	A1827237	Hs.362919	Hs.362919:ESTs	3.74
	437156	A1916600	Hs.121194	Hs.121194:Homo sapiens cDNA: FLJ21569 fi	3.74
	452833	BE559681	Hs.30736	(locustink)NM_015201:Homo sapiens block	3.73
65	426831	BE286216	Hs.172673	NM_000687:Homo sapiens S-adenosylthiomocys	3.73
	428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid ind	3.72
	443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	3.71
	408832	AW085690	Hs.63428	Hs.63428:Homo sapiens cDNA FLJ34457 fis	3.71
	440300	N39760	Hs.8859	NM_138793:Homo sapiens apyrase (SHAPY),	3.71
70	425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	3.71
	432575	AA553722	Hs.194346	Hs.194346:Spir-2 protein	3.71
	412104	AW205197	Hs.240951	(locustink)NM_033120:Homo sapiens naked	3.71
	417001	AU076648	Hs.80741	NM_000282:Homo sapiens propionyl Coenzym	3.69
	421225	AA463758	Hs.102696	Hs.102696:ACT-1 protein	3.69
	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	3.69
75	428330	L22524	Hs.2256	NM_002423:Homo sapiens matrix metallopro	3.67
	447472	AW207347	Hs.211101	Hs.211101:ESTs	3.67
	423349	AF010258	Hs.127428	NM_002142:Homo sapiens homeo box A9 (HOX	3.67
	422026	U80736	Hs.110826	Hs.110826:trinucleotide repeat containin	3.66
80	419574	AK001989	Hs.91165	Hs.91165:hypothetical protein FLJ11127	3.66
	417720	AA205625	Hs.208067	Hs.208067:ESTs	3.66
	411257	AA628957	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	3.66
	421515	Y11339	Hs.105352	(locustink)NM_018414:Homo sapiens GalNAc	3.65
	433675	AW977653	Hs.75319	Hs.75319:ribonucleotide reductase M2 pol	3.65

5	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	3.65
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis,	3.64
	412140	AA219691	Hs.73625	NM_005733:Homo sapiens RAB6 interacting,	3.64
	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	3.63
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	3.63
	414798	AI286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	3.62
	428862	NM_000346	Hs.2316	Hs.2316:SRF (sex determining region Y)-b	3.62
	414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	3.62
10	412056	T28160	Hs.778	Hs.778:guanylate cyclase activator 2A (g	3.61
	401519				3.60
	428011	BE387514	Hs.181418	NM_014730:Homo sapiens KIAA0152 gene pro	3.60
	450505	NM_004572	Hs.25051	NM_004572:Homo sapiens plakophilin 2 (PK	3.60
	421903	AW079940	Hs.15951	(locuslink)NM_145202:Homo sapiens prolif	3.58
15	413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystei	3.58
	424544	M88700	Hs.150403	NM_000790:Homo sapiens dopa decarboxylas	3.58
	413563	AI027643	Hs.120912	Hs.120912:ESTs	3.57
	435602	AF217515	Hs.283532	NM_018455:Homo sapiens uncharacterized b	3.57
	434369	AI650363	Hs.116462	Hs.116462:ESTs	3.57
20	439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	3.56
	447334	AA515032	Hs.91109	Hs.91109:ESTs, Weakly similar to putativ	3.56
	422150	AI867118	Hs.279607	Hs.279607:Homo sapiens cDNA FLJ34399 fis	3.56
	450663	H43540	Hs.25292	Hs.25292:ribonuclease H2, large subunit	3.56
	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	3.56
25	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	3.55
	422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr	3.55
	422532	AL008726	Hs.118126	(locuslink)NM_000308:Homo sapiens protec	3.55
	425860	L29339	Hs.1964	NM_000343:Homo sapiens solute carrier fa	3.55
	442053	R35343	Hs.24968	Hs.24968:hypothetical protein BC016683	3.55
30	437386	W52452	Hs.356766	Hs.356766:Homo sapiens mRNA; cDNA DKFZp7	3.54
	415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	3.53
	446372	AB020644	Hs.14945	Hs.14945:fatty-acid-Coenzyme A ligase, I	3.53
	432378	AI493046	Hs.146133	Hs.146133:ESTs	3.53
	434171	BE247688	Hs.347349	(locuslink)NM_004749:Homo sapiens cell c	3.52
35	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	3.52
	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	3.51
	414918	AI219207	Hs.72222	Hs.72222:fer-1-like 4 (C. elegans)	3.51
	440340	AW895503	Hs.125276	Hs.125276:Homo sapiens cDNA FLJ25833 fis	3.51
40	418384	AW149266	Hs.25130	Hs.25130:Homo sapiens cDNA FLJ14923 fis,	3.51
	418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kin	3.51
	429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	3.51
	409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	3.50
	431567	N51357	Hs.260855	(locuslink)NM_145175:Homo sapiens NSE1 (3.50
	453883	AI638516	Hs.347524	Hs.347524:Homo sapiens, clone MGC:24665	3.50
45	442700	AA377618	Hs.103834	NM_024056:Homo sapiens hypothetical prot	3.50
	410237	AI750589	Hs.61258	Hs.61258:argininosuccinate lyase	3.50
	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	3.49
	436213	AA325512	Hs.71472	NM_024662:Homo sapiens hypothetical prot	3.49
	442923	AW248322	Hs.95835		3.49
50	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	3.48
	452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with sequa	3.48
	448993	AI471630	Hs.355952	Hs.355952:ESTs, Weakly similar to 080320	3.48
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23656	3.48
	414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	3.47
55	420996	AK001927	Hs.100895	(locuslink)NM_018099:Homo sapiens hypoth	3.47
	439580	AF086401	Hs.293847	Hs.293847:ESTs	3.46
	422158	L10343	Hs.112341	NM_002638:Homo sapiens protease inhibito	3.46
	418266	AW845318	Hs.12271	(locuslink)NM_012162:Homo sapiens F-box	3.46
	400157		Hs.356473	NM_006713:Homo sapiens activated RNA pol	3.46
60	406709	AI355761	Hs.242463	Hs.242463:keratin 8	3.46
	453751	R38762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.46
	421526	AL080121	Hs.105460	NM_015393:Homo sapiens DKFZP564O0823 pro	3.45
	415164	AW084352	Hs.157123	Hs.157123:ESTs	3.45
	405451				3.44
65	414361	AI086138	Hs.204044	Hs.204044:ESTs	3.44
	422237	M13149	Hs.1498	NM_000412:Homo sapiens histidine-rich gl	3.44
	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphonitrosylgly	3.44
	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25- dihydroxyvitami	3.43
	450983	AA305384	Hs.25740	NM_014584:Homo sapiens ERO1-like (S. cer	3.43
70	421828	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	3.42
	418588	BE387040	Hs.182476	NM_031295:Homo sapiens Williams Beuren s	3.42
	417348	AI940507	Hs.318526	NM_025138:Homo sapiens hypothetical prot	3.42
	423554	M90516	Hs.1674	NM_002056:Homo sapiens glutamine-fructos	3.42
	451310	AW250651	Hs.26213	NM_052951:Homo sapiens chromosome 20 ope	3.41
75	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	3.41
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	3.40
	437575	AW954355	Hs.36529	NM_024320:Homo sapiens hypothetical prot	3.40
	432677	NM_004482	Hs.278611	NM_004482:Homo sapiens UDP-N-acetyl-aph	3.40
	439955	AW203959	Hs.149532	Hs.149532:ESTs	3.40
80	443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interne	3.40
	435745	AW967059	Hs.374342	Hs.374342:Homo sapiens clone 24711 mRNA	3.40
	403532				3.39
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	3.39
	425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	3.39

	424996	AF006005	Hs.154104	NM_002657:Homo sapiens pleiomorphic aden	3.38
	402944				3.37
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	3.37
	427528	AU077143	Hs.179565	NM_002388:Homo sapiens MCM3 minichromosome	3.37
5	426711	AA383471	Hs.343800	(locuslink)NM_033255:Homo sapiens epithe	3.37
	439186	AI697274	Hs.105435	Hs.105435:GDP-mannose 4,6-dehydratase	3.36
	444783	AK001468	Hs.62180	NM_018685:Homo sapiens anillin, actin bi	3.36
	426174	AA547959	Hs.115838	Hs.115838:ESTs	3.36
	421585	U95826	Hs.302043	NM_003965:Homo sapiens chemokine (C-C mo	3.36
10	421605	BE440108	Hs.106127	NM_015972:Homo sapiens RNA polymerase I	3.36
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	3.36
	438746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	3.36
	403219				3.36
	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	3.34
15	456946	T29678	Hs.166068	Hs.166068:villin 1	3.33
	425580	L11144	Hs.1907	Hs.1907:galanin	3.33
	412605	AW410734	Hs.74111	Hs.74111:RNA binding protein (autoantige	3.33
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	3.33
20	416782	L35035	Hs.79886	(locuslink)NM_144563:Homo sapiens ribose	3.33
	426761	AI015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	3.33
	441633	AW958544	Hs.112242	NM_032413:Homo sapiens normal mucosa of	3.32
	416975	NM_004131	Hs.1051	NM_004131:Homo sapiens granzyme B (granz	3.31
	428874	W32133	Hs.194366	Hs.194366:transferrin (prealbumin, amy	3.31
25	431192	AI670056	Hs.137274	Hs.137274:ESTs, Weakly similar to hypo	3.30
	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cla	3.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	3.30
	410639	BE269047	Hs.65234	(locuslink)NM_017895:Homo sapiens DEAD/H	3.29
	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	3.29
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	3.29
30	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	3.29
	437810	BE246399	Hs.367646	NM_016617:Homo sapiens hypothetical prot	3.29
	403381				3.28
	434031	BE384165	Hs.23723	(locuslink)NM_025215:Homo sapiens pseudo	3.28
35	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	3.28
	452299	AW206330	Hs.355663	Hs.355663:ESTs	3.28
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	3.28
	412994	D32257	Hs.75113	Hs.75113:general transcription factor II	3.28
	443162	T49951	Hs.9029	(locuslink)NM_015515:Homo sapiens type I	3.28
40	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3)-glycoprote	3.28
	424010	AL080188	Hs.137556	NM_033100:Homo sapiens MT-protocadherin	3.28
	428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	3.27
	419359	AL043202	Hs.90073	Hs.90073:CSE1 chromosome segregation 1-1	3.27
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	3.27
	444371	BE540274	Hs.239	Hs.239:forkhead box M1	3.27
45	450221	AA328102	Hs.24641	NM_018204:Homo sapiens cytoskeleton asso	3.27
	449207	AL044222	Hs.23255	NM_004298:Homo sapiens nucleoporin 155kD	3.27
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens slalidase 1 (lyso	3.27
	403485				3.27
	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	3.26
50	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	3.26
	405484				3.26
	435849	BE305242	Hs.16098	Hs.16098:claudin 2	3.26
	449139	BE268315	Hs.23111	NM_004461:Homo sapiens phenylalanine-IRN	3.26
	404684				3.25
55	447188	H65423	Hs.17631	NM_030804:Homo sapiens hypothetical prot	3.25
	423226	AA323414	Hs.146109	Hs.146109:ESTs, Weakly similar to T28937	3.24
	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	3.24
	424243	AI949359	Hs.143600	Hs.143600:golgi phosphoprotein 4	3.24
	435014	BE560898	Hs.10026	NM_022061:Homo sapiens ribosomal protein	3.24
60	452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fis	3.24
	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	3.23
	427333	AF067797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	3.23
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	3.23
	432035	AA524725	Hs.162108	Hs.162108:ESTs	3.23
65	408868	AW292286	Hs.255058	Hs.255058:ESTs	3.23
	429504	X99133	Hs.204238	Hs.204238:lipocalin 2 (oncogene 24p3)	3.22
	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	3.22
	426991	AK001536	Hs.214410	Hs.214410:Homo sapiens cDNA FLJ31573 fis	3.22
70	408901	AK001330	Hs.48855	(locuslink)NM_018101:Homo sapiens hypoth	3.22
	439979	AW600291	Hs.6823	NM_018092:Homo sapiens neuropilin (NRP)	3.22
	453968	AA847843	Hs.62711	Hs.62711:Homo sapiens, clone IMAGE:33512	3.22
	457465	AW301344	Hs.122908	NM_030928:Homo sapiens DNA replication f	3.22
	426317	AA312350	Hs.169294	NM_003202:Homo sapiens transcription fac	3.21
	414639	X67055	Hs.76716	NM_002217:Homo sapiens pro-alpha (globul	3.21
75	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	3.20
	444261	AA298958	Hs.10724	Hs.10724:mitochondrial ribosomal protein	3.20
	454033	AF107457	Hs.37035	NM_005515:Homo sapiens homeo box HB9 (HL	3.20
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	3.20
80	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	3.20
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	3.19
	400130		Hs.155560	NM_001746:Homo sapiens calnexin (CANX),	3.19
	422283	X94453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synthe	3.19
	400290	H18836	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	3.18

5	419239	AA468183	Hs.335798	(locuslink)NM_033103:Homo sapiens rhophi	3.18
	426215	AW963419	Hs.155223	NM_003714:Homo sapiens stannocalcin 2 (3.18
	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	3.17
	413313	NM_002047	Hs.293885	NM_002047:Homo sapiens glycyl-tRNA synth	3.17
	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	3.17
	408353	BE439838	Hs.44298	NM_015959:Homo sapiens mitochondrial rib	3.17
	400203		Hs.1390	NM_002794:Homo sapiens proteasome (proso	3.16
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	3.16
10	426088	AF038007	Hs.166196	NM_005603:Homo sapiens ATPase, Class I,	3.16
	416984	H38765	Hs.80708	NM_000903:Homo sapiens NAD(P)H dehydroge	3.16
	450635	AW403954	Hs.25237	NM_016647:Homo sapiens mesenchymal stem	3.16
	406708	AI282759		AI282759:qt84a01.x1 NCL CGAP Co14 Homo s	3.16
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	3.16
15	430127	AA219498	Hs.233952	Hs.233952:proteasome (prosome, macropain	3.16
	417308	H60720	Hs.81892	NM_014736:Homo sapiens KIAA0101 gene pro	3.15
	408116	AA251393	Hs.289052	NM_052842:Homo sapiens BCL2-like 12 (pro	3.15
	402474				3.15
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/huc	3.15
20	446595	T57448	Hs.15467	NM_017943:Homo sapiens hypothetical prot	3.15
	444954	AW247076	Hs.12163	NM_003908:Homo sapiens eukaryotic transl	3.15
	434263	N34895	Hs.79187	Hs.79187:coxsaclike virus and adenovirus	3.15
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	3.15
	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	3.15
25	436391	AJ227892	Hs.146274	Hs.146274:ESTs	3.15
	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	3.14
	445873	AA250970	Hs.251946	Hs.251946:Homo sapiens cDNA FLJ11840 fis	3.14
	432370	AA308334	Hs.274424	NM_018946:Homo sapiens N-acetylneuramin	3.14
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antige	3.14
30	417791	AW965339	Hs.44269	Hs.44269:Homo sapiens cDNA FLJ37972 fis,	3.14
	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	3.13
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	3.13
	456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	3.13
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomulas	3.13
35	408056	AA312329	Hs.42331	Hs.42331:ephrin-A4	3.13
	446386	AI032108	Hs.54424	Hs.54424:hepatocyte nuclear factor 4, al	3.12
	407804	AF228603	Hs.39957	NM_016445:Homo sapiens pleckstrin 2 (mou	3.12
	412723	AA648459	Hs.335951	Hs.335951:hypothetical protein AF301222	3.12
	407233	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	3.11
40	407168	R45175	Hs.117183	Hs.117183:Homo sapiens mRNA; cDNA DKFZp5	3.11
	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	3.11
	426427	M86699	Hs.169840	Hs.169840:TTK protein kinase	3.11
	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	3.10
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (3.10
45	434881	AA206153	Hs.4209	NM_016491:Homo sapiens mitochondrial rib	3.10
	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	3.10
	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	3.09
	454464	AW811606	Hs.271819	Hs.271819:mucin 17	3.09
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	3.09
50	422816	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.09
	421470	R27496	Hs.1378	NM_005139:Homo sapiens annexin A3 (ANXA3	3.09
	419551	AW582256	Hs.91011	NM_006408:Homo sapiens anterior gradient	3.09
	418691	AW752389	Hs.87296	Hs.87296:Homo sapiens cDNA FLJ20269 fis,	3.08
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	3.08
55	447760	AI431328	Hs.348605	NM_052953:Homo sapiens mitochondrial top	3.08
	405506				3.08
	429957	AW204530	Hs.99500	Hs.99500:ESTs	3.08
	410166	AK001376	Hs.59346	NM_018122:Homo sapiens hypothetical prot	3.08
60	422880	AF228704	Hs.193974	Hs.193974:glutathione reductase	3.08
	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	3.08
	431722	AF161528	Hs.268049	(locuslink)NM_016101:Homo sapiens hypoth	3.08
	421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	3.08
	433659	AK001301	Hs.3487	NM_018093:Homo sapiens hypothetical prot	3.07
	439492	AF086310	Hs.103159	Hs.103159:ESTs, Weakly similar to T06291	3.07
65	417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	3.07
	412530	AA766268	Hs.266273	(locuslink)NM_024918:Homo sapiens chromo	3.07
	412869	AA280712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.06
	453132	AW951952	Hs.293724	Hs.293724:Homo sapiens cDNA FLJ12683 fis	3.06
	424971	AA479005	Hs.154036	NM_003311:Homo sapiens tumor suppressing	3.06
70	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	3.05
	439273	AW139099	Hs.367692	Hs.367692:Homo sapiens cDNA FLJ25668 fis	3.05
	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	3.05
	435703	AW630133	Hs.83313	(locuslink)NM_020192:Homo sapiens GK003	3.05
	407289	AA135159	Hs.203349	Hs.203349:Homo sapiens cDNA FLJ12149 fis	3.04
75	403739				3.04
	444664	N26362	Hs.11615	NM_016086:Homo sapiens map kinase phosph	3.04
	409152	AA176585	Hs.194346	Hs.194346:Spr-2 protein	3.04
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.04
	406545				3.03
80	450553	AW850613	Hs.8715	Hs.8715:hypothetical protein MGC3232	3.03
	418887	D31771	Hs.89404	NM_002449:Homo sapiens msh homeo box hom	3.03
	422976	AU076657	Hs.1600	Hs.1600:chaperonin containing TCP1, subu	3.03
	434523	AA703709	Hs.23410	(locuslink)NM_016539:Homo sapiens skt1	3.03
	440088	BE559877	Hs.183232	NM_024839:Homo sapiens hypothetical prot	3.02

5	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	3.02
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	3.02
	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	3.02
	422283	AW411307	Hs.114311	NM_003504:Homo sapiens CDC45 cell divisi	3.02
	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	3.02
10	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	3.02
	417975	AA641836	Hs.30085	NM_024616:Homo sapiens hypothetical prot	3.02
	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.01
	436561	BE560135	Hs.5232	NM_014165:Homo sapiens HSPC125 protein (3.01
	426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens cispla	3.01
15	417678	X06560	Hs.82396	(locuslink)NM_002534:Homo sapiens 2,5-	3.01
	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	3.00
	429983	W92620	Hs.260855	(locuslink)NM_145175:Homo sapiens NSE1 (3.00
	417526	AA568906	Hs.82240	Hs.82240:syntaxin 3A	3.00
	414732	AW410976	Hs.77152	Hs.77152:MCM7 minichromosome maintenance	3.00
20	409614	BE297412	Hs.55189	NM_016489:Homo sapiens 5'-nucleotidase,	3.00
	439053	BE244588	Hs.6456	Hs.6456:chaperonin containing TCP1, subu	3.00
	411096	U80034	Hs.68583	NM_005932:Homo sapiens mitochondrial int	2.99
	433312	AI241331	Hs.131765	Hs.131765:ESTs, Moderately similar to l3	2.99
	420767	AF072711	Hs.99918	Hs.99918:carboxyl ester lipase (bile sal	2.99
25	429523	AK000788	Hs.205280	Hs.205280:Homo sapiens cDNA FLJ20781 fis	2.99
	423242	AL039402	Hs.125783	Hs.125783:chromosome 1 open reading fram	2.99
	420552	AK000492	Hs.98806	Hs.98806:hypothetical protein FLJ20485	2.99
	413380	AA904232	Hs.75323	Hs.75323:prohibitin	2.99
	421533	N71826	Hs.105465	NM_003095:Homo sapiens small nuclear rib	2.99
30	439352	BE614347	Hs.169615	NM_023080:Homo sapiens hypothetical prot	2.98
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fi	2.98
	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	2.98
	457211	AW972565	Hs.32399	(locuslink)NM_145240:Homo sapiens simlia	2.98
	410467	AF102546	Hs.63931	NM_080759:Homo sapiens dachshund homolog	2.97
35	422066	AW249275	Hs.343521	Hs.343521:malate dehydrogenase 2, NAD (m	2.97
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	2.97
	453012	T95804	Hs.31334	NM_012469:Homo sapiens chromosome 20 ope	2.97
	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	2.97
	413813	M96956	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	2.97
40	418362	AL031714	Hs.84285	NM_003345:Homo sapiens ubiquitin-conjuga	2.97
	431350	AI192528	Hs.164537	Hs.164537:ESTs	2.96
	417911	AA333387	Hs.82916	Hs.82916:chaperonin containing TCP1, sub	2.96
	413597	AW302885	Hs.117183	Hs.117183:Homo sapiens mRNA; cDNA DKFZp5	2.96
	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (2.96
45	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	2.96
	418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	2.96
	408194	AA601038	Hs.191797	Hs.191797:ESTs	2.96
	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	2.96
	459306	AW578452		AW578452:RC1-CT0252-030100-023-b07 CT025	2.96
50	425209	AL049761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	2.96
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	2.95
	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	2.95
	432843	BE250865	Hs.279529	NM_013237:Homo sapiens p19-like protein	2.95
	406584	X16354	Hs.50984	(locuslink)NM_001712:Homo sapiens carcin	2.95
55	410006	AW732308	Hs.57783	NM_003751:Homo sapiens eukaryotic transl	2.94
	442577	AA292998	Hs.163900	Hs.163900:ESTs, Highly similar to winged	2.94
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap	2.94
	449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	2.94
	427779	AA906997	Hs.180780	NM_021238:Homo sapiens TERA protein (TER	2.94
60	446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	2.94
	414549	BE393069	Hs.183506	NM_024841:Homo sapiens hypothetical prot	2.93
	410817	AI262789	Hs.93659	(locuslink)NM_004911:Homo sapiens protei	2.93
	418378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	2.93
	428376	AF119665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	2.93
65	414416	AW409985	Hs.76084	(locuslink)NM_032737:Homo sapiens hypoth	2.93
	434094	AA305599	Hs.238205	Hs.238205:hypothetical protein PRO2013	2.93
	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	2.93
	429048	AI372949	Hs.44241	Hs.44241:Homo sapiens cDNA: FLJ21447 fis	2.93
	428378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	2.92
70	422397	AJ223366	Hs.116051	(locuslink)NM_138768:Homo sapiens myelom	2.92
	426715	AB037855	Hs.171917	Hs.171917:hypothetical protein FLJ11085	2.92
	429539	AK001839	Hs.206501	(locuslink)NM_020467:Homo sapiens hypoth	2.92
	443715	AI583187	Hs.9700	NM_001238:Homo sapiens cyclin E1 (CCNE1)	2.92
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transl	2.92
75	433888	BE176078	Hs.30819	Hs.30819:hypothetical protein C40	2.92
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	2.92
	422558	NM_006420	Hs.118249	Hs.118249:ADP-ribosylation factor guanin	2.92
	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	2.92
	429626	U36787	Hs.211571	NM_005333:Homo sapiens holocytochrome c	2.92
80	413374	NM_001034	Hs.75319	NM_001034:Homo sapiens ribonucleotide re	2.92
	442159	AW163390	Hs.278554	NM_007276:Homo sapiens chromobox homolog	2.92
	400133		Hs.184893	NM_005648:Homo sapiens transcription elo	2.91
	419381	AB023420	Hs.90093	Hs.90093:heat shock 70kD protein 4	2.91
	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guanin	2.91
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	2.91
	436278	BE396290	Hs.5097	Hs.5097:synaptogyrin 2	2.91
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	2.91

5	433487	U31814	Hs.3352	NM_001527:Homo sapiens histone deacetylase	2.91
	416933	BE561850	Hs.80506	NM_003090:Homo sapiens small nuclear rib	2.90
	430287	AW182459	Hs.125759	Hs.125759:likely ortholog of mouse RING	2.90
	434026	R15486	Hs.285218	(locuslink)NM_021213:Homo sapiens phosph	2.90
	447698	AI420156	Hs.326733	NM_052858:Homo sapiens similar to RUKEN	2.90
	411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinase-like 6 (m	2.90
	432754	BE241691	Hs.3100	Hs.3100:luciferase synthetase	2.90
	437016	AU076916	Hs.5398	Hs.5398:guanine monophosphate synthetase	2.90
10	446228	NM_016046	Hs.14415	NM_016046:Homo sapiens exosomal core pro	2.90
	420421	AF281133	Hs.343589	Hs.343589:exosome component Rrp41	2.89
	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	2.89
	414420	AA043424	Hs.76095	NM_052815:Homo sapiens immediate early r	2.89
	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisi	2.89
	401405				2.89
15	453111	AB014598	Hs.31720	NM_014789:Homo sapiens hephaestin (HEPH)	2.89
	400247		Hs.356473	NM_006713:Homo sapiens activated RNA pol	2.89
	421910	NM_014586	Hs.109437	NM_014586:Homo sapiens hormonally upregu	2.89
	413610	AL117554	Hs.119908	NM_015934:Homo sapiens nucleolar protein	2.89
20	413588	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine mono	2.89
	418661	NM_001949	Hs.1189	NM_001949:Homo sapiens E2F transcription	2.88
	427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated	2.88
	417634	W27202	Hs.82327	NM_000178:Homo sapiens glutathione synth	2.88
	435099	AC004770	Hs.4756	NM_004111:Homo sapiens flap structure-sp	2.88
25	425811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha	2.88
	446849	AU076617	Hs.16251	(locuslink)NM_016207:Homo sapiens cleava	2.88
	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	2.88
	413179	N99692	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenas	2.88
	407770	AW607831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN1	2.88
30	408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	2.87
	448250	NM_016034	Hs.20776	(locuslink)NM_016034:Homo sapiens mitoch	2.87
	428810	AF068236	Hs.193788	NM_000625:Homo sapiens nitric oxide synt	2.87
	427505	AA361562	Hs.178761	Hs.178761:26S proteasome-associated pad1	2.87
	418443	NM_005239	Hs.85146	Hs.85146:v-ets erythroblastosis virus E2	2.87
35	447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	2.87
	409262	AK000631	Hs.52256	Hs.52256:hypothetical protein FLJ20624	2.87
	443323	BE560621	Hs.9222	Hs.9222:estrogen receptor binding site a	2.87
	450378	AW249181	Hs.154796	Hs.154796:Homo sapiens cDNA FLJ37976 fis	2.86
	411761	AI733848	Hs.71935	NM_021220:Homo sapiens zinc finger prote	2.86
40	415691	AW963979	Hs.24723	Hs.24723:ESTs	2.86
	417715	AW969587	Hs.86366	Hs.86366:ESTs	2.86
	452099	BE612992	Hs.27931	Hs.27931:hypothetical protein FLJ10607 s	2.86
	436138	H53323	Hs.25717	Hs.25717:Homo sapiens cDNA: FLJ23454 fis	2.86
	432858	BE618609	Hs.279591	Hs.279591:Homo sapiens, Similar to RNA p	2.86
45	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	2.86
	444237	AA336878	Hs.9842	Hs.9842:ESTs	2.85
	456362	AW973003	Hs.179909	(locuslink)NM_024831:Homo sapiens nuclea	2.85
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properd	2.85
	424270	AK001818	Hs.144407	NM_018283:Homo sapiens hypothetical prot	2.85
50	414396	BE548266	Hs.76057	(locuslink)NM_000403:Homo sapiens galact	2.85
	426120	AA325243	Hs.166887	Hs.166887:copine I	2.85
	448663	BE614599	Hs.356501	(locuslink)NM_032335:Homo sapiens hypoth	2.85
	443802	AW504924	Hs.9805	Hs.9805:exportin 5	2.85
	445863	R12234	Hs.13396	Hs.13396:Homo sapiens clone 25028 mRNA s	2.85
55	434808	AF155108	Hs.256150	Hs.256150:NY-REN-41 antigen	2.85
	440334	BE276112	Hs.7165	NM_003904:Homo sapiens zinc finger prote	2.85
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	2.85
	432680	T47364	Hs.278613	(locuslink)NM_005532:Homo sapiens Interf	2.84
	446421	BE297434	Hs.15071	Hs.15071:chaperonin containing TCP1, sub	2.84
60	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCCA	2.84
	425649	U30930	Hs.158540	(locuslink)NM_003360:Homo sapiens UDP gl	2.84
	429638	AI916662	Hs.211577	(locuslink)NM_004986:Homo sapiens kinect	2.84
	435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphata	2.84
	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	2.84
65	407833	AW955632	Hs.66666	Hs.66666:chromosome 7 open reading frame	2.84
	415083	AI632683	Hs.27179	Hs.27179:Homo sapiens cDNA FLJ12933 fis	2.83
	421462	AF016495	Hs.104624	NM_020980:Homo sapiens aquaporin 9 (AQP9	2.83
	443572	AA025610	Hs.9605	Hs.9605:cleavage and polyadenylation spe	2.83
	443180	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN1	2.83
70	413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (2.83
	453028	AB006532	Hs.31442	NM_004260:Homo sapiens RecQ protein-like	2.83
	425047	U34038	Hs.164299	NM_005242:Homo sapiens coagulation facto	2.83
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	2.83
	410197	NM_005518	Hs.59889	(locuslink)NM_005518:Homo sapiens 3-hydr	2.83
75	413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	2.83
	417677	NM_016055	Hs.82389	NM_016055:Homo sapiens mitochondrial rib	2.83
	425263	NM_001197	Hs.155419	NM_001197:Homo sapiens BCL2-interacting	2.82
	437430	W44871	Hs.124	NM_014628:Homo sapiens gene predicted fr	2.82
	428289	M26301	Hs.2253	Hs.2253:complement component 2	2.82
80	407137	T97307			2.82
	400750				2.82
	428788	AF082283	Hs.193516	NM_003921:Homo sapiens B-cell CLL/lympho	2.82
	432633	AI796390	Hs.210667	Hs.210667:ESTs	2.82
	432816	N38913	Hs.221575	Hs.221575:ESTs	2.82

5	410045	AA806930	Hs.58189	Hs.58189:eukaryotic translation initiati	2.82
	454144	BE280478	Hs.182695	NM_024026:Homo sapiens mitochondrial rib	2.82
	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	2.81
	434583	AA095761	Hs.349092	Hs.349092:ESTs, Weakly similar to A42442	2.81
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	2.81
10	428093	AW594506	Hs.104830	Hs.104830:ESTs	2.81
	416047	BE439894	Hs.78991	NM_012080:Homo sapiens DNA segment, nume	2.81
	447495	AW401884	Hs.18720	NM_004208:Homo sapiens programmed cell d	2.81
	452199	BE255643	Hs.110695	Hs.110695:hypothetical protein MGC3133	2.80
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	2.80
15	445921	AW015211	Hs.153799	Hs.153799:Homo sapiens cDNA FLJ38333 fis	2.80
	422809	AK001379	Hs.121028	NM_018136:Homo sapiens hypothetical prot	2.80
	417869	BE076254	Hs.82793	Hs.82793:proteasome (prosome, macropain)	2.80
	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 cpe	2.80
	418731	AI264688	Hs.1197	NM_002157:Homo sapiens heat shock 10kD p	2.80
20	432840	AK001403	Hs.279521	Hs.279521:hypothetical protein FLJ20530	2.80
	428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associa	2.80
	441181	AA416925	Hs.374811	Hs.374811:Homo sapiens, similar to 4-1BB	2.80
	409463	AI458165	Hs.17296	NM_023930:Homo sapiens hypothetical prot	2.79
	450010	AW293801	Hs.255052	Hs.255052:ESTs	2.79
25	418960	NM_004494	Hs.89525	(locuslink)NM_004494:Homo sapiens hepato	2.79
	401179				2.79
	419252	AW138434	Hs.129805	Hs.129805:ESTs	2.79
	434750	BE019254	Hs.4112	Hs.4112:complex 1	2.79
	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	2.79
30	400529				2.79
	436414	BE264633	Hs.143638	NM_033661:Homo sapiens WD repeat domain	2.79
	436291	BE568452	Hs.344037	(locuslink)NM_003981:Homo sapiens protei	2.79
	427963	AJ042582	Hs.181271	NM_016057:Homo sapiens CGI-120 protein (2.79
	426459	AF151812	Hs.169992	NM_015966:Homo sapiens serologically def	2.79
35	413880	AI660842	Hs.110915	NM_021258:Homo sapiens interleukin 22 re	2.79
	442468	N77737	Hs.8349	NM_136933:Homo sapiens apobec-1 compleme	2.79
	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	2.79
	413278	BE563085	Hs.833	Hs.833:Interferon-stimulated protein, 15	2.79
	430120	AW675298	Hs.233694	(locuslink)NM_018396:Homo sapiens putati	2.79
40	452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	2.79
	417164	AA338283	Hs.81361	Hs.81361:heterogeneous nuclear ribonucle	2.79
	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	2.79
	409636	AA305729	Hs.18272	(locuslink)NM_030674:Homo sapiens solute	2.78
	447619	AI174800	Hs.19054	(locuslink)NM_018530:Homo sapiens hypoth	2.78
45	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	2.78
	414862	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	2.78
	443639	BE269042	Hs.9661	Hs.9661:proteasome (prosome, macropain)	2.78
	414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	2.78
	430512	AF182294	Hs.241578	NM_016200:Homo sapiens U6 snRNA-associat	2.78
50	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	2.78
	414697	BE266134	Hs.76927	Hs.76927:translocase of outer mitochondr	2.78
	420665	AW489240	Hs.371581	Hs.371581:ESTs	2.78
	428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lik	2.78
	448093	AW977382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	2.77
55	443343	BE409809	Hs.301005	Hs.301005:histone H2A.F/Z variant	2.77
	418313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L	2.77
	424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	2.77
	456950	AF111170	Hs.308165	Hs.308165:ESTs, Highly similar to unknow	2.77
	432543	AA562690	Hs.152423	Hs.152423:Homo sapiens cDNA: FLJ21274 fi	2.77
60	423271	W47225	Hs.126256	NM_000576:Homo sapiens interleukin 1, be	2.77
	410595	AW629223	Hs.64794	NM_006978:Homo sapiens zinc finger prote	2.77
	448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte acti	2.77
	457757	AA434109	Hs.12271	NM_012162:Homo sapiens F-box and leucine	2.77
	420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	2.77
65	410094	BE147897	Hs.58593	NM_004128:Homo sapiens general transcrip	2.77
	403817				2.77
	459125	AA811363	Hs.29464	Hs.29464:Homo sapiens cDNA: FLJ23460 fis	2.77
	432705	AI879473	Hs.157123	Hs.157123:ESTs	2.77
	446658	AI440137	Hs.164989	NM_138492:Homo sapiens hypothetical prot	2.76
70	419485	AA489023	Hs.99807	Hs.99807:Homo sapiens mRNA; cDNA DKFZp31	2.76
	432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility comple	2.76
	428438	NM_001955	Hs.2271	NM_001955:Homo sapiens endothelin 1 (EDN	2.76
	414767	BE541381	Hs.178705	NM_033515:Homo sapiens MacGAP protein (M	2.76
	406830	AI829848	Hs.342389	Hs.342389:peptidylprolyl isomerase A (cy	2.76
75	432320	AW411066	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	2.76
	430450	R23553	Hs.241489	(locuslink)NM_015913:Homo sapiens hypoth	2.76
	433808	NM_014062	Hs.3566	Hs.3566:ART-4 protein	2.75
	431890	X17033	Hs.271986	NM_002203:Homo sapiens Integrin, alpha 2	2.75
	433369	Z49254	Hs.3254	NM_021134:Homo sapiens mitochondrial rib	2.75
80	446946	AI878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DN	2.75
	432204	AI916132	Hs.121593	Hs.121593:Homo sapiens cDNA FLJ13123 fis	2.75
	424438	AA340724	Hs.271912	Hs.271912:Homo sapiens cDNA FLJ38690 fis	2.75
	433952	D86960	Hs.3610	NM_014873:Homo sapiens KIAA0205 gene pro	2.75
	417080	BE392846	Hs.1063	Hs.1063:small nuclear ribonucleoprotein	2.75
	428242	H55709	Hs.2250	Hs.2250:leukemia inhibitory factor (chol	2.75
	416188	BE157260	Hs.79070	NM_002467:Homo sapiens v-myc myelocytoma	2.75
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	2.75

	419489	AW411280	Hs.90693	NM_013400: Homo sapiens replication initi	2.75
	407971	AA69117	Hs.62918	Hs.62918: CDC91 cell division cycle 91-B	2.75
	432403	AA550815	Hs.124840	(locuslink)NM_138456: Homo sapiens hypoth	2.75
5	410775	AB014460	Hs.66196	NM_002528: Homo sapiens rth endonuclease	2.75
	444197	BE266947	Hs.10590	NM_018683: Homo sapiens zinc finger prot	2.75
	447250	AI878909	Hs.17883	NM_002707: Homo sapiens protein phosphata	2.75
	406806	AW088535	Hs.350108	Hs.350108: ribosomal protein, large, P0	2.75
	411580	AL080088	Hs.70877	NM_015421: Homo sapiens DKFZP564K2062 pro	2.75
10	433662	W07162	Hs.150826	NM_020387: Homo sapiens RAB25, member RAS	2.74
	426235	AI631964	Hs.34447	Hs.34447: Homo sapiens cDNA FLJ38512 fis,	2.74
	413186	AU077141	Hs.374548	Hs.374548: solute carrier family 16 (mono	2.74
	419713	AW968058	Hs.92381	NM_019094: Homo sapiens nudix (nucleoside	2.74
	410174	AA306007	Hs.59461	Hs.59461: DKFZP434C245 protein	2.74
	430720	U85768	Hs.247838	NM_002991: Homo sapiens small inducible c	2.74
15	429345	R11141	Hs.199695	Hs.199695: hypothetical protein MAC30	2.74
	452767	AW014195	Hs.61472	Hs.61472: Homo sapiens, clone IMAGE:51841	2.74
	414561	AI064813	Hs.195155	Hs.195155: solute carrier family 38, memb	2.73
	423198	MB1933	Hs.1634	Hs.1634: cell division cycle 25A	2.73
20	421038	AL080192	Hs.101282	Hs.101282: Homo sapiens mRNA; cDNA DKFZp4	2.73
	444708	AK000398	Hs.11747	(locuslink)NM_017788: Homo sapiens chromo	2.73
	423908	AJ006422	Hs.135183	NM_006869: Homo sapiens centaurin, alpha	2.73
	433412	AV653729	Hs.8185	NM_021199: Homo sapiens sulfide dehydroge	2.73
	438485	W57578	Hs.378718	Hs.378718: Homo sapiens cDNA FLJ33433 fis	2.73
25	452461	N78223	Hs.108106	Hs.108106: ubiquitin-like, containing PHD	2.73
	407699	AA825974	Hs.32646	NM_024622: Homo sapiens hypothetical prot	2.73
	412258	AA376768	Hs.96125	(locuslink)NM_025151: Homo sapiens Rab co	2.73
	450256	AA268887	Hs.24724	Hs.24724: Homo sapiens cDNA FLJ39185 fis,	2.72
	443905	AJ215948	Hs.143969	Hs.143969: ESTs	2.72
30	413274	NM_004893	Hs.75258	NM_004893: Homo sapiens H2A histone famil	2.72
	408885	C02741	Hs.48712	NM_017948: Homo sapiens hypothetical prot	2.72
	424685	W21223	Hs.151734	Hs.151734: nuclear transport factor 2	2.72
	424692	AA429834	Hs.151791	NM_014679: Homo sapiens KIAA0092 gene pro	2.72
	413762	AW411479	Hs.848	NM_002014: Homo sapiens FK506 binding pro	2.72
35	418054	NM_002318	Hs.83354	NM_002318: Homo sapiens lysyl oxidase-like	2.72
	450164	AJ239923	Hs.63931	NM_080759: Homo sapiens dachshund homolog	2.71
	412115	AK001763	Hs.73239	Hs.73239: hypothetical protein FLJ10901	2.71
	450897	W16741	Hs.351629	NM_014017: Homo sapiens HSPC003 protein (2.71
40	447349	AA375546	Hs.12677	BE743847: 601577765F1 NIH_MGC_9 Homo sapi	2.71
	445413	AA151342	Hs.12677	(locuslink)NM_016077: Homo sapiens CGI-14	2.71
	448826	AI580252	Hs.255565	Hs.255565: Homo sapiens cDNA FLJ33892 fis	2.71
	406671	AA129547	Hs.285754	NM_000245: Homo sapiens met proto-oncogene	2.71
	433604	NM_013442	Hs.34339	Hs.34339: stomatin (EPB72)-like 2	2.71
45	441020	W79283	Hs.35962	Hs.35962: Homo sapiens mRNA; cDNA DKFZp68	2.70
	458933	AI638429	Hs.24763	NM_002882: Homo sapiens RAN binding prote	2.70
	423787	AJ295745	Hs.236204	Hs.236204: nuclear pore complex protein	2.70
	430462	AI584156	Hs.105640	Hs.105640: hypothetical protein BC007772	2.70
	439555	AW138241	Hs.160602	Hs.160602: Homo sapiens cDNA FLJ36008 fis	2.70
	425236	AW067800	Hs.155223	NM_003714: Homo sapiens stannocalcin 2 (2.70
50	420085	AJ741909	Hs.44680	Hs.44680: hypothetical protein FLJ20979	2.70
	448296	BE622756	Hs.10949	Hs.10949: Homo sapiens cDNA FLJ14162 fis,	2.70
	430200	BE613337	Hs.234896	Hs.234896: geminin	2.70
	424308	AW975531	Hs.154443	Hs.154443: MCM4 minichromosome maintenanc	2.70
55	423453	AW450737	Hs.128791	NM_015939: Homo sapiens CGI-09 protein (L	2.70
	421344	AW631030	Hs.103665	(locuslink)NM_015873: Homo sapiens villin	2.70
	446607	AI691065	Hs.155780	Hs.155780: ESTs	2.70
	418558	AW082268	Hs.86131	Hs.86131: Fas (TNFRSF6)-associated via de	2.70
	443835	AF016371	Hs.9880	NM_006347: Homo sapiens peptidyl prolyl	2.70
	413794	AF234532	Hs.61638	NM_012334: Homo sapiens myosin X (MYO10),	2.70
60	451481	AA300228	Hs.295866	(locuslink)NM_030974: Homo sapiens hypoth	2.70
	458820	BE552151	Hs.108118	Hs.108118: hypothetical protein FLJ22474	2.70
	425805	AB032959	Hs.318584	NM_032173: Homo sapiens hypothetical prot	2.69
	408089	H59789	Hs.42644	Hs.42644: thioredoxin-like 2	2.69
	431201	AA678405	Hs.8854	Hs.8854: Pvt1 oncogene homolog, MYC activ	2.69
65	437897	AA770561	Hs.146170	Hs.146170: hypothetical protein FLJ22969	2.69
	441703	AW390054	Hs.192843	NM_022145: Homo sapiens leucine zipper pr	2.69
	433916	AW732839	Hs.3631	NM_001551: Homo sapiens immunoglobulin (C	2.69
	422516	BE258862	Hs.117950	NM_006452: Homo sapiens phosphoribosylam	2.69
	416084	L16991	Hs.78006	NM_012145: Homo sapiens deoxythymidylate	2.69
70	427484	BE282956	Hs.178292	Hs.178292: protein O-fucosyltransferase 1	2.69
	453876	AW021748	Hs.110406	Hs.110406: ESTs	2.69
	424373	AJ133798	Hs.146219	NM_014427: Homo sapiens copine VII (CPNE7	2.69
	411619	AI418609	Hs.71040	NM_017816: Homo sapiens hypothetical prot	2.69
	413004	T35901	Hs.75117	Hs.75117: interleukin enhancer binding fa	2.69
75	420062	AW411096	Hs.94785	(locuslink)NM_021809: Homo sapiens TGF-beta	2.69
	446077	BE251048	Hs.22579	Hs.22579: Homo sapiens clone CDABP0036 mR	2.68
	446269	AW263155	Hs.14559	NM_018131: Homo sapiens hypothetical prot	2.68
	428728	NM_016625	Hs.191381	Hs.191381: hypothetical protein LOC51319	2.68
	400263		Hs.75309	NM_001961: Homo sapiens eukaryotic transl	2.68
80	421933	R98881	Hs.109655	NM_006746: Homo sapiens sex comb on middle	2.68
	417750	AI267720	Hs.260523	Hs.260523: neuroblastoma RAS viral (v-ras	2.68
	429671	BE379335	Hs.211594	Hs.211594: proteasome (prosome, macropain	2.68
	421720	AF155098	Hs.107213	Hs.107213: formin binding protein 3	2.68
	425601	AW629485	Hs.140720	NM_012083: Homo sapiens frequently rearra	2.68

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5	425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenanc	2.68
	433159	AB035898	Hs.150587	NM_020242:Homo sapiens kinesin-like 7 (K	2.68
	406673	M34996	Hs.198253	Hs.198253:major histocompatibility compl	2.68
	428206	AB020643	Hs.183006	Hs.183006:likely homolog of mouse hepar	2.68
	429344	R94038	Hs.374664	NM_005538:Homo sapiens inhibin, beta C (2.68
10	427719	AI393122	Hs.134726	(locuslink)NM_145060:Homo sapiens hypoth	2.68
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20669 fi	2.68
	457313	AF047002	Hs.241520	NM_005782:Homo sapiens transcriptional c	2.67
	413142	M81740	Hs.75212	(locuslink)NM_002538:Homo sapiens ornith	2.67
	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	2.67
15	432391	AI732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	2.67
	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA: cDNA DKFZp56	2.67
	447913	AW438602	Hs.191179	Hs.191179:ESTs	2.67
	418738	AW388633	Hs.6682	Hs.6682:solute carrier family 7, (cation	2.67
	439586	AA922936	Hs.110039	Hs.110039:ESTs	2.67
20	427477	AW973119	Hs.178391	NM_021029:Homo sapiens ribosomal protein	2.67
	421839	BE258778	Hs.108809	NM_008429:Homo sapiens chaperonin contai	2.67
	400448				2.67
	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu++ tran	2.67
	445304	BE613206	Hs.279607	Hs.279607:Homo sapiens cDNA FLJ34399 fis	2.67
25	417601	NM_014735	Hs.82292	NM_014735:Homo sapiens KIAA0215 gene pro	2.66
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	2.66
	431021	AI869664	Hs.351863	(locuslink)NM_003312:Homo sapiens thiloso	2.66
	453157	AF077036	Hs.31989	NM_015449:Homo sapiens NICE-3 protein (N	2.66
	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	2.66
30	422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, protein	2.66
	456248	AL035788	Hs.82425	NM_005717:Homo sapiens actin related pro	2.66
	427691	AW194426	Hs.20726	Hs.20726:ESTs, Moderately similar to hyp	2.66
	419705	AW368634	Hs.154331	Hs.154331:ESTs	2.66
	421254	AK001724	Hs.102950	NM_016128:Homo sapiens coal protein gamm	2.66
35	422719	BE017985	Hs.102558	Hs.102558:Homo sapiens cDNA FLJ40369 fis	2.66
	446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	2.66
	432435	BE218886	Hs.282070	Hs.282070:ESTs	2.66
	433020	AI375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	2.65
	436106	AI050715	Hs.2331	Hs.2331:E2F transcription factor 5, p130	2.65
40	431127	U66818	Hs.250581	Hs.250581:SW/SNF related, matrix associ	2.65
	425568	AW963118	Hs.161784	Hs.161784:ESTs	2.65
	430508	AI015435	Hs.104637	Hs.104637:solute carrier family 1 (gluta	2.65
	414761	AU077228	Hs.77256	NM_004456:Homo sapiens enhancer of zeste	2.65
	412738	N34731	Hs.74562	NM_078480:Homo sapiens fuse-binding prot	2.65
45	409893	AW247090	Hs.57101	Hs.57101:MCM2 minichromosome maintenanc	2.65
	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	2.64
	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protel	2.64
	417957	H53497	Hs.83006	NM_016071:Homo sapiens mitochondrial rib	2.64
	409119	AA531133	Hs.4253	Hs.4253:hypothetical protein MGC2574	2.64
50	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	2.64
	409214	AW405967	Hs.333388	Hs.333388:similar to CG3714 gene product	2.64
	414883	AA926960	Hs.348669	Hs.348669:CDK28 protein kinase 1	2.64
	433570	AI580053	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC16	2.64
	408633	AW963372	Hs.222088	NM_014109:Homo sapiens PRO2000 protein (2.64
55	447769	AW873704	Hs.320831	Hs.320831:chromosome 20 open reading fra	2.64
	432964	AF118395	Hs.279865	NM_014317:Homo sapiens trans-prenyltrans	2.63
	444855	BE409261	Hs.12084	Hs.12084:Tu translation elongation facto	2.63
	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	2.63
	408137	AI694131	Hs.29002	Hs.29002:KIAA1706 protein	2.63
60	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	2.63
	446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	2.63
	430024	AI808780	Hs.227730	NM_000210:Homo sapiens Integrin, alpha 6	2.63
	406122				2.63
	420988	AW006352	Hs.159643	Hs.159643:ESTs, Weakly similar to putail	2.63
65	436433	AW631437	Hs.5184	(locuslink)NM_016397:Homo sapiens TH1-i	2.63
	417129	AI381800	Hs.300684	Hs.300684:calcitonin gene-related peptid	2.63
	410397	AF217517	Hs.63042	NM_018457:Homo sapiens DKFZp564J157 prot	2.63
	419420	AA355435	Hs.30724	(locuslink)NM_001516:Homo sapiens genera	2.63
	400298	AA032279	Hs.61635	Hs.61635:six transmembrane epithelial an	2.63
70	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	2.63
	436199	R38946	Hs.127951	Hs.127951:Homo sapiens cDNA FLJ14503 fis	2.63
	425081	X74794	Hs.154443	Hs.154443:MCM4 minichromosome maintenanc	2.62
	442025	AW887434	Hs.11810	NM_032026:Homo sapiens CDA11 protein (CD	2.62
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	2.62
75	409703	NM_006187	Hs.56009	Hs.56009:2'-5'-oligoadenylate synthetase	2.62
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens integral membrane	2.62
	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	2.62
	451926	AW134519	Hs.96125	(locuslink)NM_025151:Homo sapiens Rab co	2.62
	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (i	2.62
80	407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	2.62
	421405	AA251944	Hs.104058	NM_015957:Homo sapiens CGI-29 protein (L	2.62
	429491	NM_012111	Hs.204041	NM_012111:Homo sapiens chromosome 14 ope	2.62
	453335	AW857376	Hs.169238	NM_000149:Homo sapiens fucosyltransferas	2.62
	441126	NM_000429	Hs.323715	(locuslink)NM_000429:Homo sapiens methio	2.62
	417404	NM_007350	Hs.82101	(locuslink)NM_007350:Homo sapiens plecks	2.62
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	2.62
	446766	AF083208	Hs.16178	NM_012138:Homo sapiens apoptosis antagon	2.62

	437033	AW248364	Hs.5409	(locustlink)NM_004875:Homo sapiens RNA po	2.62
	412123	BE251328	Hs.73291	NM_018256:Homo sapiens WD repeat domain	2.62
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	2.61
5	433037	NM_014158	Hs.279938	NM_014158:Homo sapiens HSPC067 protein (2.61
	414438	AJ879277	Hs.76136	(locustlink)NM_003329:Homo sapiens thione	2.61
	416221	BE513171	Hs.79086	(locustlink)NM_007208:Homo sapiens mitoch	2.61
	443898	AW804296	Hs.9950	NM_014302:Homo sapiens Sec61 gamma (SEC6	2.61
	410007	AW950887	Hs.57813	NM_014596:Homo sapiens zinc ribbon domai	2.61
10	412715	NM_000947	Hs.74519	NM_000947:Homo sapiens primase, polypept	2.61
	449864	BE276386	Hs.111429	NM_032486:Homo sapiens dynactin 4 (MGC32	2.61
	448625	AW970786	Hs.178470	NM_024829:Homo sapiens hypothetical prot	2.61
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	2.61
	410686	AJ733735	Hs.114905	NM_033266:Homo sapiens ER to nucleus sig	2.60
15	411400	AA311919	Hs.69851	NM_018983:Homo sapiens nucleolar protein	2.60
	429770	AI766047	Hs.99736	Hs.99736:hypothetical protein MGC39350	2.60
	425983	AK000226	Hs.165619	NM_031265:Homo sapiens mucin and cadheri	2.60
	430237	AJ272144	Hs.236522	Hs.236522:DKFZP434P106 protein	2.60
	419607	RS2557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	2.60
20	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	2.60
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger prote	2.60
	457234	AW988360	Hs.14355	Hs.14355:Homo sapiens cDNA FLJ13207 fis,	2.60
	420911	U77413	Hs.100293	Hs.100293:O-linked N-acetylglucosamine (2.60
	418478	U38945	Hs.1174	NM_000077:Homo sapiens cyclin-dependent	2.60
25	438533	AI440266	Hs.170673	NM_138969:Homo sapiens retinal short cha	2.60
	421699	AL161994	Hs.107003	NM_021178:Homo sapiens enhancer of Invas	2.60
	452220	BE158006	Hs.212296	Hs.212296:ESTs	2.60
	439148	AA372280	Hs.178576	(locustlink)NM_030877:Homo sapiens cateni	2.60
	453949	AU077146	Hs.36927	(locustlink)NM_006644:Homo sapiens heat s	2.59
30	451110	AI955040	Hs.265398	Hs.265398:ESTs, Moderately similar to hy	2.59
	446291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	2.59
	411125	AA151647	Hs.68877	Hs.68877:cytochrome b-245, alpha polypep	2.59
	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	2.59
	442990	AA197226	Hs.19347	NM_032351:Homo sapiens mitochondrial rib	2.59
35	424197	AF096834	Hs.142989	NM_015982:Homo sapiens germ cell specifi	2.59
	445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	2.59
	410219	T98226	Hs.171952	Hs.171952:occludin	2.59
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	2.59
	441153	BE562828		BE562828:601336534F1 NIH_MGC_44 Homo sap	2.59
40	410570	AI133096	Hs.64593	NM_006356:Homo sapiens ATP synthase, H+	2.58
	430594	AK000790	Hs.246885	NM_017958:Homo sapiens hypothetical prot	2.58
	410315	AI638871	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	2.58
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	2.58
	445725	NM_012243	Hs.159322	(locustlink)NM_012243:Homo sapiens solute	2.58
45	449019	AI949095	Hs.67776	Hs.67776:Homo sapiens, clone IMAGE:54556	2.58
	410442	X73424	Hs.63788	Hs.63788:propionyl Coenzyme A carboxylas	2.58
	456629	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	2.58
	454417	AI244459	Hs.110826	Hs.110826:trinucleotide repeat containin	2.58
	416330	AU077101	Hs.79222	Hs.79222:galactosidase, beta 1	2.58
50	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	2.58
	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	2.58
	412641	M16650	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	2.58
	406180				2.58
	416297	AA157634	Hs.79172	Hs.79172:solute carrier family 25 (mitoc	2.58
55	418803	U50079	Hs.88556	NM_004984:Homo sapiens histone deacetyla	2.58
	447532	AK000614	Hs.18791	NM_017899:Homo sapiens hypothetical prot	2.57
	420309	AW043637	Hs.21768	Hs.21768:ESTs, Weakly similar to hypoth	2.57
	447418	AA063074	Hs.18552	Hs.18552:E2IG2 protein	2.57
	424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	2.57
60	428342	AI739168	Hs.349283	Hs.349283:Homo sapiens cDNA FLJ31763 fis	2.57
	427254	AL121523	Hs.97774	Hs.97774:ESTs	2.57
	458778	AW451034	Hs.326525	NM_001669:Homo sapiens arylsulfatase D (2.57
	425689	W16480	Hs.24283	Hs.24283:Homo sapiens cDNA FLJ25952 fis,	2.57
	452700	AI859390	Hs.286940	NM_021259:Homo sapiens transmembrane pro	2.57
65	427678	BE267756	Hs.180312	NM_016065:Homo sapiens mitochondrial rib	2.57
	444656	AI277924	Hs.145199	Hs.145199:ESTs, Weakly similar to hypoth	2.57
	425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	2.57
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	2.56
	427648	AI376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	2.56
70	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	2.56
	409964	AW368226	Hs.67928	Hs.67928:ESTs	2.56
	431910	AK000142	Hs.101774	Hs.101774:hypothetical protein FLJ23045	2.56
	413010	AA393273	Hs.75133	NM_003201:Homo sapiens transcription fac	2.56
	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	2.56
75	419423	D26488	Hs.90315	Hs.90315:KIAA0007 protein	2.56
	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	2.56
	437623	D63880	Hs.5719	NM_014865:Homo sapiens chromosome conden	2.56
	444184	T87841	Hs.282990	(locustlink)NM_033550:Homo sapiens chromo	2.56
	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	2.56
80	425368	AB014595	Hs.155976	(locustlink)NM_003588:Homo sapiens cullin	2.56
	420614	AL110291	Hs.99364	Hs.99364:abhydrotase domain containing 1	2.56
	427876	AJ494291	Hs.369171	Hs.369171:ESTs	2.56
	418862	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	2.56
	416432	BE391787	Hs.79322	(locustlink)NM_005051:Homo sapiens glutam	2.55

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5	458814	AI498957	Hs.351937	Hs.351937:ribosomal protein, large P2	2.55
	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	2.55
	454003	AA058944	Hs.116602	Hs.116602:hypothetical protein BC009115	2.55
	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	2.55
	457400	AF032906	Hs.252549	NM_001336:Homo sapiens cathepsin Z (CTSZ	2.55
10	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	2.55
	402829				2.55
	425843	BE313280	Hs.159627	NM_004632:Homo sapiens death associated	2.55
	400995				2.55
	452945	AW978187	Hs.79103	NM_030579:Homo sapiens cytochrome b5 out	2.55
15	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	2.55
	422192	AA305159	Hs.113019	NM_015831:Homo sapiens fts485 (LOC51066)	2.55
	424755	AB033094	Hs.152925	Hs.152925:KIAA1268 protein	2.55
	410012	AW015832	Hs.57898	(locuslink)NM_017819:Homo sapiens hypoth	2.55
	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	2.55
20	449042	AW294985	Hs.30715	Hs.30715:potassium voltage-gated channel	2.55
	420281	AI623693	Hs.323494	(locuslink)NM_017964:Homo sapiens hypoth	2.55
	186881	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	2.55
	406629	AW277078	Hs.181165	Hs.181165:eukaryotic translation elongat	2.55
	421612	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens 8D6 an	2.54
25	446715	AI337735	Hs.173919	Hs.173919:ESTs, Weakly similar to neuron	2.54
	431183	NM_006855	Hs.250696	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	2.54
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyrido	2.54
	427368	BE041451	Hs.177507	Hs.177507:hypothetical protein HSPC155	2.54
	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	2.54
30	409632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cystei	2.54
	442875	BE623003	Hs.23625	Hs.23625:Homo sapiens clone TCCCTA00142	2.54
	456031	AA335995	Hs.355907	Hs.355907:ESTs, Weakly similar to protei	2.54
	442432	BE093589	Hs.38178	NM_024629:Homo sapiens hypothetical prot	2.54
	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	2.54
35	448775	AB025237	Hs.388	NM_002452:Homo sapiens nudix (nucleoside	2.54
	414368	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	2.54
	432876	AW248272	Hs.279652	NM_015956:Homo sapiens mitochondrial rib	2.53
	431731	BE266322	Hs.211374	(locuslink)NM_145061:Homo sapiens hypoth	2.53
	425994	AK000207	Hs.165803	NM_017708:Homo sapiens hypothetical prot	2.53
40	445982	BE410233	Hs.13501	(locuslink)NM_014303:Homo sapiens pescad	2.53
	444232	W56010	Hs.347297	(locuslink)NM_013397:Homo sapiens over-e	2.53
	435655	AW105663	Hs.6947	(locuslink)NM_014159:Homo sapiens Huntin	2.53
	417686	AA769155	Hs.235498	Hs.235498:hypothetical protein FLJ14075	2.53
	417933	X02308	Hs.82962	NM_001071:Homo sapiens thymidylate synth	2.53
45	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	2.53
	452313	Y00486	Hs.28914	Hs.28914:adenine phosphoribosyltransfera	2.53
	438317	AA826401	Hs.122393	Hs.122393:ESTs	2.53
	409299	AA045650	Hs.53125	NM_004597:Homo sapiens small nuclear rib	2.53
	423599	AI805664	Hs.31731	(locuslink)NM_012094:Homo sapiens perox	2.53
50	412525	AA581439	Hs.152328	Hs.152328:ESTs	2.53
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	2.53
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif	2.53
	414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	2.53
	434274	AA628539	Hs.57783	Hs.57783:eukaryotic translation Initiat	2.53
55	400282		Hs.289101	NM_005313:Homo sapiens glucose regulated	2.53
	425322	U63630	Hs.155837	NM_006904:Homo sapiens protein kinase, D	2.53
	453344	BE349075	Hs.44571	Hs.44571:ESTs	2.53
	449915	NM_004529	Hs.404	NM_004529:Homo sapiens myeloid/lymphoid	2.52
	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	2.52
60	439012	BE383814	Hs.6455	NM_006666:Homo sapiens RuvB-like 2 (E. c	2.52
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	2.52
	411678	AI907114	Hs.71465	NM_003129:Homo sapiens squalene epoxidase	2.52
	442315	AA173992	Hs.7956	Hs.7956:ESTs	2.52
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	2.52
65	422385	BE549407	Hs.115823	(locuslink)NM_006638:Homo sapiens ribonu	2.52
	433517	AW022133	Hs.189838	Hs.189838:ESTs	2.52
	450230	AW016607	Hs.201582	Hs.201582:ESTs	2.52
	432866	BE395875	Hs.279609	NM_014342:Homo sapiens mitochondrial car	2.52
	433001	AF217513	Hs.279905	NM_016359:Homo sapiens nucleolar protein	2.52
70	440773	AA352702	Hs.37747	NM_022767:Homo sapiens hypothetical prot	2.52
	440587	AL138461	Hs.323084	(locuslink)NM_031209:Homo sapiens tRNA-g	2.52
	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transmem	2.52
	424259	AK001776	Hs.143954	(locuslink)NM_018270:Homo sapiens chromo	2.52
	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	2.52
75	453204	R10799	Hs.191990	Hs.191990:ESTs	2.52
	453665	AA626250	Hs.326184	Hs.326184:Homo sapiens nuclear protein p	2.52
	432353	NM_016558	Hs.274411	NM_016558:Homo sapiens SCAN domain conta	2.51
	433271	BE621697	Hs.14317	NM_018648:Homo sapiens nucleolar protein	2.51
	431770	BE221880	Hs.268555	NM_012255:Homo sapiens 5'-3' exonuclease	2.51
80	444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	2.51
	428839	AI767756	Hs.82302	(locuslink)NM_147174:Homo sapiens hepara	2.51
	404826				2.51
	429669	BE185499	Hs.2471	NM_014878:Homo sapiens KIAA0020 gene pro	2.51
	434474	AL042936	Hs.211571	(locuslink)NM_005333:Homo sapiens holoxy	2.51
	424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens volta	2.51
	450422	AA743525	Hs.60300	NM_033414:Homo sapiens hypothetical prot	2.51
	440214	AA247118	Hs.7049	(locuslink)NM_018386:Homo sapiens hypoth	2.51

5	421168	AF182277	Hs.330780	Hs.330780:cytochrome P450, subfamily IIB	2.51
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	2.51
	452101	T60298	Hs.10844	NM_052972:Homo sapiens leucine-rich alph	2.51
	436043	AW963838	Hs.168830	Hs.168830:Homo sapiens cDNA FLJ12136 fis	2.51
	424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	2.51
10	435677	AA694142	Hs.6685	Hs.6685:thyroid hormone receptor interac	2.51
	406363				2.51
	452018	AW102941	Hs.211265	Hs.211265:ESTs	2.51
	409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	2.51
	421937	AJ878857	Hs.109706	NM_016185:Homo sapiens hematological and	2.51
15	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	2.51
	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	2.50
	434584	D57341	Hs.188361	Hs.188361:Homo sapiens cDNA FLJ12807 fis	2.50
	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	2.50
	426053	U88105	Hs.172182	NM_002568:Homo sapiens poly(A) binding p	2.50
20	432642	BE297635	Hs.3069	NM_004134:Homo sapiens heat shock 70kD p	2.50
	452390	AJ864142	Hs.29288	(locuslink)NM_022759:Homo sapiens endo-b	2.50
	429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inacti	2.50
	400076				2.50
	420596	NM_002692	Hs.99185	NM_002692:Homo sapiens polymerase (DNA d	2.50
25	422244	Y08890	Hs.113503	NM_002271:Homo sapiens karyopherin (impo	2.50
	410723	AA100683	Hs.372108	Hs.372108:ESTs	2.50
	435496	AW840171	Hs.265398	Hs.265398:ESTs, Moderately similar to hy	2.50
	425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	2.50
	433626	AF078859	Hs.85347	NM_013341:Homo sapiens hypothetical prot	2.50
	448391	H71025	Hs.21075	NM_016328:Homo sapiens GTF2I repeat doma	2.50

TABLE 10B

30	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
35	Accession:	Genbank accession numbers		
	Pkey	CAT Number	Accession	
40	406685	0_0	M18728	
	434414	35978_1	AF134164 BF809407 AA218567 BF842863 AJ267168 BF876178 BG999253 AW861851 AW858362 AJ817548 BF771300 AA113928 AA223422 AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298 AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AJ694265 AA045564 BG950256 AJ829309 BG987850 BE093175 BF854337	
45	432407	MH1429_12	BG036575 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BF714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AJ732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 B1861466 AA663341 AA457691 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771288 AJ075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 B1055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592	
50	406708	0_0	AJ282759	
	459306	223120_4	AW578452	
55	447349	1063443_1	BE743847 AW809603 BM469626 AJ375546	
	441153	264480_3	BE562826 BE378727	

TABLE 10C

55	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
60	Strand:	Indicates DNA strand from which exons were predicted.		
	NL_position:	Indicates nucleotide positions of predicted exons.		
65	Pkey	Ref	Strand	NL_position
	404519	8152000	Plus	12817-13000
	405399	9256288	Minus	63448-63554
	403220	7630969	Plus	64338-64517
	404661	9797073	Plus	33374-33675,33769-34008
70	402496	9797769	Minus	8615-9103
	403055	8748904	Minus	109532-110225
	400965	7770576	Minus	173043-173564
	403218	7630969	Plus	58039-68149
	401866	8018106	Plus	73126-73623
75	403221	7630969	Plus	66294-66438,66936-67124
	401519	6649315	Plus	157315-157950
	405451	7622517	Minus	145949-146227
	403532	8076842	Minus	81750-81901
	402944	9368423	Plus	110411-110716,111173-111640
80	403219	7630969	Plus	61858-61995
	403381	9438267	Minus	26009-26178
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	405484	6922025	Plus	199214-199579,199672-199920,200262-20049
	404684	9797403	Minus	110881-111020
85	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	405506	6466489	Plus	80014-80401,80593-81125
	403739	7630882	Plus	44563-44766,48209-48483,52265-52495

5	406545	7711510	Plus	145662-145781,147854-147984,148098-14824
	401405	7768126	Minus	69276-69452,69548-69958
	400750	8119067	Plus	198991-199168,199316-199548
	401179	9438647	Plus	113477-113893
	400529	9796988	Plus	138232-138423
	403817	8962055	Plus	110297-111052
	400448	9887687	Minus	177372-177674
	406122	9144087	Minus	30940-31386
10	406180	7283201	Minus	38923-39107
	402829	8918414	Plus	101532-101852,102005-102263
	400695	8090994	Plus	141188-141601
	404826	6572184	Plus	47726-48046
	406363	9256114	Plus	14403-14602,17000-17147,17241-17368

15

20 Table 11A lists about 958 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium) that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 3.0, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 70th percentile value amongst non-malignant tissues minus the colonic derived samples, the "average" colon value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of have an oncogenic function or of transducing an intracellular signal, or of being modulatable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, Trn, phosphatase, or ion transporter). In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

25

TABLE 11A: 958 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium)

30	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor to normal adult tissues			
35	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosi	37.18
	406690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carcin	31.24
	407242	M18728		(locuslink)NM_002483:Homo sapiens carcin	24.81
	406685	M18728		(locuslink)NM_002483:Homo sapiens carcin	20.54
40	431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S3B4_H	20.38
	428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	20.13
	406667	M12523			19.89
	437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel	19.68
	446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intestin	19.55
45	423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease I	18.33
	421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	17.47
	414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),	17.37
	416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating isle	16.99
	422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo	15.15
50	441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	15.02
	421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefol factor 1	14.23
	407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	14.12
	422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	13.64
	432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	13.48
55	424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	13.43
	418888	AU076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, U c	13.20
	453863	X02544	Hs.572	Hs.572:orossomucoid 1	13.06
	413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	12.58
	436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	12.34
60	421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to Z1	11.72
	409153	W03754	Hs.50813	NM_017625:Homo sapiens Intellectin (ITLN)	11.72
	452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	11.49
	406399				11.25
	414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	11.18
65	421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog	11.12
	407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	11.01
	423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	10.70
	447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	10.69
	450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	10.57
70	427583	M82962	Hs.179704	NM_005688:Homo sapiens meprin A, alpha (10.48
	418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.39
	406741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	10.20
	422424	AI186431	Hs.298638	Hs.298638:prostate differentiation facto	10.19
	423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	9.91
75	452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590	9.72
	422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr	9.70
	430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	9.65
	406687	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	9.52
	428355	BE256452	Hs.2257	NM_000638:Homo sapiens vitronectin (seru	9.47
80	422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX),	9.41
	413585	AI133452	Hs.75431	NM_000509:Homo sapiens fibrinogen, gamma	9.39
	422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	9.31
	417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:225881	9.30

5	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	9.01
	413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystei	8.99
	424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	8.80
	420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protei	8.71
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	8.67
	428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homo	8.47
	452594	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfat	8.47
	422310	AA316622	Hs.98370	(locuslink)NM_030622:Homo sapiens cytoch	8.43
10	421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	8.34
	424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysl	8.12
	435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	8.09
	413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	7.96
	443426	AF088158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	7.92
15	436972	AA284679	Hs.25640	Hs.25640:claudin 3	7.89
	430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	7.87
	409632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cystei	7.71
	423803	NM_005709	Hs.132945	(locuslink)NM_005709:Homo sapiens PDZ-73	7.58
	430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	7.48
20	451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (I iso	7.31
	422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	7.31
	425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	7.29
	411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier fa	7.23
	451917	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	7.21
25	410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	7.12
	418318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 s	7.12
	414617	AJ339520	Hs.268817	(locuslink)NM_025130:Homo sapiens hypo	7.10
	447342	AI199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	7.08
	452194	AI694413	Hs.373599	Hs.373599:EST	7.02
30	414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	6.97
	417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	6.96
	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	6.96
	403220				6.95
35	415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	6.87
	449722	BE280074	Hs.23960	Hs.23960:cyclin B1	6.87
	414798	AI286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	6.80
	415214	AI445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tr	6.78
	411975	AI916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	6.76
	422511	AU076442	Hs.117938	NM_000494:Homo sapiens collagen, type XV	6.66
40	408983	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis t	6.65
	431301	AA502384	Hs.151529	Hs.151529:ESTs	6.62
	428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid ind	6.59
	424273	W40460	Hs.144442	NM_003561:Homo sapiens phospholipase A2,	6.56
	431657	AI345227	Hs.105448	Hs.105448:protein kinase, lysine defic	6.54
45	431330	X69532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	6.53
	425983	AK000226	Hs.165619	NM_031265:Homo sapiens mucin and cadheri	6.50
	408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	6.47
	428187	AI687303	Hs.285529	Hs.285529:G protein-coupled receptor 49	6.46
	408704	AA056635	Hs.5366	NM_139053:Homo sapiens epidermal growth	6.45
50	428753	AW939252	Hs.182927	NM_017726:Homo sapiens protein phosphata	6.41
	426227	U67058	Hs.154299	(locuslink)NM_005242:Homo sapiens coagul	6.41
	419354	M62639	Hs.1252	NM_000042:Homo sapiens apolipoprotein H	6.27
	414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	6.20
	422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	6.19
55	407786	AA687538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	6.19
	414809	AI434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71	6.18
	425280	U31519	Hs.1872	NM_002591:Homo sapiens phosphoenolpyruva	6.16
	432179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPHB3), mR	6.16
	443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	6.15
60	426174	AA547959	Hs.115838	Hs.115838:ESTs	6.10
	430135	NM_000035	Hs.234234	NM_000035:Homo sapiens aldolase B, fruct	6.07
	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	6.06
	409453	AI885516	Hs.95612	Hs.95612:ESTs	6.06
	408482	NM_000876	Hs.45743	NM_000876:Homo sapiens adenosine A2b rec	6.03
65	444151	AW972917	Hs.128749	(locuslink)NM_014324:Homo sapiens alpha-	5.99
	444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	5.97
	421408	AI688223	Hs.91096	NM_052816:Homo sapiens tripartite motif-	5.95
	430204	AA618335	Hs.356664	Hs.356664:hypothetical protein FLJ32334	5.92
	443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interne	5.90
70	428874	W32133	Hs.194368	Hs.194366:transferrin (prealbumin, amy	5.88
	408908	BE296227	Hs.250822	(locuslink)NM_003158:Homo sapiens serine	5.88
	411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc6Ga	5.88
	452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fis,	5.82
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	5.77
75	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.76
	433083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20258	5.75
	403218				5.74
	412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	5.72
80	449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	5.72
	429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	5.72
	414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	5.72
	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	5.71
	425208	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	5.70
	432978	AF126743	Hs.279884	NM_013238:Homo sapiens DNAJ domain-conta	5.70

	408889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	5.67
	414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	5.67
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	5.63
	418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	5.62
5	433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apopto	5.60
	424010	AL080188	Hs.137556	NM_033100:Homo sapiens MT-protocadherin	5.59
	438746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	5.58
	414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation facto	5.56
10	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25- dihydroxyvitami	5.56
	423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical prot	5.54
	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	5.53
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	5.53
	403221				5.52
15	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	5.52
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	5.48
	418508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	5.44
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	5.42
	435251	BE515065	Hs.296585	(locuslink)NM_006392:Homo sapiens nucle	5.41
20	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	5.38
	450505	NM_004572	Hs.25051	NM_004572:Homo sapiens plakophilin 2 (PK	5.34
	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	5.33
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	5.32
	425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	5.31
25	430680	AW138724	Hs.168974	Hs.168974:ESTs	5.25
	432378	AK93046	Hs.146133	Hs.146133:ESTs	5.25
	419693	AA133749	Hs.301350	Hs.301350:FXD domain-containing ion tra	5.24
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	5.21
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23658	5.21
30	415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	5.21
	418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kin	5.20
	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	5.20
	428289	M26301	Hs.2253	Hs.2253:complement component 2	5.19
	409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	5.19
35	446051	BE048051	Hs.37054	Hs.37054:ephrin-A3	5.15
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	5.13
	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	5.11
	414639	X67055	Hs.76716	NM_002217:Homo sapiens pro-alpha (globul	5.09
	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	5.08
40	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	5.08
	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	5.07
	432575	AA553722	Hs.194346	Hs.194346:Spr-2 protein	5.07
	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	5.07
	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	5.06
45	422609	Z46023	Hs.118721	NM_000434:Homo sapiens sialidase 1 (lyso	5.06
	414381	AI086138	Hs.204044	Hs.204044:ESTs	5.04
	452940	AA029722	Hs.2173	NM_002033:Homo sapiens fucosyltransferas	5.03
	435849	BE305242	Hs.16098	Hs.16098:claudin 2	5.03
	411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	5.01
50	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	5.00
	406673	M34996	Hs.198253	Hs.198253:major histocompatibility compl	4.99
	415141	BE279383	Hs.26557	NM_007183:Homo sapiens plakophilin 3 (PK	4.99
	429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol G-	4.98
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, proper	4.98
55	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectorucleoside tr	4.98
	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	4.97
	419574	AK001989	Hs.91165	Hs.91165:hypothetical protein FLJ11127	4.97
	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	4.95
	431211	M86849	Hs.323733	Hs.323733:gap junction protein, beta 2,	4.95
60	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	4.93
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	4.93
	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	4.93
	431779	AW971178	Hs.268571	(locuslink)NM_001645:Homo sapiens apolip	4.92
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	4.91
65	414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	4.91
	422539	AJ009936	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.89
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	4.89
	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	4.89
	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	4.88
70	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	4.88
	434370	AF130988	Hs.58346	NM_022336:Homo sapiens ectodysplasin 1,	4.87
	413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (4.87
	405484				4.87
75	410639	BE269047	Hs.65234	(locuslink)NM_017895:Homo sapiens DEAD/H	4.87
	428953	AA305610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	4.86
	447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	4.83
	421462	AF016495	Hs.104624	NM_020980:Homo sapiens aquaporin 9 (AQP9	4.81
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	4.79
	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	4.79
80	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	4.79
	426761	AJ015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	4.78
	453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA: cDNA DKFZp4	4.77
	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	4.76
	424905	NM_002497	Hs.153704	NM_002497:Homo sapiens NIMA (never in mi	4.76

	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	4.75
	400529				4.75
	407233	X16354	Hs.50964	(locustlink)NM_001712:Homo sapiens carcin	4.75
5	447472	AW207347	Hs.211101	Hs.211101:ESTs	4.74
	447966	AA340605	Hs.105887	(locustlink)NM_145252:Homo sapiens simia	4.72
	439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	4.72
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	4.70
	405556				4.70
10	421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	4.70
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	4.70
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	4.70
	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	4.70
	423068	M25629	Hs.123107	NM_002257:Homo sapiens kallikrein 1, ren	4.65
15	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	4.64
	403739				4.61
	427490	Z95152	Hs.178696	NM_002754:Homo sapiens mitogen-activated	4.61
	426088	AF038007	Hs.166196	NM_005603:Homo sapiens ATPase, Class I,	4.61
	412723	AA648459	Hs.335951	Hs.335951:hypothetical protein AF301222	4.60
20	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysine	4.60
	447335	BE617696	Hs.286192	NM_032192:Homo sapiens protein phosphata	4.59
	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	4.59
	432150	AK000224	Hs.272789	NM_017716:Homo sapiens membrane-spanning	4.59
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	4.59
25	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	4.58
	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3)-glycoprote	4.57
	411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 6 (m	4.57
	408056	AA312329	Hs.42331	Hs.42331:aphrin-AA	4.55
	409964	AW368226	Hs.67928	Hs.67928:ESTs	4.54
30	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	4.54
	432407	AA221036		AF134164:Homo sapiens Human endogenous r	4.54
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	4.53
	409213	U61412	Hs.51133	NM_005975:Homo sapiens PTK6 protein tyro	4.53
	403219				4.53
35	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	4.52
	408194	AA601038	Hs.191797	Hs.191797:ESTs	4.52
	422237	M13149	Hs.1498	NM_000412:Homo sapiens histidine-rich gl	4.51
	456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	4.51
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomut	4.51
40	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	4.50
	406684	X16354	Hs.50964	(locustlink)NM_001712:Homo sapiens carcin	4.50
	439580	AF086401	Hs.293847	Hs.293847:ESTs	4.50
	411126	NM_001202	Hs.68879	(locustlink)NM_001202:Homo sapiens bone m	4.49
	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading tra	4.48
45	434263	N34895	Hs.79187	Hs.79187:coxsa-like virus and adenovirus	4.47
	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	4.47
	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	4.46
	452299	AW206330	Hs.355663	Hs.355663:ESTs	4.46
50	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	4.46
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EPN2)	4.46
	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	4.46
	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	4.45
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis	4.44
55	433662	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	4.44
	419559	Y07828	Hs.91096	NM_007028:Homo sapiens tripartite motif	4.44
	425860	L29339	Hs.1964	NM_000343:Homo sapiens solute carrier fa	4.43
	408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	4.43
	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	4.43
60	435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphata	4.42
	422867	L32137	Hs.1584	Hs.1584:cartilage oligomeric matrix prot	4.41
	431350	AI192528	Hs.164537	Hs.164537:ESTs	4.39
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	4.39
	412870	AW961017	Hs.6459	(locustlink)NM_024531:Homo sapiens hypoth	4.39
65	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	4.38
	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	4.38
	422293	X94453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synthet	4.38
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	4.38
	453082	H18835	Hs.31608	(locustlink)NM_017636:Homo sapiens transi	4.37
70	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	4.36
	432677	NM_004482	Hs.278611	NM_004482:Homo sapiens UDP-N-acetyl-alph	4.36
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	4.35
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	4.34
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (4.34
	424865	AF011333	Hs.153563	NM_002349:Homo sapiens lymphocyte antigen	4.34
75	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	4.33
	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	4.32
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	4.32
	417526	AA568906	Hs.82240	Hs.82240:syntaxin 3A	4.32
	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	4.31
80	436391	AJ227892	Hs.146274	Hs.146274:ESTs	4.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	4.29
	452017	AF109302	Hs.27495	Hs.27495:prostate cancer associated prot	4.29
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	4.29
	429638	AI916662	Hs.211577	(locustlink)NM_004986:Homo sapiens kinase	4.28

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5	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	4.29
	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	4.29
	443639	BE269042	Hs.9661	Hs.9661:proteasome (prosome, macropain)	4.28
	418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	4.27
	409636	AA305729	Hs.18272	(locuslink)NM_030674:Homo sapiens solute	4.27
10	408989	AW361666	Hs.49500	Hs.49500:KIAA0746 protein	4.27
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fi	4.27
	410199	AW377424	Hs.205126	Hs.205126:Homo sapiens cDNA: FLJ22667 fi	4.24
	431685	AW296135	Hs.267659	NM_006113:Homo sapiens vav 3 oncogene (V	4.24
	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (4.24
15	413278	BE563085	Hs.833	Hs.833:interferon-stimulated protein, 15	4.23
	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	4.23
	436856	AI469355	Hs.127310	(locuslink)NM_144624:Homo sapiens kinase	4.23
	456629	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	4.23
	426682	AV660038	Hs.2056	Hs.2056:UDP glycosyltransferase 1 family	4.23
20	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-like	4.22
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	4.22
	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	4.21
	435099	AC004770	Hs.4756	NM_004111:Homo sapiens flap structure-sp	4.21
	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	4.21
25	421585	U95626	Hs.302043	NM_003965:Homo sapiens chemokine (C-C mo	4.20
	420039	NM_004605	Hs.376147	Hs.376147:Homo sapiens cDNA FLJ39099 fis	4.20
	426427	M86699	Hs.169840	Hs.169840:TTK protein kinase	4.19
	425263	NM_001197	Hs.155419	NM_001197:Homo sapiens BCL2-interacting	4.19
	426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens cispla	4.19
30	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	4.19
	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	4.18
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antige	4.17
	431842	NM_005764	Hs.271473	Hs.271473:epithelial protein up-regulate	4.17
	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	4.17
35	404826				4.17
	414198	AW506308	Hs.75812	NM_004563:Homo sapiens phosphoenolpyruva	4.17
	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	4.17
	426378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	4.16
	433020	AI375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	4.16
40	420319	AW406289	Hs.96593	NM_019034:Homo sapiens ras homolog gene	4.15
	446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	4.15
	400130		Hs.155560	NM_001746:Homo sapiens calnexin (CANX)	4.14
	431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	4.14
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap	4.13
45	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	4.13
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	4.13
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	4.13
	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	4.12
	428471	X57348	Hs.184510	Hs.184510:stathmin	4.12
50	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	4.11
	424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	4.10
	400290	H18836	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	4.10
	409152	AA176585	Hs.194346	Hs.194346:Spir-2 protein	4.10
	427333	AF067797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	4.10
55	413835	AI272727	Hs.249163	NM_024306:Homo sapiens fatty acid hydrox	4.09
	444664	N26362	Hs.11615	NM_016086:Homo sapiens map kinase phosph	4.09
	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	4.09
	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	4.09
	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	4.08
60	421190	U95031	Hs.102482	Hs.102482:mucin 5, subtype B, tracheobro	4.08
	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	4.08
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuc	4.06
	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	4.06
	425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	4.06
65	443802	AW504924	Hs.9805	Hs.9805:exportin 5	4.04
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	4.04
	434808	AF155108	Hs.256150	Hs.256150:NY-REN-41 antigen	4.04
	428376	AF119665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	4.04
	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	4.02
70	436278	BE396290	Hs.5097	Hs.5097:synaptogyrin 2	4.02
	421910	NM_014586	Hs.109437	NM_014586:Homo sapiens hormonally upregu	4.02
	417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	4.02
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	4.01
	414561	AI064813	Hs.195155	Hs.195155:solute carrier family 38, memb	4.00
75	414812	X72755	Hs.77367	NM_002416:Homo sapiens monokine induced	4.00
	456362	AW973003	Hs.179909	(locuslink)NM_024831:Homo sapiens nuclea	3.99
	431958	X63629	Hs.2877	NM_001793:Homo sapiens cadherin 3, type	3.98
	418661	NM_001949	Hs.1189	NM_001949:Homo sapiens E2F transcription	3.98
	419092	J05581	Hs.89603	NM_002456:Homo sapiens mucin 1, transmem	3.98
80	414013	AA766605	Hs.47099	NM_024642:Homo sapiens hypothetical prot	3.98
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.97
	445873	AA250970	Hs.251946	Hs.251946:Homo sapiens cDNA FLJ11840 fis	3.96
	436485	X59135	Hs.156110	Hs.156110:immunoglobulin kappa constant	3.96
	422164	NM_014312	Hs.112377	Hs.112377:cortical thymocyte receptor (X	3.95
	437016	AU076916	Hs.5398	Hs.5398:guanine monophosphate synthetase	3.94
	449437	A702038	Hs.100057	Hs.100057:serine/threonine kinase 35	3.94
	446946	AI878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DN	3.94

	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.94
	443180	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN1	3.93
	418738	AW388633	Hs.6682	Hs.6682:solute carrier family 7, (cation	3.93
5	409463	AA58165	Hs.17295	NM_023930:Homo sapiens hypothetical prot	3.92
	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell d	3.92
	448093	AW977382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	3.91
	426598	AA852773	Hs.334838	Hs.334838:KJAA1856 protein	3.90
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433 fis	3.89
10	436827	H72187	Hs.356658	(locuslink)NM_005274:Homo sapiens guanine	3.89
	407971	AA69117	Hs.62918	Hs.62918:CDC91 cell division cycle 91-ii	3.89
	400750				3.89
	448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte acti	3.89
	413880	AI660842	Hs.110915	NM_021258:Homo sapiens Interleukin 22 re	3.89
15	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger prote	3.89
	428788	AF082283	Hs.193516	NM_003921:Homo sapiens B-cell CLL/lympho	3.88
	443044	N28522	Hs.8935	NM_014298:Homo sapiens quinolinate phosph	3.88
	413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	3.88
	417129	AI381800	Hs.300684	Hs.300684:calcitonin gene-related peptid	3.87
20	410268	AA316181	Hs.61635	NM_012449:Homo sapiens six transmembrane	3.87
	425047	U34038	Hs.154299	NM_005242:Homo sapiens coagulation facto	3.87
	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	3.86
	449667	AB023227	Hs.23860	Hs.23860:KJAA1010 protein	3.86
	400298	AA032279	Hs.61635	Hs.61635:slx transmembrane epithelial an	3.85
25	407770	AW607831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN1	3.85
	416313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L	3.85
	413380	AI904232	Hs.75323	Hs.75323:prohibitin	3.85
	452220	BE158006	Hs.212296	Hs.212296:ESTs	3.85
	413588	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine mono	3.85
30	433658	L03678	Hs.156110	Hs.156110:immunoglobulin kappa constant	3.84
	428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lik	3.84
	430237	AI272144	Hs.236522	Hs.236522:DKFZP434P108 protein	3.84
	414862	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	3.84
	437967	BE277414	Hs.5947	NM_005370:Homo sapiens mel transforming	3.84
35	427318	AF186081	Hs.175783	NM_014579:Homo sapiens solute carrier fa	3.83
	453308	AW578452		AW578452:RC1-CT0252-030100-023-b07 CT025	3.83
	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	3.83
	432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility comple	3.82
	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	3.82
40	426514	BE616633	Hs.170195	Hs.170195:bone morphogenetic protein 7 (3.82
	410315	AI638871	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	3.82
	421905	AI660247	Hs.32699	Hs.32699:Homo sapiens, Similar to RIKEN	3.81
	421481	AW391972	Hs.104696	Hs.104696:KJAA1324 protein	3.81
	445921	AW015211	Hs.153799	Hs.153799:Homo sapiens cDNA FLJ38333 fis	3.80
45	414368	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	3.80
	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisi	3.80
	413813	M96956	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	3.80
	414602	AW630088	Hs.76550	NM_052886:Homo sapiens mal, T-cell diffe	3.80
	410219	T98226	Hs.171952	Hs.171952:occludin	3.80
50	407137	T97307			3.78
	430462	AI584156	Hs.105640	Hs.105640:hypothetical protein BC007772	3.78
	432680	T47364	Hs.278613	(locuslink)NM_005532:Homo sapiens Intarf	3.78
	450010	AW293801	Hs.255052	Hs.255052:ESTs	3.78
	440334	BE276112	Hs.7165	NM_003904:Homo sapiens zinc finger prote	3.78
55	440876	NM_004987	Hs.112378	(locuslink)NM_004987:Homo sapiens LIM an	3.77
	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protel	3.77
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyrido	3.77
	426459	AF151812	Hs.169992	NM_015966:Homo sapiens serologically def	3.77
	443323	BE660621	Hs.9222	Hs.9222:estrogen receptor binding site a	3.76
60	406621	X57809	Hs.181125	Hs.181125:immunoglobulin lambda locus	3.76
	423188	M81933	Hs.1634	Hs.1634:cell division cycle 25A	3.76
	428206	AB020643	Hs.183006	Hs.183006:likely homolog of mouse hepari	3.75
	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.74
	425209	AL049761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	3.74
65	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	3.74
	418681	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	3.74
	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	3.74
	446291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	3.74
	435886	BE265839	Hs.12126	NM_018487:Homo sapiens hepatocellular ca	3.73
70	417286	AA122237	Hs.81874	NM_002413:Homo sapiens microsomal glutat	3.73
	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	3.73
	400419	AF084545		AF084545:Homo sapiens versican Vint Isof	3.73
	421357	AK000609	Hs.103808	NM_017896:Homo sapiens chromosome 20 ope	3.73
	420665	AW469240	Hs.371581	Hs.371581:ESTs	3.73
75	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	3.73
	452679	Z42387	Hs.83883	(locuslink)NM_020182:Homo sapiens transm	3.72
	419743	AW408762	Hs.5957	Hs.5957:Homo sapiens clone 24416 mRNA se	3.72
	435730	AB020635	Hs.4984	Hs.4984:KJAA0828 protein	3.72
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	3.72
80	444006	BE395085	Hs.334762	(locuslink)NM_032832:Homo sapiens hypoth	3.72
	442875	BE623003	Hs.23625	Hs.23625:Homo sapiens clone TCCCTA00142	3.71
	413431	AW246428	Hs.75355	NM_003348:Homo sapiens ubiquitin-confuga	3.71
	413950	AA249096	Hs.32793	Hs.32793:Homo sapiens cDNA FLJ31108 fis	3.71
	411125	AA151647	Hs.68877	Hs.68877:cytochrome b-245, alpha polypep	3.71

5	406722	H27498	Hs.293441	Hs.293441:Homo sapiens SNC73 protein (SN	3.71
	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu++ tran	3.71
	421038	AL080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.70
	409327	L41162	Hs.53563	NM_001853:Homo sapiens collagen, type IX	3.70
	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	3.70
10	400846				3.70
	415003	M11437	Hs.77741	Hs.77741:kininogen	3.70
	408137	AJ694131	Hs.29002	Hs.29002:KIAA1706 protein	3.70
	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	3.70
	413179	N99692	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenas	3.69
15	425843	BE313280	Hs.159627	NM_004632:Homo sapiens death associated	3.69
	432215	AU076609	Hs.2934	NM_001033:Homo sapiens ribonucleotide re	3.69
	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (i	3.69
	429344	R94038	Hs.374664	NM_005538:Homo sapiens inhibitor, beta C (3.69
	442315	AA173992	Hs.7956	Hs.7956:ESTs	3.68
20	452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	3.68
	401179				3.67
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	3.67
	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	3.67
	440086	NM_005402	Hs.6906	NM_005402:Homo sapiens v-rat simian leuk	3.66
25	409402	AF208234	Hs.695	Hs.695:cystatin B (stealin B)	3.66
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	3.66
	432633	AJ796390	Hs.210667	Hs.210667:ESTs	3.66
	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	3.66
	453857	AL080235	Hs.35861	Hs.35861:Ras-induced senescence 1	3.65
30	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	3.65
	430720	U85768	Hs.247838	NM_002991:Homo sapiens small inducible c	3.65
	432320	AW411066	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	3.64
	420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	3.64
	441128	AA570256	Hs.348504	Hs.348504:hypothetical protein BC014072	3.64
35	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	3.64
	411678	AI907114	Hs.71465	NM_003129:Homo sapiens squalene epoxidase	3.63
	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	3.62
	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	3.62
	452098	AI858183		BF755039:QV0-CT0583-181000-428-f07 CT058	3.62
40	430024	AI808780	Hs.227730	NM_000210:Homo sapiens integrin, alpha 6	3.62
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	3.61
	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	3.61
	400847				3.60
	406671	AA129547	Hs.285754	NM_000245:Homo sapiens met proto-oncogen	3.60
45	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	3.60
	404854				3.60
	400448				3.60
	453331	AJ240665	Hs.352537	Hs.352537:Homo sapiens cDNA FLJ31066 fis	3.60
	441406	Z45957	Hs.7837	Hs.7837:phosphoprotein regulated by mito	3.60
50	417389	BE260964	Hs.82045	Hs.82045:midkine (neurite growth-promoti	3.59
	419607	R52557	Hs.51579	NM_033416:Homo sapiens similar to HYPOTH	3.59
	447250	AI878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	3.59
	446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	3.59
	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	3.59
55	426722	U53823	Hs.171952	NM_002538:Homo sapiens occludin (OCLN),	3.58
	420531	AI652069	Hs.98614	NM_004587:Homo sapiens ribosome binding	3.58
	416933	BE561850	Hs.80506	NM_003090:Homo sapiens small nuclear rib	3.57
	447698	AI420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	3.57
	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	3.57
60	424241	AW995948	Hs.8364	Hs.8364:pyruvate dehydrogenase kinase, l	3.57
	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	3.57
	420614	AL110291	Hs.99364	Hs.99364:athylolase domain containing 1	3.56
	434224	AA380731	Hs.84	NM_002006:Homo sapiens interleukin 2 rec	3.56
	425322	U63630	Hs.155637	NM_006904:Homo sapiens protein kinase, D	3.56
65	438407	AI457122	Hs.129673	Hs.129673:eukaryotic translation initiat	3.56
	413859	AW992356	Hs.8364	Hs.8364:pyruvate dehydrogenase kinase, l	3.56
	427268	X78520	Hs.174139	NM_001829:Homo sapiens chloride channel	3.55
	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 ope	3.55
	411704	AI499220	Hs.71573	(locuslink)NM_017888:Homo sapiens hypoth	3.55
70	452700	AI859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	3.54
	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	3.54
	453323	AF034102	Hs.32951	NM_001532:Homo sapiens solute carrier fa	3.54
	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	3.54
	452488	N74921	Hs.184389	Hs.184389:ESTs, Moderately similar to S1	3.54
75	432268	BE311856	Hs.274230	Hs.274230:3'-phosphoadenosine 5'-phospho	3.54
	425811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha	3.53
	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	3.53
	421802	BE261458	Hs.108408	(locuslink)NM_016022:Homo sapiens CGI-78	3.53
	428582	BE336699	Hs.185055	Hs.185055:BENE protein	3.53
80	446147	AL133064	Hs.14051	(locuslink)NM_145698:Homo sapiens endoze	3.53
	408716	AI567839	Hs.151714	(locuslink)NM_033405:Homo sapiens peroxi	3.52
	450825	AC006954	Hs.25527	(locuslink)NM_014428:Homo sapiens light	3.52
	442007	AA301116	Hs.142838	NM_032390:Homo sapiens Mki67 (FHA domain	3.52
	453454	AW052506	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	3.52
	421642	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens SD6 an	3.51
	428371	AB012193	Hs.183874	NM_003589:Homo sapiens cullin 4A (CUL4A)	3.51
	421340	F07783	Hs.1369	NM_000574:Homo sapiens decay acceleratin	3.50

	429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inacti	3.50
	452862	AW378065	Hs.8687	Hs.8687:ESTs	3.50
	442993	BE018682	Hs.166196	Hs.166196:ATPase, Class I, type 8B, memb	3.50
	404240				3.50
5	424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	3.50
	429583	NM_006412	Hs.209119	NM_006412:Homo sapiens 1-acylglycerol-3-	3.50
	445937	AA52943	Hs.321231	(locuslink)NM_003779:Homo sapiens UDP-Ga	3.49
	424954	NM_000546	Hs.1846	NM_000546:Homo sapiens tumor protein p53	3.49
10	424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	3.49
	428028	US2112	Hs.182018	Hs.182018:interleukin-1 receptor-associa	3.49
	456534	X91195	Hs.100623	NM_138689:Homo sapiens protein phosphata	3.49
	424685	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	3.49
	419170	BE002798	Hs.287850	NM_002218:Homo sapiens integral membrane	3.49
15	439841	AF038961	Hs.87110	NM_004870:Homo sapiens mannosyl-P-dolicho	3.49
	428390	AI640377	Hs.350077	NM_000982:Homo sapiens ribosomal protein	3.48
	430589	AJ002744	Hs.246315	NM_017423:Homo sapiens UDP-N-acetyl-alph	3.48
	431183	NM_006855	Hs.250696	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	3.48
	422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, protein	3.48
20	457635	AV660976	Hs.3569	Hs.3569:chromosome 20 open reading frame	3.48
	419705	AW368634	Hs.154331	Hs.154331:ESTs	3.48
	454390	AB020713	Hs.56966	(locuslink)NM_024923:Homo sapiens hypoth	3.48
	402829				3.47
	451707	AW051061	Hs.60973	Hs.60973:Homo sapiens cDNA FLJ40829 fis,	3.47
25	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	3.47
	420085	AI741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	3.47
	437704	AA766142	Hs.131810	Hs.131810:Homo sapiens cDNA FLJ35976 fis	3.47
	439223	AW238299	Hs.250618	NM_025217:Homo sapiens UL16 binding prot	3.46
	452203	X57522	Hs.352018	NM_000593:Homo sapiens transporter 1, AT	3.46
30	450273	AW296454	Hs.24743	Hs.24743:hypothetical protein FLJ20171	3.46
	408089	H59799	Hs.42644	Hs.42644:thioredoxin-like 2	3.46
	446950	AA305800	Hs.5672	(locuslink)NM_030799:Homo sapiens golgi	3.46
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	3.45
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif-	3.45
35	433627	AF078866	Hs.284296	NM_033161:Homo sapiens surfeit 4 (SURF4)	3.45
	400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.45
	433570	AI580053	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC16	3.45
	410638	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.45
40	456950	AF111170	Hs.306165	Hs.306165:ESTs, Highly similar to unknown	3.44
	432391	AI732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	3.44
	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	3.44
	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	3.44
	458778	AW451034	Hs.326525	NM_001669:Homo sapiens arylsulfatase D (3.44
	425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenanc	3.44
45	448913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6),	3.44
	448847	AI587180	Hs.110906	Hs.110906:hypothetical protein BC004501	3.44
	420166	AW732276	Hs.95583	NM_012339:Homo sapiens transmembrane 4 s	3.44
	412420	AL035668	Hs.73853	NM_001200:Homo sapiens bone morphogeneti	3.43
	424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltag	3.43
50	414186	U33446	Hs.75799	Hs.75799:protease, serine, 8 (prolactin)	3.43
	422396	W21872	Hs.7907	(locuslink)NM_145059:Homo sapiens L-fuco	3.43
	428093	AW594506	Hs.104830	Hs.104830:ESTs	3.43
	428293	BE250944	Hs.183558	Hs.183558:solute carrier family 1 (neur	3.42
55	445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	3.42
	442821	BE391929	Hs.8752	Hs.8752:transmembrane protein 4	3.42
	427597	D15049	Hs.179770	NM_002842:Homo sapiens protein tyrosine	3.42
	427648	AI376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	3.41
	428734	BE303044	Hs.192023	NM_003757:Homo sapiens eukaryotic transl	3.41
	453902	BE502341	Hs.3402	NM_139177:Homo sapiens chromosome 17 ope	3.41
60	441565	AW953576	Hs.303125	Hs.303125:p53-Induced protein PIGPC1	3.41
	414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	3.41
	423323	AI951628	Hs.127007	NM_003740:Homo sapiens potassium channel	3.41
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	3.41
	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	3.40
	422256	M64673	Hs.1499	NM_005526:Homo sapiens heat shock transc	3.40
65	451129	BE072881		BE072881:RC2-BT0548-200300-012-e09 BT054	3.40
	400206		Hs.81848	NM_006265:Homo sapiens RAD21 homolog (S.	3.40
	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	3.39
	448440	AA173467	Hs.62402	Hs.62402:p21/Cdc42/Rac1-activated kinase	3.39
70	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	3.39
	417457	AA378907	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.39
	406363				3.39
	444758	AL044878	Hs.11899	NM_000859:Homo sapiens 3-hydroxy-3-methy	3.39
	423309	BE006775	Hs.126782	NM_014467:Homo sapiens sushi-repeat prot	3.38
75	426125	X87241	Hs.166994	Hs.166994:FAT tumor suppressor homolog 1	3.38
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	3.38
	419493	AF001212	Hs.90744	Hs.90744:proteasome (prosome, macropain)	3.38
	457670	AF119666	Hs.23449	NM_018842:Homo sapiens insulin receptor	3.38
	400125		Hs.125078	(locuslink)NM_004152:Homo sapiens ornith	3.38
80	429404	NM_005738	Hs.10706	NM_005738:Homo sapiens ADP-ribosylation	3.37
	410293	AK000047	Hs.61860	NM_018992:Homo sapiens hypothetical prot	3.37
	434826	AF155661	Hs.22265	Hs.22265:pyruvate dehydrogenase phosphat	3.37
	423599	AI805684	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	3.37
	427715	BE245274	Hs.180428	Hs.180428:QAAA1181 protein	3.37

5	446715	AI337735	Hs.173919	Hs.173919:ESTs, Weakly similar to neuron	3.36
	426788	U66615	Hs.172280	NM_003074:Homo sapiens SWI/SNF related,	3.36
	429747	M87507	Hs.2490	Hs.2490:caspase 1, apoptosis-related cys	3.36
	406698	X03068	Hs.73931	Hs.73931:major histocompatibility comple	3.36
	439778	AL109729	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.36
	418862	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	3.36
	421140	AA298741	Hs.102135	NM_006280:Homo sapiens signal sequence r	3.36
	451932	AA360954	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.36
10	449042	AW294985	Hs.30715	Hs.30715:potassium voltage-gated channel	3.36
	426746	J03626	Hs.2057	NM_000373:Homo sapiens uridine monophosp	3.36
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	3.35
	444734	NM_001360	Hs.11806	NM_001360:Homo sapiens 7-dehydrocholeste	3.35
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	3.35
	457329	AI634860	Hs.359682	(locuslink)NM_016442:Homo sapiens type 1	3.35
15	432169	Y00971	Hs.2910	NM_002765:Homo sapiens phosphoribosyl py	3.35
	412525	AA581439	Hs.152328	Hs.152328:ESTs	3.35
	416391	AI878927	Hs.79284	NM_002402:Homo sapiens mesoderm specific	3.35
	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	3.35
	432065	AA401039	Hs.2903	Hs.2903:protein phosphatase 4 (formerly	3.34
20	400262		Hs.75309	NM_001961:Homo sapiens eukaryotic transi	3.34
	423598	BE247600	Hs.377968	NM_020400:Homo sapiens G protein-coupled	3.34
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	3.34
	450506	NM_004460	Hs.418	(locuslink)NM_004460:Homo sapiens fibrob	3.34
	437296	AA350994	Hs.20281	Hs.20281:MAPK phosphatase-7	3.34
25	431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	3.34
	425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	3.34
	427349	AA360154	Hs.177415	(locuslink)NM_001997:Homo sapiens Finkel	3.34
	439246	AI498072	Hs.351474	Hs.351474:Homo sapiens cDNA FLJ30002 fis	3.34
	448775	AB025237	Hs.388	NM_002452:Homo sapiens nudix (nucleoside	3.34
30	407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	3.34
	445350	AF052112	Hs.12540	NM_006330:Homo sapiens lysophospholipase	3.34
	444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	3.34
	429574	BE268321	Hs.208912	Hs.208912:hypothetical protein MGC861	3.33
35	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.33
	415938	BE383507	Hs.78921	NM_003488:Homo sapiens A kinase (PRKA) a	3.33
	414271	AK000275	Hs.75871	(locuslink)NM_012408:Homo sapiens protel	3.33
	424394	BE277024	Hs.146381	Hs.146381:RNA binding motif protein, X c	3.33
	437186	AA338305	Hs.377816	Hs.377816:Homo sapiens cDNA FLJ36808 fis	3.32
40	430542	AJ557486	Hs.119122	Hs.119122:ribosomal protein L13a	3.32
	444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	3.32
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	3.32
	426158	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythro	3.32
	430393	BE185030	Hs.241305	(locuslink)NM_006470:Homo sapiens tripar	3.32
	402104				3.32
45	446520	AA128808	Hs.179902	(locuslink)NM_022109:Homo sapiens CDw92	3.32
	443425	AJ056776	Hs.133397	Hs.133397:ESTs	3.32
	414883	AA926960	Hs.348669	Hs.348669:CDK28 protein kinase 1	3.31
	413063	AL035737	Hs.75184	Hs.75184:chitinase 3-like 1 (cartilage g	3.31
50	451564	AJ076698	Hs.132760	(locuslink)NM_001467:Homo sapiens glucos	3.31
	437822	AW450485	Hs.4437	NM_000991:Homo sapiens ribosomal protein	3.31
	441866	BE464341	Hs.21201	Hs.21201:nectin 3	3.31
	438930	AW843633	Hs.343261	Hs.343261:histocompatibility (minor) 13	3.31
	422192	AA305159	Hs.113019	NM_015931:Homo sapiens tis485 (LOC51066)	3.31
55	446506	AI123118	Hs.15159	(locuslink)NM_016326:Homo sapiens chemok	3.31
	415323	BE269352	Hs.949	NM_000433:Homo sapiens neutrophil cytosol	3.31
	449644	AW960707	Hs.148324	Hs.148324:ESTs	3.31
	422611	AA158177	Hs.118722	(locuslink)NM_004480:Homo sapiens fucosy	3.31
	417640	D30857	Hs.82353	NM_006404:Homo sapiens protein C recepto	3.30
60	428157	AI738719	Hs.198427	NM_000189:Homo sapiens hexokinase 2 (HK2	3.30
	447321	AW271217	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.30
	450447	AF212223	Hs.25010	NM_018698:Homo sapiens hypothetical prot	3.30
	422691	NM_003365	Hs.119251	NM_003365:Homo sapiens ubiquinol-cytochr	3.30
	426375	AK000597	Hs.169549	NM_017893:Homo sapiens sema domain, immu	3.30
65	449230	BE613348	Hs.356392	Hs.356392:ESTs, Highly similar to S-phas	3.29
	424756	AW504657	Hs.152931	(locuslink)NM_002296:Homo sapiens lamin	3.29
	442772	AW503680	Hs.5957	Hs.5957:Homo sapiens clone 24416 mRNA se	3.29
	430281	AI878842	Hs.237924	NM_016016:Homo sapiens CGI-69 protein (L	3.29
	448163	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	3.29
70	420332	NM_001756	Hs.1305	NM_001756:Homo sapiens serine (or cystei	3.29
	417691	AJ076610	Hs.82399	NM_007357:Homo sapiens component of olig	3.29
	412926	AI879076	Hs.75061	Hs.75061:macrophage myristoylated alanin	3.28
	427308	D26067	Hs.174905	Hs.174905:KIAA0033 protein	3.28
	432026	AA524545	Hs.224630	Hs.224630:Homo sapiens cDNA FLJ33318 fis	3.28
75	449199	AI990122	Hs.196988	Hs.196988:ESTs	3.28
	442739	NM_007274	Hs.8679	(locuslink)NM_007274:Homo sapiens cytosol	3.28
	422051	AW327546	Hs.111024	(locuslink)NM_005984:Homo sapiens solute	3.28
	452714	AW770994	Hs.30340	Hs.30340:hypothetical protein KIAA1165	3.28
	431884	AA521246	Hs.210792	Hs.210792:Homo sapiens cDNA FLJ36691 fis	3.28
	402260				3.28
80	409686	AK000002	Hs.55879	(locuslink)NM_033450:Homo sapiens multidi	3.28
	409267	NM_012453	Hs.52515	NM_012453:Homo sapiens transducin (beta)	3.28
	447783	AF054178	Hs.19561	NM_005001:Homo sapiens NADH dehydrogenas	3.27
	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	3.27

	429571	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	3.27
	434521	NM_002267	Hs.3886	Hs.3886:karyopherin alpha 3 (importin al	3.27
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	3.27
5	445033	AV652402	Hs.72901	NM_078487:Homo sapiens cyclin-dependent	3.27
	448752	AA593867	Hs.300842	NM_024820:Homo sapiens KIAA1608 protein	3.26
	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymara	3.26
	440286	U29589	Hs.7138	NM_000740:Homo sapiens cholinergic recep	3.26
	413745	AW247252	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	3.26
	412338	AA151527	Hs.69485	(locuslink)NM_024661:Homo sapiens hypoth	3.26
10	426520	BE545684	Hs.343566	Hs.343566:KIAA0251 protein	3.26
	427640	AF058293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	3.26
	440943	AW082298	Hs.146161	NM_032331:Homo sapiens hypothetical prot	3.26
	425966	NM_001761	Hs.1973	NM_001761:Homo sapiens cyclin F (CCNF),	3.25
	416448	L13210	Hs.79339	NM_005567:Homo sapiens lectin, galactosi	3.25
15	449944	AF290512	Hs.58215	(locuslink)NM_033046:Homo sapiens rhotek	3.25
	424381	AA285249	Hs.146329	NM_007194:Homo sapiens CHK2 checkpoint h	3.25
	426784	U03749	Hs.172216	NM_001275:Homo sapiens chromogranin A (p	3.25
	420190	AI816209	Hs.95867	(locuslink)NM_024112:Homo sapiens chromo	3.25
	438085	R52518	Hs.7967	Hs.7967:ESTs, Weakly similar to extensin	3.24
20	419216	AIJ076718	Hs.164021	NM_002993:Homo sapiens small inducible c	3.24
	430154	AW583058	Hs.234726	NM_001085:Homo sapiens serine (or cystei	3.24
	458376	AB023179	Hs.9059	Hs.9059:KIAA0962 protein	3.24
	410800	AW575742	Hs.351676	Hs.351676:Homo sapiens cDNA FLJ25921 fis	3.24
25	420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mRNA, comple	3.24
	435640	AF220053	Hs.54960	NM_018468:Homo sapiens uncharacterized h	3.23
	427775	R28944	Hs.180777	Hs.180777:Homo sapiens mRNA; cDNA DKFZp5	3.23
	412600	L28824	Hs.74101	Hs.74101:spleen tyrosine kinase	3.23
	430250	NM_016929	Hs.283021	NM_016929:Homo sapiens chloride intracel	3.23
	432871	NM_016142	Hs.279617	Hs.279617:hydroxysteroid (17-beta) dehyd	3.23
30	432731	R31178	Hs.287820	Hs.287820:fibronectin 1	3.23
	410340	AW182833	Hs.112188	(locuslink)NM_021826:Homo sapiens hypoth	3.23
	410047	AI167810	Hs.379753	Hs.379753:Homo sapiens cDNA FLJ33176 fis	3.23
	430567	NM_003028	Hs.244542	Hs.244542:Homo sapiens cDNA FLJ38908 fis	3.23
	425907	AA365752	Hs.155965	Hs.155965:ESTs	3.23
35	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	3.22
	403912				3.22
	429782	NM_005754	Hs.220689	Hs.220689:Ras-GTPase-activating protein	3.22
	416178	AI808527	Hs.192822	NM_030949:Homo sapiens protein phosphata	3.22
40	445229	BE276013	Hs.343828	Hs.343828:Homo sapiens mRNA; cDNA DKFZp7	3.22
	422030	X51416	Hs.110849	(locuslink)NM_004451:Homo sapiens estrog	3.22
	409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	3.22
	411531	AB014511	Hs.70604	Hs.70604:ATPase, Class II, type 9A	3.22
	414820	AA371931	Hs.77422	Hs.77422:proteolipid protein 2 (colonic	3.22
45	450770	AA019924	Hs.28803	Hs.28803:ESTs	3.22
	433233	AB040927	Hs.301804	Hs.301804:KIAA1494 protein	3.22
	414172	AW954324	Hs.75790	(locuslink)NM_002642:Homo sapiens phosph	3.21
	428781	AF164799	Hs.193384	Hs.193384:putative 28 kDa protein	3.21
	432078	BE314877	Hs.24553	(locuslink)NM_022369:Homo sapiens hypoth	3.21
50	454358	AW792876	Hs.288936	NM_031420:Homo sapiens mitochondrial rib	3.21
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	3.21
	409132	AI224538	Hs.50732	NM_005399:Homo sapiens protein kinase, A	3.21
	400836				3.20
	420281	AI623693	Hs.323494	(locuslink)NM_017964:Homo sapiens hypoth	3.20
55	414343	AL036166	Hs.75914	NM_006815:Homo sapiens coated vesicle ma	3.20
	447096	BE539189	Hs.62112	(locuslink)NM_003457:Homo sapiens zinc f	3.20
	412276	BE262621	Hs.73798	Hs.73798:macrophage migration inhibitory	3.20
	425261	BE385089	Hs.355814	Hs.355814:Homo sapiens clone IMAGE:29333	3.20
	407738	N41744	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.20
	400845				3.20
60	407082	Z47055			3.20
	452012	AA307703	Hs.279766	(locuslink)NM_012310:Homo sapiens knesi	3.20
	403217				3.20
	414249	AI797994	Hs.279929	(locuslink)NM_017510:Homo sapiens gp25L2	3.19
65	431243	U46455	Hs.252189	NM_002999:Homo sapiens syndecan 4 (amphi	3.19
	417777	AI823763	Hs.7055	Hs.7055:Homo sapiens cDNA FLJ33420 fis,	3.19
	457274	AW674193	Hs.227152	NM_016391:Homo sapiens hypothetical prot	3.19
	445139	AB037848	Hs.12365	Hs.12365:synaptotagmin XIII	3.19
	430280	AA361258	Hs.237868	Hs.237868:Homo sapiens mRNA; cDNA DKFZp6	3.19
	422197	AW974265	Hs.111632	Hs.111632:Lsm3 protein	3.19
70	422938	NM_001809	Hs.1594	NM_001809:Homo sapiens centromere protel	3.18
	435575	AF213457	Hs.44234	NM_018965:Homo sapiens triggering recept	3.18
	449704	AK000733	Hs.23900	Hs.23900:Rac GTPase activating protein 1	3.18
	426925	NM_001196	Hs.172894	Hs.172894:G3H interacting domain death a	3.18
	414814	D14697	Hs.77393	(locuslink)NM_002004:Homo sapiens farnes	3.18
75	405387				3.18
	444108	R55784	Hs.140942	Hs.140942:Homo sapiens cDNA FLJ38396 fis	3.18
	424089	AL036662	Hs.144949	Hs.144949:ESTs	3.17
	414788	X78342	Hs.77313	Hs.77313:cyclin-dependent kinase (CDC2)	3.17
80	424927	AW973666	Hs.153850	Hs.153850:hypothetical protein C321D2.4	3.17
	451452	BE560065	Hs.26433	NM_001382:Homo sapiens dolichyl-phosphat	3.17
	426924	BE222542	Hs.128782	Hs.128782:Homo sapiens cDNA FLJ31512 fis	3.17
	447032	AK000310	Hs.171138	(locuslink)NM_017755:Homo sapiens hypoth	3.17
	410663	AA194952	Hs.36093	Hs.36093:Homo sapiens cDNA FLJ12885 fis,	3.17

5	415402	AA164687	Hs.177576	Hs.177576:mannosyl (alpha-1,3)-glycopro	3.17
	451032	W03692	Hs.323079	Hs.323079:Homo sapiens mRNA; cDNA DKFZp5	3.17
	412146	M92444	Hs.73722	Hs.73722:APEX nuclease (multifunctional	3.17
	417018	M16038	Hs.80887	Hs.80887:y-yes-1 Yamaguchi sarcoma viral	3.16
	425244	AK002127	Hs.155313	NM_022105:Homo sapiens death associated	3.16
10	417878	U90916	Hs.82845	Hs.82845:Homo sapiens cDNA: FLJ21930 fis	3.16
	426676	AW084791	Hs.133122	Hs.133122:hypothetical protein FLJ14524	3.16
	432728	NM_006979	Hs.278721	NM_006979:Homo sapiens HLA class II regi	3.16
	442643	U82756	Hs.374973	(locuslink)NM_004697:Homo sapiens PRP4 p	3.16
	418462	BE001596	Hs.85266	Hs.85266:integrin, beta 4	3.16
15	428922	Z97630	Hs.226117	NM_005318:Homo sapiens H1 histone family	3.16
	429556	AW139399	Hs.314807	Hs.314807:hypothetical protein MGC2555	3.15
	418127	BE243982	Hs.83532	(locuslink)NM_002389:Homo sapiens membra	3.15
	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	3.15
	435968	AW161481	Hs.111577	(locuslink)NM_030926:Homo sapiens Integr	3.15
20	414702	L22005	Hs.76932	NM_004359:Homo sapiens cell division cyc	3.15
	437672	AW748265	Hs.5741	NM_016230:Homo sapiens flavohemoprotein	3.15
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	3.14
	432710	AA609685	Hs.278672	NM_005898:Homo sapiens membrane componen	3.14
	407961	AW672939	Hs.41694	Hs.41694:origin recognition complex, sub	3.14
25	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-I	3.14
	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	3.14
	422282	AF019225	Hs.114309	(locuslink)NM_003661:Homo sapiens apolip	3.14
	450295	AI766732	Hs.210628	Hs.210628:ESTs	3.14
	413900	AW409747	Hs.75612	NM_006819:Homo sapiens stress-induced-ph	3.13
30	452695	AW780199	Hs.30327	NM_003668:Homo sapiens mitogen-activated	3.13
	407797	AK000524	Hs.39850	Hs.39850:uridine kinase-like 1	3.13
	412006	AW451618	Hs.290216	Hs.290216:ESTs	3.13
	424247	X14008	Hs.234734	NM_000239:Homo sapiens lysozyme (renal a	3.13
	447627	AF090922	Hs.152738	NM_016050:Homo sapiens mitochondrial rib	3.13
35	422753	AI928995	Hs.1575	Hs.1575:small nuclear ribonucleoprotein	3.12
	441321	H17182	Hs.7771	NM_007273:Homo sapiens repressor of estr	3.12
	411358	R47479	Hs.94761	Hs.94761:KIAA1691 protein	3.12
	438444	AI064707	Hs.301226	Hs.301226:Homo sapiens, clone IMAGE:3456	3.12
	424727	AW590378	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	3.12
40	435975	AL118990	Hs.373554	(locuslink)NM_130766:Homo sapiens alpha-	3.12
	426680	AA320160	Hs.171811	NM_001625:Homo sapiens adenylate kinase	3.12
	412326	R07566	Hs.73817	NM_002983:Homo sapiens small inducible c	3.12
	409220	BE243323	Hs.51233	(locuslink)NM_003842:Homo sapiens tumor	3.12
	428699	AW578252	Hs.190161	Hs.190161:LR8 protein	3.12
45	422675	BE018517	Hs.119140	NM_001970:Homo sapiens eukaryotic transl	3.12
	444301	AK000136	Hs.10760	NM_017680:Homo sapiens asporin (LRR clas	3.12
	409932	AI376750	Hs.57600	NM_001283:Homo sapiens adaptor-related p	3.12
	418152	L12711	Hs.89643	(locuslink)NM_001064:Homo sapiens transk	3.12
	410240	AL157424	Hs.61289	Hs.61289:synaptojanin 2	3.12
50	413073	AL038165	Hs.75187	NM_014765:Homo sapiens translocase of ou	3.11
	406865	AI025931	Hs.181357	Hs.181357:laminin receptor 1 (57kD, ribo	3.11
	405203				3.11
	441028	AI333660	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	3.11
	417211	T97617	Hs.269092	Hs.269092:ESTs	3.11
55	421684	BE281591	Hs.106768	NM_018120:Homo sapiens hypothetical prot	3.11
	429824	AA296363	Hs.121520	Hs.121520:Homo sapiens cDNA FLJ35792 fis	3.11
	426234	BE314534	Hs.168159	Hs.168159:bifunctional apoptosis regulat	3.11
	408805	H69912	Hs.48269	NM_003384:Homo sapiens vaccinia related	3.10
	417821	BE245149	Hs.82643	NM_002822:Homo sapiens protein tyrosine	3.10
60	416976	BE243985	Hs.80680	Hs.80680:major vault protein	3.10
	410013	AF067173	Hs.57904	Hs.57904:mago-nashi homolog, proliferati	3.10
	429597	NM_003816	Hs.2442	Hs.2442:a disintegrin and metalloprotein	3.10
	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.10
	429238	NM_002849	Hs.198288	NM_002849:Homo sapiens protein tyrosine	3.10
65	433409	AI278802	Hs.25561	Hs.25561:ESTs, Moderately similar to hyp	3.10
	426440	BE382756	Hs.169902	NM_006516:Homo sapiens solute carrier fa	3.10
	435472	AW972330	Hs.283022	NM_018643:Homo sapiens triggering recept	3.10
	427609	AK000436	Hs.179791	NM_017817:Homo sapiens RAB20, member RAS	3.10
	408201	AK000568	Hs.43654	NM_017882:Homo sapiens ceroid-lipofuscin	3.10
70	418181	U37012	Hs.83727	NM_013291:Homo sapiens cleavage and poly	3.10
	445176	AI878907	Hs.12379	NM_001419:Homo sapiens ELAV (embryonic l	3.10
	436906	H95980	Hs.181244	Hs.181244:major histocompatibility compl	3.10
	427337	Z46223	Hs.176663	NM_000569:Homo sapiens Fc fragment of Ig	3.10
	433435	BE545277	Hs.340959	NM_005726:Homo sapiens Ts translation el	3.09
75	408150	BE620274	Hs.43112	Hs.43112:Homo sapiens mRNA; cDNA DKFZp43	3.09
	431738	AW237726	Hs.288549	NM_032828:Homo sapiens ubiquitin UBF-4	3.09
	449703	H51001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	3.09
	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EFNA1)	3.09
	400278		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	3.09
80	449051	AW961400	Hs.333526	NM_032339:Homo sapiens hypothetical prot	3.09
	428297	AA236291	Hs.183583	NM_030666:Homo sapiens serine (or cystei	3.09
	430066	AI929659	Hs.237825	Hs.237825:signal recognition particle 72	3.09
	428044	AA083322	Hs.301404	NM_006743:Homo sapiens RNA binding motif	3.09
	426989	AI815206	Hs.100293	Hs.100293:O-linked N-acetylglucosamine (3.08
	447887	AA114050	Hs.211610	NM_001228:Homo sapiens caspase 8, apopto	3.08
	422010	AA302049	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	3.08
	444823	BE262989	Hs.12045	Hs.12045:C2f protein	3.08

	410668	BE379794	Hs.159651	NM_014452:Homo sapiens tumor necrosis fa	3.08
	415173	AW501735	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.08
	419757	AA773820	Hs.63970	Hs.63970:ESTs	3.08
5	427725	U68839	Hs.180533	NM_002756:Homo sapiens mitogen-activated	3.08
	424408	AI754813	Hs.146428	Hs.146428:collagen, type V, alpha 1	3.08
	453914	NM_000507	Hs.574	NM_000507:Homo sapiens fructose-1,6-bisph	3.08
	420187	AK001714	Hs.95744	NM_019028:Homo sapiens hypothetical prot	3.08
	431498	AK001777	Hs.258551	NM_012100:Homo sapiens aspartyl aminopep	3.07
10	411423	AW845987	Hs.68884	(locuslink)NM_139248:Homo sapiens membra	3.07
	449954	AA641636	Hs.37477	Hs.37477:ESTs, Weakly similar to T46220	3.07
	423671	AW860155	Hs.234101	Hs.234101:Homo sapiens, similar to choli	3.07
	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) proteinase	3.07
	451455	AI937227	Hs.8821	NM_021175:Homo sapiens hepcidin antimicr	3.07
15	450876	AF189062	Hs.285976	(locuslink)NM_013384:Homo sapiens LAG1 I	3.07
	432465	D56165	Hs.276163	NM_002512:Homo sapiens non-metastatic ce	3.07
	421808	AK000157	Hs.108502	NM_017688:Homo sapiens hypothetical prot	3.07
	430014	H59354	Hs.374303	(locuslink)NM_144691:Homo sapiens hypoth	3.07
	436553	AW407157	Hs.181125	Hs.181125:immunoglobulin lambda locus	3.08
	458814	AI498957	Hs.351937	Hs.351937:ribosomal protein, large P2	3.06
20	450247	AF123303	Hs.24713	NM_013386:Homo sapiens hypothetical prot	3.06
	418052	AW630656	Hs.83383	NM_005406:Homo sapiens peroxiredoxin 4 (3.06
	407223	H96850		H96850:yo03b12.s1 Soares melanocyte 2NbH	3.06
	418841	BE243136	Hs.86947	NM_001109:Homo sapiens a disintegrin and	3.06
25	450690	AA296696	Hs.333418	(locuslink)NM_014164:Homo sapiens FXD d	3.06
	408124	U89337	Hs.42853	NM_004381:Homo sapiens cAMP responsive e	3.06
	435550	AI224456	Hs.324507	Hs.324507:hypothetical protein FLJ20986	3.06
	421779	AI879159	Hs.108219	NM_004626:Homo sapiens wingless-type MMT	3.05
	440246	W52010	Hs.191379	Hs.191379:ESTs	3.05
30	446770	AV660309	Hs.154986	Hs.154986:ESTs, Weakly similar to PLLP_H	3.05
	440708	AF038962	Hs.7381	Hs.7381:voltage-dependent anion channel	3.05
	425118	AU076611	Hs.154672	Hs.154672:methylene tetrahydrofolate deh	3.05
	453830	AA534296	Hs.20953	Hs.20953:hypothetical protein BC010003	3.05
	412887	AU076861	Hs.74637	Hs.74637:testis enhanced gene transcript	3.05
35	422032	AA476966	Hs.110857	NM_016310:Homo sapiens polymerase (RNA)	3.05
	441238	AI372555	Hs.322456	NM_032039:Homo sapiens hypothetical prot	3.05
	408524	D87942	Hs.46328	Hs.46328:fucosyltransferase 2 (secretor	3.05
	408102	U46351	Hs.621	Hs.621:lectin, galactoside-binding, solu	3.05
	430508	AI015435	Hs.104637	Hs.104637:solute carrier family 1 (gluta	3.04
40	432281	AK001239	Hs.274263	Hs.274263:hypothetical protein FLJ10377	3.04
	443883	AA114212	Hs.9930	Hs.9930:serine (or cysteine) proteinase	3.04
	423570	AW838306	Hs.129819	NM_018344:Homo sapiens hypothetical prot	3.04
	443653	AA137043	Hs.9663	NM_013374:Homo sapiens programmed cell d	3.04
	451711	AK000461	Hs.26890	NM_017829:Homo sapiens cat eye syndrome	3.04
45	444736	AA533491	Hs.23317	NM_032824:Homo sapiens hypothetical prot	3.04
	407687	AK002011	Hs.37558	NM_018339:Homo sapiens hypothetical prot	3.04
	423022	AA320525	Hs.201076	Hs.201076:ESTs	3.04
	453450	AW797627	Hs.347459	Hs.347459:Homo sapiens cDNA FLJ13900 fis	3.04
50	412708	R26830	Hs.106137	Hs.106137:Homo sapiens mRNA for OKSW-CL	3.04
	448569	BE382657	Hs.21486	Hs.21486:signal transducer and activator	3.04
	443329	BE262943	Hs.9234	NM_032635:Homo sapiens seven transmembra	3.03
	439018	AW300887	Hs.26638	NM_031457:Homo sapiens membrane-spanning	3.03
	412627	BE391959	Hs.74276	Hs.74276:chloride intracellular channel	3.03
	444309	U83236	Hs.10803	Hs.10803:calcium and integrin binding 1	3.03
55	412969	AI373162	Hs.75103	NM_003406:Homo sapiens tyrosine 3-monoox	3.03
	430354	AA954810	Hs.239784	Hs.239784:scribble	3.03
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	3.03
	450607	AL050373	Hs.25213	NM_015677:Homo sapiens hypothetical prot	3.03
	421179	U72664	Hs.148495	NM_002810:Homo sapiens proteasome (proso	3.02
60	451798	BE297567	Hs.27047	Hs.27047:hypothetical protein FLJ20392	3.02
	428428	AL037544	Hs.184298	NM_001799:Homo sapiens cyclin-dependent	3.02
	447656	NM_003726	Hs.19126	NM_003726:Homo sapiens src family associ	3.02
	436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 264	3.02
	417896	AA379770	Hs.82890	Hs.82890:defender against cell death 1	3.02
65	444193	Y17801	Hs.10574	Hs.10574:solute carrier family 2, (facil	3.02
	418741	H83265	Hs.8881	Hs.8881:Homo sapiens cDNA FLJ32163 fis,	3.01
	414421	AI521130	Hs.355126	(locuslink)NM_144686:Homo sapiens hypoth	3.01
	424867	AI024860	Hs.153591	NM_005787:Homo sapiens Not56 (D. melanog	3.01
	442504	BE503373	Hs.334335	NM_022484:Homo sapiens hypothetical prot	3.01
70	437651	BE560672	Hs.13543	(locuslink)NM_145214:Homo sapiens tripar	3.01
	436540	BE397032	Hs.14468	NM_020230:Homo sapiens peter pan homolog	3.00
	438000	AI825880	Hs.5985	Hs.5985:non-kinase Cdc42 effector protai	3.00
	415697	AI365603	Hs.279696	Hs.279696:DKFZP5661024 protein	3.00
	437469	AW753112	Hs.15514	Hs.15514:hypothetical protein MGC3260	3.00
75	436319	H90727	Hs.5123	Hs.5123:hypothetical protein BC008246	3.00
	450126	BE018138	Hs.24447	(locuslink)NM_005866:Homo sapiens type I	3.00
	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	3.00
	406868	AA505445	Hs.300697	Hs.300697:immunoglobulin heavy constant	3.00
	424439	AA579635	Hs.1770	Hs.1770:Igase I, DNA, ATP-dependent	3.00
80	408452	AA054683	Hs.222728	Hs.222728:Homo sapiens cDNA FLJ39004 fis	3.00
	417831	H16423	Hs.82685	Hs.82685:CD47 antigen (Rb-related antige	3.00

TABLE 11B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	406685	0_0	M18728
	432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104
10			AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 A1732411 BG778834 BG283641 BE748279
			BE748870 BG319540 BE748864 BF739224 BG986165 AK057283 B1861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849
			AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 A1075321 L13823 AA216700 BF771864 AW861859
			BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928
			AW861687 AW821826 B1055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
15	459306	223120_4	AW578452
	452098	161393_1	BG028348 BF772844 H83066 AW817969 H90985 BF755039 A1858183
	451129	1495511_1	BE072881 A1762181 BE072946

TABLE 11C

20	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	NT_position:	Indicates nucleotide positions of predicted exons.

25	Pkey	Ref	Strand	NT_position
	406399	9256288	Minus	63448-63554
	403220	7630969	Plus	64338-64517
30	403218	7630969	Plus	58039-58149
	403221	7630969	Plus	66294-66438,66936-67124
	405484	5922025	Plus	199214-199579,199672-199920,200262-20049
	400529	9796988	Plus	138232-138423
	405556	1552511	Plus	163497-163623,164715-164968,165369-16550
35	403739	7630882	Plus	44563-44766,48209-48483,52255-52495
	403219	7630969	Plus	61858-61995
	404826	6572184	Plus	47726-48046
	400750	8119057	Plus	198991-199168,199316-199548
	400846	9188605	Plus	39310-39474
40	401179	9438647	Plus	113477-113893
	400847	9188605	Plus	44643-44835
	404854	7143420	Plus	14260-14537
	400448	9887687	Minus	177372-177674
	404240	5002624	Minus	118132-116407,116653-116922
45	402829	8918414	Plus	101532-101852,102006-102263
	406363	9256114	Plus	14403-14602,17000-17147,17241-17368
	402104	8119072	Plus	122409-122600
	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
50	400836	8954179	Plus	677-1188
	400845	9188605	Plus	34428-34612
	403217	7630969	Plus	54089-54163,55427-55623
	405387	6587915	Minus	3769-3833,5708-5895
55	405203	7230116	Plus	125295-125463

Table 12A lists about 1006 genes up-regulated in cervical cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" cervical cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" cervical cancer level was set to the 93rd percentile value amongst cervical cancers. The "average" normal adult tissue level was set to the 93rd percentile value amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 12A: 1006 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES

65	Pkey:	Unique Eos probeset identifier number
	ExAccon:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
70	R1:	Ratio of tumor to normal body tissue

	Pkey	ExAccon	UnigeneID	Unigene Title	R1
75	402075	U19557	Hs.123035	squamous cell carcinoma antigen 2 (SCCA2)	81.1
	425550	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	43.6
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial coll	38.9
	435094	A1680129	Hs.329062	EST	30.3
	439606	W79123	Hs.58561	G protein-coupled receptor 87	28.8
	452240	A1591147	Hs.61232	ESTs	27.0
80	444783	AK001468	Hs.62160	anillin (Drosophila Scraps homolog), actin bi	25.0
	417034	NM_006183	Hs.80962	neurolensin	25.5
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor, cl	24.5
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	23.7

5	435505	AF200492	Hs.211238	Interleukin-1 homolog 1	21.2
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	20.5
	418345	AJ001696	Hs.241407	serine proteinase inhibitor 13 (F113, serpin)	20.1
	452461	N78223	Hs.108106	transcription factor	19.8
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor, cl	19.2
	429432	AI678059	Hs.202676	synaptonemal complex protein 2	17.5
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-type,	16.4
	435243	AW292886	Hs.261373	hypothetical protein dJ434O14.3	16.3
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	16.2
10	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cys-X-C	15.9
	421373	AA808229	Hs.167771	ESTs	15.7
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolo	15.4
	441459	AI919142	Hs.214233	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	14.6
	447164	AF026941	Hs.17518	Homo sapiens c1g5 mRNA, partial sequence	13.8
15	412719	AW016610	Hs.129911	ESTs	13.4
	417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	13.3
	431753	X76029	Hs.2841	neuromedin U	13.2
	438817	AI023799	Hs.163242	ESTs	13.1
	404996			Target Exon	13.1
20	443211	AI128388	Hs.143655	ESTs	12.9
	414764	AW013887	Hs.72047	ESTs	12.9
	428618	AA885360	Hs.160199	Target CAT	12.7
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	12.7
25	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribosomal	12.6
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	12.6
	432666	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein produ	12.6
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaphyseal	12.6
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin D 24	12.3
30	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	12.2
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	11.6
	415989	AI267700	Hs.317584	ESTs	11.5
	452838	U65011	Hs.30743	preferentially expressed antigen in melanoma	11.4
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	11.3
35	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas	11.0
	449260	AA741180	Hs.29879	ESTs	11.0
	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN HOMEOB	10.7
	406467			Target Exon	10.5
	439926	AW014875	Hs.137007	ESTs	10.2
40	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin 1, pr	10.2
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fls, clone HEMBA10	10.2
	414422	AA147224	Hs.337232	Homeo box A13	10.2
	442660	AW138174	Hs.130651	ESTs	10.1
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu or sig	10.0
45	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN ALU SU	9.9
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDNA clo	9.8
	400195	NM_007057		NM_007057: Homo sapiens ZW10 Interactor (ZW1N	9.8
	422426	W79117	Hs.58559	ESTs	9.7
	447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypothetical p	9.7
50	458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN ALU SU	9.4
	455601	AI368880	Hs.816	SRY (sex determining region Y)-box 2	9.4
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR/MRP)	9.4
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothetical p	9.4
	419247	S65791	Hs.89764	fragile X mental retardation 1	9.1
55	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fls, clone NT2RP40	9.1
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	9.0
	428845	AL157579	Hs.163610	KIAA0751 gene product	9.0
	426427	M86699	Hs.169840	TTK protein kinase	9.0
60	429538	BE182592	Hs.11261	small proline-rich protein 2A	9.0
	446232	AI281848	Hs.194691	retinoic acid induced 3	8.9
	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	8.9
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDNA clo	8.9
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase	8.9
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	8.9
65	430486	BE062109	Hs.241551	chloride channel, calcium activated, family m	8.7
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, h	8.7
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	8.7
	407642	AW178963		gb:MR0-ST0032-200899-001-b11 ST0032 Homo sapi	8.7
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily, m	8.7
70	458027	L49054	Hs.85195	myeloid leukemia factor 1	8.4
	424086	AI351010	Hs.102267	lysyl oxidase	8.3
	420092	AA814043	Hs.88045	ESTs	8.3
	449034	AI624049		gb:ts41a09.x1 NCL CGAP_U11 Homo sapiens cDNA	8.3
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human, odont	8.2
75	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	8.2
	436279	AW900372	Hs.180793	ESTs, Weakly similar to S65657 alpha-1C-adren	8.2
	440634	AA907027	Hs.128606	ESTs	8.2
	452724	R84810	Hs.30464	cyclin E2	8.1
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (from c	8.1
80	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leucine h	8.0
	429228	AI553633	Hs.337139	ESTs	7.9
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome region 14	7.9
	425710	AF030880	Hs.159275	solute carrier family, member 4	7.8
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	7.8

	435159	AA668879	Hs.116649	ESTs	7.7
	439232	N48590	Hs.46693	ESTs	7.7
	437616	AI797163	Hs.207954	ESTs	7.6
	406554			Target Exon	7.4
5	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	7.4
	424098	AF077374	Hs.139322	small proline-rich protein 3	7.3
	418134	AA397769	Hs.86617	ESTs	7.2
	446364	AB006624	Hs.14912	KIAA0286 protein	7.2
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (yeast	7.1
10	414148	BE084049		gb:PM0-BT0651-270400-003-02 BT0651 Homo sapi	7.0
	429548	AW138872	Hs.135288	ESTs	7.0
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	7.0
	450192	AA263143	Hs.24596	RAD51-interacting protein	7.0
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophila ho	6.9
15	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone COL0454	6.9
	427821	AA470158	Hs.98202	ESTs	6.9
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794 prote	6.9
	425761	AW664214	Hs.196729	ESTs	6.9
	450028	AI912012	Hs.200737	ESTs	6.8
20	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated protein N	6.8
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane glyco	6.8
	413573	AI733859	Hs.149089	ESTs	6.8
	422330	D30783	Hs.115263	epiregulin	6.8
	454988	AW850140		gb:IL3-CT0219-261099-023-D11 CT0219 Homo sapi	6.8
25	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010317E2	6.8
	403471			Target Exon	6.7
	409041	AB033025	Hs.50081	KIAA1199 protein	6.7
	407839	AA045144	Hs.161566	ESTs	6.6
	415652	T79213	Hs.272073	ESTs	6.6
30	420900	AL045633	Hs.44269	ESTs	6.6
	444271	AW452569	Hs.149804	ESTs	6.6
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	6.5
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.5
	431622	AW979271	Hs.293184	ESTs	6.5
35	457405	AA504860		gb:ab03a10.s1 Stratagene fetal retina 937202	6.4
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT2RP20	6.4
	414812	X72755	Hs.77357	monokine induced by gamma interferon	6.4
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxygenase	6.3
	446435	AW206737	Hs.253582	ESTs	6.3
40	421948	L42583	Hs.334309	keratin 6A	6.3
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	6.3
	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-protein	6.2
	406747	AI925153	Hs.217493	annexin A2	6.2
	453884	AA355925	Hs.36232	KIAA0186 gene product	6.2
45	423735	AA330259		gb:EST33963 Embryo, 12 week II Homo sapiens c	6.2
	421773	W69233	Hs.112457	ESTs	6.2
	457435	AW972024	Hs.142653	ret finger protein	6.1
	450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HEMBB10	6.1
	427043	AA397679	Hs.3991	ESTs	6.1
50	409723	AW885757	Hs.257862	ESTs	6.1
	459462	AA481396	Hs.105167	ESTs	6.1
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif,	6.0
	427217	AA395272	Hs.144341	ESTs	6.0
	441820	AA969119	Hs.143502	ESTs, Weakly similar to envelope protein [Hs	6.0
55	437958	BE139550	Hs.121688	ESTs, Moderately similar to PC4259 ferritin a	6.0
	430791	AA486293	Hs.272068	ESTs, Weakly similar to ALU3_HUMAN ALU SUBFAM	5.9
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein [Hs	5.9
	413385	M34455	Hs.840	indoleamine-pyrole 2,3 dioxygenase	5.9
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced prote	5.9
60	414299	AA142989	Hs.71730	ESTs	5.8
	439292	AA090421	Hs.5555	hypothetical protein MGC5347	5.8
	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin (140	5.8
	413625	AW451103	Hs.71371	ESTs	5.8
	416049	AI970536	Hs.16603	hypothetical protein FLJ13163	5.8
65	415064	AA159804	Hs.149305	hypothetical protein MGC2603	5.7
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-receptor ty	5.7
	451381	BE241831	Hs.172330	hypothetical protein MGC2705	5.7
	415900	Z43758	Hs.26037	ESTs	5.7
	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.7
70	449611	AI970394	Hs.197075	ESTs	5.7
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo sapi	5.7
	438639	AI278360	Hs.31409	ESTs	5.7
	414972	BE263782	Hs.77695	KIAA0008 gene product	5.7
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-like 1	5.6
75	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone COL0042	5.6
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	5.6
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	5.5
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase 3)	5.5
80	451307	AW293207	Hs.211516	ESTs	5.5
	441531	AW291239	Hs.271111	ESTs	5.5
	418663	AK001100	Hs.41690	desmocollin 3	5.5
	410659	AI080175	Hs.68826	ESTs	5.5
	432869	AW974094		gb:EST386197 MAGE resequences, MAGN Homo sapi	5.5

5	431255	AA497043	Hs.115685	ESTs	5.5
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequen	5.5
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	5.4
	418502	R99288	Hs.35152	ESTs	5.4
	440320	AA878294		gb:ncw86e09.s1 NCI_CGAP_Pr12 Homo sapiens cDNA	5.4
10	439579	AF088400		gb:Homo sapiens full length insert cDNA clone	5.4
	420783	AI559838	Hs.99923	lectin, galactoside-binding, soluble, 7 (gate	5.4
	408536	AW381532	Hs.135188	ESTs	5.4
	408758	NM_003686	Hs.47504	exonuclease 1	5.4
	451411	AA017492	Hs.135655	EST	5.4
15	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	5.3
	407853	AA336797	Hs.40499	dickkopf (Xenopus laevis) homolog 1	5.3
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabknesin 6)	5.2
	420026	AI831190	Hs.166676	ESTs	5.2
	427356	AW023482	Hs.97849	ESTs	5.2
20	420440	NM_002407	Hs.97644	mammaglobin 2	5.2
	430082	AW514083	Hs.190135	ESTs	5.2
	445259	AI798994	Hs.152923	ESTs	5.2
	457345	AI699933	Hs.192175	ESTs	5.2
	453161	AA628608	Hs.61656	ESTs	5.2
25	445019	AI205540	Hs.281295	ESTs	5.2
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	5.2
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAPI_HUMAN DEATH-ASSO	5.2
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	5.2
	443179	AI928402	Hs.6933	hypothetical protein FLJ12684	5.2
30	432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, choline, al	5.2
	441020	W79283	Hs.35962	ESTs	5.1
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 gene	5.1
	419520	AB009303	Hs.90800	matrix metalloproteinase 16 (membrane-inserte	5.1
	430563	AA481269	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP)	5.1
35	405547			NM_018833:Homo sapiens transporter 2, ATP-bi	5.1
	435206	AI432364	Hs.160594	ESTs	5.1
	408269	AA576953	Hs.22972	hypothetical protein FLJ13352	5.1
	439223	AW238299	Hs.250618	UL16 binding protein 2	5.1
	413251	AI932903	Hs.211535	ESTs	5.1
40	426320	W47595	Hs.169300	transforming growth factor, beta 2	5.1
	458829	AI557388		gb:PT2.1_6_G03.r.tumor2 Homo sapiens cDNA 3'	5.0
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PR	5.0
	432473	AI202703	Hs.152414	ESTs	5.0
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino acid	5.0
45	423634	AW659908	Hs.1690	heparin-binding growth factor binding protein	5.0
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, protein-gl	5.0
	432867	AW016936	Hs.233364	ESTs	5.0
	449448	D60730	Hs.57471	ESTs	5.0
	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (from c	4.9
50	405657			C7000246:glj72477[pirj]DVHY1C multidrug resis	4.9
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromosomes 1	4.9
	446704	AI337228	Hs.197083	ESTs	4.9
	434376	AA631492	Hs.23921	hypothetical protein DKFZp547A023	4.9
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypothetic	4.9
55	421155	H87879	Hs.102267	lysyl oxidase	4.9
	443335	T89697	Hs.16645	ESTs	4.9
	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell growt	4.8
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-induc	4.8
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage elast	4.8
60	441720	AI348487	Hs.28739	ESTs	4.8
	442980	AA857025	Hs.8878	kinesin-like 1	4.8
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12	4.8
	417592	AA204664	Hs.182437	ESTs, Weakly similar to I54383 chromosome seg	4.8
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosyltran	4.8
65	418939	AW630803	Hs.89497	lamin B1	4.7
	417235	AA810278	Hs.24250	ESTs	4.7
	411958	AA099020		gb:zn45h01.s1 Stratagene HeLa cell s3 937216	4.7
	433858	N69243	Hs.192974	hypothetical protein FLJ12735	4.7
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	4.7
70	418379	AA218940	Hs.137516	figetin-like 1	4.7
	401747			Homo sapiens keratin 17 (KRT17)	4.7
	439769	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDNA clo	4.7
	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	4.7
	457465	AW301344	Hs.122908	DNA replication factor	4.6
75	433159	AB035898	Hs.150587	kinesin-like protein 2	4.6
	412333	AW937485		gb:QV3-DT0044-221299-045-b09 DT0044 Homo sapi	4.6
	401137			Target Exon	4.6
	401575			Target Exon	4.6
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone COL0667	4.6
80	421978	AJ243662	Hs.110196	NICE-1 protein	4.6
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	4.6
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PLACE10	4.6
	450510	AA010056	Hs.242998	ESTs	4.6
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	4.6
	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, type II	4.6
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino acid	4.5
	449416	AI651016	Hs.246311	ESTs	4.5

	416168	H23687		gb:yn72d12.r1 Soares adult brain N2b5HB55Y Ho	4.5
	447033	AI357412	Hs.157601	ESTs	4.5
	446353	AI290919	Hs.153661	ESTs	4.5
	443715	AI583187	Hs.9700	cyclin E1	4.5
5	454707	AW814989		gb:MR1-ST0206-170400-024-p05 ST0206 Homo sapi	4.5
	435435	T89473	Hs.192328	ESTs	4.5
	412099	U64198	Hs.73165	interleukin 12 receptor, beta 2	4.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma c	4.4
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	4.4
10	430919	AA489041	Hs.295448	ESTs	4.4
	435313	AI769400	Hs.189729	ESTs	4.4
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	4.4
	433322	H50621	Hs.134156	ESTs, Weakly similar to I38022 hypothetical p	4.4
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (p150)	4.4
15	408908	BE296227	Hs.250822	serine/threonine kinase 15	4.4
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated protein ho	4.4
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	4.4
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibitor, cl	4.4
	418216	AA862240	Hs.283099	AF15q14 protein	4.4
20	446252	AI283125	Hs.150009	ESTs	4.4
	447519	U46258	Hs.339665	ESTs	4.4
	425916	NM_006786	Hs.162200	urotensin 2	4.3
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalinin (10	4.3
	416320	H47867	Hs.34024	ESTs	4.3
25	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth facto	4.3
	441582	BE550200	Hs.127197	ESTs	4.3
	414132	AI801235	Hs.48480	ESTs	4.3
	424012	AW368377	Hs.137559	tumor protein 63 kDa with strong homology to	4.3
	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (RHAMM)	4.3
30	433330	AW207084	Hs.132816	hypothetical protein MGC14801	4.3
	428613	AB037749	Hs.186928	KIAA1328 protein	4.3
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter tra	4.3
	447078	AW885727	Hs.301570	ESTs	4.3
35	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEMBB10	4.3
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	4.3
	405708			Target Exon	4.3
	433405	AW157566	Hs.156892	ESTs	4.3
	456443	AW967500	Hs.133543	ESTs	4.3
40	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	4.2
	448621	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	4.2
	412608	AA247995	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequence	4.2
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.2
	455365	AW948343		gb:RC0-MT0015-130400-031-c01 MT0015 Homo sapi	4.2
45	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypothetical p	4.2
	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypothetical p	4.2
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	4.2
	427666	AI791495	Hs.180142	calmodulin-like skin protein	4.2
	444602	AI174456	Hs.271925	ESTs, Moderately similar to I38022 hypothetic	4.2
50	417791	AW985339	Hs.111471	ESTs	4.2
	444266	AI424984	Hs.125465	ESTs	4.2
	439394	AA149250	Hs.56105	ESTs	4.2
	457336	AW969657	Hs.291029	ESTs	4.2
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypothetical p	4.2
55	404440			NM_021048:Homo sapiens melanoma antigen, fami	4.2
	449228	AJ403107	Hs.148590	protein related with psoriasis	4.2
	437144	AL049466	Hs.7859	ESTs	4.2
	448599	AW860912		gb:QV0-CT0387-170200-121-c05 CT0387 Homo sapi	4.2
	431810	X67155	Hs.270845	kinesin-like 5 (mitotic kinesin-like protein	4.2
60	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.2
	444361	W76027	Hs.23920	hypothetical protein FLJ11105	4.2
	458116	AW977549	Hs.47367	KIAA1785 protein	4.1
	444105	AW189097	Hs.166597	ESTs	4.1
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	4.1
65	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor, cl	4.1
	408096	BE250162	Hs.83765	dihydrofolate reductase	4.1
	457620	AA602711	Hs.336753	EST	4.1
	402048			Target Exon	4.1
	427025	AA397589	Hs.97623	ESTs	4.1
70	423515	AA327017	Hs.162204	ESTs	4.1
	423891	AK002042	Hs.134795	Homo sapiens cDNA FLJ11180 fis, clone PLACE10	4.1
	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo sapi	4.1
	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	4.1
	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	4.1
	423738	AB002134	Hs.132195	airway trypsin-like protease	4.1
75	448243	AW369771	Hs.52620	Integrin, beta 8	4.1
	411559	BE144081		gb:MR0-HT0165-030200-007-d06 HT0165 Homo sapi	4.1
	423553	AA405635	Hs.96854	ESTs, Weakly similar to DYLYX_HUMAN CYTOPLASMI	4.1
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	4.1
80	424115	AA335497	Hs.293965	ESTs, Weakly similar to I38022 hypothetical p	4.1
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PLACE10	4.1
	424745	AA214618	Hs.152759	activator of S phase kinase	4.0
	433384	AI021892	Hs.124244	ESTs	4.0
	448995	AI613276	Hs.5662	guanine nucleotide binding protein (G protein	4.0

	448504	AI858128	Hs.171136	ESTs	4.0
	432009	AL137424	Hs.306458	Homo sapiens mRNA; cDNA DKFZp761G2123 (from c	4.0
	432441	AW292425	Hs.163484	ESTs	4.0
5	424794	M85646	Hs.210696	ESTs	4.0
	432184	AW971125		gb:EST383212 MAGE resequences, MAGL Homo sapi	4.0
	408321	AW405882	Hs.44205	coristatin	4.0
	417801	AA417383	Hs.82582	Integrin, beta-like 1 (with EGF-like repeat d	4.0
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.0
10	447724	AW298375	Hs.24477	ESTs	4.0
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y79AA10	4.0
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.0
	420252	AW270404	Hs.193161	ESTs	4.0
	412811	H05382	Hs.21400	ESTs	4.0
15	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA10	4.0
	438390	AI422017		gb:tf45f12.x1 NCL CGAP_Brn23 Homo sapiens cDN	4.0
	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	4.0
	429900	AA460421	Hs.30875	ESTs	4.0
	421270	H56037	Hs.108146	ESTs	3.9
20	430733	AW975920	Hs.283361	ESTs	3.9
	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo sapi	3.9
	424131	AA335714	Hs.199665	ESTs	3.9
	457059	BE561665	Hs.177677	exosome component Rrp40	3.9
	424717	H03754	Hs.152213	wingless-type MMTV integration site family, m	3.9
25	404959			NM_025001*-Homo sapiens hypothetical protein	3.9
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	3.9
	428536	AI143139	Hs.2288	visinin-like 1	3.9
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H.sapi	3.9
	423757	AF113013	Hs.278919	PRO0806 protein	3.9
30	418686	Z36830	Hs.87268	annexin A8	3.9
	437845	AA769678	Hs.90488	ESTs	3.9
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein produ	3.9
	415312	AA831850	Hs.58149	hypothetical protein MGC14136	3.9
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), pro	3.9
35	410553	AW016824	Hs.255527	hypothetical protein MGC14128	3.9
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.9
	438014	N71183	Hs.121806	Homo sapiens cDNA FLJ11971 fis, clone HEMBB10	3.9
	442163	AI791749	Hs.128896	ESTs	3.9
	438656	H85310	Hs.209456	ESTs, Weakly similar to NG22 [H.sapiens]	3.9
40	406560			ENSP00000016943*-C/DNA	3.8
	407395	AF005082		gb:Homo sapiens skin-specific protein (xp33)	3.8
	404132			Target Exon	3.8
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	3.8
	439238	N47305	Hs.46668	ESTs	3.8
45	433289	AF005258		gb:Homo sapiens laminin alpha 3b chain mRNA,	3.8
	436149	AI764308	Hs.159452	ESTs	3.8
	446292	AF081497	Hs.279682	Rh type C glycoprotein	3.8
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-bind)	3.8
	405545			(MDR/TAP) (TAP2)	3.8
50	442876	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequence	3.8
	409687	T61125	Hs.8493	ESTs	3.8
	407291	AA001464		gb:z45b01.r1 Soares retina N2b4HR Homo sapie	3.8
	415532	R14780	Hs.12826	ESTs	3.8
	402047	AK001921	Hs.169575	hypothetical protein MGC2550	3.8
55	415317	Z43388		gb:HSC1AF121 normalized infant brain cDNA Hom	3.8
	438777	AA825487	Hs.142179	ESTs	3.8
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.7
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolysis bu	3.7
	405943			Target Exon	3.7
60	430686	NM_001942	Hs.2633	desmoglein 1	3.7
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone HEP024	3.7
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	3.7
	418582	BE244318	Hs.213194	hypothetical protein MGC10895	3.7
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	3.7
65	433849	BE465884	Hs.280728	ESTs	3.7
	449592	AI655494	Hs.195718	ESTs	3.7
	453028	AB006532	Hs.31442	RecQ protein-like 4	3.7
	435612	AA693537	Hs.321411	ESTs	3.7
	417742	R64719		gb:EST22d11 WATM1 Homo sapiens cDNA clone 22d	3.7
70	418735	N48769	Hs.44609	ESTs	3.7
	444707	AI188613	Hs.41690	desmocollin 3	3.7
	421508	NM_004833	Hs.105115	absent in melanoma 2	3.7
	450613	AI702055		gb:tt20g10.x1 NCL CGAP_UI1 Homo sapiens cDNA	3.7
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	3.7
75	432837	AA310693	Hs.87329	HSPC072 protein	3.7
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN ALU SU	3.7
	423441	R68649	Hs.278359	absent in melanoma 1 like	3.7
	449978	AI806335	Hs.200829	ESTs, Weakly similar to T30171 nheln - mouse	3.7
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo sapi	3.7
80	409582	R27430	Hs.271565	ESTs	3.6
	428182	BE386042	Hs.283317	ESTs, Weakly similar to GGC1_HUMAN G ANTIGEN	3.6
	458446	AW394104	Hs.43744	ESTs, Moderately similar to I54374 gene NF2 p	3.6
	433040	H70423	Hs.300511	ESTs	3.6
	452193	AA987351	Hs.184993	ESTs	3.6

5	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed-rect	3.6
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.6
	459575	BE080825		gb:QV1-BT0631-180200-078-c08 BT0631 Homo sapi	3.6
	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	3.6
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	3.6
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	3.6
	427131	AA448460	Hs.112017	GE36 gene	3.6
	413278	BE563085	Hs.833	Interferon-stimulated protein, 15 kDa	3.6
10	420373	AW968228		gb:EST380198 MAGE resequences, MAGJ Homo sapi	3.6
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromosomes 2	3.6
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.6
	424639	AI917494	Hs.9812	Homo sapiens cDNA FLJ14388 fis, clone HEMBA10	3.6
	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	3.6
15	434321	AA629368		gb:zu78a11.s1 Soares_testis_NHT Homo sapiens	3.6
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic prot	3.6
	427335	AA448542	Hs.251677	G antigen 7B	3.6
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity	3.6
	408000	L11690	Hs.620	bulbous pemphigoid antigen 1 (230/240kD)	3.6
20	426749	AI823718	Hs.105618	ESTs	3.6
	443899	AW842283	Hs.79933	cyclin I	3.6
	440684	AI253123	Hs.127356	ESTs, Highly similar to S21424 nestin [H.sapi	3.6
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	3.6
	408591	AF015224	Hs.46452	mammaglobin 1	3.5
25	408867	AA437199	Hs.656	cell division cycle 25C	3.5
	428508	BE252383	Hs.184668	SBB31 protein	3.5
	431120	AA492588		gb:mg99c08.s1 NCL_CGAP_Thy1 Homo sapiens cDNA	3.5
	401780			NM_005557*:Homo sapiens keratin 16 (focal non	3.5
	409695	AA296961		gb:EST112514 Adrenal gland tumor Homo sapiens	3.5
30	456671	AB011142	Hs.114293	KIAA0570 gene product	3.5
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP10 (HT	3.5
	435244	N77221	Hs.187824	ESTs	3.5
	436246	AW450963	Hs.119991	ESTs	3.5
	431917	D16181	Hs.2868	peripheral myelin protein 2	3.5
35	443113	AI040586	Hs.132908	ESTs	3.5
	443341	AW631480	Hs.8688	ESTs	3.5
	407766	AA116021	Hs.38260	ubiquitin specific protease 18	3.5
	418347	AA216419		gb:nc16e03.s1 NCL_CGAP_Pr1 Homo sapiens cDNA	3.5
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo sapi	3.5
40	408633	AW963372	Hs.46677	PRO2000 protein	3.5
	427878	C05766	Hs.181022	CGI-07 protein	3.5
	419945	AW290975	Hs.118923	ESTs	3.5
	448372	AW445166	Hs.170802	ESTs	3.5
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen 1NFLS	3.5
45	411274	NM_002776	Hs.69423	kallikrein 10	3.5
	406666			NM_002425:Homo sapiens matrix metalloproteinase	3.5
	426920	AA393351	Hs.132121	ESTs	3.5
	402639			Target Exon	3.4
50	454891	AW837349		gb:QV2-LT0038-270300-108-d12 LT0038 Homo sapi	3.4
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet-de	3.4
	456296	AA829976	Hs.239114	mannosidase, alpha, class 1A, member 2	3.4
	450650	T65617	Hs.101257	hypothetical protein MGC3295	3.4
	429274	AI379772	Hs.99206	ESTs	3.4
	430704	AW813091	Hs.335799	ESTs	3.4
55	419807	R77402		gb:yf75f11.s1 Soares placenta Nb2HP Homo sapi	3.4
	451778	AI826131	Hs.71243	ESTs, Weakly similar to zinc finger protein [3.4
	430397	AI824533	Hs.105607	bicarbonate transporter related protein 1	3.4
	432113	AA935065	Hs.152385	ESTs	3.4
	449722	BE280074	Hs.23960	cyclin B1	3.4
60	455092	BE152428		gb:CM0-HT0323-151299-126-b04 HT0323 Homo sapi	3.4
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.4
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	3.4
	417009	AA191719	Hs.314714	ESTs	3.4
	444743	AA045648	Hs.301957	nudx (nucleoside diphosphate linked moiety X	3.4
65	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen induci	3.4
	413219	AA878200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PLACE20	3.4
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	3.4
	438993	AA828995		gb:od77b08.s1 NCL_CGAP_Ov2 Homo sapiens cDNA	3.4
	403274			Target Exon	3.4
70	435360	AF105366	Hs.4876	solute carrier family 12 (potassium/chloride	3.4
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2 prote	3.4
	443462	AI064690	Hs.171176	ESTs	3.3
	444910	AI201849		gb:qs76g04.x1 NCL_CGAP_Pr28 Homo sapiens cDNA	3.3
75	426269	HI5302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (from c	3.3
	449101	AA205847	Hs.23016	G protein-coupled receptor	3.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	3.3
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone CAE066	3.3
	419751	AW195581	Hs.93121	KIAA0761 protein	3.3
80	404782			C7001692*:gl[6724096]gb[AAF26844.1] (AF195021	3.3
	415613	R20233		gb:yg18h11.s1 Soares infant brain 1NIB Homo s	3.3
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypothetical p	3.3
	406599			Target Exon	3.3
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	3.3

	412879	BE092219		gbdL2-BT0734-240400-071-B04 BT0734 Homo sapi	3.3
	421107	AA283822	Hs.55606	ESTs, Weakly similar to S47072 finger protein	3.3
	436985	AA740946	Hs.150895	ESTs	3.3
	443903	AI220547	Hs.135223	ESTs	3.3
5	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (from c	3.3
	447153	AA805202	Hs.315562	ESTs	3.3
	450769	AA057418	Hs.33654	ESTs	3.3
	421379	Y15221	Hs.103982	small Inducible cytokine subfamily B (Cys-X-C	3.3
	402481			NM_001821*:Homo sapiens choroideremia-like (R	3.3
10	459394	BE409894	Hs.126522	Homo sapiens, clone MGC:16722, mRNA, complete	3.3
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-1 [H.	3.3
	417708	N74392	Hs.50495	ESTs	3.3
	414869	AA157291	Hs.21479	ubiquitin 1	3.3
	441690	R81733	Hs.33106	ESTs	3.3
15	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.3
	412246	AI160873	Hs.69233	zinc finger protein	3.3
	412903	BE007967	Hs.155795	ESTs	3.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placental)	3.3
	451177	AI989716	Hs.13034	ESTs	3.3
20	409990	AA079337		gb:zm95b09.r1 Stratagene colon HT29 (937221)	3.3
	418462	BE001596	Hs.85266	Integrin, beta 4	3.3
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92k	3.3
	405196			C2000662*:g 7512792 pir T12482 hypothetical	3.3
	459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA libra	3.3
25	432917	NM_014125	Hs.279812	PRO0327 protein	3.3
	448251	BE280486	Hs.84045	hypothetical protein FLJ20288	3.3
	415025	AW207091	Hs.72307	ESTs	3.3
	420218	AW958037	Hs.286	ribosomal protein L4	3.2
	429594	AK001128	Hs.210297	Homo sapiens cDNA FLJ10266 fls, clone HEMBB10	3.2
30	447762	AI939461	Hs.161370	ESTs	3.2
	414147	BE091634		gb:IL2-BT0731-240400-069-C03 BT0731 Homo sapi	3.2
	445038	AI635444	Hs.143917	dJ467N11.1 protein	3.2
	448666	NM_014953	Hs.323346	KIAA1008 protein	3.2
	402800			Target Exon	3.2
35	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated	3.2
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S. cere	3.2
	455203	AW865450		gb:PM4-SN0020-010400-008-b09 SN0020 Homo sapi	3.2
	459666	W27362		gb:30g7 Human retina cDNA randomly primed sub	3.2
	401458			Target Exon	3.2
40	432361	AI378562	Hs.159585	ESTs	3.2
	444008	BE544855	Hs.220756	ESTs, Weakly similar to SFR4_HUMAN SPLICING F	3.2
	405336			Target Exon	3.2
	446563	BE326588	Hs.141454	ESTs	3.2
45	449276	AW241510	Hs.252713	ESTs	3.2
	455838	BE145808		gb:MR0-HT0208-101299-103-f11 HT0208 Homo sapi	3.2
	420591	X53655	Hs.99171	neurotrophin 3	3.2
	401486			C4000647*:g 4758508 ref NP_004253.1 airway	3.2
	432979	AA573263	Hs.120860	ESTs	3.2
50	413833	Z15005	Hs.75573	centromere protein E (312kD)	3.2
	438325	AA804258	Hs.123229	ESTs	3.2
	421751	AW813731	Hs.159153	ESTs, Moderately similar to S65657 alpha-1C-a	3.2
	431938	AA938471	Hs.54431	specific granule protein (28 kDa); cysteine-r	3.2
	421777	BE562088	Hs.108196	HSPC037 protein	3.2
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fls, clone ADKA02	3.2
55	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fls, clone LNG004	3.2
	402337			Target Exon	3.2
	420930	AW888650		gb:CMA-NT0007-130500-551-406 NT0007 Homo sapi	3.2
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fls, clone HEMBA10	3.2
60	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.1
	437641	AA811452	Hs.291911	ESTs	3.1
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.1
	434208	T92641	Hs.127648	hypothetical protein PRO2176	3.1
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN ALU SU	3.1
65	452934	AA581322	Hs.4213	hypothetical protein MGC16207	3.1
	458923	Y12812	Hs.24422	regulatory factor X-associated protein	3.1
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A receptor, ep	3.1
	439760	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDNA clo	3.1
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevisiae,	3.1
70	445885	AI734009	Hs.127699	KIAA1603 protein	3.1
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fls, clone HEP010	3.1
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine protein k	3.1
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo sapi	3.1
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription factor	3.1
75	455987	BE178323		gb:RC3-HT0600-240400-023-g05 HT0600 Homo sapi	3.1
	421426	AA291101	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA, part	3.1
	423887	AL080207	Hs.134585	DKFZP434G232 protein	3.1
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.1
	447815	AI432199	Hs.247084	ESTs	3.1
80	441974	AI683782	Hs.128245	ESTs	3.1
	446474	AI301227	Hs.150186	hypothetical protein DKFZp566K1948	3.1
	452166	AI948607	Hs.264680	ESTs	3.1
	451659	BE379761	Hs.14248	ESTs	3.1
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.1

	447701	BE619526	Hs.255527	hypothetical protein MGC14128	3.1
	443648	AI085377	Hs.143510	ESTs	3.1
	414896	AF002020	Hs.76918	Niemann-Pick disease, type C1	3.1
	449441	AI656040	Hs.195532	ESTs	3.1
5	458145	AI239457	Hs.130794	ESTs	3.1
	444588	AI221321	Hs.167559	ESTs	3.1
	450832	AW970602	Hs.105421	ESTs	3.1
	449425	AW103433	Hs.195584	ESTs	3.1
10	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT2RP30	3.1
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	3.1
	416120	H46739		gb:yo14h02.s1 Soares adult brain N2b5HB55Y Ho	3.1
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S. cere	3.1
	404107			Target Exon	3.1
15	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HEMBB10	3.1
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (from c	3.1
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM040	3.1
	442824	BE178065	Hs.144081	ESTs	3.1
	435061	AI651474	Hs.163944	ESTs	3.0
20	420589	AA419360	Hs.192708	ESTs	3.0
	434569	AI311295	Hs.8294	KIAA0196 gene product	3.0
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B, membe	3.0
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptional act	3.0
	402892			Target Exon	3.0
	406087			Target Exon	3.0
25	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	3.0
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbHPU Ho	3.0
	435990	AI015862	Hs.131793	ESTs	3.0
	442577	AA292998	Hs.163900	ESTs	3.0
30	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitter tra	3.0
	458154	AW816379	Hs.335018	ESTs	3.0
	416809	N67253	Hs.271691	ESTs	3.0
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	3.0
	437938	AI950087		gb:wg05c02.x1 NCI_CGAP_Kd12 Homo sapiens cDN	3.0
35	413281	AA861271	Hs.222024	transcription factor BMAL2	3.0
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810027O1	3.0
	445505	AI971156	Hs.148891	ESTs	3.0
	425005	AI565851		gb:tn07g03.x1 NCI_CGAP_Bm25 Homo sapiens cDN	3.0
	435673	AF202961	Hs.284200	Homo sapiens uncharacterized gastric protein	3.0
40	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens cDNA	3.0
	453509	AL040021	Hs.252674	ESTs, Weakly similar to alternatively spliced	3.0
	455750	BE075114		gb:PM1-BT0585-110200-003-c11 BT0585 Homo sapi	3.0
	407777	AA181071	Hs.71465	squalene epoxidase	3.0
	424441	X14850	Hs.147097	H2A histone family, member X	3.0
45	417734	Z42667	Hs.6724	ESTs	3.0
	449676	AW380579	Hs.209657	ESTs	3.0
	445425	AI223511	Hs.300722	ESTs	3.0
	427061	AB032971	Hs.173392	KIAA1145 protein	3.0
	433584	AW295399		gb:UH-BI2-ahv-h-03-0-ULs1 NCI_CGAP_Sub4 Ho	3.0
50	444477	AI150548	Hs.23155	ESTs	3.0
	446255	AI283257	Hs.257090	ESTs	3.0
	400612			C10001034:gij7513113 pir T13078 KIAA0992 pro	3.0
	450841	AI741466	Hs.270515	ESTs	3.0
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone HEP091	3.0
55	433871	W02410	Hs.205555	ESTs	3.0
	401994			Target Exon	3.0
	449272	AW137658	Hs.197645	ESTs	3.0
	409703	NM_006187	Hs.55009	Z'-5'-oligoadenylate synthetase 3 (100 kD)	3.0
	400250			Eos Control	3.0
60	408015	AW136771	Hs.244349	epidermal differentiation complex protein lik	3.0
	436414	BE264633	Hs.143638	WD repeat domain 4	3.0
	432220	AI571305	Hs.232224	ESTs	3.0
	420831	AA280824	Hs.190035	ESTs	3.0
	433644	AW342028		gb:hb75d03.x1 NCI_CGAP_U12 Homo sapiens cDNA	3.0
65	447313	U92981	Hs.18081	Homo sapiens clone DT1P186 mRNA, CAG repeat r	3.0
	428262	AI651324	Hs.7298	biphenyl hydrolase-like (serine hydrolase; br	3.0
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone COL070	3.0
	417308	H60720	Hs.81892	KIAA0101 gene product	3.0
	436281	AW411194	Hs.85195	myeloid leukemia factor 1	3.0
70	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2 (dity	3.0
	423556	R72694	Hs.7720	dynein, cytoplasmic, heavy polypeptide 1	2.9
	426890	AA393167	Hs.41294	ESTs	2.9
	436333	AA709270	Hs.136672	EST	2.9
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.9
75	402556			C1001383*gi 538695 pir A61183 hypothetical	2.9
	411098	AW817238		gb:QVD-ST0247-090200-105-b07 ST0247 Homo sapi	2.9
	435399	AA679463		gb:ac50c03.s1 Stratagene hNT neuron (837233)	2.9
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.9
	427986	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone HEP016	2.9
	410658	AW105231	Hs.192035	ESTs	2.9
80	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PR	2.9
	412279	BE245511		gb:TCBAP1D3235 Pediatric pre-B cell acute lym	2.9
	405277			ENSP00000211621-Keratin, type II cytoskeleta	2.9
	423733	AA330281		gb:EST33985 Embryo, 12 week II Homo sapiens c	2.9

5	455319	AW895387		gb:QV4-NN0038-300300-157-c10 NN0038 Homo sapi	2.9
	407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	2.9
	413306	AW303544	Hs.118654	ESTs	2.9
	432215	AU076609	Hs.2934	ribonucleotide reductase M1 polypeptide	2.9
	434423	NM_006769	Hs.3844	LIM domain only 4	2.9
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	2.9
	412367	AW945964		gb:QV0-ET0001-050500-228-e09 ET0001 Homo sapi	2.9
	436148	BE005252	Hs.321583	Homo sapiens cDNA FLJ20779 fis, clone COL0507	2.9
10	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	2.9
	404981			ENSP00000252242-Keratin, type II cytoskeleton	2.9
	448796	AA147829	Hs.301431	endothelial zinc finger protein induced by tu	2.9
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA, part	2.9
	401760			Target Exon	2.9
	443859	NM_013409	Hs.9914	folistatin	2.9
15	404253			NM_021058-Homo sapiens H2B histone family, m	2.9
	432491	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	2.9
	435867	AA954229	Hs.114052	ESTs	2.9
	429035	BE549781	Hs.270475	ESTs	2.9
20	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega-hydr	2.9
	446417	AJ299050		gb:xn14d12x1 NCL_CGAP_Lu5 Homo sapiens cDNA	2.9
	437637	AJ030329	Hs.65792	syntrophin, gamma 2	2.9
	452452	BE393822	Hs.25645	Homo sapiens mRNA; cDNA DKFZp761C029 (from cl	2.9
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	2.9
25	450698	W31489	Hs.95044	ESTs, Weakly similar to I38022 hypothetical p	2.9
	439430	AF124250	Hs.6564	cervical cancer anti-estrogen resistance 3	2.9
	434876	AF160477	Hs.61460	lg superfamily receptor LNIR	2.9
	438268	AA782163	Hs.293502	ESTs	2.9
	401781			Target Exon	2.9
30	439625	AF086453	Hs.68611	ESTs	2.9
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothetical p	2.9
	410743	AA089474	Hs.272153	ESTs	2.9
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homolog o	2.9
	449746	AJ688594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOCHROME	2.9
35	443479	AF027219	Hs.9443	zinc finger protein 202	2.9
	442601	AJ684969	Hs.45772	ESTs	2.9
	405932			C15000305.gi 3806122 gb AAC69198.1 (AF097887	2.9
	405454			C12000541.gi 5729884 ref NP_006539.1 IGF-II	2.9
40	418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	2.9
	408562	AJ436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein, parti	2.9
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotransf	2.9
	414581	AA256213	Hs.72010	ESTs	2.9
	411268	AK000512	Hs.69388	hypothetical protein FLJ20505	2.9
	450024	AA005129		gb:zh90h08.r1 Soares_fetal_liver_spleen_1NFLS	2.9
45	400297	AJ127076	Hs.334473	hypothetical protein DKFZp564O1278	2.9
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugat	2.9
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.9
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein produ	2.9
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothetical p	2.9
50	435711	AF226667	Hs.58553	CTP synthase II	2.9
	419088	AJ538323	Hs.52620	Integrin, beta 8	2.8
	431629	AU077025	Hs.265827	Interferon, alpha-inducible protein (clone IF	2.8
	429299	AJ620463	Hs.293984	hypothetical protein MGC13102	2.8
	451702	AW665452	Hs.246503	ESTs	2.8
55	432162	AA584062	Hs.272798	hypothetical protein FLJ20413	2.8
	405281			NM_002864:Homo sapiens pregnancy-zone protein	2.8
	438161	BE089028	Hs.20158	ESTs, Weakly similar to S34159 transcription	2.8
	409103	AF251237	Hs.112208	XAGE-1 protein	2.8
	425599	AW366745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	2.8
60	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mms5, S	2.8
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.8
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-like	2.8
	452730	AA027952	Hs.165216	ESTs	2.8
	413083	BE064528		gb:RC4-BT0311-250200-014-h06 BT0311 Homo sapi	2.8
65	437030	AA742577	Hs.303781	EST	2.8
	438113	AJ467908	Hs.8882	ESTs	2.8
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone LNG096	2.8
	440994	AJ160011	Hs.193341	ESTs	2.8
	442295	AJ827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HEMBA10	2.8
70	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapi	2.8
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin, tissu	2.8
	424408	AJ754813	Hs.146428	collagen, type V, alpha 1	2.8
	433788	AJ810534	Hs.161275	ESTs	2.8
	403806			Target Exon	2.8
75	437182	AL080098		gb:Homo sapiens mRNA; cDNA DKFZp584C1072 (fro	2.8
	453955	AW579207	Hs.304666	ESTs, Weakly similar to I78885 serine/threonl	2.8
	420795	AA323037	Hs.128645	sorting nexin 16	2.8
	452696	AJ826645	Hs.211534	ESTs	2.8
	432656	NM_000246	Hs.3076	MHC class II transactivator	2.8
80	438052	AA776564	Hs.41891	zinc finger 1111	2.8
	441755	AW450826	Hs.127788	ESTs	2.8
	427961	AW293165	Hs.143134	ESTs	2.8
	449785	AJ225235	Hs.288300	hypothetical protein FLJ23231	2.8
	450451	AW591528	Hs.202072	ESTs	2.8

	406831	N73448	Hs.50272	ESTs, Weakly similar to RS1A_HUMAN 40S RIBOSO	2.8
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A receptor, pi	2.8
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.8
5	413582	AW295647	Hs.71331	hypothetical protein MGC5350	2.8
	448979	AI611378	Hs.192610	ESTs	2.8
	409143	AW025980	Hs.138965	ESTs, Weakly similar to I38022 hypothetical p	2.8
	410664	NM_006033	Hs.65370	lipase, endothelial	2.8
	444550	BE250718	Hs.87614	ESTs	2.8
10	422109	S73265	Hs.1473	gastrin-releasing peptide	2.8
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.8
	445941	AI267371	Hs.172636	ESTs	2.8
	459719	AW749511	Hs.301554	ESTs, Weakly similar to AF133298 1 cytochrome	2.8
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT2RP20	2.8
15	456456	AA477609	Hs.89563	nuclear cap binding protein subunit 1, 80kD	2.8
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypothetical p	2.8
	403000	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	2.8
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	2.8
	439846	T63959	Hs.228320	hypothetical protein FLJ23537	2.8
20	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	2.8
	412970	AB026436	Hs.177534	dual specificity phosphatase 10	2.8
	455091	BE079752		gb:RC6-BT0627-140200-011-A04 BT0627 Homo sapi	2.8
	410049	AW579475		gb:RC0-DT0076-110100-031-d10 DT0076 Homo sapi	2.8
	452571	W31518	Hs.34665	ESTs	2.8
25	455666	BE065813		gb:RC2-BT0318-110100-012-a08 BT0318 Homo sapi	2.8
	426343	NM_014642	Hs.169387	KIAA0036 gene product	2.8
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-associated	2.8
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromosomes 4	2.7
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.7
30	429128	AA446869	Hs.119316	ESTs	2.7
	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MAMMA10	2.7
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	2.7
	403763			NM_001059*Homo sapiens tachykinin receptor 3	2.7
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypothetic	2.7
35	406753	AA505665	Hs.217493	annexin A2	2.7
	415747	AA381209		gb:EST94257 Activated T-cells I Homo sapiens	2.7
	419875	AA853410	Hs.93557	proenkephalin	2.7
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothetical p	2.7
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.7
40	456181	L36463	Hs.1030	ras inhibitor	2.7
	416548	H62953		gb:yr47R06.r1 Soares fetal liver spleen 1NFLS	2.7
	417995	AW974175	Hs.188751	ESTs, Weakly similar to MAPB_HUMAN MICROTUBUL	2.7
	435347	AW014873	Hs.116963	ESTs	2.7
	457339	AW971949	Hs.291252	ESTs, Weakly similar to ZN91_HUMAN ZINC FINGE	2.7
45	417398	N78541	Hs.177366	ESTs	2.7
	408380	AF123050	Hs.44532	dibuliquitin	2.7
	437724	AW444828	Hs.184323	ESTs	2.7
	408680	AK000093	Hs.46821	hypothetical protein FLJ20086	2.7
50	454202	AW178363		gb:RC3-HT0105-010999-002-H06 HT0105 Homo sapi	2.7
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli RecA ho	2.7
	422278	AF072873	Hs.114218	fizzled (Drosophila) homolog 6	2.7
	406092			Target Exon	2.7
	447748	AI422023	Hs.161338	ESTs	2.7
	443236	AI079496	Hs.134169	ESTs	2.7
55	433743	AF075312	Hs.236760	Homo sapiens clone HQ0262	2.7
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related protein	2.7
	405675			Target Exon	2.7
	424825	AW904466	Hs.321197	PDZ domain protein (Drosophila InaD-like)	2.7
60	416250	AA581386	Hs.73452	hypothetical protein MGC10791	2.7
	448592	N69546	Hs.44563	hypothetical protein	2.7
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MAMMA10	2.7
	407287	AI678812		gb:tu59d08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA	2.7
	448275	BE514434	Hs.20830	kinesin-like 2	2.7
	412977	AA125910	Hs.191461	ESTs	2.7
65	431721	AB032996	Hs.268044	KIAA1170 protein	2.7
	417357	AF260257	Hs.131917	retinitis pigmentosa GTPase regulator Interac	2.7
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of the p	2.7
	416294	D86980	Hs.79170	KIAA0227 protein	2.7
	458201	AI989961	Hs.233477	ESTs, Moderately similar to A Chain A, Cyclop	2.7
70	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolog 2	2.7
	401230			NM_014191*Homo sapiens sodium channel, volta	2.7
	422058	AA862231	Hs.334443	ESTs	2.7
	452747	BE153655	Hs.61460	Ig superfamily receptor LNIR	2.7
75	430152	AB001325	Hs.234642	aquaporin 3	2.7
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	2.7
	443500	AV646388	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (from cl	2.7
	418030	BE207573	Hs.83321	neuromedin B	2.7
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapiens]	2.7
	418869	AW516565		gb:cx01d05.x1 Soares_NHCCc_cervical_tumor Hom	2.7
80	431688	AA513906		gb:ng67c08.s1 NCI_CGAP_Lip2 Homo sapiens cDNA	2.7
	427579	AA366143	Hs.175669	hypothetical protein FLJ20637	2.7
	423175	W27595	Hs.18653	hypothetical protein FLJ14627	2.7
	414737	AI60386	Hs.125087	ESTs	2.7
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.7

	446659	AI335361	Hs.226376	ESTs	2.7
	419833	AA251131	Hs.220697	ESTs	2.7
	411819	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo sapi	2.6
5	445592	AV654382	Hs.17947	ESTs, Weakly similar to T16534 hypothetical p	2.6
	446102	AW168067	Hs.252958	ESTs	2.6
	441408	AI733249	Hs.126897	ESTs	2.6
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse transc	2.6
	416283	NM_005429	Hs.79141	vascular endothelial growth factor C	2.6
10	421470	R27498	Hs.1378	annexin A3	2.6
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural arachnod	2.6
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	2.6
	431832	AW276866	Hs.192715	ESTs	2.6
	426698	AA394104	Hs.97489	ESTs	2.6
15	433288	AI368873	Hs.271257	ESTs, Weakly similar to I38022 hypothetical p	2.6
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	2.6
	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypothetical p	2.6
	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo sapi	2.6
	440048	AA897461	Hs.328737	ESTs, Weakly similar to envelope protein [H.s	2.6
20	401260			C1001031*gi7305041 ref NP_038876.1 erythro	2.6
	435136	R27289	Hs.10172	ESTs	2.6
	412108	AA100293	Hs.185043	ESTs	2.6
	434442	AA737415	Hs.152826	ESTs	2.6
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT2RP30	2.6
25	419667	AI077005	Hs.92208	a disintegrin and metalloproteinase domain 15	2.6
	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	2.6
	409594	AA076118		gb:zm18e06.s1 Stratagene pancreas (937208) Ho	2.6
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (937208) Ho	2.6
	423038	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	2.6
30	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth factor	2.6
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.6
	434444	AI765276	Hs.101257	hypothetical protein MGC3295	2.6
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP)	2.6
	411465	AW847663		gb:IL3-CT0213-280100-056-F02 CT0213 Homo sapi	2.6
35	408625	AW243323	Hs.266785	ESTs	2.6
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.6
	439245	NM_013381	Hs.6510	thyrotropin-releasing hormone degrading ectoe	2.6
	431890	X17033	Hs.271986	Integrin, alpha 2 (CD49B, alpha 2 subunit of	2.6
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin)	2.6
40	401050			NM_014155*:Homo sapiens HSPC063 protein (HSPC	2.6
	405897			Target Exon	2.6
	451153	BE082900		gb:CM2-BT0742-100400-147-h04 BT0742 Homo sapi	2.6
	407327	AA487182	Hs.269414	ESTs, Weakly similar to Z195_HUMAN ZINC FINGE	2.6
	440159	AI637599	Hs.126127	ESTs	2.6
45	404184			NM_030903*:Homo sapiens olfactory receptor, f	2.6
	428552	AW274560	Hs.129520	ESTs	2.6
	401367			Target Exon	2.6
	428450	NM_014791	Hs.184339	KIAA0175 gene product	2.6
	426698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
50	424783	AA913909	Hs.153088	TATA box binding protein (TBP)-associated fac	2.6
	449432	AW451361	Hs.196529	ESTs	2.6
	425062	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger protein)	2.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PLACE10	2.6
	450705	U90304	Hs.25351	troquels homeobox protein 5	2.6
55	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	2.6
	408391	AW859276		gb:MR1-CT0352-240200-105-d02 CT0352 Homo sapi	2.6
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mouse)	2.6
	431750	AA514986	Hs.283705	ESTs	2.6
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to ARL-	2.6
60	453331	AI240665	Hs.8895	ESTs	2.6
	447175	AI365208	Hs.293606	ESTs	2.6
	451878	AI821027	Hs.8429	ESTs	2.6
	433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	2.6
	418282	AA215535	Hs.98133	ESTs	2.6
65	434557	AW855466	Hs.271866	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	2.6
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	2.6
	420894	AA744597	Hs.88854	ESTs	2.6
	435663	AI023707	Hs.134273	ESTs	2.6
	448037	AW195634	Hs.170401	ESTs	2.6
70	418067	AI127958	Hs.83393	cystatin E/M	2.6
	439524	BE542950	Hs.155548	ESTs	2.6
	402298			Target Exon	2.6
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.6
	407471	D55644		gb:Human spleen PABL (pseudautosomal boundar	2.6
75	430994	AA490346	Hs.40530	Homo sapiens, clone MGC:17624, mRNA, complete	2.6
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (from c	2.6
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypothetical p	2.6
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp43401214 (from c	2.6
	425415	M13903	Hs.157091	Involucrin	2.6
80	444826	AI674482	Hs.148441	ESTs	2.6
	413331	BE083950		gb:PM0-BT0651-260200-001-b11 BT0651 Homo sapi	2.6
	414887	AA524394	Hs.294022	hypothetical protein FLJ14950	2.6
	405041			C3001705*gi1345652 sp P15989 CA36_CHICK COL	2.6
	413864	BE175582		gb:RCS-HT0580-100500-022-C01 HT0580 Homo sapi	2.6

	438746	AI885815	Hs.184727	ESTs	2.5
	438966	AW979074		gb:EST391184 MAGE resequences, MAGP Homo sapi	2.5
	433365	AF026944	Hs.293797	ESTs	2.5
5	412723	AA648459	Hs.335951	hypothetical protein AF301222	2.5
	422656	AI870435	Hs.1569	LIM homeobox protein 2	2.5
	411171	AW820260		gb:QV2-ST0296-150200-040-c10 ST0296 Homo sapi	2.5
	447197	R36075		gb:YH88b01.s1 Soares placenta Nb2HP Homo sapi	2.5
	459688	U72671	Hs.151250	intercellular adhesion molecule 5, telencepha	2.5
10	414883	AA926960	Hs.334883	CDC28 protein kinase 1	2.5
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.5
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (from cl	2.5
	427366	AA885108	Hs.223806	TATA box binding protein (TBP)-associated fac	2.5
	455549	AW994222		gb:RC3-BN0036-250200-012-e02 BN0036 Homo sapi	2.5
15	409676	AA077118	Hs.197298	NS1-binding protein	2.5
	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT2RP20	2.5
	429413	NM_014058	Hs.201877	DESC1 protein	2.5
	424420	BE614743	Hs.146688	prostaglandin E synthase	2.5
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, polypep	2.5
20	452834	AI638627	Hs.105585	KIAA1688 protein	2.5
	424354	NM_014314	Hs.145612	RNA helicase	2.5
	455095	AW855598		gb:CM1-CT0278-031199-032-e08 CT0278 Homo sapi	2.5
	431241	AA496799	Hs.36958	ESTs	2.5
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (connexin	2.5
25	427239	BE270447	Hs.174070	ubiquitin carrier protein	2.5
	407103	AA424881	Hs.255301	hypothetical protein MGC13170	2.5
	458175	AW296024	Hs.150434	ESTs	2.5
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein type	2.5
30	453379	AA035261	Hs.61753	ESTs	2.5
	438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypothetical p	2.5
	412313	AW936832		gb:PM2-DT0023-050400-003-h03 DT0023 Homo sapi	2.5
	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (achondro	2.5
	443757	H05479	Hs.62314	ESTs	2.5
	449300	AI656959	Hs.222165	ESTs	2.5
35	434913	AW872860	Hs.11056	RALBP1 protein	2.5
	448946	AI652855	Hs.23363	hypothetical protein FLJ10983	2.5
	437327	AL353942	Hs.306504	Homo sapiens mRNA; cDNA DKFZp761L23121 (from	2.5
	450262	AW409872	Hs.184846	Homo sapiens, Similar to zinc finger protein	2.5
	453204	R10799	Hs.191990	ESTs	2.5
40	420170	U43374	Hs.96531	Human normal keratinocyte mRNA	2.5
	449344	AI640355	Hs.312691	ESTs	2.5
	439436	BE140845	Hs.57868	ESTs	2.5
	449867	AI672379	Hs.122970	hypothetical protein FLJ21579	2.5
	452220	BE158006	Hs.212296	ESTs	2.5
45	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	2.5
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo sapien	2.5
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	2.5
	415030	D31118	Hs.191735	hypothetical protein MGC10520	2.5
	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	2.5
50	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens cDNA	2.5
	400301	X03635	Hs.1657	estrogen receptor 1	2.5
	429386	AK001795	Hs.201179	hypothetical protein FLJ10933	2.5
	423949	AI014546	Hs.130912	ESTs	2.5
	411768	NM_013371	Hs.71979	interleukin 19	2.5
55	436961	AW375974	Hs.156704	ESTs	2.5
	431124	AF284221	Hs.59506	doublesex and mab-3 related transcription fac	2.5
	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	2.5
	418717	AI334430	Hs.86984	ESTs	2.5
	443270	NM_004272	Hs.337737	Homer, neuronal immediate early gene, 1B	2.5
60	448454	NM_005879	Hs.21254	TRAF interacting protein	2.5
	430072	X13294	Hs.300592	v-myb avian myeloblastosis viral oncogene hom	2.5
	442966	AI394036	Hs.132237	ESTs, Weakly similar to DUS8_HUMAN DUAL SPECI	2.5
	451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HUMAN ALU SU	2.5
	418327	U70370	Hs.84136	paired-like homeodomain transcription factor	2.5
65	440381	AA917808	Hs.190495	ESTs	2.5
	403983			Target Exon	2.5
	451340	AW936273		gb:QV0-DT0020-090200-107-g07 DT0020 Homo sapi	2.5
	447888	BE620911	Hs.126889	ESTs	2.5
	441794	AW197794	Hs.253338	ESTs	2.5
70	424153	AA451737	Hs.141496	MAGE-like 2	2.5
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	2.5
	435647	AI853240	Hs.49823	ESTs	2.5
	428780	AI478578	Hs.50636	ESTs	2.5
	439108	AW163034	Hs.6467	synaptogyrin 3	2.5
75	422565	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fasci h	2.5
	428054	AI948688	Hs.266619	ESTs	2.5
	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	2.5
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S. cere	2.5
	443362	AK053464	Hs.166505	ESTs	2.5
80	433183	AF231338	Hs.222024	transcription factor BMAL2	2.5
	438214	H06076	Hs.25320	TRABID protein	2.5
	446745	AW118189	Hs.156400	ESTs	2.5
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.5
	426333	AW269088	Hs.118183	hypothetical protein FLJ22833	2.5

TABLE 128

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
407842	1007175_1	AW178963 AW845721 BE141041 AW806977 AW845690 AW845691 AW845724 AW176564 AW845705 AW845603 AW845729 AW845722 AW178966 AW845693 AW845685 AW845707 BE141053 BE141046 AW845570 AW845575 BE141043 BE141039 BE141070 AW062443 AW806980 AW845643 AW805969 AW845686 BE141054 BE141044 BE141042 AW845571 AW845604 BE141047 BE141071 AW062442 AW845633 AW178968
408391	1055687_1	AW859276 AW859274 AW190959 T91463
408690	107490_1	AW864542 AA056567 AW882724
409594	114249_1	AA076118 AA976618 AA076220
409695	114876_1	AA296961 AA296889 AA076945 AA077528 AA077497
409990	116644_1	AA079337 AA079338 AW272100
410008	116812_1	AA079552 BE142525 BE142527
410049	1172307_1	AW579476 AW933654 AW933655
410784	1221005_1	AW803201 BE079700 BE062940
411098	1232093_1	AW817238 AW933985 AW933998
411171	1234393_1	AW820260 AW820332 R94406
411465	1246768_1	AW847663 AW847861 AW861080
411559	1249417_1	BE144081 BE144190 AW851155
411819	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
411958	126717_1	AA090200 AW751275 AW751276 AW751289
412279	1287332_1	BE245511 BE246133 AW935247
412313	1288355_1	AW936832 AW936609 AW936657 AW936611 AW936739 AW936734 AW936779 AW936688 AW936659 AW936738 AW936827 AW936737 AW936736 AW936740 AW936833 AW936777 AW936830 AW936834 AW936829 AW936772 AW936638 AW936658 AW936636 AW936774 AW936778 AW936766 AW936776 AW936831 AW936760 AW936819
412333	1289037_1	AW937485 AW937589 AW937658 AW937654 AW937492
412367	1291505_1	AW945964 AW946020 AW946034 AW946027 AW946041 AW946044 AW946033 AW946024 AW946021 AW946029 AW946015 AW946016 AW946039 AW946045 AW946028 AW946036
412879	1334272_1	BE092219 BE092361 BE006789
413083	1348639_1	BE064528 BE064589 BE064561
413331	1361726_1	BE083950 BE084017 BE084016
413864	1395788_1	BE175582 BE175514 BE175505 BE175591 BE175530
414147	142127_1	BE091634
414148	142133_1	BE084049 AW292907 AA135984
415317	1533847_1	Z43388 F05453 R19673 R20275 H06917
415613	1540602_1	R20233 F12901 T74740
415747	155189_1	AA381209 AA381245 AA167683
416120	1571266_1	H48739 H51513 H19779
416168	1574545_1	H23687 H46460 H40239
416548	1600181_1	H62953 N76608 N72413
417742	1696282_1	R64719 Z44680 R12451
418347	174149_1	AA216419 F03238 AA229517
418869	179863_1	AW516565 AA229762 AA230035
419807	188252_1	R77402 AA262462 AA250988 R06794
420373	193194_1	AW968228 AA259146 W01465
420637	195241_1	AW976153 AA278945 AA747691
420930	197738_1	AW888650 AW888651 BE149948 BE149951 BE149947 AW888649 AA281840 AA281822 AW888652
422689	219896_1	AW856665 AA315006 AW954733
423733	231476_1	AA330281 AA330232 AW962521
423735	231498_1	AA330259 AA661806 AA502431 AW974633 AA549496
423841	232507_1	AW763967 AA370795 AA331630 AW962550
425005	245908_1	AI565851 AA349656 R24798
429163	300543_1	AA884766 AW974271 AA592975 AA447312
431120	328264_1	AA492588 AA492498 AA492571
431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
431688	336609_1	AA513906 AA847734 AI357044
432184	342677_1	AW971125 AA527731 N52655 AI821508 AA532420
432189	342819_1	AA527941 AI810608 AI620180 AA635266
432869	355475_1	AW974094 AA569074 AA602574
433289	36202_1	AF005258
433584	370400_1	AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 AA778832
433644	371919_1	AW342028 AA641080 AA603282
434321	383473_1	AA629368 AW849574 AW849573
435399	405576_1	AA679463 AW813779 AW813709
437182	43421_1	AL080098 AL037472 AA432051
437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H53937 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488954 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173588 AW150329 AI553832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA842789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA253273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613458 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005 AI422017 AI422945 AI363249 AW23113 AI925592 AI420795 AI208187 AI423279 AI423645 AI424090 AI359637 AI044732 D17003 AW979074 AA834841 AA826550 AA828995 AA834879 AI926361
438390	45662_1	
438966	467436_1	
438993	467651_1	

5	439579	47404_1	AF086400 W79232 W73990
	440320	491930_1	AA879294 N67538 A474541
	444910	624951_1	AI201849 BE069007 AW946544
	446417	676384_1	AI299050 BE256910
	447197	711623_1	R36075 AI366546 R36167
	448599	770766_1	AW860912 AI540866
	449034	794817_1	AI624049 AW117770 AI858360
	450024	82296_1	AA005129 AA679084 AA694399
10	450613	840016_1	AI702055 R89204 R86260
	451105	859083_1	AI761324 AW880941 AW880937
	451153	86054_1	BE092900 AA015877 AA018521
	451340	86540_1	AW936273 AW340350 AA017208
	454202	1050507_1	AW178363 AW846011 AW845964 AW845988 AW845977 AW846002
	454241	1087807_1	BE144666 BE184942 AW238414 BE184946
15	454707	1230250_1	AW814989 AW814852 AW814808
	454891	1239217_1	AW837349 AW837355 AW882717
	454988	1248607_1	AW850140 AW850195 AW850192
	455091	1252939_1	BE079752 BE079868 BE148989 AW855532 BE148818 BE148815 BE148796
20	455092	1252971_1	BE152428 AW855572 AW855607
	455095	1252987_1	AW855598 AW855608 BE148763 BE148764 AW855645 AW855615 AW855596 AW855610 AW855605
	455203	1259973_1	AW865450 AW865119 AW865452 AW865461 AW865325 AW865114 AW865116 AW865321 AW865590 AW865390
	455310	1278158_1	AW893961 AW893998 AW894034 AW894019
	455319	1279172_1	AW895387 AW895547 AW895564 AW895323 AW895405 AW895539 AW895538
	455365	1284681_1	AW948343 AW948341 AW902855 AW984737
25	455549	1324696_1	AW994222 AW994377
	455666	1349545_1	BE065813 BE065788 BE065889 BE065832
	455750	1355998_1	BE075114 BE075283 BE075118
	455838	1374605_1	BE145808 BE145807 BE181883
30	455987	1397735_1	BE178323 BE177978
	457405	333127_1	AA504860 AA504911
	458829	773443_1	AI557388 BE158936
	459267	966605_1	AJ003631 AJ003650 AJ003651

TABLE 12C

Pkey: Unique number corresponding to an Eos probaset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
45	400612	9929646	Minus	151513-151662
	400666	8118496	Plus	17982-18115, 20297-20456
	401050	8117628	Minus	78449-79425
	401137	2547238	Minus	598-1009
	401230	9929527	Minus	33835-34006, 34539-34592, 36461-36745, 48925-49098, 52604-52758
50	401260	8076883	Minus	86008-86355
	401367	9795198	Minus	145356-145807
	401458	9187886	Plus	78485-77597
	401486	7341763	Plus	32585-32756, 36281-36540, 40791-40933, 44018-44179
	401575	7229804	Minus	76253-76364
	401747	9789672	Minus	118598-118816, 119119-119244, 119609-119761, 120422-120990, 130161-130381, 130468-130593, 131097-131258, 131866-131932, 132451-132575, 133580-134011
55	401760	9929699	Plus	83126-83250, 85320-85540, 94719-95287
	401780	7249190	Minus	28397-28617, 28920-29045, 29135-29296, 29411-29567, 29705-29787, 30224-30573
	401781	7249190	Minus	83215-83435, 83531-83656, 83740-83901, 84237-84393, 84955-85037, 86290-86814
	401994	4153859	Minus	42904-43124, 43211-43336, 44607-44763, 45199-45281, 46337-46732
60	402048	8072512	Plus	43936-44078
	402298	6598824	Plus	36758-37953
	402337	6957691	Plus	4116-4286, 16811-16973, 17107-17256, 19715-20040, 22029-22205
	402481	9797406	Plus	87891-88991
65	402556	9863723	Plus	13579-14026
	402639	9958129	Minus	20167-22383
	402800	6010175	Plus	43921-44049, 46181-46273
	402892	8086844	Minus	194384-194645
	403274	8072441	Minus	104069-104179, 105683-105859
70	403471	9930659	Minus	85867-85983
	403763	7229888	Minus	43575-43887
	403806	8140491	Plus	146390-146678
	403983	8576059	Minus	82441-82701
	404107	8099028	Minus	201699-202363
75	404132	6981900	Plus	11307-12434
	404184	4581418	Minus	12652-13548
	404253	9367202	Minus	55675-56055
	404440	7528051	Plus	80430-81581
	404782	9910094	Minus	15455-15589
80	404959	7407964	Plus	45243-45368
	404981	4432779	Minus	20626-20770, 22513-22721
	404996	6007890	Plus	37999-38145, 38652-38998, 39727-39872, 40557-40674, 42351-42450
	405041	7547195	Plus	121230-121714
	405196	7230083	Minus	135716-135851

	405277	3980473	Plus	23471-23572
	405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47286-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
	405336	6094635	Plus	33267-33563
	405454	7656675	Plus	133807-134053
5	405545	1054740	Plus	118677-118807,119091-119296,121626-121823
	405547	1054740	Plus	124361-124520,124914-125050
	405657	4827303	Minus	104132-104293
	405675	4557087	Plus	70304-70530
10	405708	4156182	Plus	55030-55604
	405897	6758795	Plus	59828-60535
	405932	7767812	Minus	123525-123713
	405943	6758796	Plus	20605-20812
	406087	9123919	Minus	7234-7626
	406092	9123919	Plus	251370-251797,252168-252882
15	406467	9795551	Plus	182212-182958
	406554	7711566	Plus	106956-107121
	406560	7711569	Minus	35162-35292
	406599	8248616	Plus	10933-11086

TABLE 13A: 465 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES, LIKELY TO ENCODE EXTRACELLULAR OR CELL-SURFACE PROTEINS

Table 13A lists about 465 genes up-regulated in cervical cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 12A, except that the ratio was greater than or equal to 1.7, and the 96th percentile value amongst cervical cancers was greater than or equal 100 units, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. lg, fn3, egf, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 PPDomains: Predicted Protein Domains
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

	Pkey	ExAccn	UnigenelD	PPDomains	Unigene Title	R1
40	425650	NM_001944	Hs.1925	TM,cadherin,Cadherin_C_term	desmoglein 3 (periphagus vulgaris antigen)	43.6
	418007	M13509	Hs.83169	SS,hemopexin,Peptidase_M10	matrix metalloproteinase 1 (interstitial)	38.9
	439606	W79123	Hs.58561	TM,7tm_1	G protein-coupled receptor 87	28.8
	452240	AI591147	Hs.61232	TM	ESTs	27.0
	424046	AF027866	Hs.138202	SS,TM,serpin	serine (or cysteine) proteinase inhibitor	24.5
45	400289	X07820	Hs.2258	hemopexin,Peptidase_M10	matrix metalloproteinase 10 (stromelysin)	20.5
	418345	AJ001696	Hs.241407	SS,TM,serpin	serine proteinase inhibitor 13(P113; se)	20.1
	423017	AW178761	Hs.227948	SS,serpin	serine (or cysteine) proteinase inhibitor	19.2
	428227	AA321649	Hs.2248	SS,TM,IL8	small inducible cytokine subfamily B (Cys)	15.9
	447164	AF026941	Hs.17518	TM,IBR	Homo sapiens cig5 mRNA, partial sequence	13.8
50	414764	AW013887	Hs.72047	TM	ESTs	12.9
	416651	AA634543	Hs.79440	TM	IGF-II mRNA-binding protein 3	12.7
	427585	D31152	Hs.179729	SS,C1q,Collagen	collagen, type X, alpha 1 (Schmid metaphy	12.6
	406467			TM,efhand	Target Exon	10.5
	428368	BE440042	Hs.83326	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 3 (stromelysin 1	10.2
55	418882	NM_004996	Hs.89433	TM,ABC_membrane,ABC_tran	ATP-binding cassette, sub-family C (CFTR/	9.4
	419247	S65791	Hs.69764	TM,KH-domain	fragile X mental retardation 1	9.1
	446232	AI281848	Hs.194691	TM,7tm_3,Ribosomal_L13	retinoic acid induced 3	8.9
	424905	NM_002497	Hs.153704	TM,pkinase	NIMA (never in mitosis gene a)-related ki	8.9
	422420	U03398	Hs.1524	TM,tubulin,TNF	tumor necrosis factor (ligand) superfamily	8.7
60	427821	AA470158	Hs.98202	TM,7tm_1	ESTs	6.9
	436211	AK001581	Hs.334829	Ammonium_transp	hypothetical protein FLJ10719; KIAA1794 p	6.9
	444342	NM_014398	Hs.10887	Lamp	similar to lysosome-associated membrane g	6.8
	422330	D30783	Hs.115263	SS,TM,EGF	epiregulin	6.8
	447342	AI199268	Hs.19322	SS,Ipocalln	Homo sapiens, Similar to RIKEN cDNA 20103	6.8
65	407839	AA045144	Hs.161566	TM,cadherin,Cadherin_C_term	ESTs	6.6
	410153	BE311926	Hs.15830	Glycos_transf_2	hypothetical protein FLJ12691	6.5
	414812	X72755	Hs.77367	SS,TM,IL8	monokine induced by gamma interferon	6.4
	421773	W69233	Hs.112457	SS	ESTs	6.2
	413385	M34455	Hs.840	TM,IDO	indoleamine-pyrrole 2,3 dioxygenase	5.9
70	413753	U17760	Hs.75517	SS,laminin_EGF,laminin_N_term,adh_short	laminin, beta 3 (necalin (125kD), kalinin	5.8
	432239	X81334	Hs.2938	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 13 (collagenase	5.5
	418663	AK001100	Hs.41690	TM,cadherin	desmocollin 3	5.5
	407366	AF026942		TM,IBR	gb:Homo sapiens cig33 mRNA, partial seque	5.5
	433091	Y12642	Hs.3185	SS,TM,UPAR_LY6	lymphocyte antigen 6 complex, locus D	5.4
75	408536	AW381532	Hs.135188	SS,TM,E1-E2_ATPase,Cation_ATPase_C_N	ESTs	5.4
	420440	NM_002407	Hs.97644	SRCRUisogloblin	mammaglobin 2	5.2
	437044	AL035864	Hs.69517	TM	cDNA for differentially expressed CO16 ge	5.1
	405547			SS,TM,ABC_membrane,ABC_tran,Ig	NM_018833:Homo sapiens transporter 2, AT	5.1
	439223	AW238299	Hs.250618	SS	UL16 binding protein 2	5.1
80	426320	W47595	Hs.169300	SS,TM,TGF-beta,TGFb_propeptide	transforming growth factor, beta 2	5.1
	423634	AW959908	Hs.1690	TM	heparin-binding growth factor binding pro	5.0
	426350	NM_003245	Hs.2022	TM,Transglutamin_C,Transglutamin_N,Transglut_core	transglutaminase 3 (E polypeptide, protel	5.0
	409744	AW675258	Hs.56265	TM,melasthlo,Kelch	Homo sapiens mRNA; cDNA DKFZp586P2321 (fr	4.9

444461	R53734	Hs.25978	TM	ESTs, Weakly similar to 2109260A B cell g	4.8
410361	BE391804	Hs.62661	SS,TM,GBP	guanylate binding protein 1, interferon- γ	4.8
423673	BE003054	Hs.1695	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 12 (macrophage e	4.8
450375	AA009647	Hs.8850	TM,disintegrin,Pep_M12B_propep,Reprolysin	a disintegrin and metalloproteinase domai	4.6
401575	NA		TM	Target Exon	4.6
428484	AF104032	Hs.184601	TM	solute carrier family 7 (cationic amino a	4.5
425071	NM_013989	Hs.154424	SS,TM,T4_deiodinase	deiodinase, iodothyronine, type II	4.4
431808	M30703	Hs.270833	SS,TM,EGF	amphiregulin (schwannoma-derived growth f	4.3
434699	AA643687	Hs.149425	TM,Nucleoside_tra2	Homo sapiens cDNA FLJ11980 fis, clone HEM	4.3
406687	M31126	Hs.272620	SS,Peptidase_M10,hemopexin	pregnancy specific beta-1-glycoprotein 9	4.2
404440			TM,MAGE	NM_021048:Homo sapiens melanoma antigen,	4.2
449228	AJ403107	Hs.148590	TM,PAF-AH,p450	protein related with psoriasis	4.2
444105	AW189097	Hs.166597	TM,cdherin	ESTs	4.1
409632	W74001	Hs.55279	SS,serpin	serine (or cysteine) proteinase inhibitor	4.1
423515	AA327017	Hs.162204	SS,TM,UPAR_LY6	ESTs	4.1
423738	AB002134	Hs.132195	SS,TM,trypsin,SEA	airway trypsin-like protease	4.1
423553	AA405635	Hs.96854	TM	ESTs, Weakly similar to DYLL_HUMAN CYTOPL	4.1
445537	AJ245671	Hs.12844	TM,ras	EGF-like-domain, multiple 6	4.0
446989	AK001898	Hs.16740	TM	hypothetical protein FLJ11036	4.0
428536	AI143139	Hs.2288	TM,efhand,Syndecan	visinin-like 1	3.9
413801	M62246	Hs.35406	TM	ESTs, Highly similar to unnamed protein p	3.9
429441	AJ224172	Hs.204096	Uteroglobulin	lipophilin B (uteroglobulin family member),	3.9
409601	AF237621	Hs.80828	TM,filamentfilament,C2	keratin 1 (epidermolytic hyperkeratosis)	3.8
439238	N47305	Hs.46668	TM	ESTs	3.8
446292	AF081497	Hs.279682	Ammonium_transp	Rh type C glycoprotein	3.8
405545			SS,TM,proteasome,lg,ABC_memb,tranABC_tran,	(MDR/TAP) (TAP2)	3.8
422938	NM_001809	Hs.1594	TM,thiolase	centromere protein A (17kD)	3.7
423217	NM_000094	Hs.1640	SS,TM,fn3,ywa,Collagen,Kunitz_BPTI	collagen, type VII, alpha 1 (epidermolysi	3.7
430686	NM_001942	Hs.2633	SS,TM,cdherin,Cadherin_C_term	desmoglein 1	3.7
444707	AI188613	Hs.41690	TM,cdherin	desmocollin 3	3.6
409582	R27430	Hs.271565	TM	ESTs	3.6
408771	AW732573	Hs.47584	TM,K_tetra,ion_trans	potassium voltage-gated channel, delayed-	3.6
400441	M15530	Hs.99879	TM,G-alpha	B-cell growth factor 1 (12kD)	3.6
413278	BE563085	Hs.833	TM,ubiquitinlaminin_G,laminin_EGF,kazal	interferon-stimulated protein, 15 kDa	3.6
426514	BE616633	Hs.170195	SS,TGFb_propeptide,TGF-beta	bone morphogenetic protein 7 (osteogenic	3.6
424927	AW973666	Hs.153850	SS	hypothetical protein C321D2.4	3.6
408591	AF015224	Hs.46452	SS,TM,Uteroglobulin	mammaglobin 1	3.5
407756	AA116021	Hs.38260	SS,UCH-1,UCH-2	ubiquitin specific protease 18	3.5
407137	T97307		TM,GDA1_CD39	gbys53h05.s1 Soares fetal liver spleen 1	3.5
411274	NM_002776	Hs.69423	trypsin	kallikrein 10	3.5
400666			SS,hemopexin,Peptidase_M10	NM_002425:Homo sapiens matrix metalloprot	3.5
412471	M63193	Hs.73946	SS,TM,Glycos_transf_3,Cern_acyltransf	endothelial cell growth factor 1 (platelet	3.4
450650	T65617	Hs.101257	TM	hypothetical protein MGC3295	3.4
451778	AI826131	Hs.71243	lg	ESTs, Weakly similar to zinc finger prote	3.4
430397	AI924533	Hs.105607	SS,TM	bicarbonate transporter related protein 1	3.4
449722	BE280074	Hs.23960	TM,cyclin	cyclin B1	3.4
422487	AJ010901	Hs.198267	TM,vwd	mucln 4, tracheobronchial	3.4
449101	AA205847	Hs.23016	SS,TM,7tm_1	G protein-coupled receptor	3.3
418994	AA296520	Hs.89546	SS,TM,lectin_c,sushi,EGF	selectin E (endothelial adhesion molecule	3.3
421379	Y15221	Hs.103982	SS,TM,IL8	small inducible cytokine subfamily B (Cys	3.3
414774	X02419	Hs.77274	SS,kirgline,lypsin	plasminogen activator, urokinase	3.3
431958	X63629	Hs.2877	SS,TM,Cadherin_C_term,cadherin	cadherin 3, type 1, P-cadherin (placental	3.3
418462	BE001596	Hs.85266	SS,TM,Integrin_B,fn3	integrin, beta 4	3.3
424687	J05070	Hs.151738	SS,Peptidase_M10,fn2,hemopexin	matrix metalloproteinase 9 (gelatinase B,	3.3
401466	NA		SS,TM,lypsin	C4000647-gil4758508jre[1]NP_004253.1] air	3.2
408113	T82427	Hs.194101	TM,7tm_3,Ribosomal_L13	Homo sapiens cDNA: FLJ20869 fis, clone AD	3.2
427359	AW020782	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, clone LN	3.2
452934	AA581322	Hs.4213	SS,TM,lg	hypothetical protein MGC16207	3.1
448988	Y09763	Hs.22785	SS,TM	gamma-aminobutyric acid (GABA) A receptor	3.1
439750	AL359053	Hs.57664	TM,Integrin_B,FcRn_B_lectinrm	Homo sapiens mRNA full length Insert cDNA	3.1
414696	AF002020	Hs.76918	SS,TM,Patched	Niemann-Pick disease, type C1	3.1
435604	AA625279	Hs.26892	TM	uncharacterized bone marrow protein BM040	3.1
453883	AI638516	Hs.22630	TM,Elts,SAM_PNT	cofactor required for Sp1 transcriptional	3.0
448733	NM_005629	Hs.187958	SS,TM,SNF,ABC_tran,isoeth,pkinase,DSPC,Ribosomal_L	solute carrier family 6 (neurotransmitter	3.0
444946	AW139205	Hs.156457	SS,TM,abhydrolase	hypothetical protein FLJ22408	3.0
437938	AI950067		TM,histone,lg,MHC_I	gb.wq05cd2.x1 NCI_CGAP_Kid12 Homo sapiens	3.0
424441	X14850	Hs.147097	TM,histone	H2A histone family, member X	3.0
427061	AB032971	Hs.173392	TM	KIAA1145 protein	3.0
409703	NM_006187	Hs.56009	SS	2'-5'-oligoadenylate synthetase 3 (100 kD	3.0
447313	U92981	Hs.18081	TGF-beta	Homo sapiens clone DT1P1B6 mRNA, CAG repe	3.0
431070	AW408164	Hs.249184	ABC_tran	transcription factor 19 (SC1)	2.9
446269	AW263155	Hs.14559	TM	hypothetical protein FLJ10540	2.9
421190	U95031	Hs.102482	TM,vwd	mucin 5, subtype B, tracheobronchial	2.9
452732	BE300078	Hs.80449	TM	Homo sapiens, clone IMAGE:3535294, mRNA,	2.9
443859	NM_013409	Hs.9914	SS,kazal	folistatin	2.9
446733	AA863360	Hs.26040	TM,p450	ESTs, Weakly similar to fatty acid omega-	2.9
449746	AI668594	Hs.176588	SS,p450	ESTs, Weakly similar to CP4Y_HUMAN CYTOCH	2.9
418844	M62982	Hs.1200	SS,TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase	2.9
414581	AA256213	Hs.72010	TM,Cam_acyltransf,Choline_kinase,SCO1-SenC	ESTs	2.8
431629	AJ077025	Hs.265827	SS,IRNA_antiSH2,SH3,pkinase	Interferon, alpha-inducible protein (clon	2.8
445873	AA250970	Hs.251946	SS,rm,PABPpkinase,14-3-3,rm	poly(A)-binding protein, cytoplasmic 1-II	2.8
438113	AI467908	Hs.8882	TM,7tm_1	ESTs	2.8
410310	J02931	Hs.62192	SS,TM,Tissue_fac	coagulation factor III (thromboplastin, t	2.8

5	411558	AA102670	Hs.70725	SS, TM	gamma-aminobutyric acid (GABA) A receptor	2.8
	413273	U75679	Hs.75257	TM,lg, pkinase	stem-loop (histone) binding protein	2.8
	426343	NM_014642	Hs.169387	TM,SCAN7tm_1	KIAA0036 gene product	2.8
	433345	AI681545	Hs.152982	SS	hypothetical protein FLJ13117	2.7
	452234	AW084176	Hs.223296	TM	ESTs, Weakly similar to I38022 hypothetical	2.7
	456181	L36463	Hs.1030	TM,RA,VPS9	ras inhibitor	2.7
	408380	AF123050	Hs.44532	TM,ubiquitin7tm_3,ANF_receptor,sushi	diubiquitin	2.7
	422278	AF072873	Hs.114218	TM,Frizzled,Fz	frizzled (Drosophila) homolog 6	2.7
10	446839	BE091926	Hs.16244	TM	mitotic spindle coiled-coil related prote	2.7
	416250	AA581388	Hs.73452	TM,REJ,PLAT,PKD,WSC,LRRCCT,GPSPMP22_Claudin	hypothetical protein MGC10791	2.7
	407287	AI678812		TM,rascadherin	gb:tu59d08.x1 NCL_CGAP_Gas4 Homo sapiens	2.7
	412977	AA125910	Hs.191461	TGF-beta	ESTs	2.7
	400298	AA032279	Hs.61635	TM	six transmembrane epithelial antigen of t	2.7
15	425483	AF231022	Hs.158159	EGF,cadherin,laminin_G	FAT tumor suppressor (Drosophila) homolog	2.7
	430152	AB001325	Hs.234642	SS, TM, MIP	aquaporin 3	2.7
	444006	BE395085	Hs.10086	SS, TM	type I transmembrane protein Fn14	2.7
	418869	AW516565		TM, RasGAP, IQ, WW	gb:xx01d05.x1 Soares_NHCCc_cervical_tumor	2.7
	416658	U03272	Hs.79432	SS, TM, EGF, TB	fibrillin 2 (congenital contractual erac	2.6
20	410290	AA402307	Hs.322844	SS, TM, Sema, TIG, Plexin_repeat	hypothetical protein DKFZp564A176	2.6
	419567	AU077005	Hs.92208	SS, TM, disintegrin, Reprolysin, Pep_M12B_propep	a disintegrin and metalloproteinase domain	2.6
	406871	AA129547	Hs.285754	TM, pkinase, Plexin_repeat, Sema, TIG, LIM	met proto-oncogene (hepatocyte growth fac	2.6
	434444	AI755276	Hs.101257	TM	hypothetical protein MGC3295	2.6
	421817	AF146074	Hs.108660	TM, ABC_tran, ABC_membrane, Rhomboid	ATP-binding cassette, sub-family C (CFTR)	2.6
25	431890	X17033	Hs.271986	vwa, FG-GAP, Integrin_A	Integrin, alpha 2 (CD49B, alpha 2 subunit	2.6
	452281	T93500	Hs.28792	TGF-beta, TGFb_propeptide	Homo sapiens cDNA FLJ11041 fis, clone PLA	2.6
	421508	BE302798	Hs.105097	TM, TK	thymidine kinase 1, soluble	2.6
	453331	AI240665	Hs.8895	TM, disintegrin, Pep_M12B_propep, Reprolysin	ESTs	2.6
	447197	R36075		TM, SDF	gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.5
30	459688	U72671	Hs.151250	SS, TM, lg	intercellular adhesion molecule 5, telonc	2.5
	437412	BE069288	Hs.34744	TM, ABC_tran, ABC_membrane, Rhomboid	Homo sapiens mRNA; cDNA DKFZp547C136 (fro	2.5
	429413	NM_014058	Hs.201877	trypsin	DESC1 protein	2.5
	424420	BE614743	Hs.146688	TM, MAPEG	prostaglandin E synthase	2.5
	427239	BE270447	Hs.174070	TM, UQ_con	ubiquitin carrier protein	2.5
35	407103	AA424881	Hs.256301	TM, cNMP_binding, trypsin	hypothetical protein MGC13170	2.5
	431130	NM_006103	Hs.2719	SS, TM, wrap	epididymis-specific, whey-acidic protein	2.5
	453379	AA035261	Hs.61753	PAN, krtgite, trypsin	ESTs	2.5
	421733	AL119671	Hs.1420	SS, TM, lg, pkinase	fibroblast growth factor receptor 3 (acho	2.5
	452220	BE158008	Hs.212256	TM, Integrin_A, FG-GAP	ESTs	2.5
40	417975	AA641836	Hs.30085	SS, trypsin	hypothetical protein FLJ23186	2.5
	440381	AA917808	Hs.190495	TM	ESTs	2.5
	441794	AW197794	Hs.253338	TM	ESTs	2.5
	439108	AW163034	Hs.6467	SS, TM	synaptogyrin 3	2.5
	401103	NA		TM, vwd	C12001233g17305361[ref NP_038652.1] olo	2.4
45	430630	AW269920	Hs.2621	TM, cystatin	cystatin A (stefin A)	2.4
	430129	BE301708	Hs.233955	TM, Glyco_transf_11	hypothetical protein FLJ20401	2.4
	415621	AI648602	Hs.55468	TM, histone, Sec1sugar_tr	ESTs	2.4
	402745			SS, TM, EGF, kd_recept_L_b, thyroglobulin_1	NM_002508: Homo sapiens nidogen (enactin)	2.4
	407758	D50915	Hs.38365	SS, TM	KIAA0125 gene product	2.4
50	457570	AA579428		TM	gb:nf37c09.s1 NCL_CGAP_Pr2 Homo sapiens c	2.4
	429574	BE268321	Hs.208912	SS, TM	hypothetical protein MGC861	2.4
	431211	M86849	Hs.323733	SS, TM, connexin	gap junction protein, beta 2, 26kD (conn	2.4
	452865	AI924046	Hs.119587	SS, TM, PMP22_Claudin	ESTs, Weakly similar to A47582 B-cell gro	2.4
	420511	AF052692	Hs.98485	SS, TM, connexin	gap junction protein, beta 3, 31kD (conn	2.4
	437897	AA770561	Hs.146170	SS, pro_isomerase	hypothetical protein FLJ22969	2.4
55	437848	AA773868	Hs.244569	TM	esophagus cancer-related gene-2	2.4
	418432	M14156	Hs.85112	Insulin	Insulin-like growth factor 1 (somatomedin	2.3
	438108	AI471795	Hs.287776	TM	vanilloid receptor-related osmotically ac	2.3
	453408	AI192987	Hs.61784	pkinae, Furin-like, Recep_L_domain	hypothetical protein FLJ14451	2.3
	435542	AA687378	Hs.269533	pkinae, RhoGEF, lg, PH, SH3	ESTs	2.3
60	434517	AA635690	Hs.337251	TM	hypothetical protein MGC2487	2.3
	431630	NM_002204	Hs.265829	SS, TM, FG-GAP, Integrin_A	Integrin, alpha 3 (antigen CD49C, alpha 3	2.3
	422310	AA316622	Hs.98370	SS, TM, fn3, lg, pkinase, Ribosomal_L36e, p450	cytochrome P450, subfamily IIS, polypept	2.3
	441954	AI744935	Hs.8047	TM, Band_7, AAA, cdo48_N	Fanconi anemia, complementation group G	2.3
	416091	AF295370	Hs.283082	SS, TM, Defensin_beta	defensin, beta 3	2.3
65	429359	W00482	Hs.2399	SS, TM, Peptidase_M10, hemopexin	matrix metalloproteinase 14 (membrane-ins	2.3
	409402	AF208234	Hs.695	TM, cystatin	cystatin B (stefin B)	2.3
	432284	AA532807	Hs.105822	TM, pkinase	ESTs	2.3
	408243	Y00787	Hs.624	SS, TM, IL8	interleukin 8	2.3
70	423229	AC003965	Hs.125532	SS, trypsin	protease, serine, 26	2.3
	408713	NM_001248	Hs.47042	GDA1_CD39	octonucleoside triphosphate diphosphohydr	2.3
	440502	AI824113	Hs.76281	RGS, GoLoco, RBD	regulator of G-protein signalling 12	2.3
	429929	AB014583	Hs.226275	TM	KIAA0683 gene product	2.3
	439963	AW247529	Hs.6793	TM, p450Ets	platelet-activating factor acetylhydrolas	2.3
75	428953	AA306610	Hs.194676	SS, TM, TNFR_c6, arl, Stathmin, DEAD	tumor necrosis factor receptor superfamil	2.3
	439398	AA284267	Hs.221504	SS	ESTs	2.2
	440371	BE268550	Hs.80449	TM	Homo sapiens, clone IMAGE:3535294, mRNA,	2.2
	452203	X57522	Hs.158164	SS, TM, ABC_tran, ABC_membrane	transporter 1, ATP-binding cassette, sub-	2.2
	407811	AW190902	Hs.40098	SS	cysteine knot superfamily 1, BMP antagoni	2.2
80	432078	BE314877	Hs.24553	TM	hypothetical protein FLJ12541 similar to	2.2
	429113	D28235	Hs.196384	SS, TM, EGF	prostaglandin-endoperoxide synthase 2 (pr	2.2
	452755	AW138937	Hs.213436	Glyco_transf_29	ESTs, Weakly similar to A34087 hypothetic	2.2
	428434	AW363590	Hs.65551	SS	Homo sapiens, Similar to DNA segment, Chr	2.2
	429922	Z97630	Hs.226117	TM, linker_histone7tm_1	H1 histone family, member 0	2.2

5	417903	NM_002342	Hs.1116	SS,TM,ASC,TNFR_c6	lymphotoxin beta receptor (TNFR superfamily	2.2
	422012	AW403423	Hs.110746	SS,homobox,pou	HCR (a-helix coiled-coil rod homologue)	2.2
	433090	AJ720050	Hs.145362	SS,TM	immortalization-upregulated protein	2.2
	417576	AA339449	Hs.82285	TM,AIRS,formyl_transf,GARS	phosphoribosylglycinamide formyltransferase	2.2
	409994	D86864	Hs.57735	IP_transSH2,SH3	acetyl LDL receptor; SREC	2.2
	417433	BE270266	Hs.82128	SS,TM,LRRCT,LRRNT,LRR	ST4 oncofetal trophoblast glycoprotein	2.2
	416763	AJ908127	Hs.79748	TM,alpha-amylase7tm_1	solute carrier family 3 (activators of di	2.2
	425999	AW513051	Hs.332981	TM,FAD_binding_2,P53PA,Ribosomal_S2,FAD_bindi	ESTs, Weakly similar to I38022 hypothetic	2.2
10	452799	AJ948829	Hs.213786	TM	ESTs	2.2
	414733	BE514535	Hs.77171	TM,MCMHeme_oxygenase	minichromosome maintenance deficient (S.	2.2
	448153	Y10805	Hs.20521	SS,TM,Na_Ca_Ex	HMT1 (hnRNP methyltransferase, S. cerevis	2.2
	428969	AF120274	Hs.194589	SS	artemin	2.2
	443171	BE281128	Hs.9030	SS,TM,7tm_1,mm	TONDU	2.2
	408308	AL033377	Hs.44197	TM,7tm_2	hypothetical protein DKFZp564D0462	2.2
15	409533	AW969643	Hs.21291	TM	mitogen-activated protein kinase kinase k	2.2
	408201	AK000568	Hs.43654	TM	hypothetical protein FLJ20561	2.1
	408995	AJ979168	Hs.82226	TM	glycoprotein (transmembrane) nmb	2.1
	417900	BE250127	Hs.82906	TM,WD40_pro_Isomerase	CDC20 (cell division cycle 20, S. cerevis	2.1
	437191	NM_006846	Hs.331555	SS,TM,kazal	serine protease inhibitor, Kazal type, 5	2.1
20	412834	R77123	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, clone LN	2.1
	431117	AF003522	Hs.250500	SS,TM,DSL,EGF	delta (Drosophila)-like 1	2.1
	447674	BE270640	Hs.19192	TM,kinaseras,arf	cyclin-dependent kinase 2	2.1
	409651	H96643	Hs.283565	bZIPcofilin_ADF,EGF	FOS-like antigen-1	2.1
25	440495	AA887212	Hs.14161	TM,NSFN_Ca_Ex	hypothetical protein DKFZp434I1930	2.1
	429415	NM_002593	Hs.202097	SS,CUB,NTR,MAM,TIL,TLA,vwd,EPO_TPO	procollagen C-endopeptidase enhancer	2.1
	421013	M62397	Hs.1345	TM	mutated in colorectal cancers	2.1
	447827	U73727	Hs.19718	SS,TM,Y_phosphatase,fn3,jg,MAM	protein tyrosine phosphatase, receptor ty	2.1
	449224	AW995911	Hs.299883	fn3	hypothetical protein FLJ23399	2.1
	452679	Z42387	Hs.83883	TM	transmembrane, prostate androgen induced	2.1
30	409956	AW103364	Hs.727	SS,TGF-beta,TGFB_propeptide	inhibin, beta A (activin A, activin AB al	2.1
	438580	AA811262	Hs.299202	TM,kinasesugar_tr	ESTs	2.1
	406400			SS,TM,trypsin	NM_007196:Homo sapiens kallikrein 8 (neur	2.1
	424955	AW956282	Hs.144609	TM	Homo sapiens, Similar to RIKEN cDNA 57305	2.1
35	412270	AC005262	Hs.73797	TM,G-alpha	guanine nucleotide binding protein (G pro	2.1
	428471	X57348	Hs.184510	TM,14-3-3	stratfin	2.1
	427375	AL035460	Hs.177536	SS,Zn_carbOpept,hormone5Reprolysin	metallocarboxypeptidase CPX-1	2.1
	416498	U33632	Hs.79351	TM	potassium channel, subfamily K, member 1	2.1
	423453	AW450737	Hs.128791	SS,Granin,CDP-OH_P_transf	CGI-09 protein	2.1
40	417944	AU077196	Hs.82985	SS,COLFI,Collagen,vwc	collagen, type V, alpha 2	2.1
	424197	AF096834	Hs.142989	SS,TM,CSD	germ cell specific Y-box binding protein	2.1
	446163	AA026880	Hs.25252	TM,fn3	prolactin receptor	2.1
	417331	AW411297	Hs.81972	TM,SH2,PID	SHC (Src homology 2 domain-containing) tr	2.1
	430413	AW842182	Hs.241392	IL8,PX	small inducible cytokine A5 (RANTES)	2.1
45	421685	AF189723	Hs.106778	TM,E1-E2_ATPase,HydrolaseE1-E2_ATPase	ATPase, Ca transporting, type 2C, member	2.1
	407305	AA715284		TM,kinase,Sema,Plaxin_repeat,TIG,LIM	gb:mv3503.r1 NCI_CGAP_Br5 Homo sapiens c	2.1
	407792	AJ077715	Hs.39384	SS	putative secreted ligand homologous to f	2.0
	418695	AA447014	Hs.193261	SS	hypothetical protein MGC2991	2.0
	439738	BE245502	Hs.9598	TM,RasGAP,IQ,WW	sema domain, immunoglobulin domain (Ig).	2.0
50	433398	AW843150	Hs.112412	TM,PMP22_Claudin	ESTs	2.0
	456327	H68741	Hs.38774	TM,Glyco_transf_8	ESTs	2.0
	445872	X97058	Hs.16362	TM	pyrimidinergic receptor P2Y, G-protein co	2.0
	419726	U50330	Hs.1274	SS,TM,Astacin,CUB,EGF	bone morphogenetic protein 1	2.0
	410116	AW630671	Hs.58636	SS,TM	squamous cell carcinoma antigen recognize	2.0
55	426500	NM_014638	Hs.170156	TM	KIAA0450 gene product	2.0
	452194	AJ694413	Hs.332649	TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfamily 1	2.0
	418140	BE613836	Hs.83551	TM,E1-E2_ATPase	microfibrillar-associated protein 2	2.0
	425855	AF135025	Hs.159679	SS,trypsin	kallikrein 12	2.0
	434346	AA630445	Hs.116773	TM,Ferri_reduct	ESTs	2.0
60	426274	D38122	Hs.2007	TM,TNF	tumor necrosis factor (ligand) superfamily	2.0
	440008	AW051683	Hs.277686	TM,RhoGEF,FYVE,PH	ESTs	2.0
	424634	NM_003613	Hs.151407	lg,isp_1	cartilage intermediate layer protein, nuc	2.0
	446641	AL049229	Hs.15787	TM,kinase,mm	Homo sapiens mRNA: cDNA DKFZp564O1016 (tr	2.0
	418851	AJ417828	Hs.192435	TM	ESTs	2.0
65	440351	AF030933	Hs.7179	TM,Rad1,Cadherin_C_lem	RAD1 (S. pombe) homolog	2.0
	439496	BE616501	Hs.32343	SS	Homo sapiens, Similar to RIKEN cDNA 11100	2.0
	454197	BE140966		TM,Ammonium_transpkinasin,Ammonium_transp	gb:MR0-HT0065-081199-002-b06 HT0065 Homo	2.0
	433573	AF234887	Hs.57652	TM,7tm_2,GPSIRNA-synL_2b,SeryLIRNA_N	cadherin, EGF LAG seven-pass G-type recep	2.0
	429211	AF052693	Hs.198249	TM,connexin	gap junction protein, beta 5 (connexin 31	2.0
70	420737	L08096	Hs.99899	SS,TM,TNF	tumor necrosis factor (ligand) superfamily	2.0
	455333	AW897851		TM,Glyco_hydro_2	gb:RC1-NN0063-100500-022-c08 NN0063 Homo	2.0
	414784	NM_000344	Hs.288986	SS,TM,BIR	survival of motor neuron 1, telomeric	2.0
	435836	AW292532	Hs.250175	TM,GNS1_SUR4	homolog of yeast long chain polyunsaturat	2.0
	411789	AF245505	Hs.72157	TM,jg,LRRCT	DKFZP564I1922 protein	2.0
75	441455	AJ271671	Hs.7854	TM,Ras,DENN	zinc/iron regulated transporter-like	2.0
	426068	AF029778	Hs.166154	SS,TM,DSL,EGF,NUDIX	jagged 2	2.0
	439733	AL365412	Hs.107203	TM,Sm	hypothetical protein from EUROIMAGE 17593	2.0
	435014	BE560899	Hs.10026	TM,Ribosomal_L17	mitochondrial ribosomal protein L17	1.9
	457819	AA057484	Hs.35406	TM	ESTs, Highly similar to unnamed protein p	1.9
80	422737	M26939	Hs.119571	SS,Collagen,COLFI	collagen, type III, alpha 1 (Ehlers-Danto	1.9
	431104	AW970859	Hs.313503	Sema,jg	ESTs	1.9
	432210	AJ567421	Hs.273330	TM,laminin_G,laminin_EGF,kazalubiquitin	Homo sapiens, clone IMAGE:3544662, mRNA,	1.9
	436511	AA721252	Hs.291502	TM,disintegrin,Reprolysin,Pepp_M12B_propep,kinase,	ESTs	1.9
	419216	AJ076718	Hs.164021	SS,IL8	small inducible cytokine subfamily B (Cys	1.9

	432169	Y00971	Hs.2910	TM,Prbbsyltran	phosphoribosyl pyrophosphate synthetase 2	1.9
	441128	AA570256	Hs.54628	TM,ras	ESTs, Weakly similar to T23273 hypothetical	1.9
	447160	AA330310	Hs.24181	TM	ESTs	1.9
5	419138	U48508	Hs.89631	TM,RYDR,ITPR,RyR,SPRY	ryanodine receptor 1 (skeletal)	1.9
	457817	AA247751	Hs.79572	TM,hemopexin,Peptidase_M10	cathepsin D (lysosomal aspartyl protease)	1.9
	431009	BE149762	Hs.48956	SS,TM,connexin	gap junction protein, beta 6 (connexin 30)	1.9
	428957	NM_003881	Hs.194679	SS,TM,vwc,IGFBP,isp_1	WNT1 inducible signaling pathway protein	1.9
	418546	AA224827		TM,vwa,FG-GAP,integrin_A	gbnrc32g04.s1 NCL_CGAP_P2 Homo sapiens c	1.9
10	400749			SS,TM,ldl_recept_a,fn3,ldl_recept_b	NM_003105-Homo sapiens sortilin-related	1.9
	408369	R38438	Hs.182575	F-protein	solute carrier family 15 (H777) transporte	1.9
	422765	AW409701	Hs.1578	TM,BIR	baculoviral IAP repeat-containing 5 (surv	1.9
	417409	BE272508	Hs.82109	TM,Syndecan	syndecan 1	1.9
	407720	AB037776	Hs.38002	TM,calponin,CH	KIAA1355 protein	1.9
15	418830	BE513731	Hs.88959	TM,CDP-OH_P_transf,MCM	hypothetical protein MGC4816	1.9
	434769	AA648884	Hs.134278	TM,CDP-OH_P_transf,MCM	Homo sapiens cDNA FLJ12676 fis, clone NT2	1.9
	421593	NM_017436	Hs.105956	SS,TM	globotriaosylceramide/CD77 synthase; Gb3/	1.9
	426064	BE387014	Hs.166146	TM,WH1	Homer, neuronal immediate early gene, 3	1.9
	404604	NA		TM	Target Exon	1.9
20	422753	AI928995	Hs.1575	SS,TM,Sm	small nuclear ribonucleoprotein D3 polype	1.9
	422739	H20106	Hs.119591	SS,Cist_adaptor_s	adaptor-related protein complex 2, sigma	1.9
	433068	NM_008456	Hs.288215	SS,Prbbsyltran	stalytransferase	1.9
	419594	AA013051	Hs.91417	TM	topoisomerase (DNA) II binding protein	1.9
	428188	M98447	Hs.22	TM,Transglutamin_C,Transglutamin_N,Transglu_core	transglutaminase 1 (K polypeptide epiderm	1.9
25	428343	AL043021	Hs.12705	TM,Rhomboid,HMG_boxTPR	ESTs	1.9
	429592	AB029041	Hs.209646	Troponin	KIAA1118 protein	1.9
	431620	AA126109	Hs.264981	C2,PH,RasGAP,NTP_transf_2	Z'-S'-oligoadenylate synthetase 2 (69-71	1.9
	424670	W61215	Hs.116651	Ig	epithelial V-like antigen 1	1.9
	428373	AI751656	Hs.183986	SS,TM,Ig	poliovirus receptor-related 2 (herpesviru	1.9
30	453449	W16752	Hs.32581	SS,Ig,Sema	sema domain, immunoglobulin domain (Ig).	1.9
	432304	AA932186	Hs.69297	TM,7m_1	ESTs	1.9
	432673	AB028859	Hs.278605	TM,DnaJ,DnaJ_CDnaJ	DnaJ (Hsp40) homolog, subfamily B, member	1.9
	416207	NM_014745	Hs.336433	SS,TM,zf-OHHC	Homo sapiens, clone MGC2908, mRNA, comp	1.9
	408988	AL119844	Hs.49476	TM,Plexin_repeat,Sema,isp_1	Homo sapiens clone TUAB C1-du-chat regio	1.9
35	417426	NM_002291	Hs.82124	SS,Laminin_EGF,laminin_Nterm	laminin, beta 1	1.9
	443883	AA114212	Hs.9930	SS,TM,serpin,Marek_A	serine (or cysteine) proteinase inhibitor	1.9
	433328	AW298159	Hs.23644	SS,TM	ESTs, Weakly similar to S65824 reverse tr	1.9
	419981	AA897581	Hs.128773	TM,Skl_Sno	ESTs	1.8
	420931	AF044197	Hs.100431	SS,TM,IL8	small inducible cytokine B subfamily (Cys	1.8
40	415023	AA932146	Hs.133494	TM,Ribosomal_S17Ribosomal_L13	Homo sapiens clone TCCCA00164 mRNA seque	1.8
	413644	BE154910	Hs.278793	TM,Glyco_hydro_2	ESTs, Weakly similar to Z195_HUMAN ZINC F	1.8
	449987	AW079749	Hs.184719	TM,ABC_tran,ABC_membrane1on_trans	ESTs, Weakly similar to ALU1_HUMAN ALU SU	1.8
	421340	F07783	Hs.1369	SS,sush1	decay accelerating factor for complement	1.8
	417866	AW067903	Hs.82772	SS,TM,Collagen,COL1,TPSP	collagen, type XI, alpha 1	1.8
45	430259	BE550182	Hs.127826	TM,transmembrane4RasGEF,RA	RalGEF-like protein 3, mouse homolog	1.8
	432998	AA835948	Hs.153307	TM,SDF	ESTs	1.8
	431871	NM_016937	Hs.267289	TM,NA	polymerase (DNA directed), alpha	1.8
	411773	NM_006789	Hs.72026	trypsin	protease, serine, 21 (testisin)	1.8
	425247	NM_005940	Hs.155324	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 11 (stromelysin	1.8
50	422976	AU076657	Hs.1600	TM,cpn60_TCP1,Sema	chaperonin containing TCP1, subunit 5 (ep	1.8
	425159	NM_004341	Hs.154868	SS,TM,GATase,OTCase,CPSase_L_chain,Dihydrooro	carbamoyl-phosphate synthetase 2, asparta	1.8
	447776	AI525625	Hs.130181	Ricin_B_lectin	UDP-N-acetyl-alpha-D-galactosamine:polype	1.8
	426908	AW815163	Hs.172851	SS,TM,fusion_gly,Myosin_tailadh_short	arginase, type II	1.8
	408116	AA251393	Hs.289052	TM,Na_Ca_ExCam_acyltransf	Homo sapiens, Similar to RIKEN cDNA 54304	1.8
55	417847	AI521558	Hs.7331	Uteroglobulin	hypothetical protein FLJ122316	1.8
	415791	H09366	Hs.78853	SS,TM,UNG	uracil-DNA glycosylase	1.8
	407903	AI287341	Hs.154029	TM,ubiquitin,laminin_G,laminin_EGF,kazal	bHLH factor Has4	1.8
	422511	AU076442	Hs.117938	TM,p450	collagen, type XVII, alpha 1	1.8
	414117	W88559	Hs.1787	TM,ion_trans,K_tetra	proteolipid protein 1 (Pelizaeus-Merzbach	1.8
60	426841	AI052358	Hs.193726	TM,asp	ESTs	1.8
	415272	AA164215	Hs.203186	TM,TPR,plknase,Ig,B56	ESTs	1.8
	426440	BE382756	Hs.169902	TM,sugar_tr,Fork_head	solute carrier family 2 (facilitated gluc	1.8
	419488	AA316241	Hs.90691	FGF	nucleophosmin/nucleoplasmn 3	1.8
	418452	BE379749	Hs.85201	SS,TM,lectin_c	C-type (calcium dependent, carbohydrate-r	1.8
65	431363	M86528	Hs.266902	SS,NGF	neurotrophin 5 (neurotrophin 4/5)	1.8
	440975	AW499914	Hs.7579	SS,TM	hypothetical protein FLJ10402	1.8
	438962	BE046594		TGF-beta,bZIP	gbnrc41c11.x1 NCL_CGAP_RDF2 Homo sapiens	1.8
	414602	AW630088	Hs.76550	SS	Homo sapiens mRNA; cDNA DKFZp564B1264 (tr	1.8
	418054	NM_002318	Hs.83354	TM,milo_carr,Lysyl_oxidase	lysyl oxidase-like 2	1.8
70	440501	AA887391	Hs.202229	TM,Galactosyl_T	ESTs	1.8
	449309	AW589823	Hs.224189	TM	ESTs	1.8
	421461	AW291023	Hs.97255	TM,Lysyl_oxidase,SCP2,Band_7	ESTs, Weakly similar to A46010 X-linked r	1.8
	412584	X54870	Hs.74085	TM,lectin_c	DNA segment on chromosome 12 (unique) 248	1.8
	441565	AW953575	Hs.303125	TM	p53-induced protein PIGPC1	1.8
75	431837	T79326	Hs.326553	TM,7m_3,ANF_receptor,sush1	olfactory receptor, family 2, subfamily I	1.8
	438251	BE515065	Hs.285885	SS,Y_phosphataseTIG	nucleolar protein (KKE/O repeat)	1.8
	448633	AA311426	Hs.21635	TM,EGF,laminin_G,fibrinogen_C,F5_F8_type_C,tubulin	tubulin, gamma 1	1.8
	424291	AL120051	Hs.144700	TM,Ephrin,Hist_deacetyl	ephrin-B1	1.8
	415388	AF018081	Hs.78409	SS,TM,TSPN,Collagen	collagen, type XVIII, alpha 1	1.8
80	435550	AI224456	Hs.4934	TM,LRR,LRRCT	Hsapiens polyA site DNA	1.8
	448568	AA149121	Hs.71947	TM,LRRCT	ESTs	1.8
	439246	AA490072	Hs.77783	SS,TM,REJ,PLAT,PKD,WSC,LRRCT,GPSPMP22_Cla	membrane-associated tyrosine- and threonil	1.8
	410001	AB041036	Hs.57771	SS,TM,tryptsin	kallikrein 11	1.8
	417312	AW888411	Hs.81915	SS,Stathmin	leukemia-associated phosphoprotein p18 (s	1.8

5	444152	AI125694	Hs.149305	TM	hypothetical protein MGC2603	1.8
	453454	AW052006	Hs.8551	TM	PRP4/STKWD splicing factor	1.8
	449320	AB030835	Hs.23476	SS,adenylatekinase	Cip1-interacting zinc finger protein	1.8
	428329	AA426091	Hs.98453	TM,Gal-bind,Jectin	ESTs, Moderately similar to R27328 2 [Hs	1.8
	452875	BE275760	Hs.30928	TM,Apolipoprotein	DNA segment on chromosome 19 (unique) 117	1.8
10	444031	BE271513	Hs.25303	TM,Peptidase_M10,hemopexin	hypothetical protein FLJ13154	1.8
	443534	AI076123		TM	gb:ay92e04.x1 Scores_fetal_liver_spleen_1	1.8
	413313	NM_002047	Hs.75280	TM,WHEP-TRS,7tm_2	glycyl-LRNA synthetase	1.8
	452874	AK001061	Hs.30925	SS	hypothetical protein FLJ10199	1.8
	453140	AA032238	Hs.170531	TM	ESTs	1.8
15	418641	BE243136	Hs.86947	SS,TM,disintegrin,Pep_M12B_propep,Reprolysin	a disintegrin and metalloproteinase domain	1.8
	432925	AA878324	Hs.192734	SS	ESTs	1.8
	453857	AL080235	Hs.35861	TM	DKFZP586E1621 protein	1.8
	457663	AW371946	Hs.337459	TM	ESTs	1.8
	452873	AK001247	Hs.30922	TM	hypothetical protein FLJ10385	1.8
20	436396	AI683487	Hs.152213	SS,wnt	wingless-type MMTV integration site family	1.8
	452835	AK001269	Hs.30738	TM	hypothetical protein FLJ10407	1.7
	459647	R34107	Hs.198287	Ig	pregnancy specific beta-1-glycoprotein 11	1.7
	418245	AA088767	Hs.83883	TM,PEPCK	transmembrane, prostate androgen induced	1.7
	448484	BE613340	Hs.334725	TM	Homo sapiens, Similar to RIKEN cDNA 94300	1.7
25	431369	BE184455	Hs.251754	SS,wap	secretory leukocyte protease inhibitor (a	1.7
	434877	AW974792	Hs.292171	TM	ESTs	1.7
	428923	BE047698	Hs.188785	TM	ESTs	1.7
	402915	NA		TM,HCO3_cotransp	ENSP00000202587-Bicarbonate transporter-	1.7
	420185	AL044056	Hs.158047	TM	ESTs	1.7
30	445739	AW136354	Hs.145303	TM	ESTs	1.7
	409435	AI810721	Hs.95424	TM,p450	ESTs	1.7
	408688	AI634522	Hs.152925	TM	KIAA1268 protein	1.7
	420085	AI741909	Hs.44680	TM	hypothetical protein FLJ20979	1.7
	433933	AI754389	Hs.133494	TM,Ribosomal_S17Ribosomal_L13	Homo sapiens clone TCCCA00164 mRNA sequence	1.7
35	430965	AA489732	Hs.154918	hormone_rec,Prog_receptor,zf-C4	ESTs	1.7
	414703	BE243877	Hs.76941	SS,TM,Na_K-ATPaseE2F_TDP	ATPase, Na ⁺ transporting, beta 3 polypept	1.7
	423464	NM_016240	Hs.128856	TM,Collagen	CSR1 protein	1.7
	416737	AF154335	Hs.79691	SS,TM,LIM,PDZsugar_tr,PDZ,LIM	LIM domain protein	1.7
	409012	AL117435	Hs.48725	TM,RhoGEFzf-DHHC,adh_short	DKFZP434I216 protein	1.7
40	423804	AW403448	Hs.1705	TM,IRF	interferon-stimulated transcription factor	1.7
	410418	D31382	Hs.63325	SS,TM,trypsin,ldl_recept_a	transmembrane protease, serine 4	1.7
	440028	AW473675	Hs.125843	TM	ESTs, Weakly similar to T17227 hypothetical	1.7
	457646	AA725650	Hs.112948	TM,SPRY	ESTs	1.7
	445439	BE243084	Hs.12719	SS,TGF-beta	regulator of nonsense transcripts 1	1.7
45	420426	AA262045	Hs.36567	TM,Galactosyl_T_2ATP-synt_C	Homo sapiens cDNA FLJ14227 fis, clone NT2	1.7
	431341	AA307211	Hs.251531	TM,proteasome	proteasome (prosome, macropain) subunit,	1.7
	412338	AA151527	Hs.69485	TM,Sema,Plaxin_repeat,TIG,Plaxin_repeat	hypothetical protein FLJ12436	1.7
	414799	AI752416	Hs.77326	SS,thyroglobulin_1,JGFBP	insulin-like growth factor binding protein	1.7
	452700	AI859390	Hs.288940	TM,DIX,RGS,thioredo	five-span transmembrane protein M83	1.7
50	430877	NM_005269	Hs.2693	GST_C,IRNA-synt_L_1,WHEP-TRS,TGF-beta	glioma-associated oncogene homolog (zinc	1.7
	428624	AI125222	Hs.98712	TM,thioredo,Y_phosphatase,MAM,Ig,fn3MSP_domain	hypothetical protein DKFZp434H0311	1.7
	444065	AW449415	Hs.10260	TM,Ion_trans	Homo sapiens cDNA FLJ11341 fis, clone PLA	1.7
	416319	AI815601	Hs.79197	SS,TM,Ig	CD83 antigen (activated B lymphocytes, tm	1.7
	429367	AB007867	Hs.278311	Sema,Plaxin_repeat,TIG	plexin B1	1.7
55	430425	AA531428	Hs.241412	TM	apolipoprotein L, 2	1.7
	441668	AI611973	Hs.127525	TM,Ammonium_transp	ESTs	1.7
	418469	U34879	Hs.85279	SS,TM,adh_short	hydroxysteroid (17-beta) dehydrogenase 1	1.7
	450835	BE262773	Hs.25584	TM,ArfGap	hypothetical protein FLJ10767	1.7
	418859	AA229558		TM	gb:ncf15d10.1 NCL_CGAP_P1 Homo sapiens c	1.7
60	425304	AA463844	Hs.31339	TM,Ig,ITAM	fibroblast growth factor 11	1.7
	423635	X85019	Hs.130181	TM,Rickn_B_Jectin	UDP-N-acetyl-alpha-D-galactosamine:polype	1.7
	414820	AA371931	Hs.77422	TM,Ion_trans,LIM,Synaptophysin	proteolipid protein 2 (colonic epithelium	1.7
	440654	AW014242	Hs.159998	TM,connexin	ESTs	1.7
	412276	BE262621	Hs.73798	SS,MIF	macrophage migration inhibitory factor (g	1.7
65	422087	X58968	Hs.111301	SS,Peptidase_M10,fn2,hemopexin	matrix metalloproteinase 2 (gelatinase A,	1.7
	407151	H25836	Hs.301527	SS,TNF	ESTs, Moderately similar to unknown [Hsa	1.7
	410726	AI623659	Hs.15936	TM,PX	ESTs	1.7
	452012	AA307703	Hs.279766	TM,kinesin	kinesin family member 4A	1.7
	433627	AF078866	Hs.284296	TM,SURF4,SURF1,DEADilipocalin	Homo sapiens cDNA: FLJ22993 fis, clone KA	1.7
70	409220	BE243323	Hs.51233	TM,death,TNFR_c6	tumor necrosis factor receptor superfamily	1.7
	427082	AB037858	Hs.173484	TM,mito_carr	hypothetical protein FLJ10337	1.7
	426410	BE298446	Hs.305890	TM,Bcl-2,BH4	BCL2-like 1	1.7
	433598	AI762836	Hs.271433	TM,Cytidylyltransf,SIR27tm_2	ESTs, Moderately similar to ALU2_HUMAN AL	1.7
	436495	BE285948	Hs.290874	TM,Armadillo_seg	ESTs, Weakly similar to ALU8_HUMAN ALU SU	1.7
75	422032	AA476966	Hs.110857	TM,TFIIS,RNA_POL_M_15KDsperin,hormone_rec,zf-C4	polymerase (RNA) III (DNA directed) polyp	1.7
	429736	AF125304	Hs.212680	SS,TNFR_c6	tumor necrosis factor receptor superfamily	1.7
	427600	AW630918	Hs.179774	TM,Transglutamin_C,Transglutamin_N,Transglut_core	proteasome (prosome, macropain) activator	1.7
	431981	AA664069	Hs.115779	laminin_B,laminin_EGF	ESTs	1.7
	407736	N41744	Hs.19978	TM,Sulfatase	CGI-30 protein	1.7
80	420187	AK001714	Hs.95744	TM	hypothetical protein similar to ankryrin r	1.7
	424620	AA101043	Hs.151254	SS,TM,trypsin	kallikrein 7 (chymotryptic, stratum come	1.7
	430488	D19589	Hs.13453	TM	hypothetical protein FLJ14753	1.7
	423393	R37772	Hs.21420	TM,thioredoxokinase	p21-activated protein kinase 6	1.7
	444051	N48373	Hs.10247	SS,Ig		

TABLE 13B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
408344	105240_1	AA053843 BE162213
418546	176677_1	AA224827 T59708 T59843 BE156903
418859	179717_1	AA229558 AA345492 AA229582
418869	179863_1	AW516565 AA229762 AA230035
437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875
		AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493
		AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062
		AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539542
		AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499
		AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996
		AA293273 AA969759 N75628 N22388 H84729 H50052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531
		H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
438952	467390_1	BE046594 BE046667 AA828585 AI207343
443534	572957_1	AI076123 AI244834 AI695239
447197	711623_1	R36075 AI366546 R36167
454197	1050392_1	BE140966 BE140961 BE140967 BE141006 BE140985 BE140970 BE141669 BE141653 BE141664 BE141655 BE141661 BE141660 BE140969
		BE141673 BE141650 BE141674 BE141550 BE141688 AW178241 BE140994 BE141666 BE140998 BE141008 BE140988 BE141011 BE140975
		BE141667 BE141675 BE141657 BE141681 BE141656 BE141672 BE141680 AW178237 BE141012 BE140990 BE141658 BE141648 BE141013
		BE141668 BE140973 BE141004 BE140963 BE140984 BE141009 AW178232 BE141007 BE141649 AW178293 BE140993 AW178233 BE141646
		BE141005 BE141691 BE141000 BE141652 BE140965 BE141562 BE140960 BE140962 BE141001 BE140978 AW178229 AW178239 BE141671
		AW178230 BE141547 AW178235 BE141663 BE141549 BE140996 BE141003 AW178236 BE141002 BE141556
455333	1281044_1	AW897851 AW897852
457570	357443_1	AA579426 AA579436 AA573736

TABLE 13C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400666	8118466	Plus	17982-18115,20297-20456
400749	7331445	Minus	9162-9293
401103	8568122	Minus	98330-98449
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
401575	7229804	Minus	76253-76364
402745	9212200	Minus	76516-76690
402915	7406502	Minus	140-276
404440	7528051	Plus	80430-81581
404604	9212537	Minus	72019-72509
405545	1054740	Plus	118677-118807,119091-119298,121626-121823
405547	1054740	Plus	124361-124520,124914-125050
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
406467	9795551	Plus	182212-182958

TABLE 14A: 209 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES THAT ARE LIKELY TO ENCODE EITHER ENZYMES OR PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES

Table 14A lists about 209 genes up-regulated in cervical cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 12A, except that the ratio was greater than or equal to 2.0, and the 96th percentile value amongst cervical cancers was greater than or equal 40 units, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modifiable by small molecules (e.g. kinase, peptidase, phosphatase, ATPase, or ion transporter domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 PPDomains: Predicted Protein Domains
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

Pkey	ExAccn	UnigenelD	PPDomains	Unigene Title	R1
418007	M13509	Hs.83169	SS,hemopexin,Peptidase_M10	matrix metalloproteinase 1 (interst	38.9
439606	W79123	Hs.58561	TM,7tm_1	G protein-coupled receptor 87	28.8
400289	X07820	Hs.2258	hemopexin,Peptidase_M10	matrix metalloproteinase 10 (stroma	20.5
415817	U88967	Hs.78867	SS,TM,Y_phosphatase,carb_anhyd	protein tyrosine phosphatase, recep	16.4
416209	AA236776	Hs.79078	TM,HORMA	MAD2 (mitotic arrest deficient, yea	15.4
404996	NM_001333	Hs.87417	Peptidase_C1	CTSL2 Cathepsin L2	13.1

5	429618	AA885360	Hs.160199	kinase	Target CAT	12.7
	429486	AF155827	Hs.203963	helicase_C,SNF2_Nhelicase_C	hypothetical protein FLJ10339	12.6
	419183	U60669	Hs.69663	p450	cytochrome P450, subfamily XXIV (vi	12.3
	428368	BE440042	Hs.83326	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 3 (stromel	10.2
	420759	T11832	Hs.127797	helicase_C	Homo sapiens cDNA FLJ11381 fis, clo	10.2
10	458194	AW383618	Hs.265459	p450	ESTs, Moderately similar to ALU2_HU	9.4
	446232	AI281848	Hs.194691	TM,7tm_3Ribosomal_L13	retinoic acid induced 3	8.9
	424905	NM_002497	Hs.153704	TM,pkinase	NIMA (never in mitosis gene a)-rela	8.9
	452291	AF015592	Hs.28853	TM,pkinase	CDC7 (cell division cycle 7, S. cer	8.7
	424086	AI351010	Hs.102267	Lysyl_oxidase	lysyl oxidase	8.3
15	425710	AF030880	Hs.159275	TM,Sulfate_transp,STAS	solute carrier family, member 4	7.8
	433133	AB027249	Hs.104741	TM,Collagen,pkinase	PDZ-binding kinase; T-cell originat	7.4
	447254	NM_004153	Hs.17908	SS,AAA,BAH	origin recognition complex, subunit	7.1
	431941	AK000106	Hs.272227	kinase,Furin-like,Recap_L_dom	Homo sapiens cDNA FLJ20099 fis, clo	6.9
	427821	AA470158	Hs.98202	TM,7tm_1	ESTs	6.9
20	436211	AK001581	Hs.334828	Ammonium_transp	hypothetical protein FLJ10719; KIAA	6.9
	403471	NA		SS,TM,trypsin	Target Exon	6.7
	410153	BE311926	Hs.15830	Glycos_transf_2	hypothetical protein FLJ12691	6.5
	457405	AA504860		TM,7tm_2	gb:ab03a10.s1 Stratagene fetal reti	6.4
	421948	L42583	Hs.334309	filament,HCO3_cotransfilament	keratin 6A	6.3
25	439292	AA090421	Hs.5555	TM,AAA,Ferri_reduct	hypothetical protein MGC5347	5.8
	413625	AW451103	Hs.71371	TM,E1-E2_ATPase,Hydrolase	ESTs	5.8
	425695	NM_005401	Hs.159238	TM,Band_41_Y_phosphatase	protein tyrosine phosphatase, non-r	5.7
	436394	BE379623	Hs.27693	SS,pro_isomerase	peptidylprolyl isomerase (cyclophil	5.6
	432239	X81334	Hs.2936	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 13 (collag	5.5
30	408536	AW381532	Hs.135188	SS,TM,E1-E2_ATPase,Cation_ATPa	ESTs	5.4
	432226	AW182766	Hs.273558	Cytidyllyltransf	phosphate cytidyllyltransferase 1, c	5.2
	419520	AB009303	Hs.90800	TM,hemopexin,Peptidase_M10	matrix metalloproteinase 16 (membra	5.1
	426350	NM_003245	Hs.2022	TM,Transglutamin_C,Transglutam	transglutaminase 3 (E polypeptide,	5.0
	421155	H87879	Hs.102267	SS,Lysyl_oxidase,Aldose_epim,E	lysyl oxidase	4.9
35	423673	BE003054	Hs.1695	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 12 (macrop	4.8
	450375	AA009647	Hs.8850	TM,disintegrin,Pep_M12B_propep	a disintegrin and metalloproteinase	4.8
	418379	AA218940	Hs.137516	AAA	fidgetin-like 1	4.7
	457465	AW301344	Hs.122508	Pribosyltran,Sulfatase	DNA replication factor	4.6
	412333	AW937485		TM,7tm_1	gb:QV3-DT0044-221299-045-b09 DT0044	4.6
40	450510	AA010056	Hs.242998	DNA_topoisomII,DNA_topoisomVIGF	ESTs	4.6
	436291	BE558452	Hs.5101	abhydrolase	protein regulator of cytokinesis 1	4.5
	446353	AI290919	Hs.153681	HECTkinase	ESTs	4.5
	435435	T89473	Hs.192328	lipase,PLAT	ESTs	4.4
	425071	NM_013989	Hs.154424	SS,TM,T4_deiodinase	deiodinase, liothyronine, type II	4.4
45	433322	H50621	Hs.134156	TM,ion_transNB-ARC,CARD,milo_c	ESTs, Weakly similar to I38022 hypo	4.4
	408908	BE296227	Hs.250822	TM,pkinase	serine/threonine kinase 15	4.4
	444781	NM_014400	Hs.11950	PHLactamase_B	GPI-anchored metastasis-associated	4.4
	428479	Y00272	Hs.184572	kinase	cell division cycle 2, G1 to S and	4.2
	406687	M31126	Hs.272620	SS,Peptidase_M10,hemopexin	pregnancy specific beta-1-glycoprot	4.2
50	423035	AW449579	Hs.156739	TM,Glyco_transf_8	H.sapiens XG mRNA (clone PEP11)	4.2
	449228	AJ403107	Hs.148590	TM,PAF-AH,p450	protein related with psoriasis	4.2
	423738	AB002134	Hs.132195	SS,TM,trypsin,SEA	airway trypsin-like protease	4.1
	457030	AJ301740	Hs.173381	TM,Dihydroorotase	dihydropyrimidinase-like 2	4.1
	448995	AI613276	Hs.5662	adenylatekinase	guanine nucleotide binding protein	4.0
55	415857	AA866115	Hs.127797	helicase_C	Homo sapiens cDNA FLJ11381 fis, clo	4.0
	438390	AI422017		TM,DSL,7tm_17tm_1	gb:U45f12x1 NCI_CGAP_Bm23 Homo s	4.0
	429900	AA460421	Hs.30875	kinase	ESTs	4.0
	446292	AF081497	Hs.279682	Ammonium_transp	Rh type C glycoprotein	3.8
	422938	NM_001809	Hs.1594	TM,thiolase	centromere protein A (17kD)	3.7
60	408771	AW732573	Hs.47584	TM,K_tetra,ion_trans	potassium voltage-gated channel, de	3.6
	424286	AI631874	Hs.155140	kinase	casein kinase 2, alpha 1 polypeptid	3.6
	436246	AW450963	Hs.119991	connexinhormone_rec,zf-C4	ESTs	3.5
	411274	NM_002776	Hs.69423	trypsin	kalikrein 10	3.5
	406666			SS,hemopexin,Peptidase_M10	NM_002425:Homo sapiens matrix metal	3.5
65	426920	AA393351	Hs.132121	PDEase	ESTs	3.4
	412471	M63193	Hs.73946	SS,TM,Glycos_transf_3,Cam_acy	endothelial cell growth factor 1 (p	3.4
	430704	AW813091	Hs.335799	Epimerase	ESTs	3.4
	455092	BE152428		Sulfatase	gb:CMO-HT0323-151299-126-b04 HT0323	3.4
	453775	NM_002916	Hs.35120	AAA,PI3_P14_kinase,PI3Ka,PI3K_	replication factor C (activator 1)	3.4
70	438993	AA828995		Integrin_B	gb:od77b08.s1 NCI_CGAP_Ov2 Homo sap	3.4
	426572	AB037783	Hs.170623	hormone_rec,zf-C4	hypothetical protein FLJ11183	3.4
	449101	AA205847	Hs.23016	SS,TM,7tm_1	G protein-coupled receptor	3.3
	427660	A1741320	Hs.114121	hormone_rec,zf-C4	Homo sapiens cDNA: FLJ23228 fis, ci	3.3
	402481			TM,GDI,7tm_1	NM_001821*:Homo sapiens choroiderem	3.3
75	414774	X02419	Hs.77274	SS,kringle,trypsin	plasminogen activator, urokinase	3.3
	412246	AI160873	Hs.69233	SulfotransferaseCOX	zinc finger protein	3.3
	418462	BE001596	Hs.85266	SS,TM,Integrin_B,in3	integrin, beta 4	3.3
	424687	J05070	Hs.151738	SS,Peptidase_M10,in2,hemopexin	matrix metalloproteinase 9 (gelatin	3.2
	401486	NA		SS,TM,trypsin	C4000647:gi4758508 ref NP_004253.	3.2
80	408113	T82427	Hs.194101	TM,7tm_3Ribosomal_L13	Homo sapiens cDNA: FLJ20869 fis, ci	3.2
	427359	AW020782	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, ci	3.2
	402337			SS,p450	Target Exon	3.2
	420930	AW888650		ribonuclease_T2	gb:CM4-NT0007-130500-551-f05 NT0007	3.1
	443426	AF098158	Hs.9329	kinase	chromosome 20 open reading frame 1	3.1
	439750	AL359053	Hs.57664	TM,Integrin_B,Ricin_B_lectinrr	Homo sapiens mRNA full length inser	3.1
	420039	NM_004605	Hs.94581	CARD,SulfotransferaseDAGKc	sulfotransferase family, cytosolic,	3.0
	448733	NM_005629	Hs.187958	SS,TM,SNF,ABC_tran,iodh,pkina	solute carrier family 6 (neurotrans	3.0

	444946	AW139205	Hs.156457	SS,TM,abhydrolase	hypothetical protein FLJ22408	3.0
	450841	AI741466	Hs.270515	pro_isomerase	ESTs	3.0
	428262	AI651324	Hs.7298	death, pkinase	biphenyl hydrolase-like (serine hyd	3.0
5	435399	AA679463		kinase	gbac50c03.s1 Stratagene hNT neuron	2.9
	446733	AA863360	Hs.26040	TM,p450	ESTs, Weakly similar to fatty acid	2.9
	449746	AI668594	Hs.176588	SS,p450	ESTs, Weakly similar to CP4Y_HUMAN	2.9
	418844	M52982	Hs.1200	SS,TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase	2.9
	414581	AA256213	Hs.72010	TM,Cam_acyltransf,Choline_kin	ESTs	2.9
10	431629	AJ077025	Hs.265827	SS,IRNA_antiSH2,SH3,kinase	interferon, alpha-inducible protein	2.8
	445873	AA250970	Hs.251946	SS,rm,PABPkinase,14-3-3,rm	poly(A)-binding protein, cytoplasmic	2.8
	438113	AA67908	Hs.8882	TM,7tm_1	ESTs	2.8
	422689	AW856665		helicase_C,SNF2_Nhelicase_C	gb:RC3-CT0297-290100-013-d03 CT0297	2.8
	439453	BE264974	Hs.6566	SS,AAA	thyroid hormone receptor Interactor	2.8
15	413582	AW295647	Hs.71331	carb_anhydrase	hypothetical protein MGC5350	2.8
	410664	NM_006033	Hs.65370	TM,lipase,PLAT	lipase, endothelial	2.8
	456456	AA477609	Hs.89563	FBPase	nuclear cap binding protein subunit	2.8
	413273	U75679	Hs.75257	TM,lg,kinase	slam-loop (histone) binding protein	2.8
	426343	NM_014642	Hs.169387	TM,SCAN7tm_1	KIAA0036 gene product	2.8
20	403763			TM,7tm_1	NM_001059*:Homo sapiens tachykinin	2.7
	408380	AF123050	Hs.44532	TM,ubiquitin7tm_3,ANF_receptor	diubiquitin	2.7
	401230			SS,TM,ion_trans,IQ	NM_014191*:Homo sapiens sodium chan	2.7
	418030	BE207573	Hs.83321	SS,TM,Peptidase_S26,Bombesin	neuromedin B	2.7
	445640	AW869626	Hs.31704	TM,alpha-amylase	ESTs, Weakly similar to KIAA0227 [H	2.7
25	432865	AI753709	Hs.152484	TM,ion_transNB-ARC,CARD,WD40,m	ESTs, Weakly similar to I38022 hypo	2.6
	419667	AJ077005	Hs.92208	SS,TM,disintegrin,Reprolysin,P	a disintegrin and metalloproteinase	2.6
	406671	AA129547	Hs.285754	TM,kinase,Plexin_repeat,Sema,	mat proto-oncogene (hepatocyte grow	2.6
	412530	AA766268	Hs.266273	abhydrolase	hypothetical protein FLJ13346	2.6
	431890	X17033	Hs.271986	vwa,FG-GAP,Integrin_A	Integrin, alpha 2 (CD49B, alpha 2 s	2.6
30	404184	NA		SS,TM,7tm_1	NM_030903*:Homo sapiens olfactory r	2.6
	428450	NM_014791	Hs.184339	kinase,KA1	KIAA0175 gene product	2.6
	425698	NM_018112	Hs.159241	TM,kinase,ion_trans	polycystic kidney disease 2-like 1	2.6
	453331	AI240665	Hs.8895	TM,disintegrin,Pep_M12B_propep	ESTs	2.6
	444826	AI674482	Hs.148441	kinase,SAM	ESTs	2.6
35	414987	AA524394	Hs.294022	connexin,hormone_rec,zf-C4,conn	hypothetical protein FLJ14950	2.6
	438746	AI885815	Hs.184727	Ribosomal_S2,transferrin	ESTs	2.5
	429413	NM_014058	Hs.201877	trypsin	DESC1 protein	2.5
	407103	AA424881	Hs.256301	TM,cNMP_bindingtrypsin	hypothetical protein MGC13170	2.5
	453379	AA035261	Hs.61753	PAN,kringle,trypsin	ESTs	2.5
40	421733	AL119671	Hs.1420	SS,TM,lg,kinase	fibroblast growth factor receptor 3	2.5
	452220	BE158006	Hs.212296	TM,Integrin_A,FG-GAP	ESTs	2.5
	417975	AA641836	Hs.30085	SS,trypsin	hypothetical protein FLJ23186	2.5
	400301	X03635	Hs.1657	TM,Oest_recep,zf-C4,hormone_re	estrogen receptor 1	2.5
	408938	AA059013	Hs.22607	Y_phosphatase	ESTs	2.4
45	411643	AI924519	Hs.192570	DEAD,helicase_C	hypothetical protein FLJ22028	2.4
	446638	AL133063	Hs.15783	TM,kinase	Homo sapiens mRNA; cDNA DKFZp434P11	2.4
	430129	BE301708	Hs.233955	TM,Glyco_transf_11	hypothetical protein FLJ20401	2.4
	417655	AA780791	Hs.14014	Peptidase_M41,AAApkinase	hypothetical protein FLJ14813	2.4
	448005	AW207437	Hs.170378	kinase	ESTs	2.4
50	423973	AF038461	Hs.136574	TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase, 12R1	2.4
	437897	AA770561	Hs.146170	SS,pro_isomerase	hypothetical protein FLJ22969	2.4
	425397	J04088	Hs.156346	DNA_topoisomII,DNA_topoisomI/IGF	topoisomerase (DNA) II alpha (170kD	2.4
	432777	AA564991	Hs.269477	alpha-amylase	ESTs	2.4
	421247	BE391727	Hs.102910	TM,IRNA-synt_1,SPRYF5_F8_type_	general transcription factor IIH, p	2.4
55	425465	L18964	Hs.1904	TM,kinase,DAG_PE-bind,OPR,pi	protein kinase C, tota	2.4
	419281	H96452	Hs.42189	TM,E1-E2_ATPase,HMA,Hydrolase	ESTs	2.4
	434205	AF119861	Hs.283032	SH3,efhand,C2,PH,RhoGEF,AAA,PG	hypothetical protein PRO2015	2.4
	453406	AI192987	Hs.61784	kinase,Furin-like,Recep_L_dom	hypothetical protein FLJ14451	2.3
	435542	AA687376	Hs.269533	kinase,RhoGEF,lg,PH,SH3	ESTs	2.3
60	443151	AI827193	Hs.132714	DNA_mis_repair,HATPase_cAcylph	ESTs	2.3
	431630	NM_002204	Hs.265829	SS,TM,FG-GAP,Integrin_A	integrin, alpha 3 (antigen CD49C, a	2.3
	422310	AA316622	Hs.98370	SS,TM,tn3,lg,kinase,Ribosomal	cytochrome P450, subfamily IIS, poi	2.3
	4141954	AI744935	Hs.8047	TM,Band_7,AAA,cdc48_N	Fanconi anemia, complementation gro	2.3
	414907	X90725	Hs.77597	SS,TM,kinase,POLO_box	pclo (Drosophila)-like kinase	2.3
65	439810	AL109710	Hs.85568	aconitase,Aconitase_C	EST	2.3
	429359	W00482	Hs.2399	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 14 (membra	2.3
	432284	AA532807	Hs.105822	TM,kinase	ESTs	2.3
	452947	AW130413		alpha-amylase	gbcd50f04.x1 NCL_CGAP_Gas4 Homo sa	2.3
	423229	AC003965	Hs.125532	SS,trypsin	protease, serine, 26	2.3
70	453941	U39817	Hs.36820	DEAD,HRDC,helicase_C	Bloom syndrome	2.3
	439963	AW247529	Hs.6793	TM,p450Ets	platelet-activating factor acetylth	2.3
	424439	AA579635	Hs.1770	DNA_ligase	ligase I, DNA, ATP-dependent	2.2
	452755	AW138937	Hs.213436	Glyco_transf_29	ESTs, Weakly similar to A34087 hypo	2.2
	429922	Z97630	Hs.226117	TM,linker_histone7tm_1	H1 histone family, member 0	2.2
75	434149	Z43829	Hs.19574	TM,EPH_lbd,tn3,kinase,SAM	hypothetical protein MGC5469	2.2
	417576	AA339449	Hs.82285	TM,AIRS,formyl_transf,GARS	phosphoribosylglycinamide formyltra	2.2
	409994	D86864	Hs.57735	IP_transSH2,SH3	acetyl LDL receptor; SREC	2.2
	416763	AI908127	Hs.79748	TM,alpha-amylase7tm_1	solute carrier family 3 (activators	2.2
	414733	BE514535	Hs.77171	TM,MCMHeme_oxygenase	minichromosome maintenance deficien	2.2
80	443171	BE281128	Hs.9030	SS,TM,7tm_1,rm	TONDU	2.2
	430637	BE160081	Hs.256290	S_100Peptidase_M16	S100 calcium-binding protein A11 (c	2.2
	452367	U71207	Hs.29279	SS,Hydrolase	eyes absent (Drosophila) homolog 2	2.2
	408308	AL033377	Hs.44197	TM,7tm_2	hypothetical protein DKFZp584D0462	2.2
	417900	BE250127	Hs.82906	TM,WD40,pro_isomerase	CDC20 (cell division cycle 20, S. c	2.1

5	424490	AJ278016	Hs.55565	TM,pkinase,ank	ankyrin repeat domain 3	2.1
	412834	R77123	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, cl	2.1
	410855	X97795	Hs.66718	SNF2_N,helicase_C	RAD54 (S.cerevisiae)-like	2.1
	418804	AA809632		HATPase_c,HSP90,PHD,zf-C2H2	gb:nz17h04.s1 NCL_CGAP_GCB1 Homo sa	2.1
	447674	BE270640	Hs.19192	TM,pkinaseras,arf	cyclin-dependent kinase 2	2.1
	450663	H43540	Hs.25292	SS,TM,RNase_HII	ribonuclease H1, large subunit	2.1
	408805	H69912	Hs.48269	TM,pkinase	vaccinia related kinase 1	2.1
	429415	NM_002593	Hs.202097	SS,CUB,NTR,MAM,TIL,TiLa,vwd,EP	procollagen C-endopeptidase enhance	2.1
	447827	U73727	Hs.19718	SS,TM,Y_phosphatase,fn3,jg,MAM	protein tyrosine phosphatase, recep	2.1
10	428273	AI867228	Hs.303211	Glycos_transf_2	ESTs	2.1
	404274			SS,TM,pkinase,fn3	NM_002944*:Homo sapiens v-ros avian	2.1
	403133			pkinase,K_tetra,Band_41,RhoGEF	Target Exon	2.1
	440249	AI246590	Hs.337275	VHL,TatD_DNase	ESTs	2.1
	438580	AA811262	Hs.299202	TM,pkinasesugar_tr	ESTs	2.1
15	406400			SS,TM,tryptin	NM_007196:Homo sapiens kallikrein 8	2.1
	427375	AL035460	Hs.177536	SS,Zn_carbOpept,hormone5Reprol	metallocarboxypeptidase CPX-1	2.1
	423453	AW450737	Hs.128791	SS,Granin,CDP-OH_P_transf	CGI-09 protein	2.1
	433716	AA608808	Hs.225118	Acylphosphatase	ESTs	2.1
	420757	X78592	Hs.99915	TM,hormone_rec,Androgen_recep,	androgen receptor (dihydrotestoster	2.1
20	425018	BE245277	Hs.154196	DNase_I,K_tetra	E4F transcription factor 1	2.1
	421685	AF189723	Hs.106778	TM,E1-E2_ATPase,HydrolaseE1-E2	ATPase, Ca transporting, type 2C, m	2.1
	457288	AA521458	Hs.192738	pro_isomerase	ESTs	2.1
	407305	AA715284		TM,pkinase,Sema,Plaxin_repeat,	gb:nv35f03.r1 NCL_CGAP_Br5 Homo sap	2.1
	456327	H68741	Hs.38774	TM,Glyco_transf_8	ESTs	2.0
25	422429	AA310527		pkinase,RGS,PHkinase,PH,RGS	gb:EST181333 Jurkat T-cells V Homo	2.0
	402974	NM_001501	Hs.129715	GnRHhormone5,hormone4	gonadotropin-releasing hormone 2	2.0
	458016	AW188099	Hs.131813	pkinase	ESTs	2.0
	452194	AI694413	Hs.332649	TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfa	2.0
30	428028	U52112	Hs.182018	TM,pkinase,MBD	interleukin-1 receptor-associated k	2.0
	427747	AW411425	Hs.180655	pkinase,lipoxygenase,PLATipox	serine/threonine kinase 12	2.0
	452841	T17431	Hs.65412	TM,DEAD,helicase_C	DEAD/H (Asp-Glu-Ala-Asp/His) box po	2.0
	449539	W80363	Hs.58446	pkinase,Furin-like,Recep_L_dom	ESTs	2.0
	418140	BE613838	Hs.83551	TM,E1-E2_ATPase	microfibrillar-associated protein 2	2.0
35	430076	AA465115	Hs.318773	AAA,BAH	KIAA1836 protein	2.0
	425749	AW328587	Hs.159448	Ribosomal_L7Ae,LRR,LRRCT,pkina	surfeit 2	2.0
	425855	AF135025	Hs.159679	SS,tryptin	kallikrein 12	2.0
	400135	L40027	Hs.118890	pkinase	glycogen synthase kinase 3 alpha	2.0
40	TABLE 14B					
	Pkey:	Unique Eos probeset Identifier number				
	CAT number:	Gene cluster number				
	Accession:	Genbank accession numbers				
45	Pkey	CAT number	Accessions			
	412333	1289037_1	AW937485 AW937589 AW937658 AW937654 AW937492			
	418804	179138_1	AA809632 AI917245 AI701732 AA228406			
50	420930	197736_1	AW888650 AW888651 BE149946 BE149948 BE149951 BE149947 AW888649 AA281840 AA281822 AW888652			
	422429	216469_1	AA310527 AW962295 Z44865 H06641			
	422689	218896_1	AW856665 AA315006 AW954733			
	435399	405576_1	AA679463 AW813779 AW813709			
55	438390	45662_1	AI422017 AI422945 AI363249 AI423113 AI925592 AI420795 AI208187 AI423279 AI423645 AI424090 AI359637 AL044732 D17003			
	438993	467651_1	AA828995 AA834879 AI926361			
	452947	939810_1	AW130413 AI932362			
	455092	1252971_1	BE152428 AW855572 AW855607			
	457405	333127_1	AA504860 AA504911			
60	TABLE 14C					
	Pkey:	Unique number corresponding to an Eos probeset				
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.				
65	Strand:	Indicates DNA strand from which exons were predicted.				
	Nt_position:	Indicates nucleotide positions of predicted exons.				
70	Pkey	Ref	Strand	Nt_position		
	400666	8118496	Plus	17982-18115,20297-20456		
	401230	9929527	Minus	33835-34006,34539-34592,35461-36745,48925-49068,52604-52758		
	401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179		
75	402337	6957691	Plus	4116-4286,16811-16973,17107-17256,19715-20040,22029-22205		
	402481	9797406	Plus	87891-88991		
	403133	7331427	Plus	38314-38634		
	403471	9930659	Minus	85867-85983		
	403763	7229888	Minus	43575-43887		
	404184	4581418	Minus	12652-13548		
80	404274	9885189	Plus	104127-104318		
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077		

TABLE 15A: 752 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT CERVIX

5 Table 15A lists about 752 genes up-regulated in cervical cancer compared to normal adult cervix. These were selected as for Table 12A, except that the ratio was greater than or equal to 7.0, the denominator was the median value for three non-malignant cervical specimens, and the 96th percentile value amongst cervical cancers was greater than or equal 80 units.

10	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of cervical cancer to normal cervix			
15	Pkey	ExAccn	UnigeneID	Unigene Title	R1
20	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homolog of murine	58.3
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HEMBA1004341	36.2
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cys-X-Cys), mem	35.6
	421508	NM_004833	Hs.105115	absent in melanoma 2	33.6
	443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit, beta type, 1	32.0
	454390	AB020713	Hs.56966	KIAA0906 protein	30.5
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	30.4
	433226	AW503733	Hs.9414	KIAA1488 protein	30.0
25	413503	BE410228	Hs.75410	heat shock 70kD protein 5 (glucose-regulated protein,	29.4
	411669	BE612676	Hs.303116	stromal cell-derived factor 2-like 1	28.9
	414132	AI801235	Hs.48480	ESTs	28.3
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	28.1
	448569	BE382657	Hs.21486	signal transducer and activator of transcription 1, 9	27.4
	432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog 2	27.2
30	418963	BE304571	Hs.89529	aldo-keto reductase family 1, member A1 (aldehyde red	26.9
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrolase, isoform I	26.5
	449722	BE280074	Hs.23960	cyclin B1	26.2
	414812	X72755	Hs.77367	monokine induced by gamma interferon	25.3
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	25.1
35	432817	NM_014125	Hs.279812	PRO0327 protein	24.6
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	23.6
	457465	AW301344	Hs.122908	DNA replication factor	23.1
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone COL06049	22.9
	429083	Y09397	Hs.227817	BCL2-related protein A1	22.9
40	401405			Target Exon	22.8
	426272	AW450671	Hs.189284	ESTs	22.7
	424878	H57111	Hs.221132	ESTs	22.6
	412140	AA219691	Hs.73625	RAB6 Interacting, kinesin-like (rakinesin 6)	22.5
	444371	BE540274	Hs.239	forkhead box M1	22.2
45	418030	BE207573	Hs.83321	neuromedin B	22.0
	452291	AF015592	Hs.28853	ODC7 (cell division cycle 7, S. cerevisiae, homolog)-	21.6
	400198			Eos Control	21.3
	416795	AI497778	Hs.20509	HBV pX associated protein-8	21.2
50	424865	AF011333	Hs.153563	lymphocyte antigen 75	21.0
	438011	BE466173	Hs.145696	splicing factor (CC1.3)	20.7
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin 1, progelatin	20.3
	436923	AW293704	Hs.122658	ESTs	20.2
	415791	H09366	Hs.78853	uracil-DNA glycosylase	20.0
55	448775	AB025237	Hs.388	nucleoside diphosphate linked moiety X)-type m	19.6
	435647	AI653240	Hs.49823	ESTs	19.6
	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to gene trap PA	19.5
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	19.5
	428433	AA521410	Hs.41371	ESTs	19.4
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK2-associated	19.3
60	417308	H60720	Hs.81892	KIAA0101 gene product	19.2
	429574	BE268321	Hs.208912	hypothetical protein MGC861	19.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	19.0
	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	19.0
	438899	AF085833	Hs.135624	ESTs	19.0
65	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	18.9
	438598	AI805943	Hs.326067	hypothetical protein MGC5178	18.8
	408908	BE286227	Hs.250822	serine/threonine kinase 15	18.8
	427488	M91401	Hs.178658	RAD23 (S. cerevisiae) homolog B	18.6
	400195			NM_007057~Homo sapiens ZW10 Interactor (ZWINT), tran	18.5
70	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin)	18.4
	410324	AW292539	Hs.30177	ESTs	18.3
	453028	AB006532	Hs.31442	RecQ protein-like 4	18.1
	410608	AI538438	Hs.159087	ESTs	18.1
	432503	AA551196	Hs.188952	ESTs	17.9
75	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	17.7
	430709	R34356		gbyh85d01.s1 Soares placenta Nb2HP Homo sapiens cDNA	17.6
	449962	AA004879	Hs.187820	ESTs	17.3
	425408	AB002375	Hs.156814	KIAA0377 gene product	17.1
	440774	AI420611	Hs.127832	ESTs	16.8
80	408201	AK000568	Hs.43654	hypothetical protein FLJ20561	16.7
	436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypothetical protein [16.7
	426897	AW976570	Hs.97387	ESTs	16.5
	447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypothetical protein F	16.5

5	433159	AB035898	Hs.150587	kinesin-like protein 2	16.3
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	16.3
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptional activation,	16.3
	453941	U39817	Hs.36820	Bloom syndrome	16.1
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	16.0
10	407999	AI126271	Hs.49433	ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTE	16.0
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT2RP2006454	15.7
	407720	AB037776	Hs.38002	KIAA1355 protein	15.6
	425316	AA354977	Hs.191565	ESTs, Moderately similar to T14342 NSD1 protein - mou	15.6
	423673	BE030354	Hs.1695	matrix metalloproteinase 12 (macrophage elastase)	15.5
15	419777	D60134	Hs.270975	ESTs	15.3
	453886	R66282	Hs.20247	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	15.2
	443715	AI583187	Hs.9700	cyclin E1	15.2
	407786	AA687538	Hs.38972	tetraspan 1	15.2
	431910	AK000142	Hs.101774	hypothetical protein FLJ23045	15.1
20	417634	W27202	Hs.82327	glutathione synthetase	15.1
	432692	AW974944	Hs.200577	ESTs	15.1
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cys-Cys), membe	15.0
	427999	AI435128	Hs.181369	ubiquitin fusion degradation 1-like	15.0
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	14.9
25	431629	AU077025	Hs.265827	Interferon, alpha-inducible protein (clone IFI-6-16)	14.8
	435354	AA678267	Hs.117115	ESTs	14.8
	406836	AW514501	Hs.156110	immunoglobulin kappa constant	14.8
	416109	AI420311	Hs.126550	suppressor of K transport defect 1	14.7
	417933	X02308	Hs.82962	thymidylate synthetase	14.7
30	438970	AA837782	Hs.321058	ESTs	14.7
	409680	W31092	Hs.55847	mitochondrial ribosomal protein 64	14.6
	432401	NM_013330	Hs.274479	NME7	14.5
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.5
	420734	AW972872	Hs.293736	ESTs	14.5
35	434256	AI378817	Hs.191847	ESTs	14.3
	418269	AA806113	Hs.189025	ESTs	14.3
	427372	AW960673	Hs.177530	ATP synthase, H transporting, mitochondrial F1 comple	14.2
	427081	AI474533	Hs.170528	ESTs, Moderately similar to ALUC_HUMAN III ALU CLASS	14.2
	420309	AW043637	Hs.21768	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC S	14.2
40	429966	BE081342	Hs.283037	HSPC039 protein	14.1
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-inducible, 67	14.0
	443957	AA521049	Hs.34487	hypothetical protein FLJ23412	14.0
	418803	U50079	Hs.88556	histone deacetylase 1	14.0
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	13.9
45	420139	NM_005357	Hs.95351	lipase, hormone-sensitive	13.9
	444783	AK001458	Hs.62180	anillin (Drosophila Scraps homolog), actin binding pr	13.9
	433255	A274270	Hs.96840	KIAA1527 protein	13.8
	431838	AI097229	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	13.8
	449801	AA477355	Hs.288300	hypothetical protein FLJ23231	13.8
50	447078	AW885727	Hs.301570	ESTs	13.8
	441240	AA923749	Hs.132442	ESTs	13.6
	439398	AA284267	Hs.221504	ESTs	13.6
	404630			Target Exon	13.6
	408321	AW405882	Hs.44205	cortistatin	13.5
55	426427	M86699	Hs.169840	TTK protein kinase	13.5
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	13.5
	403055			C2002219:gl[12737280]ref[XP_006682.2] keratin 18 [Ho	13.5
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	13.3
	425261	BE385099	Hs.334727	hypothetical protein MGC3017	13.3
60	439926	AW014875	Hs.137007	ESTs	13.2
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated kinesin	13.2
	451141	AW772713	Hs.247186	ESTs	13.2
	447390	X95384	Hs.18426	translational inhibitor protein p14.5	13.2
	419828	T81422	Hs.14922	ESTs	13.2
65	428147	AW629965	Hs.234983	ESTs, Weakly similar to 2109260A B cell growth factor	13.1
	410068	AI633888	Hs.58435	FYN-binding protein (FYB-120/130)	13.1
	407595	BE350012	Hs.248365	ESTs	13.1
	432721	AL121478	Hs.180532	glucose phosphate isomerase	13.0
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associ	13.0
70	413314	BE081585		gb:CV2-BT0635-210400-156-b07 BT0635 Homo sapiens cDNA	12.9
	430929	AA489166	Hs.156933	ESTs	12.9
	449571	AW016812	Hs.200266	ESTs	12.8
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of the prostate	12.6
	417105	X60992	Hs.81226	CD6 antigen	12.6
75	434263	N34895	Hs.44648	ESTs	12.6
	412059	AA317962	Hs.249721	ESTs, Moderately similar to PC4259 ferritin associate	12.5
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	12.5
	437056	AI147061		gb:ok33a11.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapien	12.5
	438768	AI307416	Hs.184675	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY	12.5
80	444478	W07318	Hs.240	M-phase phosphoprotein 1	12.4
	450738	AA010907	Hs.184456	hypothetical protein	12.4
	418205	L21715	Hs.83760	tropomyosin 1, skeletal, fast	12.4
	442994	AI026718	Hs.16954	ESTs	12.4
	433301	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone HEP20977	12.4
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	12.3
	435327	BE301871	Hs.4867	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylgl	12.3
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (survivin)	12.3

	410245	C17908	Hs.194125	ESTs	12.3
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	12.3
	418941	AA452970	Hs.155218	E1B-55kDa-associated protein 5	12.3
5	432325	AW973209	Hs.261782	ESTs	12.3
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	12.3
	418618	U66097	Hs.85724	GTP cyclohydrolase 1 (dopa-responsive dystonia)	12.2
	449296	AL137257	Hs.23458	Homo sapiens cDNA: FLJ23015 fis, clone LNG00818	12.2
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501	12.2
10	427295	AW291212	Hs.283943	hypothetical protein MGC11266	12.2
	415443	T07353	Hs.7948	ESTs	12.1
	429770	AI766047	Hs.99736	ESTs	12.1
	428955	AA579297	Hs.26937	brain and nasopharyngeal carcinoma susceptibility pro	12.1
	435244	N77221	Hs.187824	ESTs	12.1
15	432810	AA863400	Hs.23054	ESTs	12.1
	434423	NM_006769	Hs.3844	LIM domain only 4	12.0
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit, beta type, 9	12.0
	459273	AW608906	Hs.334767	hypothetical protein MGC5629	12.0
	419945	AW290975	Hs.118923	ESTs	11.9
20	442159	AW163390	Hs.278554	heterochromatin-like protein 1	11.9
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MAMMA1002566	11.9
	407804	AF228603	Hs.39957	pleckstrin 2 (mouse) homolog	11.8
	401557			Target Exon	11.8
25	434408	AI031771	Hs.132586	ESTs	11.8
	406747	AI925153	Hs.217493	annexin A2	11.8
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein (EGP) (KSA)	11.8
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor 1	11.8
	445655	AA873830	Hs.167746	B cell linker protein	11.7
	419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal)	11.7
30	427527	AI809057	Hs.302063	immunoglobulin heavy constant mu	11.7
	432287	AK001057	Hs.274268	Homo sapiens cDNA FLJ10195 fis, clone HEMBA1004771	11.6
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!! ALU CLASS C W	11.6
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 kD)	11.6
	447082	T85314	Hs.42644	thioredoxin-like	11.5
35	409931	BE293233	Hs.129771	ESTs	11.4
	426172	AA371307	Hs.125056	ESTs	11.4
	424723	BE408813	Hs.152337	protein arginine N-methyltransferase 3(hnRNP methyltr	11.4
	456880	AW015644	Hs.155005	TEA domain family member 1 (SV40 transcriptional enha	11.4
40	433849	BE465884	Hs.280728	ESTs	11.4
	430519	AF129534	Hs.49210	F-box only protein 4	11.4
	434442	AA737415	Hs.152826	ESTs	11.3
	457205	AI905780	Hs.198272	Target CAT	11.3
	422713	AA902780	Hs.119325	Huntingtin-interacting protein A	11.3
	443491	AW499665	Hs.9456	SWI/SNF related, matrix associated, actin dependent r	11.3
45	424339	BE257148	Hs.145416	endoglycan	11.3
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	11.3
	450208	AI686945	Hs.272062	ESTs	11.2
	446849	AU076617	Hs.16251	cleavage and polyadenylation specific factor 3, 73kD	11.2
	424965	AW956282	Hs.144609	Homo sapiens, Similar to RIKEN cDNA 5730578N08 gene,	11.2
50	442737	AB002319	Hs.8663	KIAA0321 protein	11.2
	409113	AA074897		gb:zm85a05.r1 Stratagene ovarian cancer (937219) Homo	11.2
	415782	AA169345	Hs.123177	ESTs	11.1
	417958	AA767382	Hs.193417	ESTs	11.1
	402539	AW502761	Hs.30909	KIAA0430 gene product	11.0
55	413677	AW503116	Hs.301819	zinc finger protein 146	11.0
	414706	AW340125	Hs.76989	KIAA0097 gene product	11.0
	421632	AA825426	Hs.238832	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	11.0
	438995	AI277986	Hs.164875	ESTs	11.0
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	10.9
60	432363	AA534489		gb:nf76g11.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone 3'	10.9
	451655	H85689	Hs.225560	ESTs	10.9
	429237	AA448417	Hs.104990	ESTs	10.9
	427719	AI393122	Hs.134726	ESTs	10.9
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	10.8
65	410093	AW589558	Hs.296120	ESTs, Weakly similar to KIAA0970 protein [H.sapiens]	10.8
	400080			Eos Control	10.8
	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643	10.8
	401539			NM_002675:Homo sapiens promyelocytic leukemia (PML),	10.8
	446099	T93096	Hs.17126	hypothetical protein MGC15912	10.7
70	451066	AI758660	Hs.206132	ESTs	10.7
	409235	AA188827	Hs.7988	ESTs, Weakly similar to I38022 hypothetical protein [10.7
	451730	AF095687	Hs.26937	brain and nasopharyngeal carcinoma susceptibility pro	10.7
	428054	AI948688	Hs.266619	ESTs	10.6
	441636	AA081846	Hs.7921	Homo sapiens mRNA: cDNA DKFZp566E183 (from clone DKFZ	10.6
75	438654	AI005270	Hs.123543	ESTs	10.6
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kinase	10.6
	449035	AI815728	Hs.19980	DNA polymerase epsilon p12 subunit	10.6
	436137	AI056769	Hs.133512	ESTs	10.6
	417863	AB000450	Hs.82771	vaccinia related kinase 2	10.6
80	439975	AW328081	Hs.6817	inosine triphosphatase (nucleoside triphosphate pyrop	10.6
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen inducible gene	10.6
	454355	AW812535		gb:CM4-ST0182-051099-021-c09 ST0182 Homo sapiens cDNA	10.6
	435542	AA687378	Hs.269533	ESTs	10.6
	431386	AA504359	Hs.110067	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC S	10.5

5	416564	AW795793	Hs.179827	Homo sapiens cDNA FLJ12257 fis, clone MAMMA1001501, h	10.5
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT2RM4002390	10.5
	408329	AF155510	Hs.44227	heparanase	10.5
	410146	AW592655		gb:hl45f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA c	10.4
	427600	AW630918	Hs.179774	proteasome (prosome, macropain) activator subunit 2 (10.4
10	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial collagenase)	10.4
	407241	M34516		gb:Human omega light chain protein 14.1 (lg lambda ch	10.4
	435061	AI651474	Hs.163944	ESTs	10.4
	409653	AW451693	Hs.220826	ESTs	10.4
	428294	AA425488		gb:zw46d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapie	10.4
15	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sensitivity prote	10.4
	408809	AW274673	Hs.279706	ESTs, Weakly similar to A47582 B-cell growth factor p	10.4
	410174	AA306007	Hs.59461	DKFZP434C245 protein	10.4
	424792	U92538	Hs.153138	origin recognition complex, subunit 5 (yeast homolog)	10.3
	422406	AF025441	Hs.116206	Opa-interacting protein 5	10.3
20	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92kD gelati	10.3
	413809	L25851	Hs.851	Integrin, alpha E (antigen CD103, human mucosal lymph	10.3
	413507	BE145360	Hs.190064	ESTs, Weakly similar to I38022 hypothetical protein [10.3
	448119	H98587	Hs.82295	dedicator of cyto-kinesis 1	10.2
	457288	AA521458	Hs.192738	ESTs	10.2
25	402025			NM_021624:Homo sapiens histamine H4 receptor (HRH4),	10.2
	440572	AW183778	Hs.249584	ESTs, Weakly similar to MYSA_HUMAN MYOSIN HEAVY CHAIN	10.2
	453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside transporters), m	10.2
	443780	NM_012068	Hs.9754	activating transcription factor 5	10.1
	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapiens cDNA 5' en	10.1
30	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	10.1
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	10.1
	430848	AW021726		gb:d27e02.y1 Morton Fetal Cochlea Homo sapiens cDNA	10.1
	422470	AB017919	Hs.117232	peptidyl arginine deiminase, type V	10.1
	449501	AI652924	Hs.231942	ESTs	10.1
35	420731	AL042052	Hs.104432	ESTs	10.1
	404345	AA730407	Hs.159156	protocadherin 11	10.1
	400438	AF185611		Target	10.1
	438170	AI916685	Hs.194601	ESTs	10.1
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	10.1
40	458715	AK000973	Hs.16725	hypothetical protein FLJ10111	10.1
	427766	AA412258	Hs.188817	ESTs	10.1
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	10.0
	403038			Target Exon	10.0
	434674	AA831879	Hs.136985	ESTs	10.0
45	439685	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_HUMAN FORKHEAD BOX PROTE	10.0
	439428	AA835825	Hs.190490	ESTs	10.0
	403310			Target Exon	9.9
	408392	U28831	Hs.44566	KIAA1641 protein	9.9
	421849	AW410872	Hs.108894	hypothetical protein FLJ20411	9.9
50	433384	AI021992	Hs.124244	ESTs	9.9
	443343	BE409809	Hs.301005	purine-rich element binding protein B	9.9
	437267	AW511443	Hs.258110	ESTs	9.9
	455978	AI310151	Hs.173524	ESTs	9.9
	435851	AA700946	Hs.191933	ESTs	9.9
55	452243	AL355715	Hs.26555	programmed cell death 9	9.9
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	9.9
	414001	AI610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY	9.8
	438669	AA535975	Hs.174308	Homo sapiens, clone IMAGE:3453347, mRNA, partial cds	9.8
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate), member 2	9.8
60	417087	AA193193	Hs.188325	Homo sapiens cDNA FLJ11484 fis, clone HEMBA1001835	9.8
	455855	BE147440		gb:RC1-HT0229-060100-015-f09 HT0229 Homo sapiens cDNA	9.8
	410390	AA876905	Hs.125286	ESTs	9.8
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic acid transpo	9.8
	442660	AW138174	Hs.130651	ESTs	9.8
65	436186	BE390717	Hs.5074	similar to S. pombe dim1	9.8
	426773	NM_015556	Hs.172180	KIAA0440 protein	9.7
	413476	U25849	Hs.75393	acid phosphatase 1, soluble	9.7
	418347	AA216419		gb:nc16e03.s1 NCL_CGAP_Py1 Homo sapiens cDNA clone sl	9.7
	448752	AA593867	Hs.300842	KIAA1608 protein	9.7
70	440349	AA884196	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone THYRO1001322	9.7
	431363	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	9.7
	430752	AA485330	Hs.303278	ESTs	9.7
	436523	BE512990	Hs.5212	single-strand selective monofunctional uracil DNA gly	9.7
	415740	N80486	Hs.39911	Homo sapiens mRNA for FLJ00089 protein, partial cds	9.7
75	411930	F06485	Hs.7740	oxysterol binding protein-like 1	9.7
	430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior gradient-2 [H	9.6
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothetical protein [9.6
	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA1011 protein	9.6
	434957	AF283775	Hs.35380	x 001 protein	9.6
80	407292	AA876638		gb:nc45e06.s1 NCL_CGAP_Py12 Homo sapiens cDNA clone s	9.6
	459109	AW292447	Hs.140821	ESTs	9.6
	457892	AA744389		gb:ny51e10.s1 NCL_CGAP_Py18 Homo sapiens cDNA clone s	9.6
	432074	AA525248	Hs.149723	ESTs	9.6
	440463	AI733087	Hs.129994	ESTs	9.6
	420851	AA281052	Hs.29493	hypothetical protein FLJ20142	9.6
	445326	AI220072	Hs.165893	ESTs	9.6
	434953	BE049102	Hs.121573	ESTs, Weakly similar to TRHY_HUMAN TRICHOHYAL [Hsap	9.6

5	420361	N92054	Hs.194718	zinc finger protein 265	9.6
	415853	H06016	Hs.100855	ESTs	9.6
	429599	AA806106	Hs.123564	ESTs	9.6
	417037	BE083936	Hs.80976	antigen identified by monoclonal antibody K-67	9.6
	449317	AW293413	Hs.132906	19A24 protein	9.6
10	436588	AA759233	Hs.126506	ESTs	9.6
	409261	BE315042	Hs.19210	hypothetical protein MGC11308	9.5
	401069			C11000374:gi10764778[gb]AAG22817.1[AF302150.1 (AF30	9.5
	414085	AW515373	Hs.271249	Homo sapiens cDNA FLJ13580 fis, clone PLACE1008851	9.5
	409902	AI337658	Hs.156351	ESTs	9.5
15	432258	AW973078	Hs.293039	ESTs	9.5
	438581	AW977766	Hs.292133	ESTs, Moderately similar to I78885 serine/threonine-s	9.5
	405536			NM_005805:Homo sapiens 26S proteasome-associated pad1	9.5
	418216	AA662240	Hs.283099	AF15q14 protein	9.5
	434573	AW372340	Hs.159717	ESTs	9.5
20	439354	AF086174		gb:Homo sapiens full length insert cDNA clone ZB94A08	9.5
	455410	AW936678		gb:PM2-DT0023-080300-004-a04 DT0023 Homo sapiens cDNA	9.5
	400736			Target Exon	9.5
	419474	AW968619	Hs.155849	ESTs	9.4
	406464			C17000168:gi17294725[gb]AAF50062.1 (AE003544) CG7547	9.4
25	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	9.4
	427258	AA400091	Hs.39421	ESTs	9.4
	404680			Target Exon	9.4
	433840	AA129782	Hs.3576	Homo sapiens mRNA full length insert cDNA clone EURO1	9.4
	423842	AW452650	Hs.157148	hypothetical protein MGC13204	9.4
30	457008	AA410446	Hs.112011	ESTs, Weakly similar to unknown [Hsapiens]	9.4
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	9.4
	451846	T65840	Hs.11762	ESTs	9.4
	419988	W39388	Hs.55336	Homo sapiens, clone MGC:17421, mRNA, complete cds	9.4
	402967			Target Exon	9.3
35	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	9.3
	441075	AA915991	Hs.179214	els variant gene 3	9.3
	451107	AA235108	Hs.17639	Homo sapiens ubiquitin protein ligase (UBE3B) mRNA, p	9.3
	404649			Target Exon	9.3
	420897	AW139261	Hs.232280	ESTs	9.3
40	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	9.3
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ S	9.3
	449893	T97999	Hs.18214	ESTs, Weakly similar to B34087 hypothetical protein [9.3
	420101	AW500529	Hs.95180	KIAA0767 protein	9.3
	428166	AA423849	Hs.79530	MS-14 protein	9.3
45	420022	AA256253	Hs.120817	ESTs	9.3
	444020	R92962	Hs.35052	ESTs	9.3
	454765	AW819629		gb:RCS-ST0293-140200-014-H05 ST0293 Homo sapiens cDNA	9.3
	415021	R54409	Hs.301693	Homo sapiens, clone IMAGE:3638994, mRNA, partial cds	9.3
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	9.3
50	415009	C75253	Hs.220950	ESTs	9.3
	428845	AL157679	Hs.153610	KIAA0751 gene product	9.3
	433348	AA877996	Hs.125376	ESTs, Weakly similar to JCS314 CDC28cdc2-like kinase	9.2
	417881	AI879117		gb:au54g09.y1 Schnelder fetal brain 00004 Homo sapien	9.2
	446354	AW449650	Hs.202249	ESTs	9.2
55	427018	AA397638	Hs.136280	Homo sapiens cDNA: FLJ22288 fis, clone HRC04157	9.2
	434410	AA632644		gb:np87b07.s1 NCI_OGAP_Thy1 Homo sapiens cDNA clone s	9.2
	448072	AI459306	Hs.24908	ESTs	9.2
	457322	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HEP08257	9.2
	424317	AI865032	Hs.26017	ESTs	9.2
60	433001	AF217513	Hs.278905	clone HQ0310 PRO0310p1	9.2
	404112	BE302729	Hs.173162	neighbor of COX4	9.2
	433334	AI927208	Hs.231958	matrix metalloproteinase 28	9.1
	434960	AW374941	Hs.72545	ESTs	9.1
	431658	BE409917	Hs.266935	IRNA selenocysteine associated protein	9.1
65	439158	R60323	Hs.193888	ESTs	9.1
	443081	H86858	Hs.132909	ESTs	9.1
	429432	AI678059	Hs.202676	synaptonemal complex protein 2	9.1
	452706	AW449390	Hs.257150	ESTs, Moderately similar to SUR1_HUMAN SURFET LOCUS	9.1
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 gene	9.1
70	430780	N95102	Hs.334858	hypothetical protein MGC12250	9.1
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defective, S. cere	9.1
	418379	AA218940	Hs.137516	fidgetin-like 1	9.1
	431405	AI470895	Hs.252574	ribosomal protein L10a	9.0
	405454			C12000541:gi15728884[ref]NP_006539.1 IGF-II mRNA-bin	9.0
75	438362	AA805678	Hs.12326	ESTs	9.0
	401940			Target Exon	9.0
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	9.0
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	9.0
	459086	AA021163	Hs.22287	ESTs	9.0
80	418653	AI734064	Hs.136212	ESTs	9.0
	444152	AI125694	Hs.149305	hypothetical protein MGC2603	9.0
	437534	AA814471	Hs.291800	ESTs	9.0
	435074	AI760944	Hs.116937	ESTs	9.0
	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA, complete cds	9.0
	442829	AW263123	Hs.127554	ESTs	9.0
	431675	AA699965	Hs.202375	ESTs	9.0
	447164	AF026941	Hs.17518	Homo sapiens clg5 mRNA, partial sequence	8.9

	420183	W92885	Hs.143408	ESTs	8.9
	421133	AA814971	Hs.257634	ESTs	8.9
	407605	W03512	Hs.6479	hypothetical protein MGC13272	8.9
	441370	AI242433	Hs.270085	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	8.9
5	437966	AW891130	Hs.38173	ESTs	8.8
	426360	AW290981	Hs.211296	ESTs, Weakly similar to 2109260A B cell growth factor	8.8
	448111	AA053486	Hs.20315	Interferon-induced protein with tetratricopeptide rep	8.8
	408021	AW137133	Hs.245867	ESTs	8.8
	429228	AI553633	Hs.337139	ESTs	8.8
10	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1) mRNA, partial	8.8
	431184	AW970116	Hs.310616	ESTs	8.8
	425219	AF207881	Hs.155185	cytosolic ovarian carcinoma antigen 1	8.8
	439774	AL360257	Hs.213493	Homo sapiens mRNA full length insert cDNA clone EURO1	8.8
	432573	AA553612	Hs.324696	KIAA1594 protein	8.8
15	450881	W80462	Hs.270521	ESTs, Highly similar to ALU2_HUMAN ALU SUBFAMILY SB S	8.8
	437835	AI146771	Hs.158008	ESTs	8.7
	453204	R10799	Hs.191990	ESTs	8.7
	412719	AW016610	Hs.129911	ESTs	8.7
	408805	H69912	Hs.48269	vaccinia related kinase 1	8.7
20	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuolar proton pu	8.7
	422583	AA410506	Hs.27973	KIAA0874 protein	8.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	8.7
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapiens]	8.7
	454132	AW131759	Hs.248266	ESTs	8.7
25	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-inducing)	8.7
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolog)-like	8.7
	441525	AW241867	Hs.127728	ESTs	8.7
	459539	AI279186		gb:qm24a04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone 3'	8.7
	443148	AI034357	Hs.211194	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX S	8.7
30	424255	AI192657	Hs.143897	dysferlin, limb girdle muscular dystrophy 2B (autosom	8.7
	459435	AA320038		gb:EST22383 Adipose tissue, white II Homo sapiens cDN	8.6
	443117	AI248826	Hs.42029	ESTs	8.6
	457434	AW268192	Hs.18851	hypothetical protein FLJ10875	8.6
35	442505	AW003775	Hs.198248	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, p	8.6
	430901	AA488833	Hs.126711	ESTs, Weakly similar to 138588 reverse transcriptase	8.6
	439223	AW238299	Hs.250618	UL16 binding protein 2	8.6
	417739	Z43995		gb:HSC1QB121 normalized infant brain cDNA Homo sapien	8.6
	415961	H10983	Hs.155919	ESTs	8.6
40	424042	Y10601	Hs.137674	ankyrin-like with transmembrane domains 1	8.6
	451035	AU076785	Hs.430	plastin 1 (I isoform)	8.6
	447155	AA100605	Hs.121557	ESTs, Weakly similar to DP1_HUMAN POLYPOSIS LOCUS PRO	8.6
	412688	AA456195	Hs.10056	hypothetical protein FLJ14621	8.6
	458042	AW058464	Hs.6430	protein with polyglutamine repeat; calcium (ca2) home	8.6
45	456530	AI049437	Hs.100292	Homo sapiens mRNA; cDNA DKFZp586E1120 (from clone DKF	8.6
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	8.6
	445006	W91903	Hs.124814	ESTs	8.5
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeast homolo	8.5
	455161	BE145900		gb:MRQ-HT0208-Z21299-204-b12 HT0208 Homo sapiens cDNA	8.5
50	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S. cerevisiae)	8.5
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	8.5
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interacting protein	8.5
	416018	U49395	Hs.77807	purinergic receptor P2X, ligand-gated ion channel, 5	8.5
	404534			C11001758:gl 12621132 ref NP_075243.1 MEGF1 [Rattus	8.5
55	438451	AI081972	Hs.220261	ESTs	8.5
	435176	AA744875	Hs.189413	ESTs	8.5
	443245	AI040955	Hs.151973	hypothetical protein FLJ23511	8.5
	443162	T49951	Hs.9029	DKFZP434G032 protein	8.5
	457478	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), catalytic subuni	8.5
60	403839			Target Exon	8.5
	434932	BE613162	Hs.284135	hypothetical protein MGC3038	8.4
	420991	AW504814	Hs.121004	Homo sapiens mRNA for FLJ00111 protein, partial cds	8.4
	457854	BE547674	Hs.204169	ESTs, Weakly similar to S65557 alpha-1C-adrenergic re	8.4
	456994	BE179190		gb:RCO-HT0613-210300-032-07 HT0613 Homo sapiens cDNA	8.4
65	402796			Target Exon	8.4
	423426	AW389579	Hs.128434	Homo sapiens ELISC-1 mRNA, partial cds	8.4
	429568	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (from clone DKF	8.4
	404110			NM_020245: Homo sapiens lubby super-family protein (T	8.4
	424441	X14850	Hs.147097	H2A histone family, member X	8.4
70	433155	AI037035	Hs.100426	Homo sapiens cervical cancer metastasis-suppressor 1 (B	8.4
	414839	X63692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	8.4
	406867	AA157857	Hs.182265	keratin 19	8.4
	418278	AI088489	Hs.83937	hypothetical protein	8.4
	458696	AW375333	Hs.199890	ESTs	8.4
75	456248	AL035786	Hs.82425	actin related protein 2/3 complex, subunit 5 (16 kD)	8.4
	403152	AA576664	Hs.37078	v-crk avian sarcoma virus CT10 oncogene homolog-like	8.4
	407649	BE066724	Hs.37427	erythrocyte membrane protein band 4.1 (elliptocytosis	8.4
	448387	AI874402	Hs.170810	ESTs	8.4
	433671	AW138797	Hs.132906	19A24 protein	8.4
80	425891	AI041717	Hs.132141	ESTs	8.4
	447347	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 protein [H.sapie	8.4
	439079	AF085937	Hs.38348	ESTs	8.4
	458115	BE091587		gb:LL2-BT0731-240400-069-H04 BT0731 Homo sapiens cDNA	8.4
	428144	BE269243	Hs.182625	VAMP (vesicle-associated membrane protein)-associated	8.4

	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	8.3
	443056	AI457996	Hs.132578	ESTs	8.3
	410391	H17881	Hs.15043	Homo sapiens clone FLB5227 PRO1367 mRNA, complete cds	8.3
	407989	AW135208	Hs.256092	ESTs	8.3
5	410536	N39533		gb:yy27d04.s1 Soares fetal liver spleen 1NFLS Homo sa	8.3
	452273	AI870685	Hs.231022	ESTs	8.3
	454297	AI223335	Hs.50651	Janus kinase 1 (a protein tyrosine kinase)	8.3
	453718	AL119317	Hs.120360	phospholipase A2, group VI (cytosolic, calcium-indepe	8.3
	401654			NM_007242:Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) b	8.3
10	432891	AF161483	Hs.279761	HSPC134 protein	8.2
	419923	AW081455	Hs.120219	ESTs	8.2
	433627	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone KAT11914	8.2
	435452	AA831004	Hs.124874	ESTs	8.2
	418683	U90908	Hs.87241	hypothetical protein from clones 23549 and 23762	8.2
15	440065	W03476	Hs.266331	hypothetical protein MGC4595	8.2
	439752	T78968	Hs.14411	ESTs	8.2
	447983	AW612726	Hs.282113	ESTs, Weakly similar to I38022 hypothetical protein [8.2
	441966	AA568689	Hs.16131	hypothetical protein FLJ12876	8.2
20	408182	AA047854		gb:zf49g04.r1 Soares retina N2b4HR Homo sapiens cDNA	8.2
	432180	Y18418	Hs.272822	RuvB (E coli homolog)-like 1	8.2
	436005	BE551650	Hs.158126	Homo sapiens cDNA FLJ13350 fis, clone OVARC1002143	8.2
	414962	AF273304	Hs.235376	XPMC2 protein	8.2
	444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), soluble	8.2
25	408175	W29089	Hs.19056	hypothetical protein DKFZp667O2416	8.2
	413940	AI633205	Hs.159914	ESTs, Weakly similar to I78885 serine/threonine-speci	8.2
	437277	AA748016	Hs.123370	ESTs	8.2
	431445	AA505135	Hs.44037	ESTs	8.1
	418927	BE349635	Hs.190284	ESTs	8.1
30	452446	AA086123	Hs.297856	ESTs	8.1
	445380	AI222019	Hs.144838	ESTs	8.1
	421174	AW969058	Hs.291974	ESTs, Moderately similar to A46010 X-linked retinopat	8.1
	444374	AA009841	Hs.11039	hypothetical protein MGC2722	8.1
	417247	N58024		gb:yy63c01.s1 Soares fetal liver spleen 1NFLS Homo sa	8.1
35	438335	AI498421	Hs.243168	ESTs	8.1
	445235	AI564022	Hs.138207	ESTs	8.1
	422585	NM_016186	Hs.118620	protein Z-dependent protease inhibitor precursor	8.1
	442522	AI087038	Hs.146592	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ S	8.1
	430684	AI808979	Hs.293193	ESTs	8.1
40	446442	BE221533	Hs.257858	ESTs	8.1
	441410	AA932689	Hs.233304	ESTs, Weakly similar to I38022 hypothetical protein [8.0
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein product [H.sa	8.0
	449539	W80363	Hs.58446	ESTs	8.0
	406663	U24683	Hs.302063	Immunoglobulin heavy constant mu	8.0
45	423767	H18283	Hs.132753	F-box only protein 2	8.0
	450937	R49131	Hs.26267	ATP-dependant interferon response protein 1	8.0
	430977	AA490069	Hs.306676	Homo sapiens cDNA FLJ14302 fis, clone PLACE2000003	8.0
	455677	BE068081	Hs.8867	cysteine-rich, angiogenic inducer, 61	8.0
	436706	AA725808	Hs.194609	ESTs	8.0
50	459407	N92114		gb:za22h11.r1 Soares fetal liver spleen 1NFLS Homo sa	8.0
	444132	AK000452	Hs.10340	hypothetical protein FLJ20445	8.0
	437149	AI686651	Hs.202234	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAMILY SB2	8.0
	418499	AI627392	Hs.302023	hypothetical protein FKSG25	8.0
	411298	AW835858		gb:PMO-LT0017-031299-001-h07 LT0017 Homo sapiens cDNA	8.0
55	432571	AF151054	Hs.278429	hepatocellular carcinoma-associated antigen 59	8.0
	416295	AI064824	Hs.193385	ESTs	8.0
	427485	AF039652	Hs.178655	ribonuclease H1	8.0
	409857	AW501908		gb:UH-HF-BR0p-ajp-c-12-0-UI.r1 NIH_MGC_52 Homo sapien	7.9
60	433854	AA610649	Hs.333239	ESTs	7.9
	423573	AA328504		gb:MR0-HT0157-021299-004-d08 HT0157 Homo sapiens cDNA	7.9
	404495			gb:EST31993 Embryo, 12 week I Homo sapiens cDNA 5' en	7.9
	443135	AI376331	Hs.156103	C8001441*gl 8923061 ref NP_060114.1 hypothetical pr	7.9
	448939	BE267795	Hs.22595	ESTs	7.9
65	413283	R78669	Hs.23756	hypothetical protein FLJ10637	7.9
	443987	AW163123	Hs.10071	hypothetical protein similar to swine acyneuraminase	7.9
	434197	AA827223		seven transmembrane protein TM7SF3	7.9
	436882	AW016722	Hs.194976	gb:nq63b04.s1 NCL_OGAP_Ov6 Homo sapiens cDNA clone si	7.9
	434502	AW974915	Hs.116550	SH2 domain-containing phosphatase anchor protein 1	7.9
70	435507	AI143579	Hs.26510	ESTs	7.9
	444896	AI201480	Hs.144856	vacuolar protein sorting 33B (yeast homolog)	7.9
	419320	H96666	Hs.6137	ESTs	7.9
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	7.9
	425569	AA359597	Hs.301701	Homo sapiens cDNA FLJ12073 fis, clone HEMBB1002387	7.9
75	445209	AW294230	Hs.80988	collagen, type VI, alpha 3	7.9
	449193	AI637997	Hs.195653	ESTs	7.9
	447397	BE247676	Hs.18442	E-1 enzyme	7.9
80	455037	BE144549		gb:MR0-HT0167-081199-001-a02 HT0167 Homo sapiens cDNA	7.9
	453367	AW732847	Hs.70573	PKC-1-related HIT protein	7.8
	439317	AF086127	Hs.50600	ESTs, Weakly similar to T47156 hypothetical protein D	7.8
	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	7.8
	406562			NM_004520:Homo sapiens kinesin heavy chain member 2	7.8
	435192	AK000739	Hs.4835	eukaryotic translation initiation factor 3, subunit 8	7.8
	413500	BE144914		gb:CM3-HT0183-181099-023-b05 HT0183 Homo sapiens cDNA	7.8

5	436216	AA380887	Hs.5085	dolichyl-phosphate mannosyltransferase polypeptide 1,	7.8
	418623	AW194757	Hs.266804	ESTs	7.8
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo sapiens cDNA	7.8
	430146	AW815330		gb:QV0-ST0215-060100-083-a09 ST0215 Homo sapiens cDNA	7.8
	441841	AA971819	Hs.176083	ESTs	7.8
10	457677	AA628890	Hs.158701	ESTs	7.8
	421090	BE301870	Hs.101813	solute carrier family 9 (sodium/hydrogen exchanger),	7.8
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugating enzy	7.8
	434407	AW815333		gb:QV0-ST0215-060100-083-g01 ST0215 Homo sapiens cDNA	7.8
	406410			CS000010*:g[10440464]dbj BAB15765.1 (AK024475) FLJ0	7.8
15	453579	AI204463	Hs.61857	ESTs	7.7
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogene homolog-lik	7.7
	452139	AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 fs, clone COL05135	7.7
	405510			ENSP00000233779*:Hypothetical 68.0 kDa protein.	7.7
	440777	AA994020	Hs.128553	ESTs	7.7
20	446424	AW134529	Hs.244647	ESTs	7.7
	448004	AW451477	Hs.257455	ESTs	7.7
	430610	AI821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP S	7.7
	427080	AW068287	Hs.173466	ras-related C3 botulinum toxin substrate 2 (rho fami	7.7
	451693	BE220445	Hs.279635	ESTs	7.7
25	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	7.7
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	7.7
	427735	AA916785	Hs.180610	splicing factor proline/arginine rich (polypyrimidin	7.7
	425423	NM_005897	Hs.157180	intracisternal A particle-promoted polypeptide	7.7
	450663	HA3540	Hs.25292	ribonuclease H1, large subunit	7.7
30	432585	AA705591	Hs.190209	ESTs	7.7
	402682			Target Exon	7.7
	400247			Eos Control	7.7
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	7.7
	426761	AI015709	Hs.172089	Homo sapiens mRNA: cDNA DKFZp58612022 (from clone DKF	7.7
35	405514			ENSP00000241075:TRRAP PROTEIN.	7.7
	412406	AW948172		gb:RCO-MT0013-280300-021-b06 MT0013 Homo sapiens cDNA	7.7
	440226	AA873387	Hs.207330	ESTs	7.7
	435625	H50654	Hs.113999	ESTs	7.6
	418529	AW005695	Hs.250897	TRK-fused gene	7.6
40	407758	D50915	Hs.38365	KIAA0125 gene product	7.6
	447276	AL049795	Hs.17987	hypothetical protein MGC1203	7.6
	449938	AW970612	Hs.172635	Homo sapiens cDNA: FLJ21367 fs, clone COL03051	7.6
	422893	X58411	Hs.121555	myosin IIF	7.6
	451593	AF151879	Hs.26706	CGI-121 protein	7.6
45	424148	BE242274	Hs.1741	integrin, beta 7	7.6
	447519	U46258	Hs.339665	ESTs	7.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolog 1	7.6
	436279	AW900372	Hs.180793	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	7.6
	426523	S68616	Hs.170222	solute carrier family 9 (sodium/hydrogen exchanger),	7.6
50	456926	AB018284	Hs.158688	KIAA0741 gene product	7.6
	416294	D86980	Hs.79170	KIAA0227 protein	7.6
	409206	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo sapiens cDNA	7.6
	417086	AA194446	Hs.73451	ESTs, Weakly similar to S55024 nebulin, skeletal musc	7.5
	418181	U37012	Hs.83727	cleavage and polyadenylation specific factor 1, 160kD	7.5
55	436910	AA926944		gb:om68g01.s1 NCL_CGAP_GC4 Homo sapiens cDNA clone 3'	7.5
	401008			Target Exon	7.5
	413245	BE244334	Hs.75249	ADP-ribosylation factor-like 6 interacting protein	7.5
	446820	AW295037	Hs.254986	ESTs	7.5
	439279	AI039473	Hs.130636	ESTs	7.5
60	426116	AA868729	Hs.144694	ESTs	7.5
	410098	BE326839	Hs.17433	hypothetical protein FLJ20967	7.5
	422326	AI114875	Hs.78592	eukaryotic translation initiation factor 2B, subunit	7.5
	435513	AW404075	Hs.42785	DC11 protein	7.4
	421629	N80121	Hs.4983	ESTs	7.4
65	434663	AA641972	Hs.130058	ESTs	7.4
	452461	N78223	Hs.108106	transcription factor	7.4
	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	7.4
	405417			CX001144*:g[7242973]dbj BAA92547.1 (AB037730) KIAA1	7.4
	414076	AA467738		gb:nc74e05.s1 NCL_CGAP_Pr2 Homo sapiens cDNA clone, m	7.4
70	435014	BE560898	Hs.10026	mitochondrial ribosomal protein L17	7.4
	449610	AI242042	Hs.14044	ESTs	7.4
	403397			Target Exon	7.4
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	7.4
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant; spastin)	7.4
75	404914			NM_004046*:Homo sapiens ATP synthase, H+ transporting	7.4
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-activating fact	7.4
	432820	AI554057	Hs.152477	ESTs	7.4
	418978	T85295	Hs.268606	ESTs	7.4
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonine kinase 21)	7.4
80	454639	AW811633		gb:RC2-ST0158-091099-011-d05 ST0158 Homo sapiens cDNA	7.4
	434522	AF189259	Hs.283081	gamma-aminobutyric acid (GABA) receptor, theta	7.4
	458236	AW297043	Hs.255604	ESTs, Weakly similar to A47234 homeobox protein H6 [H	7.4
	441043	AA913422	Hs.192104	ESTs	7.4
	422838	AA524065	Hs.93670	Homo sapiens cDNA: FLJ22654 fs, clone HSI08202	7.3
	455096	AW855718		gb:RC1-CT0279-070100-021-a06 CT0279 Homo sapiens cDNA	7.3
	442307	AW027690	Hs.90037	ESTs	7.3
	425453	AW374284	Hs.297215	Homo sapiens chromosome 19, cosmid R26894	7.3

	455327	AW896238	Hs.334805	Homo sapiens cDNA FLJ14604 fis, clone NT2RP1000363, m	7.3
	420982	AW576160	Hs.100729	KIAA0692 protein	7.3
	424563	AA446932	Hs.151428	ret finger protein 2	7.3
	417125	AW181998	Hs.81248	CUG triplet repeat, RNA-binding protein 1	7.3
5	453902	BE502341	Hs.3402	ESTs	7.3
	446842	AI343510	Hs.176992	ESTs	7.3
	454128	AL031259	Hs.41639	programmed cell death 2	7.3
	427011	BE302729	Hs.173162	neighbor of COX4	7.3
10	450872	AI742594		gb:wg55h05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapien	7.3
	451512	AI800236	Hs.207080	ESTs	7.3
	406708	AI282759		gb:qt84a01.x1 NCL_CGAP_Co14 Homo sapiens cDNA clone I	7.3
	432576	AW157424	Hs.165954	ESTs, Weakly similar to I38022 hypothetical protein {	7.3
	459304	AW005809	Hs.281076	ESTs, Weakly similar to CHD4_HUMAN CHROMODOMAIN HELIC	7.3
15	401375			NM_020999-Homo sapiens neurogenin 3 (NEUROG3), mRNA	7.3
	413258	BE075114		gb:PM1-8T0585-110200-003-c11 BT0585 Homo sapiens cDNA	7.3
	406016			Target Exon	7.3
	421508	BE302796	Hs.105097	thymidine kinase 1, soluble	7.3
	422742	AA316117	Hs.337128	ESTs	7.3
20	440031	BE045970	Hs.244746	ESTs	7.3
	429389	AA454779	Hs.201441	Homo sapiens cDNA FLJ11079 fis, clone PLACE1005111	7.3
	449656	AA002008	Hs.188633	ESTs	7.3
	444310	AI140432	Hs.175936	ESTs	7.3
	459274	AA382590	Hs.170980	KIAA0948 protein	7.3
25	425404	BE048060	Hs.133494	Homo sapiens clone TCCCA00164 mRNA sequence	7.3
	431150	T63857		gb:yc16e01.s1 Stratagene lung (937210) Homo sapiens c	7.2
	443217	NM_001545	Hs.9078	Immature colon carcinoma transcript 1	7.2
	413405	AW022253	Hs.215976	ESTs	7.2
	447653	BE327277	Hs.161145	ESTs	7.2
30	414704	NM_014757	Hs.76986	mastamind (Drosophila), homolog of	7.2
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor, clade B (o	7.2
	409188	AW363284	Hs.32553	ESTs	7.2
	453493	AL039478	Hs.304447	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.2
	456111	AK000150	Hs.78185	MAX-like bHLHZIP protein	7.2
35	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	7.2
	446364	AB006624	Hs.14912	KIAA0286 protein	7.2
	432215	AU076609	Hs.2934	ribonucleotide reductase M1 polypeptide	7.2
	436943	AA773838	Hs.5353	caspase 10, apoptosis-related cysteine protease	7.2
	446336	AW816038	Hs.151251	ESTs	7.2
40	418469	U34879	Hs.85279	hydroxysteroid (17-beta) dehydrogenase 1	7.2
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	7.2
	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT2RP3002304	7.2
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polypeptide 1	7.2
	416450	AA180467		gb:zcp14g08.s1 Stratagene fetal retina 937202 Homo sep	7.2
45	449714	AB033015	Hs.23941	KIAA1189 protein	7.2
	455447	AW947507		gb:RCO-MT0002-140300-011-a12 MT0002 Homo sapiens cDNA	7.2
	437154	AI023133	Hs.10739	ESTs	7.2
	423059	AW378445	Hs.123080	Homo sapiens unknown protein mRNA, partial cds	7.2
	419092	J05581	Hs.89603	mucln 1, transmembrane	7.2
50	426736	AA431615	Hs.130722	ESTs	7.2
	417748	Z43011	Hs.21169	ESTs	7.2
	434748	AI862604	Hs.211884	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.2
	438929	AW195515	Hs.253177	ESTs	7.2
	452081	AI074259	Hs.469	succinate dehydrogenase complex, subunit A, flavoprot	7.1
55	446416	AV658299	Hs.163959	ESTs	7.1
	415023	AA932146	Hs.133494	Homo sapiens clone TCCCA00164 mRNA sequence	7.1
	434766	AA742222	Hs.120634	ESTs	7.1
	432566	AW439330	Hs.256889	ESTs, Weakly similar to 2109260A B cell growth factor	7.1
	420252	AW270404	Hs.193161	ESTs	7.1
60	435403	AA779987	Hs.269658	ESTs	7.1
	430151	AW968203		gb:EST380398 MAGE resequences, MAGJ Homo sapiens cDNA	7.1
	427908	AA417272	Hs.24122	ESTs	7.1
	417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitter transporter	7.1
	400098			Eos Control	7.1
65	412647	AW975090		gb:EST387196 MAGE resequences, MAGN Homo sapiens cDNA	7.1
	437234	AI472213	Hs.247711	hypothetical protein FLJ20557	7.1
	453366	AW958751	Hs.28921	zinc finger protein	7.1
	425803	AI825204	Hs.211408	ESTs	7.1
	447383	N24231		gb:yx22a11.r1 Soares melanocyte 2NbHM Homo sapiens cD	7.1
70	423864	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (gamma)	7.1
	450799	AW407504		gb:UL-HF-BMO-adt-g-12-0-UL.r1 NIH_MGC_38 Homo sapiens	7.1
	409592	BE280951	Hs.55058	EH-domain containing 4	7.1
	453945	NM_005171	Hs.36908	activating transcription factor 1	7.1
	425196	AL037915	Hs.155097	carbonic anhydrase II	7.0
75	439778	AL109729	Hs.99364	putative transmembrane protein	7.0
	417682	R07478	Hs.268845	ESTs	7.0
	438087	AI863770	Hs.190422	ESTs	7.0
	452724	R84810	Hs.30464	cyclin E2	7.0
	448833	AA311426	Hs.21635	tubulin, gamma 1	7.0
80	433154	AA578526	Hs.160994	ESTs	7.0
	440094	AI651558	Hs.270372	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.0
	409253	H91200	Hs.52002	CD5 antigen-like (scavenger receptor cysteine rich fa	7.0
	431270	BE046609		gb:hn41e11.x1 NCL_CGAP_RDF2 Homo sapiens cDNA clone 3	7.0
	407629	AA649242	Hs.62632	ESTs	7.0

5	408296	AL117452	Hs.44155	DKFZP586G1517 protein	7.0
	445439	BE243084	Hs.12719	regulator of nonsense transcripts 1	7.0
	427106	AA398193	Hs.97584	ESTs	7.0
	408623	AW811978	Hs.254037	ESTs	7.0
	426561	AA381437		gb:EST94514 Activated T-cells 1 Homo sapiens cDNA 5'	7.0
10	408492	AA555217	Hs.183684	eukaryotic translation initiation factor 4 gamma, 2	7.0
	428894	AA437066	Hs.271736	ESTs	7.0
	419102	AA234098	Hs.42424	ESTs, Weakly similar to 2004399A chromosomal protein	7.0
	429067	AA446019	Hs.104967	ESTs	7.0
	422684	BE561617	Hs.119192	H2A histone family, member Z	7.0
15	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase 5	7.0
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-82 protein [H.	7.0
	443599	A1079559	Hs.134125	ESTs	7.0
	400715			ENSP00000237081*-KIAA1217 PROTEIN (FRAGMENT).	7.0
	446514	AW449233	Hs.150847	ESTs	7.0
20	413992	W26276	Hs.136075	RNA, U2 small nuclear	7.0
	402442			Target Exon	7.0
	419497	NM_006410	Hs.90753	Tat-interacting protein (30kD)	7.0
	439575	W79259		gb:zdd75c06.r1 Soares_fetal_heart_NbHH19W Homo sapiens	7.0
	407027	U63312		gb:Human cosmid LL12NC01-242E1, ETV6 gene, exons 1B a	7.0

Table 15B

25	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
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	409113	110079_2	AA074897 AA113914 AA064871 AA079329 AA071309 AA084710 AA129030 AA075042 AA074794 AA071453 AA078803 AA148628 AA122204	
35			AA074159 AA125185 AA079117 AA127089 AA070912 AA079280 AA131372 AA078833 AA071087 AA076131 AA071047 AA079401 AA083070	
			AA102076 AA115163 AA074198 AA134725 AA113889 AA121103 AA075041 AA065148 AA071310 AA101144 AA079659 AA078931 AA079209	
			AA070928 AA068994 AA069817 AA076187 AA069053 AA131489 AA071308 AA063317 AA070156 AA071430 AA076056 AA075684 AA070053	
40			AA126283 AA126078 AA075895 AA079208 AA074583 AA071086 AA079623 AA070627 AA078802 AA076622 AA065061 AA079143 AA071110	
			AA079434 AA148748 AA079230 AA085188 AA074485 AA070580 AA076151 AA083166 AA085118 AA079450 AA085044 AA120938 AA079200	
			AA100188 AA081472 AA122355 AA129031 AA085362 AA069220 AA070940 AA075968 AA074563 AA084027 AA115929	
45			AW364844 AW364847 AW937534 AW937593 AW937659	
			AW501908 AW502959 AW502540	
			N39533 AW753094 AW753093	
50			AW835858 AW835836 AW835823 AW835834 AW835831 AW835832 AW835843 AW835816 AW835833 AW835815 AW835849 AW835835	
			AW835848 AW835851 AW835852 AW835862 AW835855 AW835825 AW835847 AW835838	
			AW948172 AW948178 AW948169 AW948176 AW948191 AW948182 AW948186 AW948184 AW948187 AW948188 AW948189 AW948181	
55			AW948177 AW948171 AW948183 AW948173	
			AW975090 N44182	
			BE075114 BE075283 BE075118	
60			BE081585 BE081717 BE081863 BE081794 BE081659	
			BE144914 BE394989	
			AA467736 AA135210 AW968166 AA467804	
65			AA180467 AA449184 AA464831 AA505048	
			N58024 T58194 T11693 N64222 T05848	
			Z43995 R12357 R34740	
70			AJ879117 AW161351 Z45755 BE003661 AA206949 AA476541	
			AA216419 F03238 AA229517	
			AA310527 AW952295 Z44865 H06641	
75			AA328504 AA327783 AW962370	
			AA381437 AA628833 AW407275	
			AA425488 AA496895 F23221	
80			AW815330 AW968170 AJ732687 AJ732725 AA68343 AA467817 AW063961	
			AW968203 AJ732757 AA470353 AA468025 AA68479 AJ734151	
			R34356 AW969880 AA484613	
			AW021726 AA487752 AA488085	
			T63857 AW971220 AA493469 T63699	
			BE046609 BE046118 AA501504	
			AA534489 AW970240 AW970323	
			AA627223 AA643443 AA650619 AA643463 AA643453 AA643439 AA643438 AW802964 AW821595 AW821594 AA643431 AA643432	
			AW827513	
			AW815333 AW815409 AA632563	
			AA632644 AA635376 AA664188	
			AA926944 AA767974 AA737237	
			AJ147061 AA743380 AA765223 AW976398 AJ803927	
			AF086174 W31796 WD4694	
			W79259 AF086399 W73927	
			AJ140497 AW749625 AW749626 AW749644	
			R36075 AJ366546 R36167	
			N24231 BE617964 N36313	
			AW407504 W31274 AJ738877	
			AJ742594 AJ761397 R31198 AJ819332 R31257	
			AW812535 AW812536 AW390307	
			AW811633 AW811652 AW811898	
			AW819629 AW854320	

5	455037 455096 455161 455410	1249783_1 1253078_1 1256167_1 1268380_1	BE144549 AW851677 AW851643 AW851711 AW851719 AW855718 AW855740 AW855748 BE145900 AW859906 BE145895 BE145831 BE145914 BE145820 BE145817 BE145890 BE145908 AW936678 AW936637 AW936682 AW936685 AW936817 AW936811 AW936762 AW936653 AW936815 AW936812 AW936683 AW936822 AW936823 AW936821 AW936732 AW936730 AW936781 AW947507 AW947509 AW947791 BE008335 BE147440 BE147708 BE147563 BE147456 BE179190 BE179206 BE179182 BE179185 BE179186 BE179194 AA744389 AA744270 AA744284 AA744299 AA745380 AA744337 AA846905 AA847698 BE142728 AA834047 AW937124
10	455447 455855 455994 457892 458080 458115	1292444_1 1375834_1 1398737_1 432926_1 471050_1 47705_29	BE091587 BE091730 BE091577 BE091655 BE091729 BE091640 BE091578 BE091727 BE091803 BE091660 BE091721 BE088255 BE076582 AW992312 BE008791 BE082385 BE083504 BE083466 AW997967 AW997991 BE166595 AW843686 AW844334 BE079091 AW603391 BE081427 BE079514 BE184580 BE009962 BE008722 AW579912 AW850551 AW890184 AW795276 AW860410 AW860411 AW610330 AW860564 AW860578 AW862519 BE073924 BE008687 BE073857 BE073921 AW274106 BE011050 AW268120 A1335067 AW793748 AW997736 BE080117 AW667987 A1547161 AW844767 AW393596 AW579444 BE083334 A1547158 AW799863 AA585179 AW992792 AW882215 BE011913 AW997894 A1547159 AW992772 AW581178 AA092247 AW843916 BE079190 AW878478 BE083648 BE066454 A1469937 AW393594 AW579899 AW939276 BE173265 AW878631 AW878638 AW992802 BE079913 AA633638 AW369008 BE076590 AW843456 AW992791 BE173247 AW843921 AW843333 AW876334 BE090235 BE078240 BE066325 AW603276 BE169310 AW817299 BE091641 BE000160 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BE075399 AW996628 AW578707 BE084309 AW753604 BE185916 AW842220 BE185222 BE006152 BE008795 AW578706 BE080256 BE183984 A1934532 AA449648 AW578699 BE150514 AW883580 AA493568 BE085748 AW753601 BE150562 AW882677 BE091787 AW899123 BE081679 BE080121 AW606787 AW603410 BE001317 AW905799 BE092206 AW996343 BE086922 BE008806 AW844759 AW606009 BE150487 AW070728 BE150491 BE150515 AW606010 BE150508 BE008718 AW578702 BE150509 AA436751 AW883918 BE183883 AW753607 BE008669 BE150446 AA533458 BE079219 AW838884 AW868387 AW878479 BE078815 BE008802 AW992789 BE007925 AW802204 BE011825 BE092130 BE184059 BE079087 BE150558 BE185497 BE078808 AW883761 AW842295 BE161523 AA484796 AA480390 AW994667 BE073205 AW607318 BE083201 AW802265 AW578700 BE078715 AW860403 AW897456 AW996558 AW890602 AW860413 AA425412 BE008364 BE150438 AW602606 A1435236 AA574285 A1823745 AA501773 AW002987 AW832749 BE185491 AW996489 BE001442 AW948425 BE001586 A1524864 BE085556 AW867549 AW604038 BE079832 A1752160 AW999398 AW883904 AW882376 AW467098 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BE075431 AW815917 AW998359 AW799883 AW603782 AA557480 AW841444 BE075915 AA548034 AW843393 AW391559 BE083265 AW939721
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 BE182443 BE010296 AW577806 BE008415 BE184036 BE076597 AJ817413 AW795053 AW896761 AW841433 BE182458 AW603796 AW842676
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 AA506406 AA888571 AA503568 AA507130 AA532944 AA501672 BE168634 AA492022 AA507662 AW842286 AA494226 AA776038 AA442419
 AW579900 BE171816 AA863065 AA491916 AA447490 AA461423 AA434543 AA243279 AW997466 AW603740 BE000295 AA658571

TABLE 15C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400715	8118885	Minus	80151-80297
400736	8118995	Plus	143447-143851
401008	8117391	Minus	81421-81551,82364-82512,82862-82938
401069	3927852	Minus	45682-45831
401375	7417809	Minus	6121-6766
401405	7768126	Minus	69276-69452,69548-69958
401539	8072433	Minus	62028-62808
401557	8099866	Minus	112785-112924
401654	9097132	Minus	64695-64797
401940	3738108	Plus	153460-153592
402025	7547169	Plus	173835-173998
402442	9796503	Plus	141714-141842,142010-142122
402682	8138477	Minus	147522-147795
402796	3646083	Minus	6128-6265,6416-6689
402967	5360987	Minus	33518-34546
403038	7717439	Minus	290021-290284
403055	8748904	Minus	109532-110225
403310	8139936	Minus	163883-184026
403397	9438368	Minus	84481-84655
403839	4176355	Plus	21201-22223
404110	9212839	Minus	18344-18510
404495	8151634	Minus	59449-60477
404534	8247909	Minus	147853-148086
404630	9796655	Plus	74495-74715
404649	9796926	Minus	100027-100399
404680	9797204	Minus	159810-159979,160213-160321,161023-161304,162862-163140,164490-164644,166404-166530,166936-167083,167392-167522
404914	7341760	Plus	92603-92827
405417	4753290	Minus	50704-51499
405454	7656675	Plus	133807-134053
405510	7630909	Minus	101028-101174
405514	9454624	Plus	35953-36151
405536	9795661	Plus	164091-164162,164397-164516,166720-166790,167785-167935
406016	8272661	Plus	41341-41940
406410	9256394	Minus	115806-116104
406464	9789674	Plus	72161-72562
406562	7711584	Plus	37316-37426

TABLE 16A: 200 GENES DOWN-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT CERVIX

Table 16A shows 200 genes down-regulated in cervical cancer compared to normal adult cervix. These were selected as for Table 15A, except that the numerator and denominator were switched, the median value amongst normal cervixes was greater than or equal 40 units, and the ratio was greater than or equal to 3.0 (i.e. 3-fold down-regulated in tumor vs. normal cervix).

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of cervical cancer to normal cervix

Pkey	ExAccn	UnigenelD	Unigene Title	R1
453596	AA441838	Hs.62905	hypothetical protein FLJ14834	18.1
443912	R37257	Hs.184780	ESTs	16.8
420923	AF097021	Hs.273321	differentially expressed in hematopoietic lineages	13.6
414422	AA147224	Hs.337232	Homeo box A13	13.1
420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT2RP2002672	12.9
412639	AW961284	Hs.296235	ESTs	12.4

	418994	AA285520	Hs.89546	selectin E (endothelial adhesion molecule 1)	12.4
	407938	AA905097	Hs.85050	phospholamban	11.3
	410544	AI446543	Hs.95511	ESTs	11.3
5	413802	AW984490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-adrenergic rece	11.1
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 protein [Hsapiens]	11.0
	420674	NM_000055	Hs.1327	butyrylcholinesterase	10.9
	453060	AW294092	Hs.21594	hypothetical protein MGC15754	10.6
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to hypoxia inducib	10.5
10	452106	AI141031	Hs.21342	ESTs	9.5
	428780	AI478578	Hs.50836	ESTs	9.5
	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	9.2
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PLACE1002968	9.0
	430468	NM_004673	Hs.241519	angiopoietin-like 1	9.0
15	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chain	8.7
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activin receptor inte	8.6
	401486	NA		C4000647*gi4758508ref[NP_004253.1] airway trypsin-li	8.4
	417511	AL049176	Hs.82223	chordin-like	8.3
	429900	AA460421	Hs.30875	ESTs	8.2
20	411908	L27943	Hs.72924	cytidine deaminase	8.0
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiesterase	8.0
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from clone DKFZp	8.0
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	8.0
	421666	AL035250	Hs.1408	endothelin 3	7.9
25	450164	AL239923	Hs.30098	ESTs	7.9
	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A; scatter factor	7.7
	425608	AA360486	Hs.92448	ESTs	7.6
	442748	AI016713	Hs.135787	ESTs	7.3
	415672	N53097	Hs.193579	ESTs	7.2
30	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	7.2
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	7.0
	424634	NM_003613	Hs.151407	cartilage intermediate layer protein, nucleotide pyroph	6.7
	414214	D49958	Hs.75819	glycoprotein M6A	6.5
	436637	AI783629	Hs.26766	ESTs	6.5
35	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	6.5
	432101	AI918950	Hs.123642	EphA3	6.3
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA, complete cds	6.3
	424153	AA451737	Hs.141496	MAGE-like 2	6.3
	420228	R25023	Hs.12369	ESTs	6.2
40	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myotilin)	6.1
	444931	AV652066	Hs.75113	general transcription factor IIA	6.1
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HEMBA1002970	6.1
	425849	AJ000512	Hs.286323	serum/glucocorticoid regulated kinase	6.1
45	410425	BE278367	Hs.63510	KIAA0141 gene product	6.0
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	6.0
	424973	X92521	Hs.154057	matrix metalloproteinase 19	6.0
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like 1	5.9
	429414	AI783656	Hs.202095	empty spiracles (Drosophila) homolog 2	5.9
50	440594	AW445167	Hs.126036	ESTs	5.9
	452768	AW069459	Hs.61539	ESTs	5.9
	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 protein [Hsapiens	5.9
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	5.9
	425010	T16837	Hs.4241	ESTs	5.9
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.8
55	437980	R50393	Hs.278436	KIAA1474 protein	5.8
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	5.7
	404097	NA		C5000242*gi3369379[gb]AAAF87128.1[AC006434_24 (AC00643	5.7
	422546	AB007969	Hs.301478	KIAA0500 protein	5.7
60	445872	AI681573	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HEMBB1001458	5.7
	429999	AI761802	Hs.99597	ESTs	5.6
	453354	W55946	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HEMBB1002492	5.6
	442082	RA1823	Hs.7413	ESTs	5.5
	452073	AA625150	Hs.82098	ESTs	5.4
	430032	AW936136	Hs.99610	ESTs	5.4
65	408767	AA057279	Hs.211928	ESTs	5.4
	433234	AB040928	Hs.65366	KIAA1495 protein	5.3
	431708	AI698136	Hs.108873	ESTs	5.3
	421200	AA284811	Hs.264433	ESTs	5.2
	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HEMBA1001008	5.2
70	409643	AW450866	Hs.257359	ESTs	5.1
	416676	AW392022	Hs.79507	KIAA0582 protein	5.1
	420357	U94333	Hs.97199	complement component C1q receptor	5.0
	417355	D13168	Hs.82002	endothelin receptor type B	5.0
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone COL06674	5.0
75	430965	AA489732	Hs.154918	ESTs	4.9
	419568	XD4430	Hs.93913	interleukin 6 (interferon, beta 2)	4.9
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	4.8
	404485	NA		Target Exon	4.8
	429594	AK001128	Hs.210297	Homo sapiens cDNA FLJ10266 fis, clone HEMBB1001024	4.8
80	417692	R09338	Hs.50724	Homo sapiens cDNA FLJ10934 fis, clone OVARC1000640	4.8
	432304	AA932186	Hs.69297	ESTs	4.7
	430895	U66581	Hs.248121	G protein-coupled receptor 22	4.7
	448851	AI582207	Hs.177166	ESTs	4.7
	405523			C8001409*gi7441226[ptr]S31212 collagen alpha 1(XIV)	4.7

	450656	AA010539	Hs.18912	ESTs	4.6
	422942	AF054839	Hs.122540	tetraspan 2	4.6
	401479	T49304	Hs.110950	Rag C protein	4.6
	444192	AW469413	Hs.151145	ESTs	4.5
5	439648	AW780192	Hs.267596	ESTs	4.5
	410378	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily B, member 4	4.5
	444702	AI220122	Hs.326560	hypothetical protein MGC2780	4.5
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX	4.5
10	452249	BE394412	Hs.202095	empty spiracles (Drosophila) homolog 2	4.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	4.4
	411037	BE145915	Hs.99472	ESTs	4.4
	442803	AI675298	Hs.199917	ESTs	4.4
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulatory, type II, be	4.3
15	400628	NA		C10001871:gi1705533 sp P32018 CA1E_CHICK COLLAGEN ALP	4.3
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage serine esterase	4.2
	437110	AL049240	Hs.144995	ESTs	4.2
	410646	W79408	Hs.50745	ESTs	4.2
	456304	AI820973		gbnc21c02.y5 NCI_CGAP_Pr1 Homo sapiens cDNA clone, mRN	4.2
20	401270			Target Exon	4.2
	419447	BE092696	Hs.75928	ESTs	4.2
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15 (NAD)	4.2
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	4.1
	434469	AA634806		gbab28c02.r1 Stratagene lung (937210) Homo sapiens cDN	4.1
25	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR	4.1
	418947	W52990	Hs.22860	ESTs	4.0
	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	4.0
	454736	BE184348		gb:CMO-HT0676-010500-355-e11 HT0676 Homo sapiens cDNA,	4.0
	407945	X69208	Hs.606	ATPase, Cu transporting, alpha polypeptide (Menkes synd	4.0
30	447499	AW262580	Hs.147674	protocadherin beta 16	4.0
	430686	NM_001942	Hs.2633	desmoglein 1	3.9
	409882	AJ243191	Hs.56874	heat shock 27kD protein family, member 7 (cardiovascula	3.9
	419047	AW952771	Hs.90043	ESTs	3.9
	414272	AI651603	Hs.46988	ESTs	3.9
35	443808	AW377736	Hs.12420	ESTs	3.9
	426883	H21520	Hs.35088	ESTs	3.9
	410659	AI080175	Hs.68826	ESTs	3.9
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	3.9
	432181	AA527650	Hs.156037	ESTs	3.8
40	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	3.8
	453296	AA034413	Hs.62560	ESTs	3.8
	400878	NA		Target Exon	3.8
	401103	NA		C12001233:gi17305361 ref NP_038652.1 otogelin [Mus mus	3.7
45	436670	AI690021	Hs.201536	ESTs	3.7
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface receptor	3.7
	408793	BE258371	Hs.254660	ESTs	3.7
	419093	AI804054	Hs.112885	spinal cord-derived growth factor-B	3.7
	434844	AF157116	Hs.22350	hypothetical protein LOC55757	3.7
	450776	NM_007250	Hs.320861	Kruppel-like factor 8	3.6
50	437140	AA312799	Hs.283689	activator of CREM in testis	3.6
	418421	R58620	Hs.85050	phospholamban	3.6
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOTHETICAL PROTEIN	3.6
	417194	N53793		gb:yz07a01.r1 Soares_multiple_sclerosis_2NbHMSP Homo sa	3.6
	443567	AI077540	Hs.134090	ESTs	3.6
55	451879	AI821030		gb:yb52f11.y5 Stratagene ovary (937217) Homo sapiens cD	3.6
	421013	M62397	Hs.1345	mutated in colorectal cancers	3.5
	451896	AF196304	Hs.27197	SUMO-1-specific protease	3.5
	413237	AI468574	Hs.171965	ESTs	3.5
	424636	AA453734	Hs.10198	ESTs	3.5
60	432650	AI288430	Hs.64004	ESTs	3.5
	414681	AL079440	Hs.74002	nuclear receptor coactivator 1	3.5
	400802	NA		Target Exon	3.5
	430015	AW768399	Hs.112157	ESTs	3.5
65	451978	AW813747	Hs.27371	Homo sapiens mRNA; cDNA DKFZp566J123 (from clone DKFZp5	3.5
	449088	AI654048	Hs.198556	ESTs	3.5
	425113	AI936992	Hs.154658	plackstrin and Sec7 domain protein	3.5
	458459	AI124553	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone COL09609	3.5
	420249	BE262895	Hs.276916	nuclear receptor subfamily 1, group D, member 1	3.5
	401159	NA		Target Exon	3.5
70	442789	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQ	3.4
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2/G5 [H.sapiens]	3.4
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC FINGER PROTEIN	3.4
	423587	AA328074	Hs.284256	hypothetical protein FLJ14033 similar to hypoxia induci	3.4
	443178	AI631241	Hs.47312	ESTs	3.4
75	430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTONE H2B H [H.sap	3.4
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Drosophila) homol	3.3
	437950	U79244	Hs.112642	ESTs	3.3
	419368	AI753518	Hs.209464	KIAA1604 protein	3.3
	447335	BE167695	Hs.286192	hypothetical protein FLJ20940	3.3
80	451398	AI793124	Hs.144479	ESTs	3.3
	452814	AI092790	Hs.334703	hypothetical protein FLJ14529	3.3
	407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, expressed in pro	3.3
	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	3.3
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	3.3

444216	D25303	Hs.222	Integrin, alpha 9	3.3
418771	AA807881	Hs.25329	ESTs	3.3
433036	AA574091	Hs.105964	ESTs	3.2
404584			Target Exon	3.2
404195			NM_015718*:Homo sapiens NADPH oxidase 3 (NOX3), mRNA. V	3.2
428819	AL135623	Hs.193914	KIAA0575 gene product	3.2
425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
420833	R47948	Hs.188732	ESTs	3.1
413156	AA127133		gb:z187e03.r1 Stratagene colon (937204) Homo sapiens cD	3.1
413607	T64741		gb:yc48111.r1 Stratagene liver (937224) Homo sapiens cD	3.1
443960	AI093577	Hs.255416	hypothetical protein FLJ21986	3.1
428790	AF023456	Hs.193558	protein phosphatase, EF hand calcium-binding domain 2	3.1
434520	AA205273	Hs.177011	hypothetical protein	3.1
432247	AA531287	Hs.105805	ESTs	3.1
428303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-adrenergic rece	3.1
439734	AC005013	Hs.149	cAMP response element-binding protein CRE-BPa	3.1
433546	AI075877	Hs.125461	hypothetical protein FLJ11539	3.0
430317	AB020645	Hs.239189	glutaminase	3.0
425130	AA448208	Hs.99163	ESTs	3.0
444195	AB002351	Hs.10587	KIAA0353 protein	3.0
409007	AL122107	Hs.49599	Homo sapiens mRNA: cDNA DKFZp434G0827 (from clone DKFZp	3.0
453773	AL133761		gb:DKFZp761C1413_r1 761 (synonym: hamy2) Homo sapiens c	3.0
442974	AI025670	Hs.109308	ESTs, Weakly similar to leucine-rich glioma-inactivated	3.0
446936	H10207	Hs.47314	ESTs	3.0
454086	AW885909	Hs.6975	PRO1073 protein	3.0
420271	AI954365	Hs.42892	ESTs	3.0
435545	AA687415	Hs.28107	ESTs	3.0
445175	AV652851	Hs.20255	ESTs	3.0

30 TABLE 16B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
413156	135116_1	AA127133 AA384396 AW958912 T72119
413607	1379911_1	T64741 BE158393 BE152805
417194	1657323_1	N53793 N53716 N53739
434469	387447_1	AA634806 C18732 AA729161 AA729860
451879	888642_1	AI821030 T47126 AI821318
453773	980699_1	AL133761 AL133767
454736	1232235_1	BE184348 AW817453 BE011068
456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225060 AA225101

50 TABLE 16C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:469-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400628	3818355	Plus	41851-41984
400802	8567867	Minus	174571-174856
400878	9864757	Plus	31493-32842
401103	8568122	Minus	98330-98449
401159	6067118	Minus	3180-3953
401270	9797168	Minus	141659-141813
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
404097	7770701	Plus	55512-55781
404195	3805917	Minus	39186-39332
404485	8095921	Plus	75166-75264,124036-124232
404584	9857511	Plus	138651-139153
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217

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TABLE 17A: 605 genes upregulated in testicular cancer relative to normal body tissues

Table 17A lists about 605 genes upregulated in cervical cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccon: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Protdomains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M,

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	likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
UniGene Title:	UniGene gene title
R1	95th percentile of cervical cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator
5	Pkey; ExAcct; UnigenelD; Unigene Title; Pred.Prod.Domains; R1
10	408522; A1541214; Hs.46320; Small proline-rich protein SPRK (human, ; none, Cornifin; 33.942 422168; AA586894; Hs.112408; S100 calcium-binding protein A7 (psorias; ethand_S_100; TM=M; SS=N; 33.05 424098; AF077374; Hs.139322; small proline-rich protein 3; Cornifin; TM=M; SS=N; 32.856 422158; L10343; Hs.112341; protease inhibitor 3, skin-derived (SKAL; wap; TM=M; SS=Y; 29.604 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR_LY6,toxin,Activin_recpt; TM=M; SS=Y; 27.95064945 421948; L42583; Hs.334309; keratin 6A; filament, RhoGAP, DUF286, bZIP, Tropomyosin, tubulin, DUF164, TBCA, Collagen; TM=M; SS=N; 26.778 446292; AF081497; Hs.279882; Rh type C glycoprotein; Ammonium_transp, FecCD; TM=Y; SS=M; 26.1133829 407242; M18728; ; gb:Human nonspecific crossreacting anti; lg; TM=M; SS=M; 23.382 424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2, hemopexin, Peptidase_M10; 22.522 412719; AW016610; Hs.816; ESTs; none, none; 21.198 406890; M29540; Hs.220529; carcinoembryonic antigen-related cell ad; lg; TM=M; SS=M; 20.028 402075; ; ENSP00000251056*; Plasma membrane calcium; none; 19.038 431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placenta; cadherin, Cadherin_C_term; TM=Y; SS=M; 17.92061281 412471; M63193; Hs.73946; endothelial cell growth factor 1 (platelet; Glycos_transf_3, Glycos_trans_3N; TM=M; SS=M; 17.8978979 417308; H60720; Hs.81892; KIAA0101 gene product; none; TM=M; SS=N; 17.08333333 429259; AA420450; Hs.380088; Plakophilin; none, none; 17.0823294 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; 16.91568628 439826; AW014875; Hs.137007; ESTs; none, none; 16.69 419693; AA133749; Hs.301350; FYD domain-containing ion transport reg; ATP1G1, PLM_MAT8; TM=Y; SS=M; 16.365 413753; U17760; Hs.75517; laminin, beta 3 (nlcn (125kD), kalinin; laminin_EGF, laminin_Nterm; 15.75294118 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin; 15.48600509 401781; ; Target Exon; filament; TM=M; SS=N; 15.43668831 420440; NM_002407; Hs.97644; mammaglobin 2; Uterogloblin; 15.394 441633; AW958544; Hs.112242; normal mucosa of esophagus specific 1; none; TM=M; SS=M; 15.12264151 452240; A1591147; Hs.61232; ESTs; none, none; 14.63 428957; NM_003881; Hs.194679; WNT1 inducible signaling pathway protein; tsp_1, vwc, IGFBP; TM=M; SS=M; 14.49772727 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2; TM=M; SS=N; 14.4389313 432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 fs, clone PL; none, none; 14.00909091 400289; X07820; Hs.2258; matrix metalloproteinase 10 (stromelysin; hemopexin, Peptidase_M10, Astacin; 13.824 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8; TM=M; SS=Y; 13.7754386 421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz, NTR; 13.74595843 400284; ; NM_000125*; Homo sapiens estrogen receptor; hormone_rec, zf-C4, Oest_recep; TM=M; SS=M; 13.31578947 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Oy; IL8; TM=M; SS=Y; 13.05294118 411274; NM_002776; Hs.69423; kallikrein 10; trypsin; TM=M; SS=N; 13.038 406687; M31126; Hs.352054; matrix metalloproteinase 11 (stromelysin; hemopexin, Peptidase_M10; 13.00311527 427666; A1791495; Hs.180142; calmodulin-like skin protein (CLSP); ethand; TM=M; SS=N; 12.79 400301; X03635; Hs.1857; estrogen receptor 1; F-box, hormone_rec, zf-C4, Oest_recep, adh_zinc, ketoacyl-synt, pp-binding, Acyl_transf, Thioesterase, ketoacyl-synt_C, AAA_E7, RFX_DNA_binding; TM=M; SS=N; 12.472 410001; AB041036; Hs.57771; kallikrein 11; trypsin; TM=M; SS=M; 12.47 422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypept; none, pkinase, fn3, lg; 12.28597122 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin; TM=M; SS=N; 12.13379205 437044; AL035864; Hs.69517; differentially expressed in Fanconi's an; none; TM=M; SS=M; 12.04945055 418462; BE001598; Hs.85266; Integrin, beta 4; fn3, Integrin_B, Catx-beta, EGF; TM=M; SS=M; 11.95538462 443359; NM_013409; Hs.9914; follistatin; kazal; 11.95467422 426350; NM_003245; Hs.2022; transglutaminase 3 (E polypeptide, prole; Transglutamin_N, Transglutamin_C, Transglutamine; TM=M; SS=N; 11.61 408243; Y00787; Hs.624; interleukin 8; HLH, PAS, IL8; TM=M; SS=N; 11.564 444781; NM_014400; Hs.11950; GPI-anchored metastasis-associated prote; UPAR_LY6, lactamase_B; 11.55285714 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino; aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, P13, P14_kinase, FAT, FATC, BoiA, RUN; TM=M; SS=N; 11.47956989 418663; AK001100; Hs.41690; desmocollin 3; cadherin, Cadherin_C_term; none; 11.456 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; none; 11.45352113 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epididymolys; Kunitz_BPTI, fn3, vwa, Collagen, beta-lactamase; TM=M; SS=M; 11.32234432 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7m; 3; TM=Y; SS=M; 11.26686327 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fs, clone NT; none, none; 11.076 451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg; TM=M; SS=N; 11.0381579 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank; 11 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage; hemopexin, Peptidase_M10; TM=M; SS=M; 11 425071; NM_013989; Hs.154424; delodinease, lodothyronine, type II; T4_delodinease; TM=M; SS=Y; 10.93859649 437938; A1950087; Hs.369628; gb:wc05c02x1 NCL_CGAP_Kid12 Homo sapiens; none, none; 10.78064516 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none; TM=M; SS=Y; 10.74825175 439706; AW872527; Hs.59781; ESTs, Weakly similar to DAPI_HUMAN DEATH; none, none; 10.542 437897; AA770561; Hs.146170; hypothetical protein FLJ22959; zf-DHHC; none; 10.49538462 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none; TM=M; SS=Y; 10.48210736 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A receptor; Neur_chan_LBD, Neur_chan_membr; TM=Y; SS=M; 10.26714286 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran, M_SMC, N_SMC_C, DUF164; none; 10.142 421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN, HIN; TM=M; SS=N; 10.1 418641; BE243136; Hs.86947; a disintegrin and metalloproteinase doma; disintegrin, Reprolysin, Pep_M12B_propep, EGF; TM=Y; SS=M; 10.072 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB, DNA_topoisomerase IV, HATPase_c; 9.996363636 414035; Y00630; Hs.75716; serine (or cysteine) proteinase inhibitor; serpin; 9.896825397 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK; TM=M; SS=N; 9.888888889 407786; AA687538; Hs.38972; tetraspan 1; transmembrane4; TM=Y; SS=M; 9.876066338 424441; X14850; Hs.147097; H2A histone family, member X; histone, CBFD_NFYB_HMF; 9.851635514 438091; AW373052; Hs.351546; nuclear receptor subfamily 1, group 1, m; hormone_rec, zf-C4; none; 9.840720222 413859; AW992358; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT; none; 9.823170732 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (Z30/240kD); ethand, spectrin, GAS2, SH3, Plactin, RA_Xylose_isom, FIB, bZIP, Tropomyosin, Myc-LZ, M_kh_C, CHAIP3; TM=M; SS=N; 9.812

- 409893; AW247090; Hs.57101; minichromosome maintenance deficient (S; MCM,aldo_ket_red;TM=M;SS=N; 9.787878788
442559; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank;TM=M;SS=N; 9.637037037
425650; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgaris antigen; cadherin;TM=M;SS=M; 9.596
5 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevis; WD40;TM=M;SS=N; 9.558
444946; AW139205; Hs.156457; hypothetical protein FLJ22408; abhydrolase,abhydrolase_2;TM=Y;SS=M; 9.55
421481; AW391972; Hs.104696; KIAA1324 protein; none;TM=M;SS=M; 9.529085873
408591; AF015224; Hs.46452; mamaglobin 1; Uteroglobulin;TM=M;SS=M; 9.506
444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen;TM=M;SS=M; 9.477961433
10 444006; BE395055; Hs.334762; type I transmembrane protein Fn14; krl_recept_La_PKD,MHC_I;TM=M;SS=Y; 9.415151515
413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8; 9.408
424364; AW383226; Hs.163834; ESTs, Weakly similar to G01763 atrophin; ras;TM=M;SS=N; 9.36
429002; AW248439; Hs.2340; junction plakoglobin; Armadillo_seg;TM=M;SS=N; 9.315693431
421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 9.31
15 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member; aldedh;TM=M;SS=M; 9.29
454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member; aldedh; 9.264
417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK;TM=M;SS=Y; 9.241561181
445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 9.207272727
443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M;SS=N; 9.195167286
439223; AW238299; Hs.250618; UL18 binding protein 2; krl_recept_La_PKD,MHC_I;TM=M;SS=Y; 9.108
20 428758; AA433988; Hs.98502; CA125 antigen; mucin 16; SEA;TM=Y;SS=N; 9.028
421777; BE562088; Hs.108196; HSPC037 protein; none;TM=M;SS=N; 9.004
448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A receptor; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 9.001096491
418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M;SS=N; 8.942
25 455601; A1368580; Hs.816; SRY (sex determining region Y)-box 2; HMG_box; 8.87
429211; AF052693; Hs.198249; gap junction protein, beta 5 (connexin 3; connexin;TM=Y;SS=M; 8.77131783
456908; AF117646; Hs.155637; Cas-Br-M (murine) ecotropic retroviral b; z-C3HC4,ChL_N3,ChL_N3;TM=M;SS=N; 8.738
430397; A1924533; Hs.105607; bicarbonate transporter related protein; HCO3_cotransp;TM=Y;SS=N; 8.738
417034; NM_006183; Hs.80962; neurotensin; none; 8.592
30 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 8.536
408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm_3;none; 8.49
439285; AL133916; Hs.47860; hypothetical protein FLJ20093; lg,kinase,LRR,LRRNT,LRRCT;none; 8.46055738
409420; Z15008; Hs.54451; laminin, gamma 2 (nicotin (100kD), kalin; laminin_B,laminin_EGF; 8.414
438746; AB85815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin,Guanylate_kin,PDZ,SH3; 8.376205788
35 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1;TM=Y;SS=M; 8.37
430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none;TM=Y;SS=M; 8.364
429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanesa,DSPc,Y_phosphatase,Ribosomal_S3_N;TM=M;SS=N; 8.266
417771; AA804698; Hs.82547; retinoic acid receptor responder (lazarus; none,none; 8.248314607
40 431620; AA126109; Hs.264981; Z-5-oligoadenylate synthetase 2 (69-71; NTP_transf_2;TM=M;SS=N; 8.156
412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha,prf;TM=M;SS=N; 8.142857143
448733; NM_005629; Hs.187958; solute carrier family 6 (neurotransmitter; SNF;TM=Y;SS=N; 8.137559809
427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6,ET,PLA2_inh; 8.043478261
424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; DNA_ligase; 8.038194444
418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase,DSPc;TM=M;SS=N; 8.024752475
45 453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1); none;TM=Y;SS=M; 8
424046; AF027866; Hs.138202; serine (or cysteine) proteinase inhibitor; serpin;TM=M;SS=N; 7.982
418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 7.973684211
413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH,death,TNFR_c6,Acyl-CoA_hydro; 7.892
422809; AK001379; Hs.121028; hypothetical protein FLJ10549; IQ;TM=M;SS=N; 7.824
50 452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, sub; ABC_tran,ABC_membrane,SRP54,Thymidylate_kin;TM=Y;SS=M; 7.823874755
431630; NM_002024; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha; FG-GAP,Rhabd_glycop,Integrin_A;TM=Y;SS=M; 7.758985201
432874; W94322; Hs.279551; melanoma inhibitory activity; SH3;TM=M;SS=Y; 7.75887574
439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,CoaE;TM=M;SS=N; 7.757751938
452747; BE153855; Hs.61460; lg superfamily receptor LVR; lg,Rhabd_glycop;TM=Y;SS=M; 7.624
55 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4;none; 7.605660377
427747; AW411425; Hs.180655; serine/threonine kinase 12; kinase;TM=M;SS=N; 7.578
430280; AA361258; Hs.237868; Interleukin 7 receptor; fn3;none; 7.476
429299; AI620463; Hs.347408; hypothetical protein MGC13102; none;TM=Y;SS=N; 7.442528738
441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3;none; 7.442495127
60 446163; AA026880; Hs.25252; prolactin receptor; none;NA;NA; 7.436781609
414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,lypsin,plant_thionins; 7.435897436
439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like,kinase,Recep_L_domain,YLP;none; 7.398360656
432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 7.394039735
431890; X17033; Hs.271986; Integrin, alpha 2 (CD49B, alpha 2 subunit; vwa,Integrin_A,FG-GAP;TM=Y;SS=M; 7.383419689
65 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none,none; 7.382
436972; AA284678; Hs.25640; claudin 3; PMP22_Claudin;TM=Y;SS=M; 7.327160494
409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M;SS=N; 7.316
448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2,STAT,STAT_bind,STAT_prot;TM=M;SS=N; 7.315412186
428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,kinase;TM=M;SS=N; 7.2984375
70 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevis; CDC45;TM=M;SS=N; 7.28
451253; H48299; Hs.26126; claudin 10; PMP22_Claudin,Peptidase_M1,K_tetra;TM=Y;SS=M; 7.256802721
416819; U77735; Hs.80205; plin-2 oncogene; plkinase; 7.234455959
421817; AF146074; Hs.108660; ATP-binding cassette, sub-family C (CFTR; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 7.162534435
451035; AU076785; Hs.430; plaslin 1 (I isoform); efnad,CH,Adaptin_N; 7.145454546
424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm_1;TM=Y;SS=M; 7.126
75 414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1;TM=Y;SS=M; 7.122413793
425003; AF119048; Hs.154149; epurinic/pyrimidinic endonuclease(APEX; Troporin,Exo_endo_phos,IQ;TM=M;SS=N; 7.106719368
430890; X54232; Hs.2699; glypican 1; Glypican;TM=M;SS=M; 7.088937093
407792; A1077715; Hs.39384; putative secreted ligand homologous to f; none;TM=M;SS=Y; 7.052
80 426514; BE616633; Hs.170195; bone morphogenetic protein 7 (osteoogenic; TGF-beta,TGFb_propeptide; 7.042
431241; AA496799; Hs.36958; ESTs; SH2,RasGEF;none; 7.03
437139; W73685; Hs.118513; ESTs, Weakly similar to RTA RAT PROBABLE; 7tm_1;TM=Y;SS=M; 7.03
420311; AW445044; Hs.38207; Human DNA sequence from clone RP4-530115; none,none; 7.026
439979; AW600291; Hs.6823; hypothetical protein FLJ10430; none;TM=M;SS=N; 7.008

- 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chr; SH3,PX;TM=M;SS=N; 6.991626794
 416250; AA581388; Hs.73452; Kremen 2; kringle,CUB,WSC; 6.972
 430770; AA765694; Hs.123295; ESTs; none;none; 6.95
 418869; AW516565; ; gb:qx01d05.x1 Soares_NHCeC_cervical_tumo; none,RasGAP,VW,IQ; 6.948
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfamily; 60s_ribosomal,Ribosomal_L10,TNFR_c6,DEAD; 6.914
 418283; S79895; Hs.83942; cathepsin K (pseudosyndactyl); Peptidase_C1; 6.876190476
 419667; AU077005; Hs.92208; a disintegrin and metalloproteinase domain; disintegrin,Reprolysin,Pep_M12B_propep;TM=M;SS=M; 6.862970711
 421143; AB024536; Hs.102171; immunoglobulin superfamily containing Ig; Ig_LRR,LRRNT,LRRCT;TM=M;SS=M; 6.849056604
 456181; L36463; Hs.1030; ras inhibitor; RA,SH2,VPS9;TM=M;SS=N; 6.762
 436856; A1469355; Hs.127310; ESTs; pkinase,rm;TM=M;SS=N; 6.721428571
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 6.720348837
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C,IMPDH_N,CBS,integrin_B,Ricin_B_lectin; 6.717307692
 450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2;TM=Y;SS=M; 6.715240642
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg,UQ_con,none; 6.688194444
 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema,PSI,integrin_B;TM=Y;SS=N; 6.670553936
 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3; 6.662921348
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; LIM,PDZ,pkinase; 6.653713299
 425289; AW139342; Hs.155530; Interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN; 6.652671766
 426500; NM_014638; Hs.170156; KIAA0450 gene product; C2,PI-PLC-Y;TM=M;SS=N; 6.639555172
 438113; A1467908; Hs.8882; ESTs; 7tm_1,none; 6.6
 444783; AK001468; Hs.62180; anillin (Drosophila Scraps homolog); act,PH,none; 6.6
 408482; NM_000676; Hs.45743; adenosine A2b receptor; 7tm_1;TM=Y;SS=M; 6.548148148
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,integrin_B;TM=Y;SS=M; 6.532763533
 414809; A1434699; Hs.77356; transferrin receptor (p90, CD71); PA;TM=Y;SS=N; 6.526951673
 426440; BE382758; Hs.169902; solute carrier family 2 (facilitated glx; sugar_tr;TM=Y;SS=M; 6.512704174
 420039; NM_004605; Hs.376147; sulfotransferase family, cytosolic, 2B; ; Sulfotransfer; 6.496
 423031; A1278995; Hs.374579; ESTs; none;none; 6.447658402
 421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion_trans,K_tetra,asp; 6.426666667
 433933; A1754389; Hs.355397; Homo sapiens clone TCCIA00164 mRNA sequ; none;NA;NA; 6.4
 435094; A1560129; Hs.289008; EST; none;none; 6.312
 432106; N58323; Hs.269098; ESTs, Weakly similar to RETROVIRUS-RELAT; SH3,PDZ,Guanlylate_kin,none; 6.276556777
 427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Fizzled,calreticulin,7tm_2,rm,PAP_assoc;TM=Y;SS=M; 6.272727273
 435232; NM_001262; Hs.4854; cyclin-dependent kinase inhibitor 2C (p1; ank;TM=M;SS=N; 6.269720102
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 6.219081272
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associ; kinesin;TM=M;SS=N; 6.19
 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD,helicase_C,CARD;TM=M;SS=N; 6.188888889
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; Ig_isodh,Ribosomal_L6,F-box;TM=Y;SS=M; 6.188046647
 440008; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF-1; AAA,NB-ARC,PAAD_DAPIN;NA;NA; 6.15503876
 450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta,TGFb_propeptide; 6.152
 432314; AA533447; Hs.285173; ESTs; Xlink,none; 6.123040752
 418844; M62982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase,PLAT;TM=M;SS=N; 6.12
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (ech; Ig,pkinase;TM=Y;SS=M; 6.095758355
 422051; AW327646; Hs.111024; solute carrier family 25 (mitochondrial; mito_carr;TM=M;SS=N; 6.089164786
 452683; A1089575; Hs.374574; progesterone membrane binding protein; homeobox,none; 6.06284153
 445537; A1245671; Hs.12844; EGF-like-domain, multiple 6; EGF,MAM; 6.05513308
 444309; U83236; Hs.10803; calcium and integrin binding protein (DN; ehfand; 6.04015544
 414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD,helicase_C,rm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,R1a,abhydrolase,TGF-beta,DUF139,TPR,DSPc,isp_1,Ribosomal_S21,rvp;TM=M;SS=N; 6.009562842
 438108; A1471795; Hs.287776; vanilloid receptor-related osmotically a; ank,ion_trans;TM=Y;SS=N; 6.004
 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; none;TM=Y;SS=M; 5.984536083
 405484; ; C3002124; gi12737280[ref]XP_009682.2; k; none; 5.978964401
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal_L37ae,pkinase,POLO_box,IRNA-syn1_1b,dynamln,dynamln_2,GED,bZIP,M; 5.978431373
 419216; AU076718; Hs.164021; small inducible cytokine subfamily B (Cy; IL8; 5.976
 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPc,Y_phosphatase;TM=M;SS=N; 5.969387755
 411756; BE294350; Hs.71891; discoidin domain receptor family, member; pkinase,F5_F8_type_C;TM=Y;SS=M; 5.95184136
 424291; AL120051; Hs.144700; ephrin-B1; Ephrin;TM=Y;SS=M; 5.951550388
 453458; BE047032; Hs.257789; ESTs; none;none; 5.95
 456373; BE247706; Hs.86693; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=N; 5.938
 429359; W00482; Hs.2399; matrix metalloproteinase 14 (membrane-in; hemopexin,Peptidase_M10;TM=M;SS=M; 5.917857143
 414703; BE243877; Hs.380063; ATPase, Na7 transporting, beta 3 polypep; Na_K-ATPase;TM=Y;SS=M; 5.910455487
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moi; NUDIX;TM=M;SS=M; 5.901888793
 452239; AW379378; Hs.356289; protein tyrosine phosphatase, receptor t; none;none; 5.868362832
 418345; AJ001698; Hs.241407; serine (or cysteine) proteinase inhibitor; serpin;TM=Y;SS=M; 5.842
 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 11; Euk_porin;TM=M;SS=M; 5.816363636
 439625; AF086453; Hs.58611; ESTs; Fork_head,glycolytic_enzy,Na_sulph_symp; 5.811594203
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none;none; 5.81
 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR;TM=M;SS=N; 5.806
 415198; AW009480; Hs.943; natural killer cell transcript 4; none;TM=M;SS=N; 5.804137931
 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone CO; pkinase,Furin-like,Recep_L_domain,none; 5.8
 457001; J03258; Hs.2062; vitamin D (1,25-dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metallothio_5;TM=M;SS=N; 5.794
 439335; AA742697; Hs.62492; NM_052863;Homo sapiens secretogloblin, fax; none; 5.77858808
 439246; A1498072; Hs.351474; membrane-associated tyrosine- and threon; ank,pkinase,UPF0073; 5.763492064
 452461; N78223; Hs.108106; transcription factor; zf-C3HC4,ubiquitin,PHD,YDG_SRA;TM=M;SS=N; 5.728
 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS; 5.714634146
 424517; A1539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MA; SH2,STAT,STAT_bind,STAT_pro,none; 5.701666667
 419056; M89957; Hs.89575; CD79B antigen (immunoglobulin-associated; Ig,ITAM;TM=Y;SS=M; 5.692
 432269; NM_002447; Hs.2942; macrophage stimulating 1 receptor (c-met; pkinase,Sema,PSI,TIG,AA_EXTRA;TM=M;SS=M; 5.686
 452688; A1826645; Hs.211534; ESTs; ArfGap,PH,ank,Guanlylate_kin,PDZ,SH3; 5.683673469
 411030; BE387193; Hs.67896; 7-60 protein; none;TM=M;SS=N; 5.676767677
 447131; NM_004585; Hs.17466; retinoic acid receptor responder (tazaro; none;TM=Y;SS=N; 5.672977625
 426227; U67058; Human proteinase activated receptor-2 mR; 7tm_1;TM=Y;SS=M; 5.666
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinas; ptkB;TM=M;SS=N; 5.655616943

- 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase; TM=M;SS=N; 5.6485623
 415010; NM_004203; Hs.77783; membrane-associated tyrosine- and threonine kinase; UPF0073; 5.648
 452690; A1536070; Hs.15085; ESTs; pou, homeobox, ligand, ANF receptor; 5.646
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kinase; SH2, SH3, pkinase; TM=M;SS=N; 5.642405063
 418703; NM_014448; Hs.87435; Rho guanine exchange factor (GEF) 16; SH3, PH, RhoGEF, BimA, VP3; TM=M;SS=N; 5.636
 426108; A622037; Hs.166468; programmed cell death 5; DUF122; TM=M;SS=N; 5.635087719
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank, pkinase; TM=M;SS=N; 5.620930233
 432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catalytic; Metallophos; TM=M;SS=N; 5.608352145
 417018; M16038; Hs.80887; v-src-1 Yamaguchi sarcoma viral related 5; SH2, SH3, pkinase; TM=M;SS=N; 5.596052632
 430699; AA531276; Hs.59509; ESTs; pkinase, PP2C, none; 5.575112108
 435017; AA336522; Hs.12854; angiotensin II, type I receptor-associated; none; TM=Y;SS=M; 5.556910569
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase; PAF-AH, Lpase, GDSL; TM=M;SS=N; 5.556195965
 415012; NM_004383; Hs.77793; c-src tyrosine kinase; SH2, SH3, pkinase; TM=M;SS=N; 5.555421687
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese; 5.549751244
 413969; X14034; Hs.75648; phospholipase C, gamma 2 (phosphatidylinositol); SH2, SH3, C2, PH, PI-PLC-Y, PI-PLC-X, PDGF; 5.541366907
 406621; X57809; Hs.181125; immunoglobulin lambda locus; Ig, HSP70, Ppx-GppA; TM=M;SS=N; 5.54076087
 417700; M36542; Hs.1101; POU domain, class 2, transcription factor; homeobox, pou; TM=M;SS=N; 5.536
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none; TM=M;SS=N; 5.52661597
 436576; A458213; Hs.77542; ESTs; 7tm_1, DnaI; 5.52638181
 425465; L18964; Hs.1904; protein kinase C, iota; pkinase, DAG, PE-bind, pkinase, G, OPR; TM=M;SS=N; 5.519672131
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor 3; MIF, sugar, j, none; 5.516453382
 417433; BE270266; Hs.82128; ST4 oncofetal trophoblast glycoprotein; LRR, LRRNT, LRRCT; TM=Y;SS=M; 5.514964789
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor type 3; Ig, Y, phosphatase, MAM; TM=Y;SS=M; 5.494202899
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR); ABC, trans, ABC, membrane; TM=Y;SS=M; 5.471947195
 410608; A1538438; Hs.159087; ESTs; ubiquitin, integrin, B, UBA, none; 5.465384615
 448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin; TM=M;SS=N; 5.450076046
 408716; A1567839; Hs.151714; Homo sapiens mRNA for KIAA1769 protein; UvrD-helicase, RNB, Runt; TM=M;SS=N; 5.450413223
 426410; BE298446; Hs.305890; BCL2-like 1; Bcl-2, Bcl-4, none; 5.444805195
 457819; AA057484; Hs.35406; FLJ20522 Hypothetical protein FLJ20522; none, none; 5.444281525
 422597; BE245909; Hs.118634; ATP-binding cassette, sub-family B (MDR); ABC, trans, ABC, membrane, PRK; TM=Y;SS=N; 5.437831035
 429191; AF065215; Hs.198161; phospholipase A2, group IVB (cytosolic); C2, PLA2, B, jmq; TM=M;SS=N; 5.4375
 449561; AW265634; Hs.133100; ESTs; pkinase, Furin-like, Recept_L, domain, none; 5.435211268
 409012; AL117435; Hs.49725; DKFZP434I216 protein; PH, RhoGEF; TM=M;SS=M; 5.433333333
 443466; BE243123; Hs.321045; IKK-related kinase epsilon; Inducible Ik; pkinase, RIO1; TM=M;SS=N; 5.429657795
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C, none; 5.423322684
 423189; M59371; Hs.171596; EphA2; fn3, pkinase, SAM, EPH, jbd; TM=Y;SS=M; 5.421621622
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae); pkinase; TM=M;SS=N; 5.412
 432527; AW975028; Hs.102754; ESTs; none, none; 5.40625
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz, Frizzled, 7tm_2; TM=Y;SS=M; 5.405504587
 410024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3; TM=M;SS=N; 5.396
 434467; BE552368; Hs.231853; Homo sapiens cDNA FLJ13445 f1s, clone PL; 7tm_1, none; 5.391472868
 438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ; 5.389250814
 439670; AF088076; Hs.59507; ESTs; Weakly similar to AC004858 3 U1 sm; none, none; 5.382
 437016; AU076916; Hs.5398; guanine monophosphate synthetase; PHD, SET, zf-
 CXXC, EGF, ank, notch, WW, FCH, GATase, GMP_synth, C, Occludin, YEATS, metallothionein, EB, heme_1, RCC1, ZZ, FeHRed_A, ENTH, Band_41, HECT; TM=M;SS=N; 5.373937677
 424848; A1263231; Hs.327090; EST; SH3, PDZ, Guanylate_kinase, none; 5.36
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate); MORN, sugar, tr; TM=Y;SS=M; 5.35971223
 405932; ; C15000305; g13806122[gb]AAC69198.1 [AF0]; res; TM=M;SS=N; 5.349226804
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated); Ig, ITAM, Zn_cus; TM=Y;SS=M; 5.346153846
 453143; AA382234; Hs.356289; protein tyrosine phosphatase, receptor type 1; serpin; 5.333667335
 423973; AF038461; Hs.136574; arachidonate 12-lipoxygenase, 12R type; lipoxygenase, PLAT; TM=M;SS=N; 5.33
 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0462; none, none; 5.328
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; Ig; TM=Y;SS=M; 5.316
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, re; Ig; TM=Y;SS=M; 5.309638554
 410165; BE560228; Hs.71869; apoptosis-associated speck-like protein; PAAD, DAPIN, CARD; TM=M;SS=N; 5.293560606
 415817; U88987; Hs.78867; protein tyrosine phosphatase, receptor type 3; Y, phosphatase, carb_anhydrase; TM=Y;SS=M; 5.28
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f, none, spectrin, SH3, PH, CH; 5.278947368
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC; TM=Y;SS=N; 5.274746193
 416207; NM_014745; Hs.79077; Homo sapiens, clone MGC:2908, mRNA, comp; none; TM=Y;SS=M; 5.272222222
 415117; AF120499; Hs.78016; polynucleotide kinase 3'-phosphatase; Viral_helicase1; TM=M;SS=N; 5.27
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3, RhoGAP, FCH; TM=M;SS=N; 5.251865672
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 6; DSPC, Rhodanese, none; 5.248
 431846; BE019924; Hs.271580; uropod 1B; transmembrane4; TM=Y;SS=M; 5.232
 422017; NM_003877; Hs.110776; STAT induced STAT inhibitor-2; SH2; 5.212418301
 436469; AK001455; Hs.5188; Down syndrome critical region gene 2; none; 5.209259259
 421502; AF111856; Hs.105039; solute carrier family 34 (sodium phosphate); Ribosomal_L20, Na, PL_cotrans; TM=Y;SS=N; 5.202
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 14; Exo_endo_phos, SH2; TM=M;SS=N; 5.19979716
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C138 (f, ABC, trans, GTP, EFTU, ABC, membrane, none; 5.199074074
 416602; NM_008159; Hs.367895; Protein kinase C-binding protein NEEL2; EGF, wwc, TSPN; 5.198224852
 429556; AW139399; Hs.314807; ESTs; none; TM=M;SS=N; 5.192439863
 427857; AL133017; Hs.288679; hypothetical protein FLJ22865; myosin_head, IQ, z, MYND; TM=M;SS=M; 5.190251572
 400517; ; lensgln; none; TM=M;SS=N; 5.18
 413438; AF238083; Hs.68061; sphingosine kinase 1; DAGK; TM=M;SS=N; 5.172881356
 423527; A1206965; Hs.105861; hypothetical protein FLJ13824; none; TM=M;SS=N; 5.165060241
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ion_trans, SPRY, RYDR, JTPR, RyR, MIR; TM=Y;SS=N; 5.156976744
 437809; AL137723; Hs.5855; Homo sapiens mRNA; cDNA DKFZp434D0818 (f, none, none; 5.154676259
 452069; AB028949; Hs.183994; KIAA1026 protein; Metallophos; TM=M;SS=N; 5.152360515
 409340; BE174629; Hs.321130; hypothetical protein MGC2771;
 aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, PI3_PI4_kinase, FAT, FATC, BclA, RUN; TM=M;SS=N; 5.144859813
 442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA seq; K_tetra, DUF51, none; 5.142
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; SH3, PH, WW, RhoGAP; 5.141534392
 434808; AF155108; Hs.256150; NY-REN-41 antigen; none; TM=M;SS=N; 5.14
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome; TM=M;SS=N; 5.13968254

- 431685; AW296135; Hs.267659; vav 3 oncogene; CH,DAG_PE-bind,PH,RhoGEF,SH2,SH3,DC1;TM=M;SS=N; 5.129476584
- 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase,pkinase_C,HR1;TM=M;SS=N; 5.121527778
- 433573; AF234887; Hs.57652; cadherin, EGF LAG seven-pass G-type recs; 7tm_2,EGF,cadherin,laminin_EGF,laminin_G,Trypan_glycop,GPS,HRM;TM=Y;SS=M; 5.107438017
- 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene family; ras,ABC_tran,art;TM=M;SS=M; 5.10251046
- 419493; AF001212; Hs.90744; proteasome (prosome, macropain) 26S subu; CDK5_activator,PCI,none; 5.095194085
- 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor; ; inositol_P,ig;TM=M;SS=N; 5.092
- 435243; AW292886; Hs.348932; hypothetical protein dJ434O14.3; IRF,none; 5.092
- 434417; AL110157; Hs.3843; Homo sapiens mRNA; cDNA DKFZp586F2224 (f); DSPc,none; 5.091922006
- 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3,TPR;TM=M;SS=N; 5.088932806
- 418629; BE247550; Hs.86859; growth factor receptor-bound protein 7; SH2,PH,RA; 5.082840237
- 420030; BE503994; Hs.146233; KIAA0418 gene product; SH3,none; 5.080845161
- 444065; AW449415; Hs.10260; Homo sapiens cDNA FLJ11341 fs, clone PL; SH3; 5.063953488
- 421677; H64092; Hs.38282; ESTs; A1pp,Armadillo_seg,IBB; 5.056
- 411165; NM_000169; Hs.69089; galactosylase, alpha; Melibiase; 5.054133858
- 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 5.054
- 423883; AF250238; Hs.134514; ATP-binding cassette, sub-family A (ABC1); ABC_tran,photoRC,SRP54,Ca_channel_B,Pterin_4a;TM=Y;SS=M; 5.051724138
- 421917; AB028943; Hs.109445; KIAA1020 protein; BTB,zf-C2H2,PI3_P14_kinase,PI3Ka;TM=M;SS=N; 5.051282051
- 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin,fn3,Y_phosphatase;TM=M;SS=N; 5.047311828
- 410026; AI912061; Hs.55016; hypothetical protein FLJ21935; none,none; 5.04674221
- 426395; BE151985; Hs.355669; hypothetical protein FLJ23316; pkinase,none; 5.040298508
- 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 5.039039039
- 444895; AJ574383; Hs.22891; solute carrier family 7 (cationic amino; ASC,death,TNFR_c6; 5.037151703
- 413472; U33632; Hs.75379; solute carrier family 1 (glial high aff; SDF;TM=Y;SS=M; 5.034
- 446272; BE268912; Hs.14801; hematopoietic cell-specific Lyn substrat; SH3,HS1_rep;TM=M;SS=N; 5.03030303
- 410772; BE275297; Hs.194685; Homo sapiens clone 24675 mRNA sequence; Topoisom_bac,Toprim; 5.027985075
- 418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase; pkinase,CNH;TM=M;SS=N; 5.014652015
- 415166; NM_003652; Hs.78068; carboxypeptidase Z; Zn_carbOpept,Dioxygenase,Fz; 5.012269939
- 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans;TM=Y;SS=M; 5.001811694
- 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase; 4.997983871
- 430024; AB089780; Hs.227730; integrin, alpha 6; Integrin_A,FG-GAP;TM=Y;SS=M; 4.994871795
- 409220; BE243323; Hs.51233; tumor necrosis factor receptor superfam; TNFR_c6,death,Lipoprotein_5,TIL;TM=Y;SS=M; 4.987135506
- 423804; AW403448; Hs.1706; Interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M;SS=N; 4.985185185
- 423011; NM_000683; Hs.123022; adrenergic, alpha-2C-, receptor; 7tm_1;TM=Y;SS=M; 4.984
- 419577; L36531; Hs.91296; Integrin, alpha 8; Integrin_A,FG-GAP;TM=Y;SS=N; 4.968
- 402328; ; Target Exon; pkinase;TM=M;SS=N; 4.96728972
- 421242; AW161386; Hs.13561; hypothetical protein MGC4692; none;NA;NA; 4.966334165
- 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 4.964491363
- 414203; BE262170; Hs.78629; ATPase, Na⁺ transporting, beta 1 polypep; none,none; 4.961956522
- 409582; R27430; Hs.271565; ESTs; none,Neur_chan_LBD,Neur_chan_memb; 4.946
- 451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M;SS=N; 4.943181818
- 453449; W16752; Hs.32981; sema domain, immunoglobulin domain (Ig); Ig,Sema,PSI; 4.930508475
- 425233; Z17861; Hs.155218; E1B-55kDa-associated protein 5; SPRY,SAP,pkinase,fn3,Ig; 4.925347222
- 425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin; hemopexin,Peptidase_M10; 4.92
- 422282; AF019225; Hs.114309; apolipoprotein L; MolA_ExcB;TM=Y;SS=M; 4.912181303
- 442572; AI001922; Hs.135121; hypothetical protein FLJ22415; none,HSP70; 4.910224439
- 425743; BE396495; Hs.169428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 4.909972299
- 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 4.904
- 408213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase;TM=M;SS=N; 4.897338403
- 411770; NM_014278; Hs.71992; heat shock protein (hsp110 family); HSP70;TM=M;SS=N; 4.894
- 445872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G-protein c; 7tm_1;TM=Y;SS=M; 4.886
- 423198; M81933; Hs.1634; cell division cycle 25A; Rhodanesa,none; 4.884
- 445462; AA378776; Hs.288649; hypothetical protein MGC3077; none; 4.876379691
- 448163; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevi; NusG; 4.876117497
- 427792; M63928; Hs.180841; tumor necrosis factor receptor superfam; SRP14,TNFR_c6; 4.873684211
- 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49,EGF,Ig,Neuregulin;TM=M;SS=N; 4.872641509
- 421541; NM_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C;TM=M;SS=N; 4.869318182
- 429618; AL120751; Hs.211568; eukaryotic translation Initiation factor; none,none; 4.868073879
- 458873; AW150717; Hs.345728; STAT induced STAT inhibitor 3; none,none; 4.861538462
- 437669; AI358105; Hs.123164; ESTs, Weakly similar to match lo ESTs AA; none,pkinase,pkinase_C; 4.854651163
- 405545; ; Target Exon; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 4.85
- 424779; ALD46851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 4.848387097
- 424263; M77640; Hs.1757; L1 cell adhesion molecule (hydrocephalus; fn3,Ig,IRK;TM=Y;SS=M; 4.846153845
- 425421; L11669; Hs.157145; tetracycline transporter-like protein; sugar_tr;TM=Y;SS=M; 4.843694494
- 421267; BE314724; Hs.103081; ribosomal protein S6 kinase, 70kD, polyp; pkinase,pkinase_C;TM=M;SS=N; 4.842532468
- 418736; T18979; Hs.87908; Snf2-related CBP activator protein; helicase_C,AT_hook,SNF2_N;TM=M;SS=N; 4.842
- 444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2,none; 4.841071429
- 417331; AW441129; Hs.81972; SHC (Src homology 2 domain-containing) t; SH2,PID,zf-C2H2,SCAN,AMP-binding,KRAB;TM=M;SS=N; 4.839464883
- 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fs, clone C; none,SDF,sugar_tr; 4.83783788
- 434521; NM_002267; Hs.3888; karyopherin alpha 3 (importin alpha 4); Armadillo_seg,IBB;TM=M;SS=N; 4.833333333
- 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;SS=N; 4.821666667
- 453082; H18835; Hs.31608; hypothetical protein FLJ20041; ion_trans;TM=Y;SS=N; 4.820936639
- 417949; ALD49795; Hs.83004; interleukin 14; none,Armadillo_seg,IBB,WD40; 4.814432399
- 439569; AW602168; Hs.222399; CEGP1 protein; EGF,TNFR_c6,granulin,CUB,Keratin_B2,TIL;TM=M;SS=M; 4.81
- 432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C;TM=M;SS=N; 4.805063291
- 432194; ALD40801; Hs.273219; breast cancer anti-estrogen resistance 1; SH3; 4.803191489
- 431472; AK001023; Hs.256549; nucleotide binding protein 2 (E.coli Mtr; fer4_NiH,ParA,APS_kinase,ArsA_ATPase;TM=M;SS=N; 4.800990099
- 450690; AA266698; Hs.333418; FXD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=N; 4.795480881
- 448595; BE286867; Hs.9275; CGI-152 protein; E1-E2_ATPase,Hydrolase;TM=Y;SS=N; 4.776923077
- 427681; AB018263; Hs.284232; tumor necrosis factor receptor superfam; death, TNFR_c6,PH,Xlink,RhoGEF,Metallothio_5;TM=M;SS=N; 4.772196262
- 432827; Z68128; Hs.3109; Rho GTPase activating protein 4; FCH,RhoGAP,SH3;TM=M;SS=N; 4.760115607
- 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20; 4.751162791
- 419981; AA897581; Hs.128773; ESTs; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 4.748
- 431657; AI345227; Hs.105448; ESTs, Weakly similar to B34087 hypothet; pkinase,PA28_alpha,PA28_beta,Cu_amine_oxid,Cu_amine_oxidN2,Cu_amine_oxidN3; 4.746

- 412958; BE391579; Hs.75087; Fas-activated serine/threonine kinase, none; 4.736781609
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor; lg, pkinase; TM=M; SS=N; 4.733
 419250; AW770185; Hs.356066; U5 snRNP-specific protein, 116 kD; 7tm_1,BAH,zf-CXXC,DNA_methylase; 4.725454546
 417903; NM_002342; Hs.1116; lymphotoxin beta receptor (TNFR superfam; TNFR_c6; TM=M; SS=M; 4.718858132
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK_Coae; 4.718836565
 426059; BE292842; Hs.166120; Interferon regulatory factor 7; IRF; 4.718543046
 414788; X78342; Hs.77313; cyclin-dependent kinase (CDC2-like) 10; pkinase; TM=M; SS=N; 4.708
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC; TM=Y; SS=M; 4.707920792
 448520; AB002367; Hs.21355; doublecortin and CaM kinase-like 1; pkinase,DCX; TM=M; SS=N; 4.707671958
 407143; C14076; Hs.332329; EST; none; TM=Y; SS=M; 4.682675815
 428582; BE336699; Hs.185055; BENE protein; none; TM=Y; SS=M; 4.681818182
 408806; AWA87814; Hs.75608; Homo sapiens cDNA: FLJ21532 fs, clone C; SH3,PDZ,Guanylate_kin,none; 4.680440771
 448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec,MIP; TM=M; SS=M; 4.679841897
 418836; AI655499; Hs.161712; ESTs; pkinase,Activin_rec,PDZ,ZU5,death; 4.679180887
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; lg,kringle,pkinase,Fz; TM=Y; SS=M; 4.675342466
 414665; AA160873; Hs.356307; serum amyloid A1; zf-C2H2,BTB,K_tetra,none; 4.67447496
 449843; R85337; Hs.24030; solute carrier family 31 (copper transp; none; TM=Y; SS=M; 4.673701299
 428245; AF151048; Hs.183180; anaphase promoting complex subunit 11 (y; none; 4.656756757
 417088; M54915; Hs.81170; p1m-1 oncogene; pkinase; TM=M; SS=N; 4.656190476
 420340; NM_000734; Hs.97087; CD32 antigen, zeta polypeptide (TIT3 corr; ITAM; TM=M; SS=M; 4.65
 425966; NM_001761; Hs.1973; cyclin F; cyclin_F-box,cyclin_C; TM=M; SS=N; 4.644
 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain; lg,abhydrolase; 4.640384615
 430603; AA148164; Hs.247280; HBV associated factor; zf-C3HC4,zf-RanBP,pkinase; 4.630653266
 419273; BE271180; Hs.293490; ESTs, Weakly similar to I38022 hypothet; none,none; 4.628
 453880; AI803166; Hs.135121; ESTs, Weakly similar to I38022 hypothet; HSP70,none; 4.619047619
 459399; BE407712; Hs.153998; creatine kinase, mitochondrial 1 (ubiqui; none,none; 4.618577075
 412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanesa,DSPe; 4.616
 433577; AW007080; Hs.284192; ESTs; none,none; 4.614
 444838; AV651680; Hs.208558; ESTs; Integrin_A,FG-GAP,none; 4.612149533
 408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+;pep; PTR2; TM=Y; SS=N; 4.602
 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate_kin; 4.596875
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22_Claudin,none; 4.587931035
 433083; AL042759; Hs.191762; ESTs; SH3,PX; TM=M; SS=N; 4.586
 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor; ig; TM=Y; SS=M; 4.58557047
 412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C; MARCKS; 4.578087049
 422009; AI742845; Hs.110713; DEK oncogene (DNA binding); SAP; 4.576347305
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none,lectin_c; 4.57312253
 414561; AI084813; Hs.195155; Homo sapiens amino acid transport system; Aa_trans; TM=Y; SS=N; 4.573015873
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin,ABC_tran,ABC_membrana,GTP_EFTU; TM=M; SS=M; 4.570526316
 459053; AI807052; Hs.97792; ESTs; none,7tm_2,GPS; 4.569230769
 424247; X14008; Hs.234734; lysosome (renal amyloidosis); lys,lg,FAD_Synth,ldh,ldh_C,pkinase; 4.566195373
 439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triph; Ham1p_like; TM=M; SS=N; 4.56056338
 416178; AI080527; Hs.192822; serologically defined breast cancer anti; none; TM=M; SS=N; 4.558
 408051; AI623351; Hs.172148; ESTs; PH,RhoGAP,none; 4.552307692
 421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; ethand,ldl_recept_a; 4.547761194
 439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein; 7tm_1,LRR; TM=Y; SS=N; 4.547169811
 426201; AW182614; Hs.128499; ESTs; SH3,none; 4.541666667
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase; TM=M; SS=N; 4.536
 445229; BE276013; Hs.343828; Homo sapiens mRNA for FLJ00086 protein; G-alpha; TM=M; SS=N; 4.530588235
 413109; AW389845; Hs.110855; ESTs; PHO4,none; 4.529761905
 426125; X87241; Hs.166994; FAT tumor suppressor (Drosophila) homolog; EGF_cadherin, laminin_G; TM=Y; SS=M; 4.529710145
 402330; ; Target Exon; pkinase,none; 4.528070175
 439238; N47305; Hs.302161; EDG-8 (endothelial differentiation, sph; 7tm_1; TM=Y; SS=M; 4.524
 433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE_p10,ICE_p20; 4.523715415
 413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase; CBS,IMPDH_C,IMPDH_N,NPD; TM=M; SS=N; 4.522900763
 431429; AF072813; Hs.252831; reticulin 3; Reticulin_Fz,lg,kringle,pkinase; TM=Y; SS=N; 4.512
 424078; AB006625; Hs.139033; paternally expressed 3; zf-C2H2,KRAB,none; 4.512
 420602; AF060877; Hs.99236; regulator of G-protein signalling 20; RGS; TM=M; SS=N; 4.51
 449101; AA205847; Hs.23016; G protein-coupled receptor; 7tm_1; TM=Y; SS=M; 4.506
 408157; AA047685; Hs.62946; ESTs; none,pkinase; 4.504
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT; TM=M; SS=Y; 4.50215208
 431326; AW970580; Hs.198689; KIAA0728 protein; none,none; 4.501
 428072; BE258602; Hs.182366; heat shock protein 76; HATPase_c,HSP90; TM=M; SS=N; 4.48828125
 416149; X12451; Hs.78056; cathepsin L; Peptidase_C1; 4.484375
 421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypept; p450; TM=Y; SS=M; 4.48
 445143; U29171; Hs.378918; casein kinase 1, delta; zf-C3HC4,Flamin,zf-B_box,NHL,pkinase,zf-MZ; TM=M; SS=N; 4.478092784
 421071; AI311298; Hs.104476; ESTs, Weakly similar to CGHU1E collagen; none; TM=Y; SS=M; 4.477337111
 410590; BE615216; Hs.64746; chloride intracellular channel 3; none; TM=M; SS=N; 4.476
 438774; AA431620; Hs.379034; hypothetical protein MGC2745; none,none; 4.474874372
 410726; AI623859; Hs.15936; ESTs; pkinase,pro_Isomerase,none; 4.47
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory su; CDK5_activator,none; 4.468
 426485; NM_006207; Hs.170040; platelet-derived growth factor receptor; lg; 4.464944649
 433646; AA603319; Hs.155195; ESTs; pou,homeobox,lg_chan,ANF_receptor; 4.458
 410293; AK000047; Hs.61960; hypothetical protein; K_tetra; TM=M; SS=N; 4.453020134
 453464; AI884911; Hs.32989; receptor (calcitonin) activity modifying; none; TM=Y; SS=N; 4.448198198
 410583; AW770280; Hs.36258; ESTs, Moderately similar to JC5238 galac; SH3,PDZ,Guanylate_kin,none; 4.446927374
 441455; AJ271671; Hs.7854; zinc/ferron regulated transporter-like; Zfp; TM=Y; SS=M; 4.445010183
 453064; R40334; Hs.89463; potassium large conductance calcium-act; none,none; 4.436480187
 443303; U87319; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase,ICE_p10,ICE_p20; TM=M; SS=M; 4.433411215
 411825; AK000334; Hs.352415; solute carrier family 39 (zinc transport SNF,Zfp; TM=Y; SS=N; 4.432765152
 428376; AF119665; Hs.184011; pyrophosphatase (inorganic); Pyrophosphatase; TM=M; SS=N; 4.428571429
 429592; AB029041; Hs.209846; KIAA1118 protein; Tropinin,Exo_endo_phos,JQ; TM=M; SS=N; 4.428
 419344; U94905; Hs.277445; diacylglycerol kinase, zeta (104kD); ank,DAGKa,DAGKc,DAG_PE-bind; TM=M; SS=N; 4.426229508

- 427138; N77624; Hs.173717; phosphatidic acid phosphatase type 2B; PAP2; none; 4.4234375
 414496; W73853; Hs.355424; ESTs; pkinase_F5_F8_type_C adh_short; none; 4.42114094
 429432; A1678059; Hs.202676; synaptonemal complex protein 2; none; TM=M;SS=N; 4.42
 429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone; TM=M;SS=N; 4.419207317
 446700; AW206257; Hs.156326; Human DNA sequence from clone RP11-145L2; none; TM=M;SS=N; 4.418181818
 435411; AW444619; Hs.138211; ESTs; none; pkinase; 4.414
 414581; AA256213; Hs.72010; ESTs; none; Carn_acyltransf.Choline_kinase,SCO1-SenC,Glycos_transf_3,Glycos_trans_3N; 4.41
 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domain; death.DED; 4.408523909
 442259; A1690269; Hs.201345; ESTs; Acetyltransf,RhoGAP,FCH,SH3,Kelch,fn3; 4.405
 415860; D56051; Hs.78888; diazepam binding inhibitor (GABA receptor; ACBP; TM=M;SS=N; 4.404678363
 434419; AL040606; Hs.296938; dual specificity phosphatase 7; DSPc; TM=M;SS=N; 4.404
 404440; ; NM_021048; Homo sapiens melanoma antigen; ; MAGE; TM=M;SS=N; 4.4
 435542; AA687376; Hs.351226; ESTs; SH3,Ig,pkinase,PH,spectrin,RhoGEF; none; 4.394
 413367; NM_006517; Hs.75317; solute carrier family 16 (monocarboxylic; sugar_ir; TM=Y;SS=N; 4.39028777
 435732; AF229178; Hs.123138; leucine rich repeat and death domain con; none; none; 4.38490566
 427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 fts, clone L; 7tm_1; none; 4.382129278
 425749; AW328587; Hs.159448; surfactant 2; none; 4.382
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase; TM=Y;SS=N; 4.381422925
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; PSS; TM=Y;SS=M; 4.380681818
 431837; T79326; Hs.331967; olfactory receptor, family 2, subfamily; none; 7tm_3,sushi,ANF_receptor; 4.376
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypept; Sm,pkinase; 4.370247934
 434876; AF160477; Hs.61460; Ig superfamily receptor LNIR; Ig,Rhabd_glycop; TM=Y;SS=M; 4.37
 430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; ion_trans; TM=Y;SS=M; 4.367777778
 403912; ; CS000394*gi12737280|ref|XP_006682.2|k; none; TM=M;SS=N; 4.367684478
 426268; AF083420; Hs.168913; serine/threonine kinase 24 (Sta20, yeast; pkinase; 4.366348449
 434263; N34895; Hs.79187; ESTs; Ig; none; 4.358527132
 404760; ; Target Exon; cadherin; TM=M;SS=M; 4.356
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase; TM=M;SS=N; 4.35472973
 420757; X78592; Hs.99915; androgen receptor (dihydrotestosterone r; hormone_rec_zf_C4,Androgen_recep; TM=M;SS=N; 4.354
 426812; AF105365; Hs.172613; solute carrier family 12 (potassium/chlor; none; TM=Y;SS=N; 4.353244838
 431674; AA098901; Hs.301642; G-protein coupled receptor; none; GCV_H; 4.35
 431886; L77954; Hs.271980; mitogen-activated protein kinase 6; pkinase; TM=M;SS=N; 4.347893916
 447719; BE387402; Hs.19333; hypothetical protein FLJ10349; adenylatekinase,ATP-bind; TM=M;SS=N; 4.346007605
 424837; BE276113; Hs.333034; N-acetyltransferase, homolog of S. cerev; Acetyltransf; TM=M;SS=N; 4.344
 449437; A1702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fts, clone K; none; none; 4.334722222
 411768; NM_013371; Hs.71979; Interleukin 19; IL10; 4.322
 445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase_2; TM=M;SS=N; 4.320359281
 425864; AW889928; Hs.9071; progesterone membrane binding protein; homeobox; none; 4.318867925
 450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; rrm; TM=M;SS=N; 4.316573557
 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase; 4.316
 400290; H18836; Hs.31608; hypothetical protein FLJ20041; none; Cys_knot; 4.314728582
 438899; AF085833; Hs.135624; ESTs; none; PI3_P14_Kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B; 4.314084507
 418883; BE387036; Hs.12111; acid phosphatase 5, tartrate resistant; Metallophos; TM=M;SS=M; 4.312121212
 419807; R52567; Hs.91579; Homo sapiens clone 23783 mRNA sequence; IMP4; TM=M;SS=N; 4.304407714
 421532; AW138207; Hs.146170; hypothetical protein FLJ22969; Armadillo_seg,HEAT; TM=M;SS=N; 4.304
 430017; AA263172; Hs.35; protein tyrosine phosphatase, non-recept; Y_phosphatase; TM=M;SS=M; 4.302
 447224; BE617125; Hs.142076; gb:601441664F1 NIH_MGC_65 Homo sapiens c; none; NA/NA; 4.302
 425424; NM_004954; Hs.157199; ELKL motif kinase; pkinase,UBA,KAI; TM=M;SS=N; 4.301639344
 454042; H22570; Hs.47860; hypothetical protein FLJ20093; Ig,pkinase,LRR,LRRNT,LRRCT; none; 4.30141844
 446143; BE245342; Hs.305079; sec61 homolog; NUDDI_secY,E1_dehydrog,transket_pyr; TM=Y;SS=M; 4.300872093
 428981; BE313077; Hs.93135; ESTs; Weakly similar to ALU2_HUMAN ALU S; none; rrm; 4.292620865
 432562; BE531048; Hs.278422; DKFZP586G1122 protein; zf-C2H2; TM=M;SS=N; 4.290258449
 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none; TM=M;SS=M; 4.288405797
 421921; H83363; Hs.355993; translocase of inner mitochondrial member; zf-Tim10_DDP,ethand,CH,spectrin,serpin; TM=M;SS=N; 4.284
 448564; AL044962; Hs.21453; inositol 1,4,5-trisphosphate 3-kinase C; IPK; 4.28057554
 453941; U98917; Hs.38820; Bloom syndrome; DEAD_helicase_C,HRDC; TM=M;SS=N; 4.28
 437712; X04588; Hs.85844; neurotrophic tyrosine kinase, receptor; ; Tropomyosin,pkinase,LRR,LRRCT,Hydantoinase_B,Hydantoinase_A; TM=M;SS=N; 4.277477478
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,Integrin_B; 4.276162791
 450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyros; none; none; 4.273927393
 438012; AA393254; Hs.43619; ESTs; Armadillo_seg; none; 4.273134328
 409619; AK001015; Hs.55220; BCL2-associated ethanol gene 2; BAG; TM=M;SS=N; 4.273109244
 418529; AW005695; Hs.250897; TRK-fused gene; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmn,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164; TM=M;SS=N;
 4.272123894
 415214; A1445236; Hs.125124; EphB2; fn3,pkinase,SAM,EPH_jbd; TM=Y;SS=M; 4.268
 438233; W52448; Hs.56147; ESTs; Neur_chan_LBD,Neur_chan_memb,MAGE; 4.26284585
 429019; AA443280; Hs.279907; myosin IIIA; myosin_head,pkinase,PRK,IQ; TM=M;SS=N; 4.262
 424959; NM_005781; Hs.153937; activated p21cdc42hs kinase; lkh,lkh_C,SH3,pkinase,UBA; TM=M;SS=N; 4.258695652
 453655; AW960427; Hs.342874; transforming growth factor, beta recepto; zona_pellucida; none; 4.257208766
 417414; AA434589; Hs.367676; dUTP pyrophosphatase; dUTPase,KRAB; 4.251785714
 453905; NM_002314; Hs.36556; LIM domain kinase 1; pkinase,LIM,PDZ,zf-PARP; TM=M;SS=N; 4.249116608
 424232; AB015982; Hs.143460; protein kinase C, nu; pkinase,DAG_PE-bind,PH; TM=M;SS=N; 4.247692308
 404883; ; ENSP00000216009; Sodium-glucose cotranspo; SSF; TM=Y;SS=M; 4.242424242
 412507; L36645; Hs.73964; EphA4; fn3,pkinase,SAM,EPH_jbd; TM=Y;SS=M; 4.239285714
 411089; AA456454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none; none; 4.237313433
 436997; AA902488; Hs.122952; ESTs; none; DAGKc,DAGKa,RA,DAG_PE-bind; 4.236
 452568; AA805634; Hs.300870; Homo sapiens mRNA; cDNA DKFZp547M072 (fr; PI3_P14_Kinase; TM=M;SS=M; 4.23537415
 433535; AF111106; Hs.3382; protein phosphatase 4, regulatory subunit; HEAT; TM=M;SS=N; 4.234793187
 432728; NM_006979; Hs.276721; HLA class II region expressed gene KEA; Zip,Ig_chan; TM=Y;SS=M; 4.234545455
 416350; AF188625; Hs.189507; phospholipase A2, group IId; phosph; TM=M;SS=Y; 4.234
 409533; AW969543; Hs.144609; mitogen-activated protein kinase kinase; ; Peptidase_C48; none; 4.230666667
 427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C; none; 4.228009259
 403362; ; NM_001615*-Homo sapiens actin, gamma 2, ; actin; 4.22688478
 417856; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA; 4.226388889

428897; AJ245719; Hs.194385; hypothetical protein FLJ20234; SH2;TM=M;SS=N; 4.224731183
 425771; BE561776; Hs.159494; Bruton agammaglobulinemia tyrosine kinase; GH2,SH3,pkinase,PH,BTK;TM=M;SS=N; 4.223584211
 418566; C21220; Hs.321717; hypothetical protein FLJ10875; zf-C2H2,BTB,K_tetra,7tm_1; 4.222807018
 454098; W27953; Hs.217493; Plakophilin; none,none; 4.22
 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); pkinase,FHA,DnaJ;TM=M;SS=N; 4.21875
 419223; X60111; Hs.1244; CD9 antigen (p24); transmembrane4;TM=Y;SS=M; 4.217130215
 436756; Z18364; Hs.198298; v-src avian sarcoma (Schmidt-Ruppin A-2); none,none; 4.216
 450167; AA446404; Hs.24563; NTF2-related export protein 1; NTF2;TM=M;SS=N; 4.215163934
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium binding; ehand; 4.212041885
 432539; AL138169; Hs.278378; karyopherin beta 2b, transportin; none,OS,UPF0139,Glyco_hydro_38; 4.207407407
 416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; KH-domain,rm;TM=M;SS=N; 4.206
 432284; AA532807; Hs.287740; ESTs; pkinase,none; 4.205454546
 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase,RIOT;TM=M;SS=N; 4.204142012
 450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypothetical; ABC_tran,ABC_membrane,Ig,MHC_II_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 4.202572347
 412817; AL037159; Hs.74619; proteasome (prosome, macropain) 26S subu; PC_rep;TM=M;SS=N; 4.202061856
 425394; AA356730; Hs.323949; kangai 1 (suppression of tumorigenicity); transmembrane4,none; 4.195014663
 449335; AW150717; Hs.345728; STAT induced STAT inhibitor 3; SH2;TM=M;SS=N; 4.192248062
 415023; AA932146; Hs.355397; Homo sapiens clone TCCCA00164 mRNA sequ; none,NA;NA; 4.192
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none;TM=M;SS=Y; 4.191878981
 445330; R52656; Hs.21691; ESTs; 7tm_1,none; 4.189922481
 430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX,EXS;TM=Y;SS=N; 4.188333333
 434633; AJ189587; Hs.120915; ESTs; SH3,PH,RhoGAP,none; 4.187106918
 452908; AB001451; Hs.30965; neuronal Shc adaptor homolog; SH2,PID,Zn_carbOpept;TM=M;SS=N; 4.186885246
 439318; AW837046; Hs.6527; G protein-coupled receptor 56; 7tm_2,CytC_asm,GPS;TM=Y;SS=M; 3.930957684
 432201; AJ538613; Hs.298241; Transmembrane protease, serine 3; ldl_recept_La,trypsin;TM=Y;SS=M; 3.893103448
 428969; AF120274; Hs.194689; artemin; TGF-beta; 3.884030418
 444633; AF111713; Hs.12284; junctional adhesion molecule 1; ig;TM=Y;SS=M; 3.831669044
 432305; M62402; Hs.274313; insulin-like growth factor binding prote; thyroglobulin_1,IgFBP,A2M_N;TM=M;SS=N; 3.742996346
 405547; ; NM_018833; Homo sapiens transporter 2, A; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 3.676
 407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none;TM=M;SS=Y; 3.634
 426427; M86699; Hs.169840; TTK protein kinase; pkinase; 3.662
 427585; D31152; Hs.179729; collagen, type X, alpha 1 (Schmid metaph; C1q,Collagen; 3.49
 405546; ; NM_018833; Homo sapiens transporter 2, A; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 3.422661871
 439820; AL360204; Hs.283853; Homo sapiens mRNA full length insert cDN; none,none; 3.402
 404210; ; NM_005936; Homo sapiens myeloid/lymphoid; FHA,PDZ,RA,DIL;TM=M;SS=N; 3.368807339
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 80kD, polyp; pkinase,pkinase_C; 3.213402062
 418678; NM_001327; Hs.87225; cancer/testis antigen (NY-ESO-1); none;TM=M;SS=N; 3.084
 451106; BE382701; Hs.25960; N-MYC oncogene; HLH,Myc_N_term;TM=M;SS=N; 1.55

TABLE 17B

Pkey: Unique Eos probe set identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
418869	12789_14	AA229762 AA230035

TABLE 17C

Pkey: Unique number corresponding to an Eos probe set
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
405484	5922025	Plus	199214-199579,199672-199920,200262-20049
405932	7767812	Minus	123525-123713
400517	9796686	Minus	49996-50346
402328	4464283	Minus	13758-13922,14558-14752
405545	1054740	Plus	118577-118807,119091-119296,121626-12182
402330	4464283	Minus	15325-15380,15484-15588,15842-15915
404440	7528051	Plus	80430-81581
403912	7710730	Minus	72000-72280,72431-72700,72929-73199
404760	7767724	Plus	223266-223352,224472-224585
404883	5101762	Minus	94626-94730,96998-97069
403362	8571772	Plus	64099-64260
405547	1054740	Plus	124361-124520,124914-125050
405546	1054740	Plus	124010-124183
404210	5006246	Plus	169926-170121

Table 18A: 194 Up-Regulated Genes in Uterine Cancer Versus Normal Adult Tissues

Table 18A lists about 194 genes up-regulated in uterine cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" uterine cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" uterine cancer level was set to the 2nd highest amongst uterine cancers. The "average" normal adult tissue level was set to the 90th percentile value amongst non-malignant tissues. In order to remove gene-specific background

levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor vs. normal tissue			
10	Pkey	ExAccn	UnigeneID	Unigene Title	R1
15	449034	AI624049		gb:ts41a09.x1 NCI_CGAP_U11 Homo sapiens cDNA	55.7
	435094	AI560129	Hs.277523	EST	45.2
	438817	AI023799	Hs.163242	ESTs	42.6
	421478	AI683243	Hs.97258	ESTs	35.2
	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	27.3
20	450451	AW591528	Hs.202072	ESTs	26.0
	428153	AW513143	Hs.98367	hypothetical protein FLJ22252	24.8
	428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49) (HG38)	24.2
	438993	AA828995	Hs.52620	integrin; beta 8	16.7
	436775	AA731111	Hs.291891	ESTs	14.3
25	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDNA clo	13.5
	441377	BE218239	Hs.202656	ESTs	13.5
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	12.3
	400292	AA250737	Hs.72472	BMPRII; bone morphogenetic protein receptor II	10.7
	403899			predicted exon	10.1
30	442438	AA959598		gb:os26b03.s1 NCI_CGAP_K1d5 Homo sapiens cDNA	10.0
	447350	AI375572	Hs.1939	HER4 (c-erb-B4)	9.8
	453964	AI961486	Hs.12744	ESTs	9.7
	443830	AI142095	Hs.143273	ESTs	9.1
	459325	AW088369	Hs.282184	ESTs	9.0
35	415245	N59650	Hs.27252	ESTs	8.9
	446608	N76217	Hs.257846	ESTs	8.9
	426635	BE395109	Hs.129327	ESTs	8.8
	433426	H69125	Hs.133525	ESTs	8.7
	437960	AI669586	Hs.222194	ESTs	8.5
40	441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b [H	8.3
	440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [H.s	7.3
	447835	AW591623	Hs.164129	ESTs	7.2
	440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone THYRO10	7.1
	412925	AI089319	Hs.179243	ESTs	7.0
45	408562	AI436323	Hs.31141	Roundabout homolog 2 transmembrane receptor (robo2)	7.0
	429272	W25140	Hs.110667	ESTs	6.9
	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAM	6.3
	437938	AI950087		ESTs; Weakly similar to Gag-Pol polyprotein	6.2
	420610	AI683183	Hs.99348	distal-less homeo box 5	6.2
50	448672	AI955511	Hs.225106	ESTs	6.1
	452461	N78223	Hs.108106	transcription factor	6.1
	413335	AI613318	Hs.48442	ESTs	6.1
	449611	AI970394	Hs.197075	ESTs	6.0
	449260	AA741180	Hs.29879	ESTs	6.0
55	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6)	6.0
	443715	AI583187	Hs.9700	cyclin E1	6.0
	432113	AA935065	Hs.152385	ESTs	5.9
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	5.7
	410658	AW105231	Hs.192035	ESTs	5.7
60	426465	AI758948		gb:ty16f07.x1 NCI_CGAP_U13 Homo sapiens cDNA	5.7
	446704	AI337228	Hs.197083	ESTs	5.5
	419503	AA243642	Hs.137422	ESTs	5.5
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane glyco	5.4
	436076	AI193277	Hs.120954	ESTs	5.4
65	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	5.3
	445258	AI635931	Hs.147613	ESTs	5.3
	440901	AA909358	Hs.128612	ESTs	5.3
	434636	AA083764	Hs.241334	ESTs	5.3
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone LNG020	5.2
70	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	5.2
	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapiens cDN	5.2
	436787	AA908554	Hs.192756	ESTs	5.2
	400301	X03635	Hs.1657	Estrogen receptor 1	5.1
	428771	AB028992	Hs.193143	KIAA1069 protein	5.1
75	444929	AI685841	Hs.161354	ESTs	5.0
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	5.0
	405609			predicted exon	5.0
	410102	AW248508	Hs.279727	ESTs	5.0
	433283	BE041135	Hs.175622	ESTs	4.8
80	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 18	4.8
	410247	AF181721	Hs.61345	RU2S	4.7
	422589	AA312735	Hs.179725	ESTs	4.7
	452771	T05477		gb:EST03366 Fetal brain, Stratagene (catS3620	4.7
	407275	A364186		gb:qw34h07.x1 NCI_CGAP_U14 Homo sapiens cDNA	4.7
	420440	NM_002407	Hs.97644	mammaglobin 2	4.6
	451105	AI761324		gb:w6b011.x1 NCI_CGAP_Co16 Homo sapiens cDNA	4.6

5	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate polypept	4.6
	424115	AA335497	Hs.293965	ESTs	4.6
	414245	BE148072	Hs.75850	WAS protein family, member 1	4.6
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif,	4.5
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	4.5
10	447048	AW393080	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone LNG076	4.4
	458861	AI630223		PHD finger DNA binding protein isoform 1 (int	4.4
	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE20	4.3
	420149	AA256920	Hs.88095	ESTs	4.3
	433479	AW511459	Hs.249972	ESTs	4.3
15	449416	AI651016	Hs.246311	ESTs	4.3
	457551	AW821319	Hs.288928	Homo sapiens cDNA: FLJ23296 fis, clone HEP106	4.3
	450109	AI539295	Hs.17967	ESTs	4.3
	436954	AA740151	Hs.130425	ESTs	4.3
	415511	AI732617	Hs.182362	ESTs	4.3
20	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT2RM40	4.3
	408411			predicted exon	4.2
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, hamolo	4.2
	416456	H57052	Hs.176626	hypothetical protein EDAG-1	4.2
	454692	AW813350		gb:MR3-ST0192-100100-024-g07	4.1
25	452249	BE394412	Hs.61252	ESTs	4.1
	436211	AK001581	Hs.80951	polymerase (DNA directed), gamma	4.1
	449765	N92293	Hs.206832	EST, Moderately similar to ALU8_HUMAN ALU SUB	4.1
	434988	AI418055	Hs.161160	ESTs	4.1
	423515	AA327017	Hs.162204	ESTs	4.0
30	435407	AI149774	Hs.117178	ESTs	4.0
	440886	AW511032	Hs.190516	ESTs	4.0
	444783	AK001468	Hs.62180	ESTs	4.0
	452039	AI922988	Hs.172510	ESTs	4.0
	407300	AA102616	Hs.120769	Homo sapiens cDNA FLJ20463 fis, clone KAT0614	4.0
35	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC	4.0
	449433	AI672096	Hs.9012	ESTs	3.9
	419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone NT2RP20	3.9
	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp586i1518	3.9
	453096	AW294631	Hs.11325	ESTs	3.9
40	441982	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone HEP010	3.9
	445034	AW293376	Hs.160323	ESTs	3.8
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	3.8
	422219	AW978073		gb:EST390182 MAGE resequences	3.8
	440304	BE159984	Hs.125395	ESTs	3.8
45	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228	3.8
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK	3.8
	400250			predicted exon	3.8
	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN	3.8
	420092	AA814043	Hs.88045	ESTs	3.8
50	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	3.8
	437212	AI765021	Hs.210775	ESTs	3.8
	409867	AW502161		gb:UI-HF-BR0p-ajr-g-12-0-UI.r1 NIH_MGC_52	3.7
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	3.7
	427119	AW880562	Hs.114574	ESTs	3.7
55	458154	AW816379		gb:QV4-ST0234-181199-035-g01 ST0234	3.7
	434539	AW748078	Hs.214410	ESTs	3.7
	424717	H03754	Hs.152213	wingless-type MMTV Integration site family	3.7
	412078	X69699	Hs.73149	paired box gene 8 (PAX-8)	3.7
	447342	AI199268	Hs.19322	ESTs; Weakly similar to !!! ALU SUBFAMILY J	3.7
60	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity	3.7
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin)	3.7
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDNA do	3.7
	443613	AI079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapiens c	3.6
	441285	NM_002374	Hs.187	microtubule-associated protein 2	3.6
65	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma c	3.6
	417847	AI521558	Hs.288312	Homo sapiens cDNA: FLJ22316 fis, clone HRC052	3.6
	441484	AA935481	Hs.58972	ESTs	3.6
	415802	AA169515	Hs.6006	ESTs	3.6
	448112	AW245919	Hs.301018	ESTs	3.6
70	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin)	3.6
	402606			predicted exon	3.6
	407905	AW103655	Hs.252905	ESTs	3.6
	424917	AI836208	Hs.96901	Homo sapiens cDNA: FLJ23049 fis, clone LNG025	3.6
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix p	3.6
75	451842	AI820639	Hs.267087	ESTs, Moderately similar to ALU4_HUMAN ALU SU	3.6
	455666	BE065813		gb:RC2-BT0318-110100-012-a08 BT0318 Homo sapi	3.6
	431731	BE266322	Hs.211374	ESTs, Weakly similar to SP49_HUMAN SPLICEOSOM	3.6
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retinal sh	3.6
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein produ	3.6
80	406030			predicted exon	3.5
	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA Libr	3.5
	430481	AA479678	Hs.203269	ESTs, Moderately similar to ALU8_HUMAN ALU SU	3.5
	437641	AA811452	Hs.291911	ESTs	3.5
	415211	R64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFACE PROTEIN	3.4
	443450	N66045	Hs.133529	ESTs	3.4
	457438	NM_014053	Hs.270594	FLVCR protein	3.4
	451254	AI571016	Hs.172967	ESTs	3.4

5	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HEMBB10	3.4
	427778	AA412323	Hs.105323	ESTs	3.3
	435031	AI632091	Hs.116877	ESTs	3.3
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequence.	3.3
	417411	AW500008	Hs.6966	Human DNA sequence from clone RP1-187J11 on c	3.2
10	431548	AI834273	Hs.9711	Homo sapiens cDNA FLJ13018 fis, clone NT2RP30	3.2
	432415	T16971	Hs.289014	ESTs	3.2
	423126	AA322245	Hs.290165	ESTs	3.2
	433420	AI674093	Hs.293981	ESTs	3.2
	435174	AA687378	Hs.194624	ESTs	3.2
15	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moiety X	3.2
	452588	AA889120	Hs.110637	Homeo box A10	3.2
	427304	AA761526	Hs.163853	ESTs	3.1
	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232 (from cl	3.1
	417728	AW138437	Hs.24790	KIAA1573 protein	3.1
20	419356	AI656166	Hs.7331	ESTs	3.1
	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein [3.1
	435185	AA689490	Hs.289109	dimethylarginine dimethylaminohydrolase 1	3.1
	416823	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone COL064	3.1
	405174			predicted exon	3.1
25	403776			predicted exon	3.1
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfamily, m	3.1
	431255	AA497043	Hs.115585	ESTs	3.1
	442353	BE378594	Hs.49136	ESTs	3.1
	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (formerl	3.1
30	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	3.1
	454392	BE268093		gb:601150677F1 NIH_MGC_19 Homo sapiens cDNA c	3.0
	406400			kallikrein 8 (neurosin/ovasin)	3.0
	439949	AW979197	Hs.292073	ESTs	3.0
	430704	AW813091		gb:RC3-ST0186-240400-111-407 ST0186 Homo sapi	3.0
35	401517			predicted exon	3.0
	417830	AW504786	Hs.132808	epithelial cell transforming sequence 2 oncog	3.0
	435267	N23797	Hs.110114	ESTs	3.0
	426384	AI472078		ESTs	3.0
	422797	AB033064	Hs.120908	KIAA1238 protein	3.0
40	428832	AA578229		gb:nl22b12.s1 NCI_CGAP_HSC1 Homo sapiens cDNA	3.0
	449722	BE280074	Hs.23960	cyclin B1	3.0
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A	3.0
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapi	3.0

TABLE 18B

45	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
50	Pkey	CAT number	Accession	
	409745	115237_1	AA077391 AI347618 AI361453 AI088754 AW207491 AW960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450	
	409867	1156530_1	AW502161 AW502587 AW502345	
55	422219	213547_1	AW978073 AW978072 AA807550 AA306567	
	422689	219896_1	AW856665 AA315006 AW954733	
	426384	266211_1	AI472078 AA377209 AA865807	
60	426465	267664_1	AI758948 AA379527 AA379948 AA379262 AW963933	
	428832	296144_1	AA578229 AA364342 AA481375 AA481363	
	430704	322217_1	AW813091 AW206655 AA484440	
65	431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188	
	437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA808598	
			AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493	
70			AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI850397 AI950344 AI741346 AI689062 AA282915	
			AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975	
			AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669	
75			AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628	
			N22388 H84729 H60052 T92487 AJ022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R65056	
			AJ002839 R67840 AA300207 AW959581 T63226 F04005	
80	438993	467651_1	AA828995 AA834879 AI926361	
	442438	542469_1	AA995998 AI916584 R61781 T77332 F07756 F08149 F07647	
	443613	575391_1	AJ079356 W23287	
85	449034	794817_1	AI624049 AW117770 AI858360	
	451105	859083_1	AI761324 AW880941 AW880937	
	452771	930983_1	T05477 T07855 AI917711	
90	454392	115882_1	BE260893 AA078319 R85057 AW803024 H85811 AA078293	
	454692	1229118_1	AW813350 AW816082 AW813476 AW813383	
	455666	1349545_1	BE065813 BE065788 BE065889 BE065832	
95	458154	491768_1	AW816379 AA888282 AA879046 AA879195	
	458861	798085_1	AI630223 AI630470	

TABLE 18C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L. et al., Nature (1999) 402:469-495.

Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
5	401517	7677912	Plus
	402606	9909429	Minus
	403776	7770611	Minus
	403899	7381715	Minus
10	405174	7108030	Minus
	405609	5757553	Minus
	406030	8312328	Minus
	406400	9256298	Plus
15	406411	9256407	Plus

Table 19A: 225 Up-Regulated Genes Encoding Extracellular/Cell Surface Proteins, UTERINE Cancer Versus Normal Adult Tissues

Table 19A lists about 225 genes up-regulated in uterine cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 18A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 PSDomain: Protein Structural Domain
 R1: Ratio of tumor vs. normal tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	PSDomain	R1
35	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	TM	27.3
	438993	AA828995	Hs.52620	Integrin; beta 8	SS,TM,Integrin_B	16.7
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stroma	SS,hemopexin	12.3
	446608	N75217	Hs.257846	ESTs	TM	8.9
	433426	H69125	Hs.133525	ESTs	TM	8.7
40	440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clo	TM,PAX	7.1
	408562	AI436323	Hs.31141	Roundabout homolog 2 transmembrane	SS,TM,Ig,fn3	7.0
	420610	AI683183	Hs.99348	distal-less homeo box 5	TM,homeobox	6.2
	412140	AA219691	Hs.73625	RAB6 Interacting, kinesin-like (rab	TM,kinesin	6.0
	443715	AI583187	Hs.9700	cyclin E1	TM,cyclin	6.0
45	432113	AA935065	Hs.152385	ESTs	TM	5.9
	419503	AA243642	Hs.137422	ESTs	TM	5.5
	444342	NM_014398	Hs.10887	similar to lysosome-associated memb	TM,Lamp	5.4
	436076	AI193277	Hs.120954	ESTs	TM	5.4
	405687	M31126	Hs.272620	pregnancy specific beta-1-glycoprot	TM,hemopexin	5.3
50	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	TM	5.2
	459583	AI907673		gb:BL-BT152-080399-004 BT152 Homo s	TM	5.2
	400301	X03635	Hs.1657	Estrogen receptor 1	TM,hormone_rec,zf-C4	5.1
	405609			predicted exon	TM,Myosin_tail,myosin_head	5.0
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazol	TM	5.0
55	410102	AW248508	Hs.279727	ESTs;	SS,TM,	5.0
	433283	BE041135	Hs.175622	ESTs	TM	4.8
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gen	TM	4.8
	410247	AF181721	Hs.61345	RU25	TM	4.7
	422589	AA312735	Hs.179725	ESTs	TM	4.7
60	407275	AI364186		gb:qw34h07.x1 NCL_CGAP_UA Homo sap	TM	4.7
	420440	NM_002407	Hs.97644	mammaglobin 2	TM,Uterogloblin	4.6
	453616	NM_003482	Hs.33846	dynein, axonemal, light intermediat	TM,Ribosomal_S27e	4.6
	424115	AA335497	Hs.293965	ESTs	TM	4.6
	414245	BE148072	Hs.75850	WAS protein family, member 1	TM,WH2	4.6
65	458861	AI630223		PHD finger DNA binding protein iso	TM,PHD	4.4
	449416	AI651016	Hs.246311	ESTs	SS,TM,	4.3
	420149	AA255920	Hs.88095	ESTs	TM	4.3
	433479	AW511459	Hs.249972	ESTs	TM	4.3
	457551	AW821319	Hs.288928	Homo sapiens cDNA: FLJ23296 fis, cl	TM	4.3
70	406411			predicted exon	TM,vwa,FG-GAP	4.2
	418456	H57052	Hs.176626	hypothetical protein EDAG-1	TM	4.2
	454692	AW813350		gb:MR3-ST0192-100100-024-g07 ST0192	TM	4.1
	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	TM	4.1
	434988	AI418055	Hs.161160	ESTs	TM	4.1
75	444783	AK001468	Hs.62180	ESTs	TM,PH	4.0
	440886	AW511032	Hs.190516	ESTs	TM,FG-GAP	4.0
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HU	TM,Glyco_transf_29,TEA	4.0
	445034	AW293376	Hs.160323	ESTs	TM	3.8
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box	TM,HMG_box	3.8
80	400250			predicted exon	TM,Hist_deacetyl	3.8
	428227	AA321649	Hs.2248	Interferon-gamma induced protein	TM,IL8	3.8
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 T	TM,Kunitz_BPTI,G-gamma	3.8
	458154	AW816379		gb:QV4-ST0234-181199-035-g01 ST0234	TM,VWV	3.7
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	TM	3.7

5	413472	BE242870	Hs.75379	solute carrier family 1 (glial high	TM,SDF	3.7
	447342	AI199268	Hs.19322	ESTs; Weakly similar to IIII ALU SU	TM	3.7
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopon	TM,Osteopontin	3.7
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length inser	TM	3.7
	441285	NM_002374	Hs.167	microtubule-associated protein 2	TM,tubulin-binding	3.6
10	409731	AA125985	Hs.56145	thymosin, beta, identified in neuro	TM,Thymosin	3.6
	441484	AA935481	Hs.58972	ESTs	TM,In3,ig_Y_phosphatase	3.6
	428330	L22524	Hs.2255	matrix metalloproteinase 7 (matril	SS,Peptidase_M10	3.6
	407905	AW103655	Hs.252905	ESTs	SS,TM,Ephrin	3.6
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellula	SS,TM,	3.6
15	402606			predicted exon	TM	3.6
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1	TM	3.5
	437641	AA811452	Hs.291911	ESTs	TM	3.4
	415211	R64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFA	TM,IQ,Rila	3.4
	443450	N66045	Hs.133529	ESTs	TM	3.4
20	457438	NM_014053	Hs.270594	FLVCR protein	TM	3.3
	435031	AI632091	Hs.116877	ESTs	TM,RhoGEF,PH	3.3
	417411	AW500008	Hs.6966	Human DNA sequence from clone RP1-1	TM	3.2
	435174	AA687378	Hs.194624	ESTs	TM,SPRY	3.2
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linke	TM,muT	3.2
25	433420	AI674093	Hs.293961	ESTs	TM	3.1
	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E23	TM	3.1
	417728	AW138437	Hs.24790	KIAA1573 protein	SS,TM,IL8	3.1
	403776			predicted exon	TM,TNF	3.1
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) supe	TM,Ets	3.1
30	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, cl	TM	3.1
	405174			predicted exon	TM	3.1
	431255	AA497043	Hs.115685	ESTs	TM	3.1
	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog	TM,homeobox	3.1
	416530	U62801	Hs.79351	kallikrein 6 (neurosin, zyme)	TM,trypsin_pro_isomerase	3.1
35	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapi	TM	3.0
	406400			kallikrein 8 (neuropsin/ovasins)	TM,trypsin	3.0
	401517			predicted exon	TM,HMG14_17	3.0
	417830	AW504786	Hs.132808	epithelial cell transforming sequen	TM	3.0
	435267	N23797	Hs.110114	ESTs	TM	3.0
40	449722	BE280074	Hs.23960	cyclin B1	TM,cyclin	3.0
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2	TM,ank	3.0
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297	TM,SNF2_N	2.9
	441794	AW197794	Hs.253338	ESTs	TM,ank	2.9
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractura	TM,EGF,TB	2.9
45	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic pr	SS,wap	2.9
	418113	AI272141	Hs.83484	ESTs	TM,HMG_box	2.9
	402373	AL135225	Hs.301865	dopachrome tautomerase (dopachrome	TM,TEA	2.9
	431989	AW972870	Hs.291069	ESTs	SS	2.9
	400284			Estrogen receptor 1	TM,hormone_rec_zf-C4	2.9
50	438578	AA811244	Hs.164168	ESTs	TM,formyl_L_transf_AIRS,GARS	2.8
	423513	AF035960	Hs.129719	transglutaminase 5	TM,Transglutamin_N	2.8
	448966	AW372914	Hs.287462	Homo sapiens cDNA FLJ11875 fis, clo	TM	2.8
	431870	AW449902	Hs.105500	ESTs	TM,MHC_Lig	2.8
	409457	AW818081		gb:CM4-ST0276-101299-059-b09 ST0276	TM	2.8
55	438777	AA825487	Hs.142179	ESTs; Weakly similar to ORF2 [M.mus	TM	2.8
	451807	W52854	Hs.27099	DKFZP564J0863 protein	TM	2.8
	433326	AI379486	Hs.159430	ESTs	TM	2.8
	448221	BE622615		gb:601440775T1 NIH_MGC_72 Homo sapi	TM	2.8
	448141	AI471598	Hs.197531	ESTs	TM,bZIP	2.8
60	456311	AA225632	Hs.190016	ESTs	TM,Sec7	2.8
	405454			predicted exon	TM	2.8
	459287	AL079369		gb:DKFZp564G2378_r1 564 (synonym: h	TM	2.7
	438935	H40665	Hs.31564	ESTs	TM	2.7
	421312	AA824627	Hs.291670	ESTs	TM,G-palch	2.7
65	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C	TM,ABC_membrane,ABC_tran	2.7
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clo	TM	2.7
	417956	AA210704	Hs.190465	ESTs	SS,sushi	2.7
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	SS,EGF	2.6
	448089	AI467945	Hs.173686	ESTs	SS,TM,	2.6
70	446643	AA194417	Hs.282060	ESTs	TM,ClaL_adaptor_s	2.6
	456671	AB011142	Hs.114293	KIAA0570 gene product	TM	2.6
	457256	AA459443	Hs.231816	ESTs	SS	2.5
	438986	AF085888	Hs.269307	ESTs	TM,Spin-Ssty	2.5
	435313	AI769400	Hs.189729	ESTs	TM,MBD	2.5
75	417351	T90278	Hs.15049	ESTs	TM,CH	2.5
	412198	AA937111	Hs.69165	ESTs	TM	2.5
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 k	TM,ubiquitin	2.5
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium ph	TM,Na_FL_cotrans	2.5
	418092	RA5154	Hs.106604	ESTs	TM,pkinase	2.5
80	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (TM,FG-GAP	2.5
	420362	U79734	Hs.97206	huntingtin interacting protein 1	TM,ENTH1_LWEQ	2.5
	431974	AW972689	Hs.200934	ESTs	TM,bZIP	2.5
	438209	AL120659	Hs.6111	KIAA0307 gene product	TM,HLH,PAS	2.5
	447578	AA912347	Hs.136585	ESTs	TM	2.5
	414812	X72755	Hs.77367	monokine induced by gamma Interfero	SS,IL8	2.4
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase	TM,Glyco_transf_29	2.4
	416402	NM_000715	Hs.1012	complement component 4-binding prot	TM,sushi	2.4

5	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HU	TM	2.4
	428242	H55709	Hs.2250	leukemia inhibitory factor (chole	SS,LIF_OSM	2.4
	417693	AW959741	Hs.40368	adaptor-related protein complex 1,	TM,Clat_adaptor_s	2.4
	428679	AA431765		gbzw80c03.s1 Soares_testis_NHT Hom	TM,HECT	2.4
	436311	AA708958	Hs.168732	ESTs	TM	2.4
	426920	AA393351	Hs.132121	ESTs	TM	2.4
	426698	AA394104	Hs.97489	ESTs	TM	2.4
	443426	AF098158	Hs.9329	Homo sapiens mRNA for fls353, compl	TM	2.4
10	406815	AA833930	Hs.288036	IRNA isopentenylpyrophosphate trans	TM,IPPT	2.4
	434808	AF155108	Hs.256150	ESTs, Highly similar to NY-REN-41 a	TM	2.3
	432441	AW292425	Hs.163484	EST	TM,Fork_head	2.3
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQ	TM	2.3
	402298			predicted exon	TM,zf-C2H2,KRAB	2.3
15	435542	AA687376	Hs.269533	ESTs	TM	2.3
	442952	AJ743261	Hs.131860	ESTs	TM	2.3
	418203	X54942	Hs.83758	CDC28 protein kinase 2	TM,CKS	2.3
	429228	AI553633	Hs.104965	ESTs	TM	2.3
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	TM,SH3	2.3
20	447570	AJ868315	Hs.99669	ESTs	TM,PHD	2.3
	405032			predicted exon	TM,FMO-like	2.3
	416566	NM_003914	Hs.79378	cyclin A1	TM,cyclin	2.3
	420900	AL045633	Hs.44269	ESTs	TM,FAD_binding_5	2.3
	430563	AA481269	Hs.178381	ESTs	TM,ABC_membrane,p450	2.3
25	417372	T99755	Hs.290814	ESTs	TM	2.3
	449083	AI948808	Hs.191144	ESTs	TM	2.3
	410361	BE391804	Hs.62661	guanylate binding protein 1, Interf	TM,GBP	2.3
	434131	AI858275	Hs.143659	ESTs	TM	2.3
	431846	BE019924	Hs.271580	Uroplakin 1B	TM,transmembrane4	2.3
30	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific	TM	2.3
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	TM	2.3
	445870	AW410053	Hs.13406	syntaxin 18	TM	2.3
	430639	AW025427	Hs.233552	ESTs	TM,pkinase	2.3
	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfam	SS,TM	2.3
35	422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	SS,TM,Cu-oxidase	2.2
	411558	AA102670	Hs.70725	*Human GABA-A receptor pl subunit m	TM,neur_chan	2.2
	408380	AF123050	Hs.44532	diubiquitin	TM,7tm_3,ANF_receptor	2.2
	403721			predicted exon	TM	2.2
40	440711	AA904389	Hs.143511	ESTs	TM,rm	2.2
	457285	AI038858	Hs.228780	ESTs, Highly similar to AF199597 1	TM,efhand	2.2
	422956	BE545072	Hs.122579	ESTs	TM	2.2
	433482	AI953499	Hs.152617	ESTs	TM	2.2
	431980	AA523696	Hs.222695	Homo sapiens cDNA: FLJ20986 fls, cl	TM	2.2
45	420777	AA280223	Hs.130865	ESTs	TM	2.2
	446659	AI335361	Hs.226376	ESTs	TM	2.2
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	TM	2.2
	422282	AF018225	Hs.114309	apolipoprotein L	TM	2.2
	431701	AW935490	Hs.14658	ESTs	TM,Occludin	2.2
50	426910	AA470023	Hs.190089	ESTs	TM,MMR_HSR1	2.2
	406636		Hs.163695	predicted exon	SS,TM,EGF_kl_recept_a	2.2
	401933			predicted exon	TM,ion_trans	2.1
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed pro	TM	2.1
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 pr	TM	2.1
55	410664	NM_006033	Hs.65370	lipase, endothelial	SS,TM,Ribosomal_L22,lipase	2.1
	449378	AW664026	Hs.59892	ESTs	TM	2.1
	433345	AI681545	Hs.152982	EST cluster (not in UniGene)	TM	2.1
	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase	SS,TM,Branch	2.1
	431832	AW276866	Hs.192715	ESTs	TM,Ets,SAM_PNT	2.1
60	448275	BE514434	Hs.20830	synaptic Ras GTPase activating prot	TM,kinesin_abhydrolase_2	2.1
	423049	X59373	Hs.188023	ESTs	TM,homeobox	2.1
	427510	Z47542	Hs.179312	small nuclear RNA activating comple	TM	2.1
	418076	R61388	Hs.6724	ESTs	TM	2.1
	413670	AB000115	Hs.75470	hypothetical protein, expressed in	TM	2.1
65	429183	AB014604	Hs.197955	KIAA0704 protein	TM	2.1
	439031	AF075079		gb:Homo sapiens full length insert	TM	2.1
	431060	AF039307	Hs.249171	homeo box A11	TM,homeobox	2.1
	451494	AJ799444	Hs.247095	ESTs, Moderately similar to ALU7_HU	TM	2.1
	419978	NM_001454	Hs.93974	forkhead box J1	TM,Fork_head	2.1
70	404535	Z25884	Hs.121483	chloride channel 1, skeletal muscl	SS	2.1
	445181	AW338972	Hs.147471	ESTs	TM	2.1
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	TM,Hydrolase	2.1
	443591	AJ078281	Hs.179240	ESTs	TM	2.1
	448105	AW691433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN	TM,trypsin	2.1
75	424310	AA338648	Hs.50334	ESTs	TM	2.0
	450193	AI916071	Hs.224823	ESTs	TM,pkinase	2.0
	436009	H57130	Hs.120925	ESTs	SS,TM,Ephrin	2.0
	453313	BE005771	Hs.153748	Homo sapiens cDNA: FLJ22490 fls, cl	TM	2.0
	419833	AA251131	Hs.220697	ESTs	TM,WHEP-TRS	2.0
	437555	AA759263	Hs.14041	ESTs	TM,Nramp	2.0
80	411828	AW161449	Hs.72290	wingless-type MMTV Integration site	TM,wnt	2.0
	440052	AI633744	Hs.195648	ESTs	TM,PAC	2.0
	410718	AI920783	Hs.191435	ESTs	TM,SQS_PSY	2.0
	404767			predicted exon	TM	2.0
	447462	AW337214	Hs.158973	ESTs	TM	2.0

442255	AI701857	Hs.202388	ESTs	TM	2.0
410292	AA843087	Hs.124194	ESTs	TM	2.0
442748	AI016713	Hs.135787	ESTs	TM	2.0
458760	AI498631	Hs.111334	ferritin, light polypeptide	TM,HCO3_cotransp	2.0
409799	D11928	Hs.76845	phosphoserine phosphatase-like	TM,Hydrolase	2.0
401324			predicted exon	TM,myosin_head	2.0
432140	AK000404	Hs.272688	hypothetical protein FLJ20397	SS	2.0
447541	AK000288	Hs.18800	hypothetical protein FLJ20281	TM,zf-CCHC	2.0
421379	Y15221	Hs.103982	small inducible cytokine subfamily	SS, TM, IL8	2.0

TABLE 19B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accession
409457	1132521_1	AW818081 AW392887 AW514700 AW392881
410008	116812_1	AA079552 BE142525 BE142527
422689	219896_1	AW856665 AA315006 AW954733
428679	294049_1	AA431765 AA432015
438993	467651_1	AA828995 AA834879 A1926361
439031	46798_1	AF075079 H48601 H48795
448221	75534_1	BE622615
454392	115882_1	BE260893 AA078319 R85057 AW803024 H85811 AA078293
454692	1229118_1	AW813350 AW816082 AW813476 AW813383
458154	491768_1	AW816379 AA888282 AA879046 AA879195
458861	798085_1	AI630223 AI630470
459287	977129_1	AL079369 D81804

TABLE 19C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NI_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NI_position
401324	9863791	Plus	234057-234174
401517	7677912	Plus	29278-29770
401933	3810668	Minus	48725-49057,51864-51955,52424-52589
402298	6598824	Plus	36758-37953
402606	9909429	Minus	81747-82094
403721	7528046	Minus	156647-157366
403776	7770611	Minus	1414-1513,1624-1756
404767	7882827	Minus	23244-23759
405032	7107731	Minus	131945-132224
405174	7108030	Minus	102814-103063
405454	7656675	Plus	133807-134053
405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
405636	5123990	Plus	56384-56587
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
406411	9256407	Plus	7400-7527

Table 20A: 56 Up-Regulated Genes Encoding Extracellular/Cell Surface Proteins, Uterine Cancer Versus Normal Adult Tissues

Table 20A lists about 56 genes up-regulated in uterine cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 18A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulated by small molecules (e.g. kinase, peptidase, isomerase, transporters). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 PSDomain: Protein Structural Domain
 R1: Ratio of tumor vs. normal tissue

Pkey	ExAccn	UnigeneID	Unigene Title	PSDomain	R1
428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49)	7tm_1	24.2
400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromelysin)	hemopexin	12.3
447350	AI375572	Hs.172634	HER4 (c-erb-B4)	kinase	9.8
420610	AI683183	Hs.99348	distal-less homeo box 5	homeobox	6.2
405609			predicted exon	Myosin_tail, myosin_head	5.0
458861	NM_007358	Hs.31016	PHD finger DNA binding protein	PHD	4.4
410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fs, clone	NA	4.3

5	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	NA	4.1
	444783	AK001468	Hs.62180	ESTs	PH	4.0
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	HMG_box	3.8
	413472	BE242870	Hs.75379	solute carrier family 1	SDF	3.7
	443613	AI079356	Hs.21807	gbx39b09.s1 Soares_NhHMPu_S1 Homo s	zf-C2H2	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin)	Peptidase_M10	3.6
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 re	NA	3.6
	435031	AI632091	Hs.116877	ESTs	RhoGEF,PH	3.3
	417411	AW500008	Hs.6966	Human DNA sequence from clone RP1-187	NA	3.3
10	435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrola	NA	3.1
	416530	U62801	Hs.79361	kalikrein 6 (neurosin, zyme)	trypsin_pro_isomerase	3.1
	406400	AA343629	Hs.104570	kalikrein 8 (neurosinovasin)	trypsin	3.0
	418478	U38945	Hs.11174	cyclin-dependent kinase inhibitor 2A	ank	3.0
	441794	AW197794	Hs.253338	ESTs	ank	2.9
15	402373	AL135225	Hs.301865	dopachrome tautomerase (dopachrome de	TEA	2.9
	423513	AF035960	Hs.129719	transglutaminase 5	Transglutamin_N	2.8
	448141	AI471598	Hs.197531	ESTs	bZIP	2.8
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	guanylate_cyc	2.7
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C	ABC_membrane,ABC_tran	2.7
20	448435	BE293439	Hs.182278	catmodulin 2	NA	2.6
	417351	T90278	Hs.15049	ESTs	CH	2.5
	430372	AI206173	Hs.211375	ESTs	SH3,efhand,C2,PH	2.5
	431974	AW972689	Hs.200934	ESTs	bZIP	2.5
25	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hy	ank	2.4
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I	Glyco_transf_29	2.4
	403095			predicted exon	homeobox,PAX	2.4
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transfe	IPPT	2.4
	435615	Y15065	Hs.4975	potassium voltage-gated channel	ion_channel	2.3
30	402298			predicted exon	zf-C2H2,KRAB	2.3
	418203	X54942	Hs.83758	CDC28 protein kinase 2	CKS	2.3
	430663	AA481269	Hs.178381	ESTs	ABC_membrane,p450	2.3
	447570	AI868315	Hs.99669	ESTs	PHD	2.3
	439018	AW300687	Hs.26638	membrane-spanning 4-domains, subfamil	NA	2.3
35	415539	AI733881	Hs.72472	BMPRIIb;	bone morphogenetic protein NA	2.2
	422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	Cu-oxidase	2.2
	408380	AF123050	Hs.44532	diubiquitin	ANF_receptor,sushi,7tm_1	2.2
	440711	AA904389	Hs.143511	ESTs	rm	2.2
	457285	AI038858	Hs.228780	ESTs, Highly similar to AF199597 1 A-	efhand	2.2
40	418506	AA084248	Hs.85339	G protein-coupled receptor 39	NA	2.2
	410664	NM_006033	Hs.65370	lipase, endothelial	Ribosomal_L22,lipase,PLAT	2.1
	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1	Branch	2.1
	448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein	kinesin,PHD,abhydrolase_2	2.1
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-dom	rm,NTF2	2.1
45	404535	Z25884	Hs.121483	chloride channel 1, skeletal muscle	NA	2.1
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2	trypsin	2.1
	446342	BE298665	Hs.14846	Cationic amino acid transporter (ecto	NA	2.0
	458760	AI498631	Hs.111334	fertilin, light polypeptide	HCO3_cotransp,zf-C3HC4	2.0
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	Hydrolase	2.0
50	401324			predicted exon	myosin_head	2.0

TABLE 20B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accession
443613	575391_1	AI079356 W23287
458861	798085_1	AI630223 AI630470

TABLE 20C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401324	9863791	Plus	234057-234174
402298	6598824	Plus	36758-37953
403095	8954339	Plus	150025-150240,151564-151690
405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51969,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 21A: 270 Up-Regulated Genes, Uterine Cancer Versus Normal Uterus

Table 21A lists about 270 genes up-regulated in uterine cancer compared to normal uterus. These were selected as for Table 18A, except that the ratio was greater than or equal to 5.0, and the denominator was the median value for six non-malignant uterine specimens.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor vs. normal tissue

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	449034	AI624049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens	55.7
	435094	AI560129	Hs.277523	EST	45.2
15	438461	AW075485	Hs.286049	phosphoserine aminotransferase	19.5
	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel	15.6
	441633	AW958544	Hs.112242	ESTs	15.2
	429183	AB014604	Hs.197955	KIAA0704 protein	14.6
	436775	AA731111	Hs.291891	ESTs	14.3
20	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	14.0
	446921	AB012113	Hs.16530	CC chemokine SCYA18 (MIP-4) (PARC)	13.0
	413753	U17760	Hs.301103	Laminin, beta 3 (nicotin (125kD), kalinin	12.9
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	12.2
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	12.0
25	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	11.7
	425196	AL037915	Hs.155097	carbonic anhydrase II	11.4
	444863	AW384082	Hs.301323	ESTs	11.3
	449785	AI225235	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C	11.1
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	10.9
30	449801	AA477355	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C	10.3
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	10.3
	414812	X72755	Hs.77367	monokine induced by gamma interferon	10.2
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	10.1
	423645	AI216632	Hs.147487	ESTs	10.1
35	442438	AA959598		gb:os26b03.s1 NCI_CGAP_KId5 Homo sapiens	10.0
	415786	AW419196	Hs.257924	ESTs	10.0
	458017	AA813426	Hs.192034	ESTs, Weakly similar to KIAA0705 protein	10.0
	435525	AI831297	Hs.123310	ESTs	9.9
	413335	AI613318	Hs.48442	ESTs	9.7
40	420297	AI628272	Hs.88323	ESTs	9.6
	452799	AI948829	Hs.213786	ESTs	9.6
	434311	BE543469	Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MA	9.4
	408243	Y00787	Hs.624	Interleukin 8	9.3
	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	9.3
45	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	9.2
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	9.2
	443830	AI142095	Hs.143273	ESTs	9.1
	442547	AA306997	Hs.288362	ESTs, Weakly similar to hypothetical pro	9.0
	421633	AF121860	Hs.106260	sorting nexin 10	9.0
50	403381			0	8.9
	426635	BE395109	Hs.129327	ESTs	8.8
	440500	AA972165	Hs.150308	ESTs	8.7
	436291	BE568452	Hs.5101	ESTs; Highly similar to protein regulati	8.7
55	431668	AW969610	Hs.151179	ESTs	8.7
	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	8.6
	424966	AU077312	Hs.153985	solute carrier family 7 (cationic amino	8.6
	425495	AA358454	Hs.78026	ESTs, Weakly similar to similar to ankyr	8.6
	428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9	8.5
	438986	AF085888	Hs.269307	ESTs	8.4
60	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: hla3)	8.4
	441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin	8.3
	415892	C05837	Hs.145807	Homo sapiens cDNA FLJ13593 fis, clone PL	8.2
	431211	M86849	Hs.5566	Homo sapiens connexin 26 (GJB2) mRNA, co	8.2
65	409865	AW502208		gb:UH-HF-BR0p-aju-e-09-0-ULr1 NIH_MGC_5	8.0
	448158	AI627292	Hs.190877	ESTs	8.0
	401519			0	7.9
	441730	AI243276	Hs.149017	ESTs	7.9
	432441	AW292425	Hs.163484	EST	7.8
70	448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein 1	7.8
	438424	AI912498	Hs.25895	ESTs, Weakly similar to PI-3 kinase [Hs	7.8
	447342	AI199268	Hs.19322	ESTs; Weakly similar to [Hs] ALU SUBFAM1	7.7
	408369	R38438	Hs.182575	solute carrier family 15 (H+)-peptide tra	7.7
	423081	AF262992	Hs.123159	sperm associated antigen 4	7.6
75	414484	BE314385		gb:601154649F1 NIH_MGC_19 Homo sapiens c	7.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	7.5
	459142	AI903396		gb:RC-BT029-120199-219_1 BT029 Homo sapi	7.5
	411094	BE066142		gb:CMA-BT0320-221199-047-g10 BT0320 Homo	7.5
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	7.5
	452607	AI160029	Hs.61436	ESTs	7.5
80	443171	BE281128	Hs.9030	TONDU	7.4
	459081	W07808		gb:zb03a12.r1 Soares_fetal_Jung_NbHL19W	7.4
	431195	AA503083	Hs.79742	ESTs	7.4
	444459	AI680624	Hs.148676	ESTs	7.4

5	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	7.3
	414918	A1219207	Hs.72222	Hypothetical protein FLJ13459	7.3
	423334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	7.3
	448865	R35027		gb:cyg60g02r1 Soares infant brain 1NIB H	7.3
	409219	AA393383	Hs.133331	ESTs	7.3
10	400491	H25530	Hs.50868	solute carrier family 22 (organic cation	7.2
	403485			0	7.2
	408350	AW183350	Hs.250127	ESTs	7.2
	445873	AA250970	Hs.251946	Homo sapiens cDNA: FLJ23107 fis, clone L	7.1
	400995			0	7.1
15	406086			0	7.1
	403378			0	7.0
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	7.0
	422038	R39098	Hs.192028	ESTs	7.0
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in cardi	6.9
20	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.9
	427494	AI628365	Hs.130412	ESTs, Weakly similar to sre-2 [C.elegans	6.9
	429272	W25140	Hs.110667	ESTs	6.9
	427258	AA400091	Hs.39421	ESTs	6.9
	449309	AW589823	Hs.224189	ESTs	6.9
25	400104			0	6.9
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	6.8
	404767			0	6.8
	406690	M29540	Hs.220529	CEA (carcinoembryonic antigen-related ce	6.8
	439750	AL359053	Hs.57664	ESTs	6.8
30	403127	AI904493	Hs.99890	polymerase (DNA directed), delta 1, cata	6.8
	418203	X54942	Hs.83758	CDC28 protein kinase 2	6.8
	425858	AA364923		gb:EST75602 Pineal gland II Homo sapiens	6.8
	421712	AK000140	Hs.107139	hypothetical protein	6.7
	456903	D49441	Hs.155981	mesothelin	6.7
35	414564	AA164803	Hs.71994	ESTs	6.7
	457942	AW665665	Hs.153034	ESTs	6.7
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	6.7
	424596	AB020639	Hs.151017	estrogen-related receptor gamma	6.7
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	6.7
40	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	6.6
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	6.6
	410664	NM_006033	Hs.65370	lipase, endothelial	6.6
	428575	M19684	Hs.184929	serine (or cysteine) proteinase inhibito	6.6
	406400			kallikrein 8 (neuropsin/ovasin)	6.6
45	426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,	6.5
	441460	AI962478	Hs.226804	ESTs, Moderately similar to ALUC_HUMAN I	6.5
	412570	AA033517	Hs.74047	electron-transfer-flavoprotein, beta pol	6.5
	424349	AF141289	Hs.145550	solute carrier family 7 (cationic amino	6.5
	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	6.4
50	445258	AI635931	Hs.147613	ESTs	6.4
	456032	AW957446	Hs.301711	ESTs	6.4
	404727			0	6.4
	422810	AA317400		gb:EST19374 Retina II Homo sapiens cDNA	6.4
	440044	AW665167	Hs.259563	EST	6.4
55	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	6.4
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	6.4
	422170	AI791949	Hs.112432	anti-Müllerian hormone	6.4
	449611	AI970394	Hs.197075	ESTs	6.4
	402539	AW502761	Hs.30909	KIAA0430 gene product	6.3
60	456983	AI081687	Hs.170225	thymopoietin	6.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	6.3
	457887	AI240007	Hs.148812	ESTs	6.3
	431765	AF124249	Hs.268541	novel SH2-containing protein 1	6.3
	420344	BE463721	Hs.97101	Putative G protein-coupled receptor GPCR	6.2
65	443494	T99719	Hs.270404	Homo sapiens cDNA: FLJ2389 fis, clone H	6.2
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	6.2
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	6.2
	413982	BE503035	Hs.279193	ESTs	6.2
	458091	AF150286		gb:AF150286 Human mRNA from cd34+ stem c	6.2
70	402104			0	6.2
	428771	AB028992	Hs.193143	KIAA1069 protein	6.1
	435313	AI769400	Hs.189729	ESTs	6.1
	441666	AI188346	Hs.301776	ESTs	6.1
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (6.1
75	427308	D26067	Hs.174905	KIAA0033 protein	6.1
	423069	W15613	Hs.1613	adenosine A2a receptor	6.1
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	6.1
	417079	U65590	Hs.81134	Interleukin 1 receptor antagonist	6.1
	449409	AI650935	Hs.301694	ESTs	6.1
80	400855			0	6.1
	454692	AW813350		gb:MR3-ST0192-100100-024-g07 ST0192 Homo	6.0
	414869	AA157291	Hs.72163	ESTs	6.0
	439662	H97552	Hs.269060	ESTs	6.0
	445181	AW338972	Hs.147471	ESTs	6.0
	437129	AL049327		gb:Homo sapiens mRNA; cDNA DKFZp664E016	6.0
	440128	AA962623	Hs.189144	ESTs, Weakly similar to NPT2_HUMAN RENAL	6.0
	443715	AI583187	Hs.9700	cyclin E1	6.0

	422355	AW403724	Hs.140	immunoglobulin heavy constant gamma 3	5.9
	405291			0	5.9
	432113	AA935065	Hs.152385	ESTs	5.9
	441236	AA923489	Hs.130432	ESTs	5.9
5	424418	BE503432	Hs.66170	HSKM-B protein	5.9
	453028	AB006532	Hs.31442	RecQ protein-like 4	5.8
	407137	T97307	Hs.199067	EST	5.8
	443462	AJ064690	Hs.171176	ESTs	5.8
	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapiens c	5.8
10	456311	AA225632	Hs.190016	ESTs	5.8
	446501	AJ302616	Hs.150819	ESTs	5.8
	433921	AA618174		gb:nq14f01.s1 NCL_CGAP_Thy1 Homo sapiens	5.8
	409615	AW444861		gb:U1-H-BI3-ajz-a-04-0-UI.s1 NCL_CGAP_Su	5.8
	459360	BE384526		gb:601277913F1 NIH_MGC_20 Homo sapiens c	5.8
15	403824			0	5.8
	428187	AJ687303	Hs.285529	G protein-coupled receptor 49 (GPR49)	5.7
	412140	AA219691	Hs.73625	RAB6 Interacting, kinesin-like (rabkines	5.7
	410658	AW105231	Hs.192035	ESTs	5.7
	426465	AJ758948		gb:ty16f07.x1 NCL_CGAP_UI3 Homo sapiens	5.7
20	443695	AW204099	Hs.112769	ESTs, Weakly similar to AF126780 1 retin	5.7
	437372	AA323958	Hs.283631	hypothetical protein DKFZp547G183	5.7
	405392			0	5.7
	437100	AJ761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	5.7
	449796	AA004321	Hs.194397	ESTs	5.7
25	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	5.7
	428987	NM_004751	Hs.194710	glucosaminyl (N-acetyl) transferase 3	5.7
	404220			0	5.6
	420973	AA743415	Hs.291368	ESTs	5.6
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	5.6
30	442549	AJ751601	Hs.8375	TNF receptor-associated factor 4	5.6
	409867	AW502161		gb:U1-HF-BR0p-ajz-g-12-0-UI.r1 NIH_MGC_5	5.6
	451110	AJ955040	Hs.301584	ESTs	5.6
	418216	AA662240	Hs.283099	AF15q14 protein	5.6
	411897	AW875066		gb:RC6-PT0001-180100-021-F04 PT0001 Homo	5.6
35	456161	BE264645	Hs.282093	Homo sapiens cDNA: FLJ21918 fis, clone H	5.6
	406636			0	5.6
	432540	AJ821517	Hs.105866	ESTs	5.6
	446315	NM_016293	Hs.14770	bridging integrator 2	5.6
40	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	5.6
	451035	AJ076785	Hs.430	plastin 1 (I isoform)	5.6
	406685	M18728		gb:Human nonspecific crossreacting antig	5.5
	454580	AW809762	Hs.222056	Homo sapiens cDNA FLJ11572 fis, clone HE	5.5
	402430			0	5.5
	446704	AJ337228	Hs.197083	ESTs	5.5
45	435282	AA677428	Hs.189731	ESTs	5.5
	426062	N57014	Hs.44013	ESTs	5.5
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	5.5
	456002	AJ628729	Hs.191450	ESTs, Weakly similar to type II membrane	5.5
	409613	AW444816	Hs.171537	Homo sapiens cDNA: FLJ21596 fis, clone C	5.5
50	430259	BE550182	Hs.127826	RaIGEF-like protein 3, mouse homolog	5.5
	434609	R76593		gb:yf60c11.r1 Soares placenta Nb2HP Homo	5.5
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	5.5
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	5.4
	400379	NM_018432	Hs.283076	Homo sapiens ovarian cancer related prot	5.4
55	436076	AJ193277	Hs.120954	ESTs	5.4
	432119	T80289		gb:yf03h04.r1 Soares infant brain 1NIB H	5.4
	417175	R44568	Hs.94002	ESTs	5.4
	445774	AJ254165	Hs.145504	ESTs	5.4
	455604	BE011183		gb:PM3-BN0218-100500-003-d09 BN0218 Homo	5.4
60	411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	5.4
	445262	AW205650	Hs.253503	ESTs	5.4
	412517	BE271584		gb:601141065F1 NIH_MGC_9 Homo sapiens cD	5.4
	434756	AA827650	Hs.259307	ESTs	5.3
	454417	AJ244459	Hs.110826	trinucleotide repeat containing 9	5.3
65	439949	AW979197	Hs.292073	ESTs	5.3
	414995	C18200		gb:C18200 Human placenta cDNA (TFujizawa	5.3
	428071	AF212848	Hs.182339	transcription factor ESE-3B	5.3
	412323	AW937143		gb:PM1-DT0041-281299-001-401 DT0041 Homo	5.3
	434283	AW235341	Hs.58715	mouse thiamin pyrophosphokinase homolog	5.3
70	447798	AJ425049	Hs.119629	ESTs, Moderately similar to ALU1_HUMAN A	5.3
	401723			0	5.3
	408270			0	5.3
	452194	AJ694413	Hs.298262	ESTs, Weakly similar to dJ88J8.1 [H.sapi	5.3
	415757	AA830854	Hs.187810	ESTs	5.2
75	430051	AA464611	Hs.52515	transducin (beta)-like 2	5.2
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-lik	5.2
	459583	AJ907673		gb:IL-BT152-080399-004 BT152 Homo sapien	5.2
	449009	BE044755	Hs.224812	ESTs	5.2
	424001	W67883	Hs.137476	KJAA1051 protein	5.2
	409479	BE163800	Hs.136912	ESTs	5.2
80	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.sa	5.2
	435928	H64345	Hs.183961	ESTs	5.2
	447397	BE247676	Hs.18442	E-1 enzyme	5.2

5	449183	AW445022	Hs.196985	Homo sapiens cDNA: FLJ21135 fis, clone C	5.2
	410146	AW592655		gb:U45M12.x1 Scores_NFL_T_GBC_S1 Homo s	5.2
	458164	AI208666	Hs.192081	ESTs	5.2
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT	5.1
	439509	AF086332	Hs.58314	ESTs	5.1
	422569	BE552132	Hs.118442	cyclin C	5.1
	430664	AW969834		gb:EST381912 MAGE resequences, MAGK Homo	5.1
	411231	AW833501		gb:QV4-TT0008-091199-025-e09 TT0008 Homo	5.1
10	412194	AW900282	Hs.115412	Homo sapiens cDNA FLJ13881 fis, clone TH	5.1
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	5.1
	417173	U61397	Hs.81424	ubiquitin-D1a 1 (senrin)	5.1
	433279	AW971745		gb:EST383834 MAGE resequences, MAGL Homo	5.1
	454112	NM_000885	Hs.301806	ESTs	5.1
15	423261	Z43509		gb:HSC1EA031 normalized infant brain cDN	5.1
	434084	AI061640	Hs.192788	hypothetical protein PRO1905	5.1
	446115	AI733075	Hs.292682	ESTs, Weakly similar to S69913 hypertens	5.1
	416719	H79731		gb:yu81112.r1 Scores fetal liver spleen	5.1
	421462	AF016495	Hs.104624	aquaporin 9	5.1
20	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	5.1
	403383			0	5.1
	430832	AI073913	Hs.100688	ESTs, Weakly similar to secreted cement	5.1
	436070	AK000073		gb:Homo sapiens cDNA FLJ20066 fis, clone	5.0
	416969	AI815443	Hs.283404	organic cation transporter	5.0
25	444929	AI685841	Hs.161354	ESTs	5.0
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	5.0
	439031	AF075079		gb:Homo sapiens full length insert cDNA	5.0
	414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens c	5.0
	425349	AA425234	Hs.78886	ribose 5-phosphate isomerase A (ribose 5	5.0
30	449986	AW864502		gb:PM4-SN0016-120400-004-b12 SN0016 Homo	5.0
	418717	AI334430	Hs.86984	ESTs	5.0
	438769	AA830684	Hs.163426	ESTs	5.0
	441859	AW194364	Hs.128022	ESTs, Weakly similar to FIG1 MOUSE FIG-1	5.0
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase	5.0
35	TABLE 21B				
	Pkey: Unique Eos probeset identifier number				
	CAT number: Gene cluster number				
	Accession: Genbank accession numbers				
40	Pkey	CAT number	Accession		
	409615	1143425_1	AW444861 BE074994 BE074966 BE074992		
	409865	1156518_1	AW502208 AW502366 AW502148		
45	409867	1156530_1	AW502161 AW502587 AW502345		
	410146	1178974_1	AW592655 R05927 R06916		
	411094	1231982_1	BE066142 AW817074		
	411231	1236356_1	AW833501 AW833506 AW833722 AW833332 AW833509 AW833511 AW833767 AW833339		
	411426	1245515_1	BE141714 AW845993 AW845989		
50	411897	1264907_1	AW875066 AW875079 AW875075 AW875062 AW875061 AW875074		
	412323	1288770_1	AW937143 AW937150 AW937141 AW937151 AW937132 AW937160 AW937191 AW937174 AW937195 AW937173		
			AW937159 AW937139 AW937171 AW937142 AW937145 AW937165 AW937163 AW937164 AW937137 AW937179		
			AW937156 AW937140 AW937135 AW937170		
55	412517	130281_1	BE271584 AA112511		
	414484	1452830_1	BE314385		
	414539	1460320_1	BE379046 BE395459		
	414995	1511736_1	C18200 D78681 T82025		
	416719	1611345_1	H79731 H79732		
60	422731	220507_1	AL138411 AL138412 AA315860		
	422810	221630_1	AA317400 AA434584		
	423261	226553_1	Z43509 H09001 AA375202 AW954383		
	425858	257265_1	AA364923 AW963483 BE182774 C21461		
	426465	267664_1	AI758948 AA379527 AA379948 AA379262 AW963933		
	430664	321423_1	AW969834 AA528493 AA483165 AW969842		
65	432119	341770_1	T80289 AF052168		
	433279	361800_1	AW971745 AA581359 AA581358		
	433921	377350_1	AA618174 AI114549 R36464 R36465		
	434609	38950_1	R76593 AF147390 R76594		
70	436070	41426_1	AK000073 AA380183 AA380181 AW963533		
	437129	43343_1	AL049327 AA847105		
	439031	46798_1	AF075079 H48801 H48795		
	442438	542469_1	AA995998 AI916584 R61781 T77332 F07756 F08149 F07647		
	448865	78535_1	R35027 R12034 BE407120		
75	449034	794817_1	AI624049 AW117770 AI858360		
	449986	821463_1	AW864502 AW864369 AI678780		
	454392	115882_1	BE260893 AA078319 R85057 AW803024 H85811 AA078293		
	454692	1229118_1	AW813350 AW816082 AW813476 AW813383		
	455604	1337197_1	BE011183 BE011170 BE011333 BE011188 BE011181 BE011324 BE011161 BE011169		
80	458091	472385_1	AF150286 AA835857		
	459081	889426_1	W07808 AI822056		
	459142	918906_1	AI903396 AI903361 AI903360		

TABLE 21C

5	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
10	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
15	400855	1931571	Minus	17801-18228
	400995	8099094	Plus	141186-141601
	401519	6649315	Plus	157315-157950
	401723	7656694	Plus	147273-147503
20	402104	8119072	Plus	122409-122600
	402430	9796372	Minus	62382-62552
	403378	9438244	Minus	44264-44443
	403381	9438267	Minus	26009-26178
25	403383	9438267	Minus	119837-121197
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	403824	9798468	Plus	473-887
	404220	6706820	Plus	46107-46439
30	404727	8081050	Plus	115534-115747
	404767	7882827	Minus	23244-23759
	405291	3845420	Plus	19999-20473,20672-21036,21147-21285,21378-21667
	405392	6624069	Minus	116167-116289,118879-119030
35	406086	7107817	Plus	9418-9573
	406270	7534217	Plus	13136-13591
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
	406536	7711478	Plus	25655-25782

TABLE 22A: 430 SIGNIFICANTLY DOWN-REGULATED GENES, UTERINE CANCER VERSUS NORMAL UTERUS

35 Table 22A lists about 430 genes significantly down-regulated in uterine cancer compared to normal uterus. These were selected as for Table 21A, except that the numerator and denominator were switched, and the ratio was greater than or equal to 14 (i.e. 14-fold down-regulated in tumor vs. normal uterus).

40	Pkey:	Unique Eos probeset Identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
45	UnigenelD:	Unigene number		
	Unigene Title:	Unigene gene title		
50	R1:	Ratio of tumor vs. normal tissue		
	Pkey	ExAccn	UnigenelD	Unigene Title
55	414063	H26904	Hs.75736	apolipoprotein D
	447990	BE048821	Hs.20144	small inducible cytokine subfamily A, member 14
	407815	AW373860	Hs.301716	ESTs
	452547	AA335295	Hs.74120	adipose specific 2
60	415165	AW887604	Hs.78065	complement component 7
	453655	AW960427	Hs.300878	ESTs, Moderately similar to TGR3_HUMAN TGF-BE
	429350	AI754634	Hs.131987	ESTs
	407228	M25079	Hs.155376	hemoglobin, beta
65	425869	AA524547	Hs.160318	FXD domain-containing ion transport regulator
	416585	X54162	Hs.79386	telomodin 1 (smooth muscle)
	408614	AL137698	Hs.46531	Homo sapiens mRNA; cDNA DKFZp434C1915 (from c
	417542	JD4129	Hs.82269	progesterone-associated endometrial protein (p
70	412295	AW088826	Hs.22971	ESTs
	421998	R74441	Hs.117176	poly(A)-binding protein, nuclear 1
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (from c
	429707	W76631	Hs.211819	matrix metalloproteinase 23B
75	416950	AL049798	Hs.80552	dermatopontin
	408221	AA912183	Hs.47447	ESTs
	406791	AI220684	Hs.272572	hemoglobin, alpha 2
	446500	U78093	Hs.15154	sushi-repeat-containing protein, X chromosome
80	407938	AA905097	Hs.85050	phospholamban
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein)
	412524	AA417813	Hs.11177	ESTs
	452426	AI904823	Hs.31297	Homo sapiens cDNA: FLJ23001 fis, clone LNG002
85	414290	AI568801	Hs.71721	ESTs
	439627	BE621702	Hs.29076	Homo sapiens cDNA: FLJ21841 fis, clone HEP018
	400258		Hs.79064	deoxyhypusine synthase
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD)
90	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3
	407663	NM_016429	Hs.37482	COP22 for nonclathrin coat protein zeta-COP
	410286	AI739159	Hs.61898	DKFZP586N2124 protein
	418986	AI23555	Hs.81796	ESTs
95	409060	AI815867	Hs.50130	necdin (mouse) homolog
	436569	BE439539	Hs.279837	glutathione S-transferase M2 (muscle)
	420674	NM_000055	Hs.1327	butyrylcholinesterase
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, member
100	450810	BE207588	Hs.25511	transforming growth factor beta 1 induced tra
	438150	AA037534	Hs.300878	ESTs, Moderately similar to TGR3_HUMAN TGF-BE

5	430468	NM_004673	Hs.130699	ESTs	31.5
	453060	AW294092	Hs.21594	ESTs	31.3
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vascular	30.8
	422126	AW973784	Hs.112028	Misschapel/NIK-related kinase	30.5
	406082	S47833	Hs.82927	adenosine monophosphate deaminase 2 (isoform	30.3
10	421639	NM_012082	Hs.297921	Homo sapiens mRNA full length insert cDNA clo	30.3
	402520				29.9
	418043	AW377752	Hs.83341	H.sapiens mRNA for tyrosine kinase receptor	29.7
	443906	AA348031	Hs.7913	ESTs	29.7
	450958	AL137669	Hs.25700	Homo sapiens mRNA; cDNA DKFZp434M0435 (from c	29.4
15	418828	AF020774	Hs.88844	Homo sapiens hair and skin epidermal-type 12-	29.4
	412828	AL133396	Hs.74621	prior protein (p27-30) (Creutzfeld-Jakob dise	29.4
	429507	NM_003102	Hs.2420	superoxide dismutase 3, extracellular	29.2
	400545				29.1
	425078	NM_002599	Hs.154437	phosphodiesterase 2A, cGMP-stimulated	29.1
20	429942	AI338993	Hs.134535	ESTs	28.9
	438303	AB028998	Hs.6147	KIAA1075 protein	28.7
	419971	AA400027	Hs.298234	ESTs, Highly similar to mitogen-activated pro	28.7
	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	28.7
	452877	AI250789	Hs.32478	ESTs	28.6
25	412442	AI983730	Hs.26530	serum deprivation response (phosphatidylserin	28.6
	424378	W28020	Hs.184367	GTPase activating protein-like	28.6
	421823	N40850	Hs.28625	ESTs	27.9
	447786	BE620810	Hs.39619	hypothetical protein LOC57333	27.6
	400023			AFFX control: 18S ribosomal RNA	27.5
30	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	27.2
	414134	X60188	Hs.861	mitogen-activated protein kinase 3	27.1
	428451	AW970451	Hs.98570	ESTs	26.9
	435520	AA297990	Hs.9315	HNOEL-iso protein	26.6
	437179	AA393508	Hs.171409	serologically defined colon cancer antigen 8	26.4
35	441481	AA935303	Hs.270553	ESTs	26.0
	450227	BE388192	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone COL001	25.6
	403731				25.5
	452814	AI092790	Hs.55016	hypothetical protein FLJ21935	25.5
	410038	R57171	Hs.57975	calsequestrin 2, cardiac muscle	25.5
40	416854	H40164	Hs.80296	Purkinje cell protein 4	25.4
	418421	R58620	Hs.85050	phospholamban	25.4
	407000	U12139		gb:Human alpha1(XI) collagen (COL11A1) gene,	25.3
	421803	NM_012205	Hs.108441	3-hydroxyanthranilate 3,4-dioxygenase	25.3
	445613	BE550889	Hs.158491	ESTs	25.1
45	432302	AA345857	Hs.274307	KIAA1442 protein	24.8
	420796	L34355	Hs.99931	sarcoglycan, alpha (50kD dystrophin-associate	24.8
	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone COL021	24.7
	417302	BE245812	Hs.8941	ESTs	24.6
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mimecan)	24.6
50	440130	AI083899	Hs.157527	ESTs	24.5
	431967	AJ243653	Hs.283404	organic cation transporter	24.5
	424580	AA446539	Hs.35092	ESTs	24.4
	406807	Z25427		gb:Hsapiens protein-serine/threonine kinase	24.2
	443745	AB039670	Hs.9728	ALEX1 protein	24.1
55	429101	AW452174	Hs.173780	ESTs	23.6
	410691	AW239226	Hs.65450	reticulum 4	23.4
	408853	AW291484	Hs.254967	ESTs	23.3
	407979	AA046306	Hs.62927	ESTs	23.1
	448619	AI867182	Hs.202255	ESTs	22.8
60	424585	AA464840		gb:zx43h11.1 Soares_total_fetus_Nb2HF8_9w Ho	22.7
	407891	AA486620	Hs.41135	Endomucin 2	22.6
	407196	D11747	Hs.177415	Finkel-Bisicks-Reilly murine sarcoma virus (FB	22.5
	426990	AL044315	Hs.173094	Homo sapiens mRNA; cDNA DKFZp564H142 (from cl	22.5
	450493	M93718	Hs.166373	nitric oxide synthase 3 (endothelial cell)	22.1
65	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-like	22.0
	423690	AA329648	Hs.23804	ESTs	22.0
	402865				21.9
	417387	AW021102	Hs.21509	ESTs	21.9
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	21.9
70	459722			Homo sapiens cDNA: FLJ23449 fis, clone HSI058	21.8
	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	21.8
	402195				21.7
	418213	AW978753	Hs.127327	ESTs	21.6
	440274	R24595	Hs.7122	scrapie responsive protein 1	21.6
75	455818	AI733747		gb:zn86d04.y5 Stratagene lung carcinoma 93721	21.4
	420861	AI039044	Hs.88827	Homo sapiens mRNA for FLJ00033 protein, part	21.4
	405228				21.3
	441292	AF131218	Hs.7765	chromosome 16 open reading frame 5	21.3
	432553	AA553334	Hs.211095	ESTs	21.3
80	417098	AB017365	Hs.173859	fritzzled (Drosophila) homolog 7	21.2
	453642	AI370936	Hs.34074	dipeptidylpeptidase VI	21.2
	405313				21.1
	410243	D83402	Hs.289006	ESTs, Weakly similar to alternatively spliced	21.1
	413186	AU077141	Hs.75231	solute carrier family 16 (monocarboxylic acid	21.1
	425954	AK000633	Hs.164476	hypothetical protein FLJ20626	21.0
	421770	AA374192	Hs.108124	ribosomal protein L41	21.0
	435265	AA779958	Hs.185932	ESTs	20.8

	430036	AL050284	Hs.227782	DKFZP586M1019 protein	20.7
	430233	AW367902	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (from c	20.7
	436130	AA341497	Hs.31408	ESTs	20.7
5	434843	R43707	Hs.133159	ESTs, Weakly similar to PIHUSD salivary prot	20.7
	429303	AW137635	Hs.44238	ESTs	20.6
	442422	AJ344415	Hs.156082	ESTs	20.5
	410399	BE068889	Hs.63236	synuclein, gamma (breast cancer-specific prot	20.5
	435869	AF255910	Hs.54650	ESTs, Weakly similar to (define not availabl	20.5
10	447384	AJ377221	Hs.40528	ESTs	20.5
	440610	AJ733098	Hs.130800	ESTs	20.5
	445806	AL137516	Hs.13323	hypothetical protein FLJ22059	20.4
	433657	AJ244368	Hs.8124	PH domain containing protein in retina 1	20.4
	436467	AW450278	Hs.91681	ESTs	20.3
15	440191	AJ990417	Hs.116107	Homo sapiens genomic DNA, chromosome 21q, sec	20.2
	417511	AL049176	Hs.82223	chordin-like	20.2
	406976	M60299		gb:Human alpha-1 collagen type II gene, exons	20.1
	443547	AW271273	Hs.23767	ESTs	20.1
	417998	AW967420		gb:EST379495 MAGI resequences, MAGI Homo sapi	20.1
20	419313	AA843387	Hs.87279	ESTs	20.1
	408322	AW181985	Hs.249986	ESTs	20.0
	448422	BE263813		gb:01194177F1 NIH_MGC_7 Homo sapiens cDNA cl	20.0
	403121				19.9
	424198	AB029010	Hs.143026	KIAA1087 protein	19.9
25	459060	H89244	Hs.79625	heterogeneous nuclear ribonucleoprotein D (AU	19.9
	457829	AJ742291	Hs.210843	ESTs, Weakly similar to dJ1039K5.2 [H.sapiens	19.9
	445029	AF196481	Hs.12256	midline 2	19.9
	424362	AL137646	Hs.146001	Homo sapiens mRNA; cDNA DKFZp586F0824 (from c	19.8
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal monoa	19.7
30	413972	BE279548	Hs.162717	ESTs, Weakly similar to HPPD_HUMAN 4-HYDROXY	19.6
	435891	AW249394	Hs.5002	copper chaperone for superoxide dismutase	19.6
	447551	BE066634	Hs.929	myosin, heavy polypeptide 7, cardiac muscle,	19.6
	400637				19.5
	409882	AJ243191	Hs.56874	heat shock 27kD protein family, member 7 (car	19.4
35	430310	U60115	Hs.239069	four and a half LIM domains 1	19.4
	402741				19.4
	401703				19.3
	409229	H60333	Hs.251928	nuclear pore complex interacting protein	19.3
	453856	AA804789	Hs.19447	Homo sapiens mRNA for FLJ00106 protein, parti	19.3
40	430342	NM_006938	Hs.239663	myeloid/lymphoid or mixed-lineage leukemia (t	19.3
	404033				19.2
	411939	AJ365585	Hs.146246	ESTs	19.2
	431227	X63755	Hs.2743	keratin, cuticle, ultrahigh sulphur 1	19.1
	452669	AA216363	Hs.262958	ESTs, Weakly similar to alternatively spliced	19.1
45	439698	AW779654	Hs.55876	ESTs	18.9
	416253	BE250659	Hs.15463	ESTs	18.9
	418556	T02850		gb:FB12A9 Fetal brain, Stratagene Homo sapien	18.9
	408877	AA479033	Hs.130315	ESTs	18.9
	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24kD	18.9
50	417054	AF017060	Hs.174151	aldehyde oxidase 1	18.8
	404654				18.8
	420174	AJ824144	Hs.23912	ESTs	18.8
	400525				18.7
	406150				18.7
55	457835	BE256338	Hs.192375	ESTs, Highly similar to dJ127B20.3 [H.sapiens	18.6
	420105	AW015571	Hs.32244	ESTs	18.6
	404619	BE514535	Hs.77171	minichromosome maintenance deficient (S. cere	18.5
	423282	AL137563	Hs.126378	putative ABC transporter	18.5
	424097	M13981	Hs.1734	inhibin, alpha	18.5
60	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from c	18.5
	427605	NM_000997	Hs.179779	ribosomal protein L37	18.4
	406535				18.4
	418947	W52990	Hs.22860	ESTs	18.4
	414323	NM_014759	Hs.239500	KIAA0273 gene product	18.3
65	457111	AA482027	Hs.142569	ESTs	18.3
	418373	AW750770	Hs.84344	CGI-135 protein	18.3
	424461	D83542	Hs.148090	cadherin 15, M-cadherin (myotubule)	18.2
	451565	NM_000897	Hs.456	leukotriene C4 synthase	18.2
	407751	BE276096	Hs.38205	from HeLa cyclin-dependent kinase 2 interact	18.2
70	432031	AF039196	Hs.284126	hairless (mouse) homolog	18.1
	404608	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PLACE10	18.1
	451962	AW078832	Hs.226806	ESTs	18.1
	424100	AJ733080	Hs.123525	ESTs, Weakly similar to NGAL RAT NEUTROPHIL G	18.1
	451509	AJ969529	Hs.171637	Homo sapiens cDNA: FLJ21937 fis, clone HEP044	18.1
75	453512	AL040160	Hs.209542	ESTs, Weakly similar to B cell linker protein	18.0
	429242	W39693	Hs.226138	Homo sapiens mRNA; cDNA DKFZp586H2446 (from c	17.9
	423780	AA352013		gb:EST59935 Infant brain Homo sapiens cDNA 5'	17.9
	427030	AA397600	Hs.97531	ESTs	17.9
	439872	T81058		gb:yd26c08.r1 Soares fetal liver spleen 1N1LS	17.9
80	407836	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone CAE112	17.9
	451427	AJ091441	Hs.26401	tumor necrosis factor (ligand) superfamily, m	17.9
	424462	AJ076666	Hs.148101	serum constituent protein	17.9
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyserin	17.8
	422319	AW403342	Hs.115232	splicing factor 3a, subunit 2, 65kD	17.8

	400489				17.8
	454421	BE409759	Hs.59563	Homo sapiens mRNA for FLJ00007 protein, part	17.8
	449282	AL048056	Hs.23437	Homo sapiens cDNA FLJ13555 fis, clone PLACE10	17.7
	420495	AJ338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (from c	17.7
5	429790	AK001352	Hs.221737	hypothetical protein FLJ10490	17.7
	422796	AW897265		gb:CM0-NN0057-150400-335-e04 NN0057 Homo sapi	17.7
	427980	AA418305		gb:zv96g05.s1 Soares_NhHMPu_S1 Homo sapiens c	17.6
	409543	AW410200		gb:th05b12.x1 NIH_MGC_17 Homo sapiens cDNA cl	17.6
	440206	AJ762232	Hs.46794	ESTs	17.6
10	455904	BE156173		gb:QV0-HT0367-201299-079-a02 HT0367 Homo sapi	17.5
	427707	NM_005578	Hs.180398	LIM domain-containing preferred translocation	17.5
	437140	AA312799	Hs.283689	activator of CREM in testis	17.5
	417637	AA204969	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HEMBB10	17.5
	419171	NM_002846	Hs.89555	protein tyrosine phosphatase, receptor type,	17.4
15	417808	AF177909	Hs.12828	twety (Drosophila) homolog 1	17.4
	426232	Z70024	Hs.168157	nuclear transcription factor Y, gamma	17.4
	440747	AW297226	Hs.137840	ESTs, Moderately similar to SIX1_HUMAN HOME08	17.4
	415307	F05232	Hs.27495	prostate cancer associated protein 7	17.3
	407049	X72632		(NONE)	17.3
20	454054	AJ336329	Hs.301519	Homo sapiens cDNA FLJ12536 fis, clone NT2RM40	17.3
	411085	AF022991	Hs.68398	period (Drosophila) homolog 1	17.3
	443104	AA088470	Hs.83135	p53-responsive gene 6	17.2
	424106	AA412442	Hs.98132	ESTs	17.2
	446716	AA436575	Hs.16602	ESTs	17.1
25	448677	AJ560769	Hs.227051	ESTs	17.0
	434919	AJ821740	Hs.116531	ESTs	17.0
	401171	AA360954	Hs.27268	Homo sapiens mRNA; cDNA DKFZp564N195 (from cl	17.0
	456804	AJ421645	Hs.139851	caveolin 2	17.0
30	453621	AW749983		gb:QV3-BT0537-280100-070-e04 BT0537 Homo sapi	16.9
	413419	BE093686	Hs.48938	Homo sapiens cDNA: FLJ21802 fis, clone HEP007	16.9
	426515	BE394222	Hs.231444	ESTs	16.9
	428937	T82221	Hs.56729	lymphocyte-specific protein 1	16.9
	424562	AJ420859	Hs.150557	basic transcription element binding protein 1	16.9
35	444655	AF088886	Hs.11580	cathepsin F	16.9
	447424	AJ681105	Hs.181641	ESTs	16.8
	425439	D38024	Hs.157425	double homeobox, 2	16.8
	446707	AJ591214	Hs.156336	ESTs	16.8
	405324				16.8
40	434340	AJ193043	Hs.128685	ESTs	16.8
	422942	AF054839	Hs.122540	tetraspan 2	16.8
	421820	AW662990	Hs.108675	heme-binding protein	16.8
	420037	BE299598	Hs.135569	ESTs, Weakly similar to NEUROD [H.sapiens]	16.7
	428818	AJ131291	Hs.98866	ESTs	16.7
45	426485	NM_006207	Hs.170040	platelet-derived growth factor receptor-like	16.7
	404947				16.6
	412677	AW029608	Hs.17384	ESTs	16.6
	401551				16.6
	408053	AW139474	Hs.246862	ESTs	16.6
50	425016	AA376049	Hs.154162	ADP-ribosylation factor-like 2	16.6
	418179	X51630	Hs.1145	Wilms tumor 1	16.6
	418994	AA296520	Hs.89546	Selectin E (endothelial adhesion molecule 1)	16.5
	457514	AA775208	Hs.136423	ESTs	16.5
	426275	BE151551		gb:RC0-HT0297-201199-031-f12 HT0297 Homo sapi	16.5
55	457924	AL390142	Hs.288697	Homo sapiens cDNA FLJ13861 fis, clone THYRO10	16.5
	430712	AW044647	Hs.196284	ESTs	16.5
	455144	AW875942		gb:CM1-PT0013-131299-067-b10 PT0013 Homo sapi	16.4
	407524	X64985		gb:H.sapiens mRNA HTPCRX11 for olfactory rece	16.4
	426712	AW173177	Hs.197755	ESTs	16.4
60	429954	AJ918130	Hs.21374	ESTs	16.4
	446208	BE258323	Hs.225795	ESTs, Highly similar to OTX1_HUMAN HOMEBOX P	16.4
	442792	AJ352340	Hs.131194	ESTs	16.3
	420485	AF218586	Hs.288835	cell death-inducing DFFA-like effector b	16.3
	426767	AA384398	Hs.192491	ESTs	16.3
65	436950	L05779	Hs.113	epoxide hydrolase 2, cytoplasmic	16.3
	415196	AK000150	Hs.78185	MAX-like bHLHZIP protein	16.3
	442197	AW837912		gb:QV3-LT0048-260100-068-c02 LT0048 Homo sapi	16.3
	433457	AA830194	Hs.199417	Homo sapiens mRNA for FLJ00027 protein, part	16.2
	402316				16.2
70	409736	AA078628		gb:7P07H07 Chromosome 7 Placental cDNA Librar	16.2
	407964	AW130334	Hs.281111	ESTs	16.2
	433677	AJ791912	Hs.190885	ESTs, Moderately similar to ALU1_HUMAN ALU SU	16.2
	425507	AJ684745	Hs.165983	hypothetical C2H2 zinc finger protein FLJ2250	16.2
	413724	AA131466	Hs.23767	Homo sapiens cDNA FLJ12666 fis, clone NT2RM40	16.2
75	408922	R87388		gb:ym88g04.r1 Soares adult brain N2b4HB55Y Ho	16.1
	413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-induc	16.1
	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	16.1
	442208	AW296984	Hs.255595	ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIA	16.1
	402426				16.0
80	412399	N53816	Hs.14394	hypothetical protein FLJ20157	16.0
	413200	AA127395	Hs.222414	ESTs	16.0
	404597				15.9
	453143	AA382234	Hs.170121	protein tyrosine phosphatase, receptor type,	15.9
	455984	BE177442		gb:RC1-HT0595-200400-012-01 HT0595 Homo sapi	15.9

5	416193	T25400		gb:PTHI069 HTCCL1 Homo sapiens cDNA 5/3' sim	15.9
	407065	Y10141		gb:H.sapiens DAT1 gene, partial, VNTR	15.9
	441785	AW138139	Hs.244598	ESTs	15.9
	413784	BE165819		gb:CM0-HT0486-220300-301-d12 HT0486 Homo sapi	15.8
	429092	AI190864	Hs.178226	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	15.8
10	408499	AW205323	Hs.253475	ESTs	15.8
	453754	AW972580	Hs.172753	ESTs	15.8
	450826	U43030	Hs.25537	cardiotrophin 1	15.7
	428486	AW583497	Hs.184604	pancreatic polypeptide	15.7
	405895				15.7
15	409108	AA339443	Hs.48793	ESTs	15.6
	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	15.6
	422948	AW810824	Hs.21351	ESTs	15.6
	447852	AW504781		gb:UL-HF-BN0-ain-c-04-0-ULr1 NIH_MGC_50 Homo	15.6
	419084	AA496539	Hs.179902	transporter-like protein	15.6
20	456771	AW016739	Hs.232201	ESTs	15.6
	438564	AA381553	Hs.198253	major histocompatibility complex, class II, D	15.6
	448705	H05072	Hs.124984	ESTs, Moderately similar to unnamed protein p	15.5
	454460	X66945	Hs.748	fibroblast growth factor receptor 1 (fms-rela	15.5
	458893	BE161733	Hs.97283	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	15.5
25	426759	AI590401	Hs.21213	ESTs	15.4
	453769	R35261	Hs.24947	ESTs	15.4
	434179	AI743448	Hs.116177	ESTs	15.4
	404111				15.4
	402056				15.3
30	458602	AI262208	Hs.276489	ESTs	15.3
	427530	AA405093	Hs.126519	ESTs	15.3
	414716	AF199598	Hs.97044	Kv channel-interacting protein 2	15.3
	400632				15.3
	443918	AA305475	Hs.22660	Homo sapiens cDNA FLJ11658 fis, clone HEMBA10	15.3
35	432037	AW450592	Hs.300459	ESTs	15.3
	412921	BE009345	Hs.128942	ESTs	15.3
	421905	AI660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein [H.sapi	15.3
	441704	AI458766	Hs.201988	ESTs	15.3
	414272	AI651603	Hs.46988	ESTs	15.2
40	448224	R48700	Hs.20733	EH-domain containing 2	15.2
	404611	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PLACE10	15.2
	448381	D61580	Hs.21036	Homo sapiens mRNA; cDNA DKFZp434A1010 (from c	15.2
	454719	BE006547		gb:RC2-BN0130-040400-011-b03 BN0130 Homo sapi	15.2
	446973	H95724	Hs.4283	ESTs	15.2
45	457760	AA668123	Hs.134170	ESTs	15.2
	440144	AW082297	Hs.88523	ESTs	15.2
	407397	AB000895		gb:Homo sapiens mRNA for cadherin FIB1, parti	15.2
	427850	AA416756	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN ALU SU	15.1
	404244				15.1
50	402959				15.1
	435487	W07343	Hs.182538	phospholipid scramblase 4	15.0
	414213	BE297765		gb:601176246F1 NIH_MGC_17 Homo sapiens cDNA c	15.0
	455916	BE156710		gb:QV0-HT0368-310300-181-d01 HT0368 Homo sapi	15.0
	448943	AI608810	Hs.193288	ESTs	15.0
55	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	14.9
	454082	AF283508	Hs.63168	cell death regulator aven	14.9
	453308	AW959731	Hs.32538	ESTs	14.9
	458823	AW207574	Hs.179501	ESTs	14.9
	452532	AI905811	Hs.110757	DNA segment on chromosome 21 (unique) 2056 ex	14.9
60	418464	R87580		gb:ym89h07.r1 Soares adult brain N2b4HB55Y Ho	14.8
	409473	AL137716	Hs.296567	Homo sapiens mRNA; cDNA DKFZp434D2030 (from c	14.8
	449779	AA004258	Hs.25218	ESTs, Weakly similar to ALU8_HUMAN III ALU C	14.8
	457546	AA568484	Hs.153632	ESTs	14.8
	403368				14.8
65	432163	AK000440	Hs.272799	hypothetical protein FLJ20433	14.8
	421531	AA713505	Hs.291769	ESTs	14.8
	428283	AI439096	Hs.25832	Homo sapiens mRNA; cDNA DKFZp564P116 (from cl	14.8
	443528	AK001778	Hs.9547	hypothetical protein FLJ10916	14.8
	402399				14.8
70	410545	U32324	Hs.54310	interleukin 11 receptor, alpha	14.7
	450300	AL041440	Hs.58210	ESTs	14.7
	403552				14.7
	406929	U04690		gb:Human olfactory receptor (OR17-210) gene,	14.7
	436365	AW444548	Hs.163118	ESTs	14.7
75	402550				14.7
	441782	AW140126	Hs.132357	ESTs	14.7
	415672	N53097	Hs.193579	ESTs	14.7
	430582	AI215509	Hs.143964	ESTs	14.7
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (sacsin	14.7
80	432683	AW995441	Hs.10475	ESTs	14.6
	441871	AI306150	Hs.153450	ESTs, Weakly similar to 1909123A Na glucose c	14.6
	447481	AF052151	Hs.18686	Mouse Mammary Tumor Virus Receptor homolog	14.6
	405114				14.6
	401082				14.6
	454316	AW366144		gb:QV0-HT0101-061099-032-b12 HT0101 Homo sapi	14.6
	421572	AA531607	Hs.125143	ESTs, Weakly similar to POL2 MOUSE RETROVIRUS	14.6
	424591	R55704	Hs.150968	hypocretin (orexin) receptor 1	14.6

5	441503	AW172263	Hs.185202	ESTs	14.6
	416199	R83537		gb:yq12a08.r1 Soares fetal liver spleen 1NFLS	14.6
	420360	U83171	Hs.97203	small inducible cytokine subfamily A (Cys-Cys	14.6
	425126	N32759	Hs.172944	chorionic gonadotropin, beta polypeptide	14.5
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, member	14.5
10	405100				14.5
	454012	M76424	Hs.37014	carbonic anhydrase VII	14.5
	402457				14.5
	454613	AW810814		gb:MR2-ST0129-201099-004-e01 ST0129 Homo sapi	14.5
	429821	AL096749	Hs.225433	Homo sapiens mRNA: cDNA DKFZp434G153 (from cl	14.5
15	431073	BE254470	Hs.249186	cone-rod homeobox	14.5
	421143	AB024536	Hs.102171	immunoglobulin superfamily containing leucine	14.5
	401223				14.4
	438627	AI087335	Hs.123473	ESTs	14.4
	407124	R08160	Hs.268857	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	14.4
20	437217	AW779241	Hs.155316	ESTs	14.4
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G protein	14.4
	410258	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-biphosp	14.4
	413237	AI468574	Hs.171955	ESTs	14.4
	412975	T70956	Hs.75105	clusterin (complement lysis inhibitor, SP-40,	14.4
25	426488	X03350	Hs.4	alcohol dehydrogenase 2 (class I), beta polyp	14.4
	416667	AK000526	Hs.79457	hypothetical protein FLJ20519	14.4
	405479				14.3
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedia C)	14.3
	426316	NM_002430	Hs.301852	Human DNA sequence from clone 437G10 on chrom	14.3
30	412171	AW897452		gb:CM0-NN0058-150400-337-b08 NN0058 Homo sapi	14.3
	447241	BE382838	Hs.19322	ESTs	14.3
	402100				14.2
	438286	AW139266	Hs.134807	Homo sapiens cDNA FLJ12057 fis, clone HEMBB10	14.2
	407947	AI500332	Hs.102367	ESTs, Weakly similar to hTcf-4 [H.sepiens]	14.2
35	402275				14.2
	402358				14.2
	439624	AA838771	Hs.124407	ESTs	14.2
	444455	AI149879	Hs.175024	Homo sapiens cDNA: FLJ23447 fis, clone HSI033	14.2
	455314	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	14.2
40	427872	AA835058	Hs.21111	ESTs	14.2
	409826	AW501112	Hs.34487	hypothetical protein FLJ23412	14.2
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene homolo	14.2
	442682	AI014545	Hs.231027	EST	14.1
	457033	AF029674	Hs.173422	KIAA1605 protein	14.1
45	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	14.1
	401007				14.1
	458274	AF149297	Hs.8087	NAG-5 protein	14.1
	454106	D19687	Hs.245146	ESTs	14.1
	432928	AA570454	Hs.186467	ESTs, Moderately similar to ALU1_HUMAN ALU SU	14.1
50	425352	NM_000939	Hs.1897	proopiomelanocortin (adrenocorticotropin/ bet	14.1
	433887	AW204232	Hs.279522	ESTs	14.1
	434927	H46612	Hs.293815	ESTs, Weakly similar to PLM_HUMAN PHOSPHOLEMM	14.1
	404282				14.1
	422581	NM_016339	Hs.118562	Link guanine nucleotide exchange factor II	14.0
55	424823	NM_006226	Hs.153322	phospholipase C, epsilon	14.0
	408107	AA806754	Hs.62835	ESTs	14.0
	401577				14.0
	433883	AI925688	Hs.222312	ESTs, Weakly similar to B24264 proline-rich p	14.0
	408104	AW972927	Hs.293968	ESTs	14.0
60	404642				14.0
	400675				14.0
	406059				14.0
	446386	AB037750	Hs.21061	KIAA1329 protein	14.0
	407287	AI678812	Hs.201658	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	14.0

TABLE 22B

65	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
70	Pkey	CAT number	Accession	
	408922	109017_1	R87388 R84328 AA058916	
	409543	1138723_1	AW410200 AW409705 AW411433 BE296786 BE270309	
75	409736	115189_1	AA078628 R09051 AA078197 AA077334 AW748808 AW748807	
	412171	1280759_1	AW897452 Z20302 D55805 D52877 D60432	
	413784	1389150_1	BE165819 BE165853 W01386	
80	414213	1426375_1	BE297765 BE262061 BE302686 T83915	
	416193	1577102_1	T25400 H26834 H44554 R73193	
	416199	1577561_1	R83537 W80940 H27368	
	417998	171375_1	AW967420 AA210915 AA236991 AA210916	
	418464	1759038_2	R87580	
	418556	1767866_1	T02850	
	422796	221500_1	AW897265 AW897274 AL119504 AW897275 AW897270 AW897312 AW897318 AW897317 AA317240 AW961361	
			T06241 AA326794 AL138130 AW407975 AW999277	
	423780	231952_1	AA352013 AA330878 AA339379 AW966303	

5	424585	241151_1	AA464840 AA343628
	426275	263712_1	BE151551 AA373783 BE182852 BE008826 BE008827 BE008781 BE008699
	427980	285225_1	AA418305 AI264351
	439872	47823_1	T81058 AL357200 T70270
	442197	535550_1	AW837912 AW837934 AA984475 AW997490
	447852	73973_1	AW504781 BE620394
	448422	762770_1	BE263813 BE253504 AI500202 BE251145
	453621	974528_1	AW749983 AL045823
10	454316	1109350_1	AW366144 AW366154 AW366142 AW366151 AW366140 AW366155 BE141715 BE141718 BE141698
	454613	1226904_1	AW810814 AW810787 AW810854 AW810773 AW810735 AW810785 AW810660 AW810834 AW810874 AW810723
			AW810881 AW810791 AW810644 AW810659 AW810676
	454719	1230646_1	BE006547 AW815578 AW815311 AW856304
	455144	1254914_1	AW875942 AW858234 AW875938 AW875941 AW858235 AW875958
	455818	137219_1	AI733747 AA129802
15	455904	1382290_1	BE156173 BE156305 BE156196
	455916	1382748_1	BE156710 BE156726 BE156712
	455984	1397288_1	BE177442 BE177439 BE177445 BE177440 BE177448 BE177444 BE177433

TABLE 22C

20	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:469-495.
25	Strand:	Indicates DNA strand from which exons were predicted.
	NL_position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
30	400489	8954013	Plus	131475-131652
	400545	9800107	Minus	124618-124881
	400625	7228177	Minus	117266-117441
	400632	3818355	Plus	72875-73447,75874-76425
	400637	8894326	Plus	68901-69507
	400675	8118750	Plus	11223-11816
35	401007	8117333	Minus	140821-141050
	401082	3242744	Plus	22937-23494,27677-27966
	401223	8099088	Plus	148940-150214
	401551	8096896	Minus	189824-190728
	401577	9280797	Minus	139377-139674,141195-141281,142217-142340
40	401703	4826475	Plus	135-1229
	402058	8084234	Plus	207002-207288
	402100	8117697	Plus	133649-133792
	402195	7689778	Minus	147901-148884
	402275	2935596	Minus	31065-31233,33680-33771,34345-34411,38890-39125,39779-39943
45	402316	7527774	Minus	10751-10919,18817-19052,22131-22328
	402358	8886976	Minus	131788-132729
	402399	1905915	Minus	24502-24666,24986-25102
	402426	9796361	Minus	73590-73824
	402457	9796782	Minus	16513-16577,16838-16926
50	402520	7596899	Minus	171761-171996
	402550	7652009	Minus	80413-80673
	402741	9212200	Minus	18603-18760,19719-19890
	402865	9716300	Plus	3197-3429,3722-3914,5795-5987,6802-6961,8653-8815,9292-9660
	402959	9368493	Plus	36729-37084
55	403121	9180223	Plus	4059-4258
	403368	4388738	Plus	70286-70429,75165-75258
	403652	6862638	Minus	117504-117662
	403731	7543752	Minus	144000-144618
	404033	8122195	Plus	7976-8156
60	404111	9408736	Plus	161506-161781
	404244	5672609	Minus	98173-98517
	404282	2276311	Plus	61503-62205
	404597	9958262	Minus	114369-114599
	404642	9796810	Plus	102999-103145
65	404654	9797010	Plus	6275-6527
	404947	7382205	Plus	29740-30105,30176-30412
	405100	8076846	Plus	144114-144234
	405114	8096938	Minus	97013-97560
	405228	7248990	Plus	92234-95905
70	405313	3638954	Plus	68924-69093
	405324	3342751	Minus	5475-5677
	405479	6453391	Plus	1668-1844
	405895	7677903	Minus	66990-67484
	406059	9103984	Minus	13856-14004
75	406150	9886026	Minus	59331-59701
	406535	7711477	Plus	83135-83362

80 TABLE 23A: 626 genes upregulated in uterine cancer relative to normal body tissues

Table 23A lists about 626 genes upregulated in uterine cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis

was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

5	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar accession number, GenBank accession number
	UniGeneID:	UniGene number
	Pred.ProT.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
10	UniGene Title:	UniGene gene title
	R1	95th percentile of uterine cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator
15	Pkey; ExAccn; UniGeneID; UniGene Title; Pred.ProT.Domains; R1	
		428330; L22524; Hs.2256; matrix metalloproteinase 7 (matrilysin, ; Peptidase_M10; 35.11
		420440; NM_002407; Hs.97644; mamaglobin 2; Uteroglobulin; 22.80
20		433335; AA742697; Hs.62492; NM_052863; Homo sapiens secretoglobulin, fa; none; 21.66
		425723; NM_014420; Hs.159311; dickkopf (Xenopus laevis) homolog 4; none; 21.11
		421481; AW391972; Hs.104696; KIAA1324 protein; none; TM=M; SS=M; 20.20
		437938; A1950087; Hs.369628; gb:wg05c02.x1 NCL_CGAP_Kid12 Homo sapiens; none, none; 19.83
		406687; M31126; Hs.352054; matrix metalloproteinase 11 (stromelysin; hemopexin; Peptidase_M10; 17.68
25		446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin, ; Osteopontin; 17.60
		418281; U09550; Hs.1154; oviductal glycoprotein 1, 120kD (mucin 9; Glyco_hydro_18; TM=M; SS=M; 17.48
		431130; NM_006103; Hs.2719; HE4; epididymis-specific, whey-acidic pr; wap; TM=M; SS=Y; 16.59
		400301; X03635; Hs.1657; estrogen receptor 1; F-box, hormone_rec, zf-C4, Oest_recep, adh_zinc, ketoacyl-synt, pp-binding, Acyl_transf, Thioesterase, ketoacyl-synt_C, AAA, E7, RFX_DNA_binding; TM=M; SS=N; 16.11
30		419356; A1656166; Hs.7331; hypothetical protein FLJ22316; Asparaginase_2, none; 15.90
		433222; AW514472; Hs.238415; dickkopf (Xenopus laevis) homolog 4; none, PHO4; 15.39
		417931; W95642; Hs.82961; trefol factor 3 (intestinal); trefol; 15.39
		400284; ; NM_000125; Homo sapiens estrogen receptor; hormone_rec, zf-C4, Oest_recep; TM=M; SS=M; 15.23
		456662; NM_002448; Hs.1494; msh (Drosophila) homeo box homolog 1 (fo; homeobox, none; 15.04
35		438817; A023799; Hs.163242; ESTs; none, none; 13.72
		453857; AL080235; Hs.35861; Ras-Induced senescence 1 (RIS1); none; TM=Y; SS=M; 13.67
		424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2, hemopexin; Peptidase_M10; 13.51
		458627; AW088642; Hs.97584; SRY (sex determining region Y)-box 17 (S; HMG_box; TM=M; SS=N; 13.44
		410001; AB041036; Hs.57771; kallikrein 11; trypsin; TM=M; SS=M; 13.41
40		421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion_trans_K_tetra, asp; 13.27
		449048; Z45051; Hs.22920; similar to S68401 (cattle) glucose induc; Lamp; TM=M; SS=M; 12.76
		436972; AA284679; Hs.25640; claudin 3; PMP22_Claudin; TM=Y; SS=M; 12.59
		450693; AW450461; Hs.203965; ESTs; Sema, lg, none; 12.52
		415457; AW081710; Hs.7369; Homo sapiens testes specific A2 homolog; MORN, sugar_tr; TM=Y; SS=M; 12.46
45		413719; BE439580; Hs.75498; small inducible cytokine subfamily A (C; IL8; 12.23
		431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none; TM=M; SS=Y; 12.09
		417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK; TM=M; SS=Y; 12.08
		407786; AA687538; Hs.38972; tetraspan 1; transmembrane4; TM=Y; SS=M; 11.91
		444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen; TM=M; SS=M; 11.86
50		446608; N75217; Hs.175622; ESTs; Armadillo_sep, HEAT_PBS; TM=M; SS=M; 11.72
		447835; AW591623; Hs.164129; ESTs, Weakly similar to I38022 hypothetical; none, UQ_con; 11.59
		420181; A1380089; Hs.158951; ESTs; none, lg, pkinase, LRR, LRRCT; 11.49
		451253; AA48299; Hs.26126; claudin 10; PMP22_Claudin, Peptidase_M1, K_tetra; TM=Y; SS=M; 11.45
		453988; AA847843; Hs.62711; High mobility group (nonhistone chromoso; HMG_box, none; 11.42
55		448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec, MIP; TM=M; SS=M; 11.37
		421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz, NTR; 11.08
		452367; U71207; Hs.29279; eyes absent (Drosophila) homolog 2; Hydrolase; 11.01
		409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7tm_1, zf-C3HC4, fn3, SPRY, KRAB, zf-C2H2, rve, zf-B_box; TM=Y; SS=M; 10.95
		415138; C18356; Hs.295944; tissue factor pathway inhibitor 2; Kunitz_BPTI, none; 10.91
60		416658; U03272; Hs.79432; fibrillin 2 (congenital contractual ara; EGF, TB, granulin, PSI, EB, TIL; TM=M; SS=M; 10.81
		411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A receptor; Neur_chan_LBD, Neur_chan_memb; TM=Y; SS=M; 10.72
		438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec, zf-C4, none; 10.68
		425071; NM_013989; Hs.154424; deiodinase, iodothyronine, type II; T4_deiodinase; TM=M; SS=Y; 10.66
		430832; A1073913; Hs.100686; ESTs, Weakly similar to JE0350 Anterior; none, none; 10.52
65		451497; H83294; Hs.284122; Wnt Inhibitory factor-1; EGF, WIF; 10.50
		421478; A1683243; Hs.97258; ESTs, Moderately similar to S29539 ribos; none, none; 10.50
		409231; AA446644; Hs.692; GA733-2 antigen; epithelial glycoprotein; thyroglobulin_1; TM=Y; SS=M; 10.35
		443785; AW449952; Hs.180125; basic-helix-loop-helix-PAS protein; HLH_PAS; TM=M; SS=N; 10.34
		409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran, M_SMC, SMC_C, DUF164, none; 10.34
70		431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4; TM=Y; SS=M; 10.34
		415539; A173881; Hs.72472; NAME OMITTED ... receptor kinase; pkinase, Activin_rec, PDZ_ZU5, death; 10.31
		411274; NM_002776; Hs.69423; kallikrein 10; trypsin; TM=M; SS=N; 10.24
		423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage; hemopexin, Peptidase_M10; TM=M; SS=M; 10.24
		441377; BE218239; Hs.202656; ESTs; none, none; 10.17
75		400292; AA250737; Hs.72472; NAME OMITTED ... receptor kinase; pkinase, Activin_rec, PDZ_ZU5, death; 10.17
		452594; AU076405; Hs.29581; solute carrier family 26 (sulfate transp; xan_ur_permease, Sulfate_transp, STAS, HMG_box; 10.12
		429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic; C2, PLA2_B; TM=M; SS=N; 9.87
		413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT, none; 9.87
		408562; A436323; Hs.31141; roundabout (axon guidance receptor, Dros; lg, fn3; TM=M; SS=N; 9.86
80		428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7tm_3; TM=Y; SS=M; 9.72
		438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec, zf-C4, none; 9.68
		411089; AA456454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none, none; 9.53
		450451; AW591528; Hs.202072; ESTs; none, none; 9.53
		456062; A1666286; Hs.71962; ESTs, Weakly similar to B36298 proline-r; none, none; 9.50

- 418113; A1272141; Hs.83484; SRY (sex determining region Y)-box 4; HMG_box,homeobox;TM=M;SS=N; 9.38
 412791; A1131192; Hs.143199; ESTs, Weakly similar to S72481 probable; pkinase,PBD:none; 9.36
 432435; BE218886; Hs.282070; ESTs; none:none; 9.35
 416530; U62801; Hs.79361; kallikrein 6 (neurosin, zyme); trypsin;TM=M;SS=M; 9.32
 439018; AW300887; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 9.23
 445537; A1245671; Hs.12844; ECF-like-domain, multiple 6; EGF,MAM; 9.19
 410407; X66839; Hs.63287; carbonic anhydrase IX; carb_anhydrase;TM=M;SS=M; 9.19
 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_transp,STAS,HMG_box; 9.17
 453459; BE047032; Hs.257789; ESTs; none:none; 9.14
 431674; AA098901; Hs.301642; G-protein coupled receptor; none,GCV_H; 9.05
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldhdh;TM=M;SS=M; 9.00
 413278; BE563085; Hs.833; Interferon-stimulated protein, 15 kDa; ubiquitin; 8.93
 436954; AA740151; Hs.130425; ESTs; none:none; 8.91
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 8.89
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisomIV,HATPase_c; 8.85
 407792; A1077715; Hs.39384; putative secreted ligand homologous to f; none;TM=M;SS=Y; 8.80
 451027; AW519204; Hs.40808; Homo sapiens, Similar to RIKEN cDNA 2810; none:none; 8.79
 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; IQ;TM=M;SS=N; 8.72
 413385; M34455; Hs.840; indoleamine-pyrrole 2,3 dioxygenase; IDO;TM=M;SS=N; 8.70
 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodi; Somatomedin_B,Endonuclease,Phosphodiester;TM=Y;SS=M; 8.69
 421502; AF111856; Hs.105039; solute carrier family 34 (sodium phosphat; Ribosomal_L20,Na_P1_cotrans;TM=Y;SS=N; 8.67
 437935; AW939591; Hs.5940; mucin 13, epithelial transmembrane; EGF,SEA;TM=Y;SS=M; 8.56
 408692; AL040127; Hs.34074; dipeptidylpeptidase VI; DPPIV_N_term,Peptidase_S9:none; 8.55
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 8.53
 428187; A1687303; Hs.285529; G protein-coupled receptor 49; 7tm_1:none; 8.49
 448672; A1955511; Hs.374290; ESTs; lig_chan,ANF_receptor,SBP_bac_3;TM=Y;SS=M; 8.44
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm_2,HRM;TM=Y;SS=M; 8.40
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M;SS=N; 8.40
 452093; AA447453; Hs.27860; Homo sapiens mRNA; cDNA DKFZp586M0723 (f; 7tm_1:none; 8.33
 407894; A1278313; Hs.41143; phosphoinositide-specific phospholipase ; C2,PI-PLC-Y,PI-PLC-X;TM=M;SS=N; 8.23
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M;SS=N; 8.21
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=M; 8.20
 424441; X14850; Hs.147097; H2A histone family, member X; histone,CBFD_NFYB_HMF; 8.20
 408243; Y00787; Hs.624; Interleukin 8; HLH,PAS,IL8;TM=M;SS=N; 8.00
 415752; BE314524; Hs.78776; putative transmembrane protein; none;TM=Y;SS=N; 7.99
 422608; AW160644; Hs.118695; potassium voltage-gated channel, subfam; ion_trans,K_tetra;TM=Y;SS=N; 7.99
 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; none; 7.95
 409649; AA159216; Hs.55505; hypothetical protein FLJ20442; Y_phosphatase,DSPc;TM=M;SS=N; 7.95
 424078; AB006525; Hs.139033; paternally expressed 3; zf-C2H2,KRAB:none; 7.86
 432179; X75208; Hs.2913; EphB3; EPH_bld,fn3,pkinase,SAM;TM=Y;SS=M; 7.85
 424581; M62062; Hs.150917; catenin (cadherin-associated protein), alpha; Vinculin,DNA_ligase_ZBD;TM=M;SS=N; 7.84
 420610; A1683183; Hs.99348; distal-less homeo box 5; homeobox;TM=M;SS=N; 7.81
 436856; A1469355; Hs.127310; ESTs; pkinase,rm;TM=M;SS=N; 7.81
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 7.80
 407811; AW190902; Hs.40098; cysteine knot superfamily 1, BMP antagon; TGF-beta,DAN; 7.78
 424399; A1905687; Hs.348419; A1905687:IL-BT095-190199-019 BT095 Homo ; none;TM=M;SS=M; 7.65
 418836; A1655499; Hs.161712; ESTs; pkinase,Activin_rec,PDZ,ZU5,death; 7.64
 435793; AB037734; Hs.4993; KIAA1313 protein; none;TM=M;SS=N; 7.61
 426201; AW182614; Hs.128499; ESTs; SH3:none; 7.59
 447400; AK000322; Hs.18457; hypothetical protein FLJ20315; zf-C3HC4;TM=Y;SS=M; 7.55
 410850; AW362867; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_transp,STAS,HMG_box; 7.55
 453464; A1884911; Hs.32989; receptor (calcitonin) activity modifying; none;TM=Y;SS=N; 7.54
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypept; Sm,pkinase; 7.52
 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC:none; 7.38
 443991; NM_002250; Hs.10082; potassium intermediate/small conductance; CaMBD,SK_channel,ion_trans;TM=Y;SS=M; 7.36
 414617; A1339520; Hs.288817; ESTs, Moderately similar to N Chain N, M; hexokinase,hexokinase2;TM=Y;SS=N; 7.35
 422017; NM_003877; Hs.110776; STAT induced STAT inhibitor-2; SH2; 7.33
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis, clone NT; none:none; 7.30
 409041; AB033025; Hs.50081; Hypothetical protein, XP_051860 (KIAA119; none;TM=M;SS=M; 7.28
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; 7.28
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc,Y_phosphatase,Ribosomal_S3_N;TM=M;SS=N; 7.28
 418506; AA084248; Hs.372651; Unknown protein for MGC:29643 (formerly ; none:none; 7.27
 448913; AA194422; Hs.22564; myosin VI; rm,zf-RanBP,pkinase,GST_C,Ets,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFIIS,AT_hook,SAM;TM=M;SS=N; 7.26
 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 7.26
 424317; A1865032; Hs.26017; ESTs; none,pkinase; 7.21
 410361; BE391804; Hs.62661; guanylate binding protein 1, Interferon-; GBP,GBP_C;TM=Y;SS=M; 7.21
 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M;SS=N; 7.14
 438707; L08239; Hs.5326; amino acid system N transporter 2; porcu; ACAT,MBOAT;TM=Y;SS=M; 7.05
 423011; NM_000683; Hs.123022; adrenergic, alpha-2C-, receptor; 7tm_1;TM=Y;SS=M; 7.03
 435021; AA922192; Hs.73962; ESTs; EPH_bld,pkinase,fn3,SAM:none; 7.02
 446163; AA026880; Hs.25252; prolactin receptor; none;NA;NA; 7.01
 447768; X86400; Hs.19520; FXD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=M;SS=N; 7.00
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,CoE;TM=M;SS=N; 6.99
 451035; AU076785; Hs.430; plastin 1 (I isoform); ehand,CH,Adaplin_N; 6.99
 450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta,TGFb_propeptide; 6.95
 424054; AA334511; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 6.93
 432519; A1221311; Hs.130704; ESTs, Weakly similar to BCHUA S-100 pro; none:none; 6.93
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-con; UQ_con;TM=M;SS=N; 6.92
 419693; AA133749; Hs.301350; FXD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 6.92
 437139; W73685; Hs.118513; ESTs, Weakly similar to RTA RAT PROBABLE; 7tm_1;TM=Y;SS=M; 6.87
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCRLysyl_oxidase;TM=M;SS=M; 6.87

- 418203; X54942; Hs.83758; CDC28 protein kinase 2; Cks; 6.86
 410467; AF102546; Hs.63931; dachshund (Drosophila) homolog; Ski_Sno; TM=M; SS=M; 6.86
 425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin; hemopexin; Peptidase_M10; 6.85
 453064; R40334; Hs.89463; potassium large conductance calcium-act; none; none; 6.83
 452046; AB018345; Hs.27657; KIAA0802 protein; none; TM=M; SS=N; 6.79
 417771; AA804698; Hs.82547; retinoic acid receptor responder (lazarus; none; none; 6.79
 422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glut; aldedh; aakkinase; TM=M; SS=N; 6.77
 431470; AA832417; Hs.139650; ESTs; none; ig, pkinase, LRR, LRRCT; 6.76
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none; none; 6.75
 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory sub; SH2; none; 6.74
 417886; AA214584; ESTs; SPRY, 7tm_3, ANF_receptor; none; 6.72
 412926; AB79076; Hs.75061; macrophage myristoylated alanine-rich C; MARCKS; 6.70
 437960; AB69586; Hs.369312; ESTs; none; none; 6.68
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfamily; 60s_ribosomal; Ribosomal_L10, TNFR_c6, DEAD; 6.66
 444006; BE395085; Hs.334762; type I transmembrane protein Fnl4; kll_recept_a, PKD, MHC_I; TM=M; SS=Y; 6.65
 413040; AA193338; Hs.12321; sodium calcium exchanger; Na_Ca_Ex; TM=Y; SS=M; 6.64
 449556; AA002008; Hs.188633; ESTs; PIP5K; none; 6.64
 447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-induc; pyr_redox; TM=M; SS=N; 6.62
 446063; A1720140; Hs.151079; ESTs; ISK_Channel; none; 6.61
 424762; AL119442; Hs.183684; eukaryotic translation initiation factor; none; none; 6.60
 421554; AW137676; Hs.97775; ESTs; none; none; 6.59
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank; 6.55
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase; TM=M; SS=N; 6.54
 448730; AB032983; Hs.21894; KIAA1157 protein; PP2C; TM=M; SS=N; 6.54
 433577; AW007080; Hs.284192; ESTs; none; none; 6.53
 422627; BE336857; Hs.118767; transforming growth factor, beta-induced; Foscidin, ABC_tran, ABC_membrane, GTP_EFTU; TM=M; SS=M; 6.53
 442133; AW874138; Hs.129017; ESTs; type Ia transmembrane protein; LRR, LRRNT, LRRCT; TM=Y; SS=M; 6.52
 430259; BE550182; Hs.375142; RalGEF-like protein 3, mouse homolog; fn3, RA, RasGEF; TM=M; SS=M; 6.52
 434263; N34895; Hs.79187; ESTs; ig; none; 6.49
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase, DSPC; TM=M; SS=N; 6.48
 419942; U25138; Hs.93841; potassium large conductance calcium-act; CaKb; TM=Y; SS=M; 6.47
 421064; AJ245432; Hs.101382; tumor necrosis factor, alpha-induced pro; none; TM=M; SS=N; 6.47
 432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin; TM=Y; SS=M; 6.45
 431685; AW296135; Hs.267659; vav 3 oncogene; CH, DAG_PE-bind, PH, RhoGEF, SH2, SH3, DC1; TM=M; SS=N; 6.44
 428832; AA578229; Hs.324239; ESTs; Moderately similar to ZN91_HUMAN Z; Osteopontin; none; 6.39
 436775; AA731111; Hs.372225; ESTs; none; none; 6.39
 424343; AW956360; Hs.4748; adenylate cyclase activating polypeptide; 7tm_2, HRM; none; 6.37
 421071; AJ311238; Hs.104476; ESTs; Weakly similar to CGH1E collagen; none; TM=Y; SS=M; 6.37
 438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nuclear trans; HLH, PAS, ILB; TM=M; SS=N; 6.37
 438993; AA828995; gb:cd77b08.s1 NCL_CGAP_Ov2 Homo sapiens; EGF, metalloth, Integrin_B, PSI; none; 6.27
 406400; ; kallikrein 8 (neuropilin/ovasin) (KLK8); trypsin; TM=M; SS=M; 6.27
 429556; AW139399; Hs.314807; ESTs; none; TM=M; SS=N; 6.26
 409269; AA576953; Hs.22972; steroid 5 alpha-reductase 2-like; H5AR g; Steroid_dh; TM=Y; SS=M; 6.25
 435732; AF229178; Hs.123136; leucine rich repeat and death domain con; none; none; 6.24
 439668; AJ091277; Hs.302634; frizzled (Drosophila) homolog 8; Frizzled_Fz, 7tm_2, twdn_2; TM=Y; SS=M; 6.24
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (MIF, sugar_tr; none; 6.23
 438961; AW375974; Hs.156704; ESTs; none; none; 6.23
 434808; AF155108; Hs.256150; NY-REN-41 antigen; none; TM=M; SS=N; 6.22
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-i; AAA, NB-ARC, PAAD, DAPIN; NA; NA; 6.20
 418224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; ehand; 6.20
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49, EGF, ig, Neuregulin; TM=M; SS=N; 6.19
 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4; TM=Y; SS=M; 6.19
 452551; L27071; Hs.29877; TXK tyrosine kinase; Beach, WD40, SH2, SH3, pkinase; TM=M; SS=N; 6.14
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3; TM=M; SS=N; 6.12
 454462; AA378776; Hs.288649; hypothetical protein MGC3077; none; 6.11
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; LIM, PDZ, pkinase; 6.11
 449700; L02857; Hs.78358; paraneoplastic antigen; none; TM=M; SS=N; 6.10
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase, ICE_p10, ICE_p20; TM=M; SS=M; 6.10
 416209; AA236778; Hs.79078; MAD2 (mitotic arrest deficient, yeast, h; HORMA; TM=M; SS=N; 6.09
 433159; AB035898; Hs.150587; kinesin-like protein 2; bZIP, kinesin; 6.08
 432432; AA541323; Hs.115831; ESTs; ig, Sema, PSI; none; 6.07
 409619; AK001015; Hs.55220; BCL2-associated athanogene 2; BAG; TM=M; SS=N; 6.04
 412723; AA648459; Hs.335951; hypothetical protein AF301222; none; TM=M; SS=N; 6.03
 424273; W40460; Hs.144442; phospholipase A2, group X; phoslip; TM=M; SS=Y; 6.03
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPC, Rhodanese; none; 6.00
 421143; AB024536; Hs.102171; immunoglobulin superfamily containing Ig; ig, LRR, LRRNT, LRRCT; TM=M; SS=M; 6.00
 428677; AJ657119; Hs.351582; troponin I, cardiac; none; TM=M; SS=N; 6.00
 450098; W27249; Hs.8109; hypothetical protein FLJ21080; SET, zif-MYND; TM=M; SS=N; 6.00
 410422; AL042014; Hs.63348; Homo sapiens, clone MGC:15203, mRNA, cont; C1q, Collagen; 5.99
 419972; AL041465; Hs.182982; golgin-67; none; none; 5.99
 421251; Z28913; Hs.102948; enigma (LIM domain protein); LIM, PDZ; 5.97
 403362; ; NM_001615; Homo sapiens actin, gamma 2; actin; 5.95
 451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg; TM=M; SS=N; 5.95
 420253; AJ656055; Hs.96200; neighbor of A-kinase anchoring protein 9; none; NA; NA; 5.93
 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK; TM=M; SS=N; 5.93
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2; TM=M; SS=N; 5.92
 450747; AI064821; Hs.12953; ESTs, Highly similar to 1818357A EWS gen; rrm, zif-RanBP, GAS2; 5.92
 415211; R64730.comp; Hs.155986; DEAD/H (Asp-Glu-Ala-Asp/His) box polypep; DEAD_helicase_C, rrm, Ndr, Oys_knot, TIL, vwa, vwc, vwd, IQ, Rila, abhydrolase, TGF-beta, DUF139, TPR, DSPC, lsp_1, Ribosomal_S21, rvp; TM=M; SS=N; 5.91
 429910; NM_000867; Hs.2507; 5-hydroxytryptamine (serotonin) receptor; 7tm_1; TM=Y; SS=N; 5.90
 447131; NM_004585; Hs.17466; retinoic acid receptor responder (lazarus; none; TM=Y; SS=N; 5.89
 437952; D63209; Hs.5944; solute carrier family 11 (proton-coupled; none; TM=Y; SS=M; 5.89
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT; TM=M; SS=Y; 5.89

- 453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz,Frizzled,7tm_2,TM=Y,SS=M; 5.87
 426761; AI015709; Hs.172089; PORIMIN Pro-oncogene receptor inducing me; none; TM=Y,SS=M; 5.85
 425367; BE271188; Hs.155875; protein tyrosine phosphatase, receptor type 1; none; TM=M,SS=Y; 5.85
 426108; AA622037; Hs.166468; programmed cell death 5; DUF122; TM=M,SS=N; 5.84
 5 450502; T08065; Hs.118262; ESTs; Ion_trans,ion_trans; 5.84
 442652; AI005163; Hs.201378; Homo sapiens cDNA FLJ40427 fis; none; TM=M,SS=N; 5.83
 424917; AI636208; Hs.96901; hypothetical protein FLJ23049; none; TM=M,SS=N; 5.83
 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2,STAT,STAT_bind,STAT_prot; TM=M,SS=N; 5.82
 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS,AIRS_C; TM=M,SS=N; 5.82
 10 445133; AW157646; Hs.198689; ESTs; ehfand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,FLID,bZIP,Tropomyosin,Myc-LZ,M,Idh_C,CH,AIP3; TM=M,SS=N; 5.79
 426215; AW963419; Hs.155223; stanniocalcin 2; Stanniocalcin; 5.78
 414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1; TM=Y,SS=M; 5.75
 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA; TM=Y,SS=N; 5.74
 452683; AI089575; Hs.374574; progesterone membrane binding protein; homeobox; none; 5.72
 15 432201; AI538613; Hs.298241; Transmembrane protease, serine 3; Idl_recept_La, trypsin; TM=Y,SS=M; 5.72
 429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 5.72
 449458; AI805078; Hs.208261; ESTs; Frizzled,Fz; none; 5.72
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none; TM=Y,SS=M; 5.71
 418848; AI820961; Hs.193465; ESTs; PDZ, pkinase; none; 5.70
 20 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1; TM=Y,SS=M; 5.69
 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase,pkinase_C,HR1; TM=M,SS=N; 5.69
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-assoc; kinesin; TM=M,SS=N; 5.69
 445136; AI348014; Hs.143949; ESTs; Weakly similar to Achaete-Scute ho; Ion_trans,ion_trans; 5.69
 409223; AA312572; Hs.362852; phosphoinositide-3-kinase, regulatory subunit; SH2,SH3,RhoGAP; none; 5.67
 25 430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX,EXS; TM=Y,SS=N; 5.66
 429638; AI916662; Hs.211577; kinecltin 1 (kinesin receptor); bZIP,Tropomyosin,spectrin,LBP,BPL,CETP,B56,M; TM=Y,SS=M; 5.65
 450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2; TM=Y,SS=M; 5.64
 453950; AA156998; Hs.348037; eukaryotic translation initiation factor; none; 5.64
 425889; M57414; Hs.161305; tachykinin receptor 2; 7tm_1; TM=Y,SS=M; 5.64
 30 432527; AW975028; Hs.102754; ESTs; none; none; 5.64
 441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3; none; 5.63
 419080; AW150835; Hs.18878; hypothetical protein FLJ21620; 2OG-Fel1_Oxy; TM=M,SS=N; 5.63
 447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5_F8_type_C; TM=M,SS=M; 5.61
 440422; AW452696; Hs.130760; myosin phosphatase, target subunit 2; BTB,Kelch,ank; none; 5.58
 35 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome; TM=M,SS=N; 5.58
 432805; X94630; Hs.3107; CD97 antigen; 7tm_2,EGF,GPS,FacCD; TM=Y,SS=M; 5.55
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; Ig,Isodh,Ribosomal_L6_F-box; TM=Y,SS=M; 5.55
 441607; NM_005010; Hs.7912; neuronal cell adhesion molecule; WD40,fn3,Ig; TM=M,SS=N; 5.54
 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulated; none; none; 5.54
 40 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C; none; 5.53
 404210; ; NM_005936; Homo sapiens myeloid/lymphoid ; FHA,PDZ,RA,DIL; TM=M,SS=N; 5.53
 408051; AI623351; Hs.172148; ESTs; PH,RhoGAP; none; 5.53
 436726; AA324975; Hs.198689; ESTs; Weakly similar to T00079 hypotheti; ehfand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,FLID,bZIP,Tropomyosin,Myc-LZ,M,Idh_C,CH,AIP3; TM=M,SS=N; 5.53
 45 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none; none; 5.52
 428667; AI375550; Hs.345888; nucleolar protein p40; homolog of yeast ; none; none; 5.51
 433907; AW296107; Hs.152686; ESTs; Armadillo_seg; none; 5.50
 442821; BE391929; Hs.8752; transmembrane protein 4; none; 5.50
 422282; AF019225; Hs.114309; apolipoprotein L; MolA_ExcB; TM=Y,SS=M; 5.49
 50 439820; AL1360204; Hs.283853; Homo sapiens mRNA full length insert cDN; none; none; 5.49
 428771; AB028992; Hs.193143; KIAA1069 protein; C2,PI-PLC-Y,PI-PLC-X; TM=M,SS=N; 5.48
 452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fis, clone HE; GDI,7tm_1; none; 5.48
 442013; AA506476; Hs.375009; Human DNA sequence from clone RP11-353C1; none; none; 5.48
 408056; AA312328; Hs.42331; ephrin-A4; Ephrin; TM=M,SS=M; 5.47
 55 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR; TM=M,SS=N; 5.47
 420297; AI628272; Hs.128757; ESTs; Weakly similar to ALU1_HUMAN ALU S; pkinase,TUDOR; none; 5.47
 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3; 5.46
 424517; AI539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MA; SH2,STAT,STAT_bind,STAT_prot; none; 5.45
 441560; F13386; Hs.7888; v-erb-a avian erythroblastic leukemia vi; pkinase,Recep_L_domain,Furin-like,YLP; none; 5.44
 60 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS; 5.43
 450402; BE218027; Hs.89969; ESTs; SH3; none; 5.42
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P14_kinase,FAT,FATC,BolA,RUN; TM=M,SS=N; 5.42
 65 430696; AA531278; Hs.59509; ESTs; pkinase,PP2C; none; 5.42
 412350; AI659306; Hs.73826; protein tyrosine phosphatase, non-recept; Y_phosphatase,Band_41,PDZ; TM=M,SS=N; 5.42
 444783; AK001468; Hs.62180; anillin (Drosophila Scraps homolog); act; PH; none; 5.41
 448379; AI097463; Hs.21035; KIAA1130 protein; none; Zip; 5.41
 410082; AA081694; Hs.158311; Musashi (Drosophila) homolog 1; rrm; TM=M,SS=N; 5.41
 70 411817; BE302900; Hs.72241; mitogen-activated protein kinase kinase ; pkinase; TM=M,SS=M; 5.40
 445413; AA151342; Hs.12677; CG1-147 protein; UPF0099; TM=M,SS=M; 5.39
 451863; AL120634; Hs.331803; ATPase, Ca transporting, plasma membrane; cpn60_TCP1,E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase; 5.38
 442875; BE623003; Hs.23625; Homo sapiens clone TCCTA00142 mRNA sequ; K_tetra,DUF51; none; 5.38
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase; PAF-AH_ib,Lipase_GDSL; TM=M,SS=N; 5.36
 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate_kin; 5.34
 75 441031; AI110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen_C,G-alpha,arf; TM=M,SS=M; 5.33
 408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+/pep; PTR2; TM=Y,SS=N; 5.33
 435391; AA704588; Hs.58934; ESTs; PIP5K; none; 5.33
 411779; AA292811; Hs.72050; non-metastatic cells 5, protein expresse; NDK; 5.33
 80 422170; AI791949; Hs.112432; anti-Müllerian hormone; TGF-beta; 5.32
 447350; AI375572; Hs.172634; v-erb-a avian erythroblastic leukemia vi; pkinase,Recep_L_domain,Furin-like,YLP; none; 5.32
 449964; AW001741; Hs.24243; hypothetical protein FLJ10706; pkinase; TM=M,SS=N; 5.31
 426427; M86699; Hs.169840; TTK protein kinase; pkinase; 5.30
 430407; H23551; Hs.30974; ESTs; pkinase,PBD; none; 5.29

- 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3; TM=M; SS=N; 5.27
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; Ig,kringle,ptkinase,Fz; TM=Y; SS=M; 5.27
 424596; AB020639; Hs.151017; estrogen-related receptor gamma; hormone_rec, zf-C4; TM=M; SS=N; 5.27
 428013; AF151020; Hs.181444; hypothetical protein; none; TM=Y; SS=M; 5.26
 447384; A1377221; Hs.40528; ESTs; SH3, Sorb, none; 5.26
 441824; AB007871; Hs.7977; KIAA0411 gene product; SH3, RhoGAP; TM=M; SS=N; 5.26
 438493; A1130740; Hs.6241; phosphoinositide-3-kinase, regulatory su; SH2, SH3, RhoGAP; TM=M; SS=N; 5.26
 428579; NM_005756; Hs.184942; G protein-coupled receptor 64; 7tm_2, GPS; TM=Y; SS=M; 5.25
 414359; M62194; Hs.75929; cadherin 11, type 2, OB-cadherin (osteob; cadherin, Cadherin_C_term; TM=Y; SS=M; 5.25
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glur, sugar_tr; TM=Y; SS=M; 5.24
 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG; TM=M; SS=N; 5.24
 423685; BE350494; Hs.49753; uveal autoantigen with coiled coil domain; ank, bZIP, M, DUF164, AIP3; 5.23
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phos; MORN, sugar_tr; TM=Y; SS=M; 5.23
 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase; TM=M; SS=N; 5.23
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; coillin_ADF; 5.23
 412507; L36645; Hs.73964; EphA4; fn3, pkinase, SAM, EPH_jbd; TM=Y; SS=M; 5.23
 426770; A1948618; Hs.150176; ESTs; Sulfate_transp, STAS; TM=Y; SS=N; 5.23
 422583; AA410506; Hs.27973; KIAA0874 protein; ank, G-alpha; TM=M; SS=N; 5.22
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK, CoaE; 5.22
 448093; AW977382; Hs.15898; 2,4-dienoyl CoA reductase 2, peroxisomal; adh_short; 5.21
 443646; A1085198; Hs.164226; Thrombospondin 1; EGF, tsp_1, vwc, TSPN, tsp_3, none; 5.18
 457916; BE085271; Hs.8834; ring finger protein 3; pkinase, none; 5.18
 433933; A1754389; Hs.355397; Homo sapiens clone TCCCA00164 mRNA sequ; none; NA; NA; 5.18
 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none; 5.17
 433652; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene family; ras, ABC, tran, arf; TM=M; SS=M; 5.17
 450511; R07423; Hs.85092; thyroid hormone receptor interactor 11; Myosin_tail, EGF; 5.16
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 no; none; TM=M; SS=N; 5.15
 454438; AA224053; Hs.172405; cell division cycle 27; SPRY, 7tm_3, ANF_receptor; 5.14
 413869; NM_000878; Hs.75596; Interleukin 2 receptor, beta; none; TM=Y; SS=M; 5.14
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial; mito_carr; TM=M; SS=N; 5.14
 415474; NM_014252; Hs.78457; solute carrier family 25 (mitochondrial; mito_carr; TM=M; SS=N; 5.14
 411704; A1499220; Hs.71573; hypothetical protein FLJ10074; pkinase; TM=M; SS=N; 5.13
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz, Frizzled, 7tm_2; TM=Y; SS=M; 5.13
 454128; AL031259; Hs.367900; programmed cell death 2; zf-MYND; TM=M; SS=N; 5.13
 431322; AW970622; Hs.376626; gb:EST382704 MAGE resequences, MAGK Homo; none, none; 5.13
 444754; T83911; Hs.11881; transmembrane 4 superfamily member 4; none; TM=Y; SS=M; 5.12
 422867; L32137; Hs.1584; cartilage oligomeric matrix protein (pse; tsp_3, EGF; 5.12
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans; TM=Y; SS=M; 5.11
 436494; AA720997; Hs.128295; ESTs; none, CAP_GLY, HCO3_cotransp, Glyco_hydro_63, PH; 5.11
 419833; AA251131; Hs.220697; Homo sapiens tryptophanyl-tRNA synthetase; WHEP-TRS, tRNA-synt_1b, none; 5.10
 453387; AJ990741; Hs.252809; ESTs; Na_Ca_Ex, none; 5.07
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase; TM=M; SS=N; 5.07
 456906; AF117646; Hs.156637; Cas-Bir-M (murine) ectropic retroviral tr; zf-C3HC4, Cbl_N, Cbl_N2, Cbl_N3; TM=M; SS=N; 5.07
 438746; A1885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin, Guanylate_kin, PDZ, SH3; 5.07
 448520; AB002367; Hs.21355; doublecortin and CaM kinase-like 1; pkinase, DCX; TM=M; SS=N; 5.06
 413745; AW247252; Hs.75514; nucleoside phosphorylase; Map_PNP; 5.06
 407235; D20569; Hs.169407; SAC2 (suppressor of actin mutations 2, y; none, Ribosomal_S13, Galactosyl_T, Zip, adh_short, zf-C3HC4; 5.06
 421369; NM_005089; Hs.171909; U2 small nuclear ribonucleoprotein auxd; rm, zf-CCCH, lectin_c, integrin_B; TM=M; SS=N; 5.06
 412170; D16532; Hs.73729; very low density lipoprotein receptor; ldl_recept_a, ldl_recept_b, EGF; TM=M; SS=M; 5.06
 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3, ank; TM=M; SS=N; 5.05
 421109; L32832; Hs.101842; AT-binding transcription factor 1; HMG14_17, homeobox, zf-C2H2; TM=M; SS=M; 5.05
 453880; A1803168; Hs.135121; ESTs, Weakly similar to 138022 hypotheti; HSP70, none; 5.05
 431512; BE270734; Hs.2795; lactate dehydrogenase A; ldn, ldn_C, SH3, pkinase, UBA; TM=M; SS=N; 5.05
 435411; AW444619; Hs.138211; ESTs; none, pkinase; 5.04
 419088; A1538323; Hs.367688; Integrin, beta 8; Integrin_B, none; 5.04
 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease/APEX; Troponin, Exo_endo_phos, IQ; TM=M; SS=N; 5.04
 428376; AF119655; Hs.184011; pyrophosphatase (inorganic); Pyrophosphatase; TM=M; SS=N; 5.03
 413073; AL038165; Hs.75187; translocase of outer mitochondrial membr; MAS20, zf-A20, VPS9; TM=M; SS=M; 5.03
 436415; BE265254; Hs.343258; proliferation-associated 2G4, 38kD; Peptidase_M24, Furin-like, pkinase, Recep_L_domain, ehand; 5.01
 449674; AW444937; Hs.233482; ESTs; C2, PI-PLC-Y, PI-PLC-X, none; 5.01
 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to; ras, arf, TK; 5.01
 412133; U83460; Hs.104557; solute carrier family 31 (copper transpo; none; TM=Y; SS=N; 5.01
 446488; AB037782; Hs.15119; KIAA1361 protein; pkinase; 5.00
 449474; AA019344; Hs.2055; ubiquitin-activating enzyme E1 (A1S9T an; Thif, UBACT, pkinase, UCH-2, UCH-1, rm, zf-C2H2, zf-RanBP, G-patch; 5.00
 416365; U15131; Hs.79265; suppression of tumorigenicity 5; DENN, dDENN, uDENN; TM=M; SS=N; 5.00
 421351; AU076667; Hs.103755; receptor-interacting serine-threonine ki; CARD, pkinase; TM=M; SS=N; 4.99
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH, death, TNFR_c6, Acyl-CoA_hydro; 4.98
 442007; AA301116; Hs.142838; nucleolar phosphoprotein Nopp34; rm, IRK; 4.95
 441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 fis, clone NT; none, none; 4.95
 426310; NM_000909; Hs.169266; neuropeptide Y receptor Y1; 7tm_1; TM=Y; SS=M; 4.95
 457718; F18572; Hs.22978; ESTs, Weakly similar to ALU4_HUMAN ALU S; pkinase, pkinase; 4.94
 408805; H69912; Hs.48269; vaccinia related kinase 1; pkinase; TM=M; SS=N; 4.94
 427541; A1798983; Hs.375835; solute carrier family 35 (CAMP-sialic aci; none, none; 4.94
 452792; AB037765; Hs.30652; KIAA1344 protein; thiod; TM=M; SS=M; 4.93
 430713; AA351647; Hs.2642; eukaryotic translation elongation factor; GTP_EFTU, GTP_EFTU_D3, GTP_EFTU_D2; 4.93
 444838; AV651680; Hs.208558; ESTs; Integrin_A, FG-GAP, none; 4.93
 440516; S42303; Hs.161; cadherin 2, type 1, N-cadherin (neuronal; HNH, cadherin, Cadherin_C_term; TM=M; SS=N; 4.92
 421302; T34462; Hs.103291; neuritin; none; TM=M; SS=Y; 4.91
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisi; pkinase; TM=M; SS=N; 4.91
 408657; AA782601; Hs.378649; ESTs; B56, none; 4.91
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C, IMPDH_N, CBS, Integrin_B, Richn_B, lectin; 4.91
 421462; AF016495; Hs.104624; aquaporin 9; MIP; TM=Y; SS=M; 4.90
 424503; NM_002205; Hs.149609; Integrin, alpha 5 (fibronectin receptor; Integrin_A, FG-GAP; TM=Y; SS=N; 4.89

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- 438564; AA381553; Hs.198253; major histocompatibility complex, class ; Ig.MHC,II_alpha,none; 4.89
 427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Fizzled,catreticul,7tm_2,rm,PAP_assoc;TM=Y;SS=M; 4.88
 434521; NM_002287; Hs.3886; karyopherin alpha 3 (importin alpha 4); Armadillo_seg,IBB;TM=M;SS=N; 4.88
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; Ig;TM=Y;SS=M; 4.88
 424118; BE269041; Hs.140452; cargo selection protein (mannose 6 phosph; perilipin; 4.88
 410639; BE269047; Hs.65234; hypothetical protein FLJ20598; DEAD,helicase_C,PRK,ALP3;TM=M;SS=N; 4.87
 417089; H52280; Hs.18612; Homo sapiens cDNA: FLJ21909 fis, clone H; voltage_CLC,CBS,none; 4.86
 429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C; Phosphodiester,Somatomedin_B,Endonuclease,none; 4.86
 417666; AJ345001; Hs.82380; menage a trois 1 (CAK assembly factor); zf-C3HC4;TM=M;SS=N; 4.86
 453864; AW021407; Hs.21068; hypothetical protein; none,none; 4.85
 453082; H18835; Hs.31608; hypothetical protein FLJ20041; ion_trans;TM=Y;SS=M; 4.85
 413407; A1356293; Hs.75339; inositol polyphosphate phosphatase-like ; SH2,SAM,Exo_endo_phos;; 4.85
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA;; 4.85
 435652; NM_032388; Hs.334370; uncharacterized hypothalamus protein HBE; none;TM=M;SS=N; 4.84
 419355; AA428520; Hs.90061; progesterone binding protein; heme_1;TM=Y;SS=M; 4.83
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y;SS=N; 4.83
 409893; NM_000492; Hs.663; cystic fibrosis transmembrane conductance; ABC_tran,ABC_membrane,PRK,Bac_export_3;TM=Y;SS=N; 4.83
 425465; U18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-blind,pkinase_C,OPR;TM=M;SS=N; 4.82
 435232; NM_001262; Hs.4854; cyclin-dependent kinase inhibitor 2C (p1; ank;TM=M;SS=N; 4.81
 424490; AJ278018; Hs.55565; ankyrin repeat domain 3; ank,pkinase;TM=M;SS=N; 4.81
 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 4.81
 453354; W55946; Hs.234863; Homo sapiens cDNA FLJ12082 fis, clone HE; transmembrane4,none; 4.81
 450883; NM_001348; Hs.25619; death-associated protein kinase 3; pkinase;TM=M;SS=N; 4.79
 429736; AF125304; Hs.212680; tumor necrosis factor receptor superfamily; TNFR_c6;TM=M;SS=M; 4.79
 431183; NM_006855; Hs.250898; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept;TM=M;SS=M; 4.79
 409960; BE261944; Hs.355264; hexokinase 1; none,none; 4.78
 422795; AB033109; Hs.375610; KIAA1283 protein; 7tm_1,kazal,A2M,A2M_N;TM=Y;SS=M; 4.78
 423619; T48691; Hs.249159; adrenergic, alpha-2A-, receptor; 7tm_1,7tm_2;TM=Y;SS=M; 4.78
 429305; AF095727; Hs.287832; myelin protein zero-like 1; Ig,transmembrane4;TM=Y;SS=M; 4.78
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPC;TM=M;SS=N; 4.77
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none,none; 4.76
 444672; Z95636; Hs.11669; laminin, alpha 5; laminin_EGF,laminin_G,EGF,TNFR_c6,laminin_B,laminin_Nterm,metalthio,Tropomyosin,DUF164,p450;TM=M;SS=N; 4.76
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinas; ptk8;TM=M;SS=N; 4.75
 438330; AW4450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH,none; 4.75
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase;; 4.75
 411165; NM_000169; Hs.69089; galactosidase, alpha; Melibiase;; 4.75
 425548; AA890023; Hs.1906; prolactin receptor; In3;TM=Y;SS=M; 4.73
 434158; T86534; Hs.14372; ESTs; adenylatekinase,none; 4.73
 459035; AW291109; Hs.332563; ESTs, Weakly similar to T31611 hypothet; none,SH3,myosin_head,IQ; 4.73
 409012; AL117435; Hs.49725; DKFZP434I216 protein; PH,RhoGEF;TM=M;SS=M; 4.73
 434503; T96231; Hs.17762; ESTs; SH3,Sorb,none; 4.73
 446342; BE298665; Hs.14846; solute carrier family 7 (cationic amino ; none;TM=M;SS=N; 4.72
 427418; AA402587; Hs.356667; LAT1-3TM protein; none,none; 4.71
 449433; A1672096; Hs.9012; ESTs, Weakly similar to S26550 DNA-bind; Fizzled,Fz,Fizzled,Fz; 4.71
 418910; Z25821; Hs.89466; Homo sapiens, Similar to dodecenoyl-Coen; ECH; 4.70
 414907; X90725; Hs.77697; polo (Drosophila)-like kinase; Ribosomal_L37ae,pkinase,POLO_box,tRNA-synt_1b,dynamlin,dynamlin_2,GED,bZIP,M; 4.70
 442199; BE277633; Hs.372542; eltoposide-induced mRNA; none;TM=Y;SS=M; 4.69
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (tus; 7tm_1,7tm_2;TM=Y;SS=M; 4.69
 453922; AF053306; Hs.36708; budding uninhibited by benzimidazoles 1 ; none;; 4.69
 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domai; death,DED;; 4.68
 434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase;TM=M;SS=N; 4.68
 443323; BE560621; Hs.9222; estrogen receptor binding site associate; none;TM=M;SS=M; 4.68
 400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin receptor; Integrin_A,FG-GAP;TM=Y;SS=N; 4.68
 418838; AW385224; Hs.35198; ectonucleotide pyrophosphatase/phosphodi; Phosphodiester;TM=Y;SS=M; 4.67
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,Integrin_B;; 4.67
 425976; C75094; Hs.334514; NG22 protein; voltage_CLC;TM=Y;SS=M; 4.66
 407844; AW073716; Hs.8037; ESTs; transmembrane4,none; 4.66
 406656; AA010539; Hs.18912; unnamed protein product; zf-C2H2;; 4.66
 420311; AW445044; Hs.38207; Human DNA sequence from clone RP4-530115; none,none; 4.65
 404287; ; FGENESH predicted novel CUB-domain contax; none,none; 4.64
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; Ig,Rhabd_glycop;TM=Y;SS=M; 4.63
 426680; AA320160; Hs.171811; adenylate kinase 2; adenylatekinase;TM=M;SS=N; 4.63
 430397; AJ924533; Hs.105607; bicarbonate transporter related protein ; HCO3_cotransp;TM=Y;SS=N; 4.63
 447658; NM_003726; Hs.19126; src kinase-associated phosphoprotein of ; SH3,PH;TM=M;SS=N; 4.63
 414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain,PHD,PWWP,zf-MYND;TM=M;SS=N; 4.62
 429126; AW172356; Hs.99083; ESTs; 7tm_1,none; 4.61
 429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Fizzled,catreticul,7tm_2,rm,PAP_assoc;TM=Y;SS=M; 4.60
 409220; BE243323; Hs.51233; tumor necrosis factor receptor superfamily; TNFR_c6,death,Lipoprotein_5,TIL;TM=Y;SS=M; 4.60
 421921; H83363; Hs.355993; translocase of inner mitochondrial memb; zf-Tim10_DDP,ethand,CH,spectrin,serpin;TM=M;SS=N; 4.60
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 4.59
 400290; H18836; Hs.31608; hypothetical protein FLJ20041; none,Cys_knot; 4.59
 430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; ion_trans;TM=Y;SS=M; 4.59
 409645; A1142255; Hs.55498; geranylgeranyl diphosphate synthase 1; polyprenyl_synt;TM=M;SS=N; 4.59
 427373; AB007872; Hs.130760; myosin phosphatase, target subunit 2; ank;TM=M;SS=N; 4.58
 437212; A1765021; Hs.210775; ESTs; UDPGT,none; 4.58
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank,death,ZU5,EGF,Iringle,trypsin,Nebulin,LIM;; 4.57
 452069; AB028949; Hs.183994; KIAA1026 protein; Metallophos;TM=M;SS=N; 4.56
 416041; AA345547; Hs.53263; hypothetical protein FLJ13287; WD40;; 4.55
 434511; R28982; Hs.18106; ESTs; pkinase,Glyco_hydro_39; 4.55
 410174; AA306007; Hs.59461; DKFZP434C245 protein; none,DSPC; 4.55
 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase,RI01;TM=M;SS=N; 4.55
 451367; AA923729; Hs.25322; cell cycle related kinase; pkinase;TM=M;SS=N; 4.54

- 417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glycoprotein; LRR, LRRNT, LRRCT; TM=Y; SS=M; 4.54
 411296; BE207307; Hs.10114; growth suppressor 1; 2OG-Fell_Oxy; TM=M; SS=M; 4.53
 439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triph); Ham1p_like; TM=M; SS=N; 4.53
 431992; NM_002742; Hs.2891; protein kinase C, mu; pkinase, DAG_PE-bind, PH; TM=M; SS=M; 4.53
 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase, ICE_p10, ICE_p20; TM=M; SS=M; 4.53
 428005; AW302245; Hs.181390; casein kinase 1, gamma 2; pkinase; TM=M; SS=N; 4.52
 407775; NM_004914; Hs.38772; RAB36, member RAS oncogene family; ras, arf; TM=M; SS=N; 4.52
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 4.51
 447321; AW271217; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HE; none, none; 4.51
 405484; ; C3002124; glij12737280[ref]XP_006682.2; k; none; 4.50
 443605; H06865; Hs.134131; ESTs; ehand, lon, trans, none; 4.50
 431738; AW237726; Hs.288549; hypothetical protein FLJ14710; 7m_1, zf-C3HC4, fn3, SPRY, KRAB, zf-C2H2, rve, zf-B_box; TM=Y; SS=M; 4.50
 422112; BE540240; Hs.111783; Lsm1 protein; Sm, BAG; 4.49
 418869; AW516565; ; gbxxq01d05.x1 Soares_NHCcC_cervical_tumo; none, RasGAP, WW, IQ; 4.48
 447898; AW969638; Hs.112318; 6.2 kd protein; none, none; 4.48
 450607; AL050373; Hs.25213; hypothetical protein; SH3; TM=M; SS=N; 4.48
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell ; lg; TM=Y; SS=M; 4.48
 424823; NM_006226; Hs.153322; phospholipase C, epsilon; C2, PH, PI-PLC-Y, PI-PLC-X; TM=M; SS=N; 4.48
 426812; AF105365; Hs.172613; solute carrier family 12 (potassium/chlor); none; TM=Y; SS=N; 4.47
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, pkinase, Recep_L_domain, YLP; none; 4.47
 435815; Y15065; Hs.4975; potassium voltage-gated channel, KQT-like; lon, trans, KCNQ1_channel; TM=Y; SS=N; 4.47
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR, LY6, ET, PLA2_inh; 4.47
 428727; AF078847; Hs.78452; general transcription factor IIH, polypep; PHO4, LIM; TM=M; SS=N; 4.46
 412760; AW379030; Hs.41324; ESTs; Cbl_N, Cbl_N2, Cbl_N3, UBA, zf-C3HC4, none; 4.46
 409093; BE243834; Hs.50441; CGI-04 protein; Ribosomal_L37ae, pkinase, POLO_box, tRNA-syn_1b, dynamn, dynamn_2, GED, bZIP, M; 4.46
 434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase, ATP-sulfonylase, PRK, Thymidylate_kin; 4.46
 447434; R16890; Hs.137135; ESTs; pkinase, fn3, lg, pkinase, fn3; 4.45
 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none, SDF, sugar_tr; 4.45
 414108; AI267592; Hs.75761; SFRS protein kinase 1; ank, PH, Oxysterol_BP, pkinase; TM=M; SS=N; 4.44
 457001; J03258; Hs.2062; vitamin D (1,25-dihydroxyvitamin D3) re; hormone_rec, zf-C4, Metallothio_5; TM=M; SS=N; 4.44
 409686; AK000002; Hs.55879; Homo sapiens mRNA; cDNA DKFZp434L0827 (f; ABC_tran, ABC_membrane; TM=M; SS=M; 4.44
 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7m_3, none; 4.44
 436823; AW749865; Hs.117077; ESTs, Weakly similar to 138022 hypotheti; aa_permeases, zf-C2H2, KRAB, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, ODT, PI3_P14_kinase, FAT, FATC, BoIA, RUN, TFIIS; TM=M; SS=N; 4.44
 450505; NM_004572; Hs.25051; plakophilin 2; Armadillo_seg; TM=M; SS=N; 4.43
 437915; AI637993; Hs.202312; Homo sapiens clone N11 NTera2D1 teratoca; none, none; 4.43
 417412; X16896; Hs.82112; Interleukin 1 receptor, type I; lg, TIR; TM=M; SS=M; 4.43
 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 4.43
 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, ; inositol_P, lg; TM=M; SS=N; 4.43
 452124; AA454220; Hs.61170; ESTs; pkinase, none; 4.43
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) ; NDK, PH, Oxysterol_BP; 4.42
 416202; AW964492; Hs.169624; ESTs; none; TM=M; SS=N; 4.42
 441518; AW161697; Hs.294150; ESTs; Y_phosphatase, DSPc, none; 4.42
 441680; AW444598; Hs.7940; RAP1, GTP-GDP dissociation stimulator 1; Armadillo_seg; TM=M; SS=N; 4.42
 431429; AF072813; Hs.252831; reticulation 3; Reticulon, Fz, lg, Iringle, pkinase; TM=Y; SS=N; 4.42
 453870; AW385001; Hs.8042; Homo sapiens cDNA: FLJ23173 fis, clone L; FG-GAP, Integrin_A, NIF; 4.41
 421242; AW161386; Hs.13561; hypothetical protein MGC4692; none; NA; NA; 4.41
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none; TM=M; SS=N; 4.41
 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death, ZU5; 4.41
 432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY_C; TM=M; SS=N; 4.41
 413367; NM_006517; Hs.75317; solute carrier family 16 (monocarboxylic; sugar_tr; TM=Y; SS=N; 4.41
 458097; AW341135; Hs.58104; ESTs; none, SH3, PID; 4.40
 458248; BE407379; Hs.108082; ESTs, Weakly similar to T31636 hypotheti; C1q, Collagen; TM=M; SS=Y; 4.40
 427681; AB018263; Hs.284232; tumor necrosis factor receptor superfamily; death, TNFR_c6, PH, Xlink, RhoGEF, Metallothio_5; TM=M; SS=M; 4.40
 443693; AJ344782; Hs.9983; DnaJ (Hsp40) homolog, subfamily C, member; rm, DnaJ, TPR; TM=M; SS=N; 4.40
 437162; AW005505; Hs.5464; thyroid hormone receptor coactivating pr; bromodomain; TM=M; SS=N; 4.39
 453891; AB037751; Hs.301242; Homo sapiens mRNA full length insert cDN; none, none; 4.39
 442572; AI001922; Hs.135121; hypothetical protein FLJ22415; none, HSP70; 4.39
 427337; Z46223; Hs.176653; Fc fragment of IgG, low affinity IIb, r; lg; TM=Y; SS=M; 4.37
 445817; NM_003642; Hs.13340; histone acetyltransferase 1; none; TM=M; SS=N; 4.37
 444895; AJ674383; Hs.22891; solute carrier family 7 (cationic amino ; ASC, death, TNFR_c6; 4.37
 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo_seg; TM=M; SS=M; 4.37
 432106; N58323; Hs.269098; ESTs, Weakly similar to RETROVIRUS-RELAT; SH3, PDZ, Guanylate_kin, none; 4.37
 418283; S79895; Hs.83942; cathepsin K (pseudodysostosis); Peptidase_C1; 4.37
 445826; BE313754; Hs.13350; Homo sapiens mRNA; cDNA DKFZp586D0918 (f; lg, isp_1, ZU5, Nucleoside_tran; 4.37
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase; TM=Y; SS=N; 4.36
 400257; ; Hs.76366; ENSP00000000452-BAD protein (BCL-2 bindi; none; TM=M; SS=N; 4.36
 431476; BE612705; Hs.256697; histidine triad nucleotide-binding prote; HIT; 4.36
 416178; AI808527; Hs.192822; serologically defined breast cancer anti; none; TM=M; SS=N; 4.36
 456829; AW891965; Hs.367942; histone deacetylase 3; HSP90, HATPase_c, zf-C2H2, PHD; none; 4.36
 427716; L38951; Hs.180446; karyopherin (Importin) beta 1; Armadillo_seg, HEAT; TM=M; SS=N; 4.35
 425843; BE313280; Hs.159627; death associated protein 3; myb_DNA-binding, PAH, BAH, bromodomain, PHD, SET; TM=M; SS=N; 4.35
 420261; AW206093; Hs.748; fibroblast growth factor receptor 1 (fms; pkinase, lg, pkinase, lg, p450, SET, PWWP; 4.35
 445926; AF054284; Hs.334826; splicing factor 3b, subunit 1, 155kd; none; TM=M; SS=N; 4.35
 410726; AI623859; Hs.15936; ESTs; pkinase, pro_isomerase, none; 4.35
 433966; AW135357; Hs.192374; ESTs; HSP90, HATPase_c, UDG; 4.34
 433592; NM_004642; Hs.3438; deleted in oral cancer (mouse, homolog) ; none; TM=M; SS=N; 4.34
 437103; AW139408; Hs.152940; ESTs; Choline_kinase, none; 4.34
 410068; AI633888; Hs.58435; FYN-binding protein (FYB-120130); SH3; TM=M; SS=N; 4.34
 427349; AA360154; Hs.177415; Finkel-Biskids-Reilly murine sarcoma virus; ubiquitin; TM=M; SS=N; 4.33
 439807; AA376417; Hs.374608; hypothetical protein MGC5244; ; abhydrolase_2; TM=M; SS=M; 4.33
 453308; AW959731; Hs.323099; ESTs; none, pkinase, Activin_rec; 4.33
 424893; AW295112; Hs.153648; Homo sapiens cDNA FLJ13303 fis, clone OV; SAM; 4.33

- 444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-S; DSPc; TM=M;SS=N; 4.33
 429655; U48959; Hs.211582; myosin, light polypeptide kinase; pkinase,fn3,jg:none; 4.32
 409121; AA802256; Hs.78979; Golgi apparatus protein 1; cys_rich_FGFR:none; 4.32
 430280; AA361258; Hs.237868; Interleukin 7 receptor; fn3:none; 4.32
 423798; AF047033; Hs.132904; solute carrier family 4, sodium bicarbon; HCO3_cotransp; TM=Y;SS=M; 4.29
 425654; AB033022; Hs.158654; KIAA1195 protein; zf-C2H2; TM=M;SS=N; 4.29
 457500; NM_002759; Hs.274382; protein kinase, interferon-inducible dou; dsrm,pkinase; TM=M;SS=N; 4.29
 427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C:none; 4.29
 447191; NM_014521; Hs.17667; SH3-domain binding protein 4; SH3; TM=M;SS=N; 4.29
 408331; NM_007240; Hs.44229; dual specificity phosphatase 12; DSPc; TM=M;SS=N; 4.29
 441130; AI160734; Hs.267604; Homo sapiens PNAS-129 mRNA, complete cds; BTB,Kelch,K_tetra,DSPc; TM=M;SS=N; 4.28
 430057; AW450303; Hs.2534; bone morphogenetic protein receptor, typ; Activin_rec.pkinase; TM=Y;SS=M; 4.28
 430250; NM_016929; Hs.283021; chloride intracellular channel 5; none; TM=M;SS=N; 4.28
 406774; AW518383; Hs.177592; ribosomal protein, large, P1; 60s_ribosomal; 4.28
 413809; L25851; Hs.851; integrin, alpha E (antigen CD103, human ; vwa,integrin_A,FG-GAP; TM=M;SS=Y; 4.27
 443960; AI093577; Hs.255416; hypothetical protein FLJ21986; TTL; TM=M;SS=N; 4.27
 427378; BE515037; Hs.177556; melanoma antigen, family D, 1; MAGE; TM=M;SS=N; 4.27
 412204; AI125507; Hs.24937; ESTs; lg_rmm:none; 4.26
 439506; AI361238; Hs.41136; ESTs; MAM,pkinase,Nucleoplasm; none; 4.26
 451295; AI557212; Hs.17132; ESTs; Moderately similar to I54374 gene ; pkinase,DAG_PE-bind,pkinase_C,OPR:none; 4.26
 452488; N74921; Hs.184389; ESTs; none; TM=M;SS=N; 4.26
 450973; AF012072; Hs.25732; eukaryotic translation initiation factor; W2,MA3,MIF4G; TM=M;SS=N; 4.26
 452437; AA026237; Hs.181272; ESTs; eifhand,ion_trans:none; 4.26
 438204; AI589645; Hs.128690; ESTs; none; 7tm_1; 4.25
 424756; AW504657; Hs.152931; lamin B receptor; ERG4_ERG24,FKBP; TM=Y;SS=N; 4.25
 430570; AI417881; Hs.292464; ESTs; 7tm_2,Fz,Frizzled:none; 4.25
 445709; H02592; Hs.74280; ESTs; PDZ:none; 4.25
 428134; AA421773; Hs.161008; ESTs; Armadillo_seg:none; 4.24
 434149; Z43829; Hs.244624; hypothetical protein MGC5469; none; TM=M;SS=M; 4.24
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb_DNA-binding,THF_DHG_CYH,THF_DHG_C,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,M_xan_ur_permease,HCO3_cotransp; TM=M;SS=N; 4.24
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20; 4.24
 447818; W79940; Hs.355279; Homo sapiens clone 24670 mRNA sequence; none,pkinase; 4.24
 450684; AA872605; Hs.25333; interleukin 1 receptor, type II; lg; TM=Y;SS=M; 4.23
 435542; AA687376; Hs.351226; ESTs; SH3,jg,pkinase,PH_spectrin,RhoGEF:none; 4.23
 426224; BE085860; Hs.374468; karyopherin (importin) beta 2; Armadillo_seg,HEAT; TM=M;SS=N; 4.23
 413284; AU077055; Hs.289107; baculoviral IAP repeat-containing 2; zf-C3HC4,CARD,BIR,death,jg; TM=M;SS=N; 4.22
 421917; AB028943; Hs.109445; KIAA1020 protein; BTB,zf-C2H2,PI3_P14_kinase,PI3Ka; TM=M;SS=N; 4.22
 431239; AI039971; Hs.251216; hypothetical protein DKFZp434A196; SH2,ank,WH2; 4.22
 419685; W76083; Hs.134185; ESTs; none; TM=M;SS=N; 4.22
 431630; NM_002204; Hs.265829; Integrin, alpha 3 (antigen CD49C, alpha ; FG-GAP,Rhabd_glycop,integrin_A; TM=Y;SS=M; 4.22
 425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none; 4.21
 422219; AW978073; Hs.1010; regulator of mitotic spindle assembly 1; pkinase:none; 4.21
 450746; D82673; Hs.278589; general transcription factor II, t; none,SH3,PX; 4.21
 428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone L; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P14_kinase,FAT,FATC,BolA,RUN; TM=M;SS=N; 4.21
 416907; W60909; ; gbzd29g10.s1 Soares_fetal_heart_NbHH19W; ion_trans:none; 4.21
 411768; NM_013371; Hs.71979; interleukin 19; IL10; 4.21
 425262; D87119; Hs.155418; GS3955 protein; pkinase; 4.21
 430035; NM_003463; Hs.227777; protein tyrosine phosphatase type IVA, m; Y_phosphatase,DSPc; TM=M;SS=N; 4.21
 411789; AF245505; Hs.72157; Adican; lg_LRR,LRRNT,LRRCT; TM=M;SS=M; 4.15
 416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic; none:none; 4.14
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; lg,pkinase; TM=Y;SS=M; 4.13
 431745; AW972448; Hs.163425; Novel FGENESH predicted cadherin repeat ; none:none; 4.10
 416955; N26223; Hs.160436; MDAC1; none;NA;NA; 3.94
 426890; AA393167; Hs.41294; ESTs; none:none; 3.88
 442438; AA995998; Hs.370007; gb.os26b03.s1 NCL_CGAP_Kid5 Homo sapiens; none,DNA_pol_B,DNA_pol_B_exo; 3.86
 412314; AA825247; Hs.356084; downstream of: G protein-coupled receptor; 7tm_1; TM=Y;SS=M; 3.84
 448243; AW369771; Hs.367688; integrin, beta 8; integrin_B:none; 3.64
 439318; AW837046; Hs.6527; G protein-coupled receptor 58; 7tm_2,CytC_asm,GPS; TM=Y;SS=M; 3.61
 415999; AA172179; Hs.294029; ESTs; none:none; 3.60
 429466; M85835; Hs.12827; ESTs; none:none; 3.45
 407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none; TM=M;SS=Y; 3.34
 400517; ; lengstin; none; TM=M;SS=N; 3.17
 439180; AI393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.88
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.84
 414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigen; DAN; TM=M;SS=M; 2.81
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C; 2.70
 438167; R28363; Hs.24286; chemokine binding protein 2 (CCBP2), mRN; none; TM=Y;SS=M; 2.68
 418888; AU076801; Hs.89436; cadherin 17, LI cadherin (liver-intestin; cadherin; TM=Y;SS=M; 2.17

TABLE 23B

75	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
80	Accession:	Genbank accession numbers
	Pkey	CAT Number Accession
	409745	MH1944_5 B1030997 AA921874 AW188822 B1027862 A1347618 A1361453 A1088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 B1007625 B1027864 B1009100 B1006275 B1006270 B1031000 B1029884 B1006277 B1007627 B1006266 B1006991 B1006990 B1007763 B1007762 BG997377 AA150760 B10033518 B1027818 BG015789 B1033807 AA341445
	417886	1031334_1 AA210987 D57294 AA214584 AA207006 D56572
	438993	2580163_1 A1926361 AA834879 AA828995

418859 12789_14 AA229762 AA230035
416907 1112245_1 W60909 W61051 M78905 BG959483

TABLE 23C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
403362	8571772	Plus	64099-64260
404210	5006246	Plus	169926-170121
404287	2326514	Plus	53134-53281
405484	5922025	Plus	199214-199579,199672-199920,200262-20049
400517	9796686	Minus	49996-50346

TABLE 24A: 571 GENES UP-REGULATED IN HEAD AND NECK TUMORS COMPARED WITH NORMAL BODY TISSUES

Table 24A lists about 571 genes up-regulated in head and neck tumors compared with normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
ExAcon: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 70th percentile of AI for head and neck cancer samples vs. the 80th percentile of the AI for normal body tissues

Pkey	ExAcon	UnigeneID	Unigene Title	R1
421155	H87879	Hs.102267	lysyl oxidase	166.00
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	156.00
434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	80.00
438274	AJ918906	Hs.55080	ESTs	28.00
401486				121.00
446999	AA151520	Hs.334822	hypothetical protein MGC4485	126.00
423887	AL080207	Hs.134585	DKFZP434G232 protein	13.00
419569	AJ971651	Hs.91143	jagged 1 (Alagille syndrome)	98.00
428505	AL035481	Hs.2281	chromogranin B (secretogranin 1)	1.00
420602	AF060877	Hs.99236	regulator of G-protein signalling 20	35.00
445019	AI205540	Hs.281295	ESTs	93.00
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	270.62
449722	BE280074	Hs.23960	cyclin B1	9.81
423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	373.00
424086	AI351010	Hs.102267	lysyl oxidase	200.00
447078	AW885727	Hs.301570	ESTs	184.00
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	177.00
409506	NM_006153	Hs.54589	NCK adaptor protein 1	170.00
426471	M22440	Hs.170009	transforming growth factor, alpha	158.00
413268	AL039079	Hs.75256	regulator of G-protein signalling 1	155.00
419948	AB041035	Hs.93847	NADPH oxidase 4	140.00
451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	139.00
442875	BE623003	Hs.23625	Homo sapiens clone TCCTA00142 mRNA sequ	111.00
452795	AW392555	Hs.18878	hypothetical protein FLJ21620	109.00
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	106.00
416283	NM_005429	Hs.79141	vascular endothelial growth factor C	95.00
450221	AA328102	Hs.24641	cytoskeleton associated protein 2	92.00
449101	AA205847	Hs.23016	G protein-coupled receptor	92.00
442611	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	86.00
438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypotheti	85.68
414132	AI801235	Hs.48480	ESTs	85.00
447164	AF026941	Hs.17518	Homo sapiens cgl5 mRNA, partial sequence	83.00
402047	AK001921	Hs.169575	hypothetical protein MGC2550	80.00
414972	BE263782	Hs.77695	KIAA0008 gene product	74.00
452943	BE247449	Hs.31082	hypothetical protein FLJ10525	74.00
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	71.00
427099	AB032953	Hs.173560	odd Ozten-m homolog 2 (Drosophila, mous	70.19
449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	66.25
418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	66.00
415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	64.00
414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	63.00
432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	60.00
431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	58.00
411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	57.00
418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	57.00
438394	BE379623	Hs.27693	peptidylprolyl isomerase (cytoplasmic)-I	54.00
452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	54.00
423020	AA383092	Hs.1608	replication protein A3 (14kD)	49.00

	422426	W79117	Hs.58559	ESTs	49.00
	406747	AI925153	Hs.217493	annexin A2	46.00
	445828	F05802	Hs.81907	ESTs	46.00
5	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfamily	44.00
	452909	NM_015368	Hs.30985	pannexin 1	43.95
	432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, cholin	43.00
	458027	L49054	Hs.85195	myeloid leukemia factor 1	43.00
	443354	AW970672	Hs.9247	protein kinase, AMP-activated, alpha 1 c	43.00
10	416049	AI970536	Hs.16603	hypothetical protein FLJ13163	42.00
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	40.00
	433859	AW896758	Hs.273789	ESTs	38.00
	426753	T89832	Hs.170278	ESTs	37.00
	400792	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	36.00
	402034				35.00
15	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	34.00
	458424	AI084049	Hs.206761	ESTs	34.00
	435159	AA688879	Hs.116649	ESTs	33.00
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	32.00
	444361	W76027	Hs.23920	hypothetical protein FLJ11105	31.00
20	439128	AI949371	Hs.153089	ESTs	29.20
	420795	AA323037	Hs.128645	sorting nexin 16	28.00
	422505	AL120862	Hs.124165	ESTs	25.00
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	24.00
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	22.10
25	423035	AW449679	Hs.156739	Hsapiens XG mRNA (clone PEP11)	19.00
	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	19.00
	414869	AA157291	Hs.21479	ubiquitin 1	17.37
	453049	BE537217	Hs.30343	ESTs	16.00
30	417801	AA417383	Hs.82582	Integrin, beta-like 1 (with EGF-like rep	14.00
	435243	AW292886	Hs.261373	hypothetical protein dJ434O14.3	13.00
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	10.80
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	10.00
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	9.60
	414231	AI468004	Hs.278956	hypothetical protein FLJ12929	9.00
35	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	8.09
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	8.07
	439999	AA115811	Hs.6838	ras homolog gene family, member E	8.07
	417791	AW965339	Hs.111471	ESTs	8.04
	436486	AA742221	Hs.120633	ESTs	7.23
40	432731	R31178	Hs.287820	fibronectin 1	7.00
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	5.18
	435039	AW043921	Hs.130526	ESTs	5.00
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	4.25
45	457001	J03258	Hs.2062	vitamin D (1,25-dihydroxyvitamin D3) re	4.24
	450684	AA872605	Hs.25333	Interleukin 1 receptor, type II	3.74
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	3.19
	458531	AA367718	Hs.159083	ESTs	3.00
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	2.53
50	411388	X72925	Hs.69752	desmocollin 1	1.00
	419760	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	1.00
	429370	C19097	Hs.89709	glutamate-cysteine ligase, modifier subu	1.00
	429921	AA526911	Hs.82772	collagen, type XI, alpha 1	1.00
	449467	AW205006	Hs.197042	ESTs	1.00
55	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1.00
	453637	NM_002589	Hs.34073	BH-protocadherin (brain-heart)	1.00
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	517.00
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	616.00
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	226.00
60	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	278.00
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	56.11
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	264.00
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	124.00
	424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	1.00
65	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	1.00
	415511	AI732617	Hs.182362	ESTs	1.00
	406467				141.00
	422330	D30783	Hs.115263	epiregulin	98.00
	452461	N78223	Hs.108106	transcription factor	159.00
70	415542	R13474	Hs.290263	ESTs, Weakly similar to I38022 hypothei	1.00
	413324	V00571	Hs.75294	corticotropin releasing hormone	1.00
	431571	AW500486	Hs.180610	splicing factor proline/glutamine rich (7.60
	443211	AI128388	Hs.143655	ESTs	99.00
	451844	T61430		gb:yc08a03.s1 Stratagene lung (937210) H	1.00
	441877	AW273802	Hs.11340	hypothetical protein FLJ23047	3.00
75	439926	AW014875	Hs.137007	ESTs	2.79
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (f	94.00
	421103	AI625835	Hs.27104	Homo sapiens mRNA; cDNA DKFZp667D226 (fr	1.22
	448062	AW295923	Hs.255472	KIAA1843 protein	1.00
80	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.27
	421577	BE465451	Hs.105925	single-minded (Drosophila) homolog 1	1.00
	421187	NM_014721	Hs.102471	KIAA0680 gene product	5.00
	408908	BE296227	Hs.250822	serine/threonine kinase 15	89.00
	437214	BE092336		gb:LL2-BT0734-240400-072-A12 BT0734 Homo	1.00

	449773	R76294	Hs.302383	ESTs	1.00
	443054	A1745185	Hs.8939	yes-associated protein 65 kDa	90.00
	432097	X51730	Hs.2905	progesterone receptor	1.00
5	453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	0.38
	430184	AB013802	Hs.234790	contactin 5	1.00
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.23
	415025	AW207091	Hs.72307	ESTs	1.00
	416575	W02414	Hs.38383	ESTs	1.00
10	443171	BE281128	Hs.9030	TONDU	0.92
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	20.30
	400844				0.60
	409402	AF208234	Hs.695	cystatin B (stefin B)	1.96
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.38
15	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2.60
	400761				1.34
	436361	AA825814	Hs.149065	ESTs	0.92
	455812	BE042896	Hs.274848	ESTs	0.81
	447437	U07225	Hs.339	purinergic receptor P2Y, G-protein coupl	1.55
20	404148				0.77
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	1.00
	446619	AJ076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.47
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	3.92
	442994	AJ026718	Hs.16954	ESTs	0.40
25	415327	H22769		gbcm54c02.r1 Soares infant brain 1NIB H	0.47
	418624	AJ734080	Hs.104211	ESTs	1.90
	452850	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-in	0.54
	401747			Homo sapiens keratin 17 (KRT17),	7.22
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	5.10
30	418259	AA215404	Hs.137289	ESTs	1.28
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	8.13
	403381				21.00
	420923	AF097021	Hs.273321	differentially expressed in hematopoiet	0.00
	418216	AA662240	Hs.283099	AF15q14 protein	11.29
35	444649	AW207523	Hs.197628	ESTs	0.10
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	4.64
	402230				1.64
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.97
40	447334	AA515032	Hs.91109	ESTs	0.62
	432829	W60377	Hs.57772	ESTs	0.86
	418686	Z36830	Hs.87268	annexin A8	8.44
	421508	NM_004833	Hs.105115	absent in melanoma 2	2.68
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	2.22
45	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	78.00
	425721	AC002115	Hs.159309	uroplakin 1A	0.88
	420370	Y13645	Hs.97234	uroplakin 2	0.87
	417720	AA205625	Hs.208067	ESTs	5.83
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 (H.sa	1.07
	431753	X76029	Hs.2841	neuromedin U	7.00
50	402075				288.00
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	363.00
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.81
	405064				1.00
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	2.00
55	441233	AA972965	Hs.135568	ESTs	1.00
	456034	AW450979		gb:UH-BI3-ala-a-12-0-UI.s1 NCL CGAP_Su	1.23
	414221	AW450979		gb:UH-BI3-ala-a-12-0-UI.s1 NCL CGAP_Su	0.65
	412296	AW936233		gb:QV0-DT0020-090200-107-a06 DT0020 Homo	1.00
	405494				1.00
60	407189	AA598927		gb:ae37e03.s1 Gessler Wilms tumor Homo s	1.00
	403085				1.00
	408633	AW963372	Hs.46677	PRO2000 protein	2.46
	435257	AA677026	Hs.191217	ESTs	1.00
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00
65	445182	AW189787	Hs.147474	ESTs	0.50
	417275	X63578	Hs.295449	parvalbumin	1.00
	418406	X73501	Hs.84905	cytokeratin 20	1.00
	421110	AJ250717	Hs.1355	cathepsin E	1.00
	406081				2.13
70	449448	D60730	Hs.57471	ESTs	123.00
	451668	Z43948	Hs.326444	cartilage acidic protein 1	0.37
	408243	Y00787	Hs.624	Interleukin 8	3.35
	436246	AW450963	Hs.119991	ESTs	51.00
	440304	BE159984	Hs.125395	ESTs	1.00
75	402778				1.00
	406117				1.00
	406360				71.00
	435347	AW014873	Hs.116963	ESTs	1.00
	445550	A1242754	Hs.137306	ESTs	1.00
80	451359	H85334	Hs.336623	ESTs	1.00
	419559	Y07828	Hs.91096	ring finger protein	1.00
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	58.00
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00
	402901				0.85

5	414918	AI219207	Hs.72222	hypothetical protein FLJ13459	0.87
	417715	AW969587	Hs.86366	ESTs	5.12
	442577	AA292998	Hs.163900	ESTs	2.19
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	1.54
	426088	AF038007	Hs.166195	ATPase, Class I, type 8B, member 1	1.11
10	412610	X90908	Hs.74126	fatty acid binding protein 6, Ilal (gas	1.27
	414683	S78296	Hs.76888	hypothetical protein MGC12702	0.67
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	0.03
	403903				0.87
	405033				0.13
15	422282	AF019225	Hs.114309	apolipoprotein L	2.13
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.05
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.59
	430168	AW968343	Hs.24255	DKFZP434I1735 protein	1.69
	459702	AI204995			1.00
20	446082	AI274139	Hs.156452	ESTs	0.60
	400843				0.76
	417409	BE272506	Hs.82109	syndecan 1	1.78
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	1.20
	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	0.50
25	404875				0.80
	436293	AI601188	Hs.120910	ESTs	1.40
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.03
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	0.94
	404977			Insulin-like growth factor 2 (somatomedi	0.99
30	431347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	1.10
	413804	T64682		gb:yc48b02.r1 StrataGene liver (S37224)	0.85
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	1.20
	420876	AA918425	Hs.177744	ESTs	0.85
	422119	AI277829	Hs.111862	KIAA0590 gene product	0.71
35	400846			sortilin-related receptor, L(DLR class)	0.75
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	4.01
	430152	AB001325	Hs.234642	aquaporin 3	1.74
	402777				0.70
	417151	AA194055	Hs.293858	ESTs	0.99
40	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	1.48
	405034	AL035754	Hs.2474	toll-like receptor 1	1.00
	406671	AA129547	Hs.285754	mel proto-oncogene (hepatocyte growth fa	18.68
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.94
	453134	AA032211	Hs.118493	ESTs	0.70
45	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.19
	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUS protein d	0.25
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	2.74
	439780	AL109688		gb:Homo sapiens mRNA full length insert	3.07
	438315	R56795	Hs.82419	ESTs	0.65
50	418937	T71508	Hs.13861	ESTs, Weakly similar to T42383 probable	1.18
	444163	AI126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	0.85
	444444	AI148332	Hs.14855	ESTs	0.59
	407581	R48402	Hs.173508	P3ECSL	0.82
	433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA	0.92
55	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	0.62
	446024	AB040946	Hs.264227	KIAA1513 protein	0.92
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.42
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.68
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptiona	1.57
60	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	0.08
	446009	AI989885	Hs.231926	ESTs	1.00
	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	0.98
	415949	H10662	Hs.21691	ESTs	0.61
	420281	AI623693	Hs.191533	ESTs	7.01
65	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	0.72
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.21
	414792	BE314949	Hs.87128	hypothetical protein FLJ23309	0.99
	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	0.54
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	0.06
70	426900	AW163564	Hs.142375	ESTs	0.48
	414595	AA641726	Hs.289015	hypothetical protein MGC4171	0.83
	402305				0.89
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	0.04
	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	0.49
75	436608	AA628980	Hs.192371	down syndrome critical region protein DS	0.65
	423916	AW993496	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ	0.63
	405932				1.76
	401760				2.61
	452240	AI591147	Hs.61232	ESTs	453.00
80	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	1.04
	421373	AA808229	Hs.167771	ESTs	17.00
	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.16
	435099	AC004770	Hs.4755	flap structure-specific endonuclease 1	1.68
	422406	AF025441	Hs.116206	Opa-interacting protein 5	3.19
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.73
	453389	BE273648	Hs.32963	cadherin 6, type 2, K-cadherin (fetal ki	1.00
	454789	BE156314		gb:QV0-HT0367-150200-114-d02 HT0367 Homo	1.00

	434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	0.06
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	2.45
	418067	AI127958	Hs.83393	cystatin E/M	1.41
5	441801	AW242799	Hs.86366	ESTs	140.00
	423536	L22075	Hs.1666	guanine nucleotide binding protein (G pr	2.45
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	58.00
	400409	AF153341	Hs.283954	Homo sapiens winged helix/forkhead trans	1.17
	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	0.86
10	427587	BE348244	Hs.202628	ESTs, Weakly similar to I78885 serine/th	0.91
	451161	AA211329	Hs.26006	hypothetical protein FLJ10559	1.00
	453204	R10799	Hs.191990	ESTs	1.13
	437240	AA747537		gbnx85c05.s1 NCI_CGAP_GC81 Homo sapiens	1.00
	405531				0.92
15	440249	AI246590	Hs.337275	ESTs	1.32
	426783	Z19084	Hs.172210	MUF1 protein	1.17
	434192	AW387314	Hs.34371	ESTs	1.00
	407881	AW072003	Hs.40958	heparan sulfate (glucosamine) 3-O-sulfot	87.14
	402001				37.00
20	433967	AF113018	Hs.284302	PRO1621 protein	1.00
	451592	AI805416	Hs.213897	ESTs	10.00
	422170	AI791949	Hs.112432	anti-Mullerian hormone	0.67
	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFp564N1662 (f	1.00
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	0.99
25	441940	AW298115	Hs.128152	ESTs	0.88
	425048	H05468	Hs.164502	ESTs	0.33
	444008	BE544855	Hs.220756	ESTs, Weakly similar to SFRA_HUMAN SPLIC	1.01
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFp434B0425 (f	1.06
	423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	0.45
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	0.62
30	410348	AW182663	Hs.95469	ESTs	1.00
	419078	M93119	Hs.89584	insulinoma-associated 1	0.04
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.04
	441795	N58115	Hs.21137	AD024 protein	10.00
35	418583	AA604379	Hs.86211	hypothetical protein	1.22
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	106.67
	413385	M34455	Hs.840	indoleamine-pyrole 2,3 dioxygenase	2.30
	441495	AW294603	Hs.127039	ESTs	0.44
	417933	X02308	Hs.82962	thymidylate synthetase	2.48
40	412661	N32860	Hs.24611	ESTs, Weakly similar to I54374 gene NF2	1.00
	411880	AW872477		gbhm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	1.00
	417771	AA804698	Hs.82547	retinoic acid receptor responder (lazar	1.44
	430034	X60155	Hs.227767	zinc finger protein 41	1.00
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.87
45	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	0.54
	429257	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase	2.27
	417599	AA204688	Hs.136201	ESTs	1.01
	438366	AA805760	Hs.303567	ESTs	1.00
	438746	AI885815	Hs.184727	ESTs	1.47
50	409691	T89983	Hs.246042	Homo sapiens, clone MGC:5437, mRNA, comp	1.00
	408827	AW275730	Hs.254825	ESTs	1.00
	414735	BE468016	Hs.281904	ESTs	1.00
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	5.21
	412719	AW016610	Hs.129911	ESTs	494.00
55	417034	NM_006183	Hs.80962	neurotensin	1.00
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	23.36
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	6.98
	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin	7.50
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	9.77
60	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	445.00
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (raklines	13.93
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	12.77
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	45.00
	418663	AK001100	Hs.41690	desmocollin 3	10.89
65	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.29
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	0.88
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	38.31
	421948	L42583	Hs.334309	keratin 6A	36.81
	431846	BE019924	Hs.271580	uropod 1B	1.37
70	424098	AF077374	Hs.139322	small proline-rich protein 3	8.85
	453964	AI961486	Hs.12744	ESTs	0.40
	446856	AI814373	Hs.164175	ESTs	1.18
	443648	AI085377	Hs.143610	ESTs	2.15
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	4.39
75	431384	BE158000		gb:MR2-HT0377-150200-202-e03 HT0377 Homo	1.18
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	4.22
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	164.00
	417366	BE185269	Hs.1076	small proline-rich protein 1B (comifin)	9.85
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	5.59
80	441020	W79283	Hs.35962	ESTs	5.75
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.97
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	1.09
	444371	BE540274	Hs.239	forkhead box M1	2.44
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	8.39

5	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.53
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	1.67
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	2.30
	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.04
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.11
10	401781				11.07
	401780				9.54
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.62
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	1.12
	423834	AW959908	Hs.1690	heparin-binding growth factor binding pr	947.00
15	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.79
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	3.16
	440704	M69241	Hs.162	insulin-like growth factor binding prote	1.08
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	5.20
	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	2.53
20	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	72.00
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	19.96
	409103	AF251237	Hs.112208	XAGE-1 protein	0.47
	417542	J04129	Hs.82269	progesterone-associated endometrial prote	0.66
	428471	X57348	Hs.184510	stratifin	3.39
25	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	1.61
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.31
	451541	BE279383	Hs.26557	plakophilin 3	1.82
	418203	X54942	Hs.83758	CDC28 protein kinase 2	5.60
	447343	AA256641	Hs.238894	ESTs, Highly similar to S02392 alpha-2-m	2.78
30	437016	AU076916	Hs.5398	guanine monophosphate synthetase	2.01
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.18
	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	2.58
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.63
	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	2.25
35	410555	U92849	Hs.64311	a disintegrin and metalloproteinase doma	11.88
	430677	Z26317	Hs.94560	desmoglein 2	1.38
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.09
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.09
	422963	M79141	Hs.13234	ESTs	2.28
40	418462	BE001596	Hs.85268	Integrin, beta 4	1.40
	450832	AW970602	Hs.105421	ESTs	13.31
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	1.25
	409353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.89
	458933	AI638429	Hs.24763	RAN binding protein 1	1.54
45	439394	AA149250	Hs.56105	ESTs	3.89
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	1.77
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	1.52
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	3.11
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.10
50	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.84
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	0.61
	439606	W79123	Hs.58561	G protein-coupled receptor 87	303.00
	453884	AA355925	Hs.36232	KIAA0186 gene product	10.55
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.38
55	451743	AW074266	Hs.23071	ESTs	2.90
	413129	AF292100	Hs.104613	RP42 homolog	2.38
	406974	M57293		gb:Human parathyroid hormone-related pep	1.00
	413281	AA861271	Hs.222024	transcription factor BMAL2	5.92
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	2.18
60	416819	U77735	Hs.80205	plm-2 oncogene	1.01
	451320	AW118072	Hs.89981	diacylglycerol kinase, zeta (104kD)	0.67
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.19
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	2.55
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	3.06
65	413004	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	1.64
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	7.04
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	203.00
	435013	H91923	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33
	430337	M36707	Hs.239600	calmodulin-like 3	1.32
70	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	81.00
	448993	AI471630	Hs.8127	KIAA0144 gene product	1.03
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	28.00
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.24
	425245	AI751768	Hs.155314	KIAA0095 gene product	1.40
75	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.55
	420462	AF050147	Hs.97932	chondromodulin I precursor	1.00
	418678	NM_001327	Hs.167379	cancer/testis antigen	0.82
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00
	427335	AA448542	Hs.251677	G antigen 7B	0.91
80	409420	Z15008	Hs.54451	laminin, gamma 2 (niclin (100kD), kalini	6.53
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	1.35
	421917	AB028943	Hs.109445	KIAA1020 protein	0.94
	404440				38.57
	409582	R27430	Hs.271565	ESTs	3.19
80	415569	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	2.45
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.61
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	1.95

	408380	AF123050	Hs.44532	diubiquitin	7.23
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.35
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	0.81
5	446102	AW168067	Hs.252956	ESTs	1.03
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	137.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.91
	423761	NM_006194	Hs.132576	paired box gene 9	36.00
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	5.35
10	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	207.00
	440659	AF134160	Hs.7327	claudin 1	3.06
	434360	AW015415	Hs.127780	ESTs	3.89
	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	1.28
	438898	AI819863	Hs.106243	ESTs	1.73
	441553	AA281219	Hs.121296	ESTs	1.47
15	418379	AA218940	Hs.137516	fidgetin-like 1	40.42
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	14.25
	429413	NM_014058	Hs.201877	DESC1 protein	5.17
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.95
20	415380	F07953	Hs.16085	putative G-protein coupled receptor	0.18
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00
	446292	AF081497	Hs.279682	Rh type C glycoprotein	2.09
	429538	BE182592	Hs.11261	small proline-rich protein 2A	6.14
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00
25	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	44.00
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	149.00
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	127.00
	408572	AA055811	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	20.00
	404996				147.00
30	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regl	1.00
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	54.00
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor	139.00
	430563	AA481269	Hs.108660	ATP-binding cassette, sub-family C (CFTR	22.00
	438702	AI879064	Hs.54618	ESTs	1.00
35	444378	R41339	Hs.12569	ESTs	1.00
	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	41.00
	407839	AA045144	Hs.161566	ESTs	7.50
	439223	AW238299	Hs.250818	UL16 binding protein 2	3.39
40	409041	AB033025	Hs.50081	KIAA1199 protein	245.00
	429228	AI553633	Hs.337139	ESTs	10.89
	409757	NM_001898	Hs.123114	cystatin SN	3.19
	411089	AA456454	Hs.183418	cell division cycle 2-like 1 (PTSLRE pr	0.78
	436511	AA721252	Hs.291502	ESTs	0.23
45	449207	AL044222	Hs.23255	nucleoporin 155kD	1.68
	453331	AI240665	Hs.8895	ESTs	5.21
	409935	AW511413	Hs.278025	ESTs	0.75
	428969	AF120274	Hs.194689	artemin	1.17
	445443	AV653838	Hs.322971	ESTs	1.00
50	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	11.42
	401785				2.76
	412723	AA648459	Hs.335951	hypothetical protein AF301222	107.00
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	2.17
	405770				2.42
55	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	4.24
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	4.50
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.95
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	1.44
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	1.00
	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.33
60	453968	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	1.11
	427441	AA412605	Hs.178053	SPANX family, member C	5.00
	403478				0.78
	400842				0.16
	441525	AW241867	Hs.127728	ESTs	0.79
65	452865	AI924046	Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	1.50
	405646				1.05
	427260	AA663848		gb:ae70b06.s1 Stratagene schizo brain S1	0.79
	431413	AA504777	Hs.105293	ESTs	1.00
	401994				3.25
70	402420				0.05
	404298				0.64
	404927				88.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	0.96
	436961	AW375974	Hs.156704	ESTs	3.58
75	429563	BE619413	Hs.2437	eukaryotic translation initiation factor	0.92
	426087	AW564691	Hs.97053	ESTs	0.97
	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	0.66
	426897	AW976570	Hs.97387	ESTs	1.29
	443892	AI889572	Hs.134791	ESTs	1.00
80	413223	AI732182	Hs.191866	ESTs	0.79
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	1.51
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f	2.59
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	1.39
	420758	AW297536	Hs.33053	ESTs	0.89

	423816	AL031985	Hs.133034	hypothetical protein	1.00
	447534	AW953935	Hs.30837	ESTs	1.88
	451919	W05086	Hs.114256	ESTs, Weakly similar to I78885 serine/th	0.11
	409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell	0.92
5	403715				0.89
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	37.00
	436839	AA767346	Hs.291614	ESTs	1.00
10	413582	AW295647	Hs.71331	hypothetical protein MGC5350	59.00
	413573	AI733859	Hs.149089	ESTs	78.00
	430686	NM_001942	Hs.2633	desmoglein 1	127.08
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	1.00
	448243	AW369771	Hs.52620	integrin, beta 8	133.00
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	232.00
15	426427	M86699	Hs.169840	TTK protein kinase	66.00
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	148.00
	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	40.75
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	13.00
20	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	106.00
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	159.00
	415989	AI267700	Hs.317584	ESTs	196.00
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	32.44
	453160	AI263307	Hs.239884	H2B histone family, member L	7.00
25	409361	NM_006982	Hs.54416	sine oculis homeobox (Drosophila) homolo	4.13
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	45.00

TABLE 24B

30 Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accessions: Genbank accession numbers

	Pkey	CAT number	Accessions
35	411880	1263110_1	AW872477 BE088101 T05990
	412296	1288043_1	AW936233 AW936272
	413804	1390710_1	T64682 BE168190 BE168256
40	414221	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
	415327	1534137_1	BE011368 BE011362 BE011215 BE011365 BE011363
	427260	276598_1	H22769 R35182 Z43545 F05783 N92089 H71928
	431322	331543_1	AA663848 AA400100 AA401424
45	431384	33264_1	AW970622 AA503009 AA502998 AA502805 T92188
	432222	343347_1	BE158000 BE157999 H75671 H70965 C18895 BE386512 BE385815 BE390298 AI341995 BE074534 AA055592 AA132265 AI733757
	437214	434730_1	AA134504 BE145037 AA055887 BE070191 R66492 AW858018 AW858058 AW817057 AW862031 AW861688 AW862029 AW858805 AW858792
	437240	435139_1	AW862028 AW858017 AW819164 AW853698 AI522161 AW854789 AW817408 BE152005 AI732411 AA133084
50	438993	467651_1	AW862028 AW858017 AW819164 AW853698 AI522161 AW854789 AW817408 BE152005 AI732411 AA133084
	439780	47673_1	BE092336 BE092259 BE092497 BE092051 AA746882 AI336378
	444163	593658_1	AA747537 BE089068 BE089070
	451844	888230_1	AA828995 AA834879 AI926361
55	453823	982526_1	AL109688 R23665 R26576
	454789	1234742_1	AI126098 AI184746 AI148521
	456034	142696_1	T61430 AI820546 AI821336
			AL137967 BE064160 BE064186
			BE156314 BE156316 AW820750
			AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
			BE011368 BE011362 BE011215 BE011365 BE011363

TABLE 24C

60 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
70	400751	7331445	Minus	35395-35533
	400842	1927148	Plus	90462-90673
	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
	400844	9188605	Plus	24746-24872,25035-25204
	400846	9188605	Plus	39310-39474
75	401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
80	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
	401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
	402001	9501818	Plus	68052-68223

	402034	7684482	Minus	86227-86451
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
	402230	9966312	Minus	29782-29932
5	402305	7328724	Plus	40832-41362
	402420	9796339	Plus	129750-129919
	402777	9588235	Plus	126786-126948
	402778	9588235	Plus	128560-128702
	402901	8894222	Minus	175426-175667
10	403085	8954241	Plus	165035-165334,165420-165713
	403381	9438267	Minus	26009-26178
	403478	9958258	Plus	116458-116564
	403715	7239669	Plus	85128-85292
	403903	7710671	Minus	101165-102597
15	404148	9863703	Plus	78218-78418,79571-79709
	404298	9944263	Minus	73591-73723
	404440	7528051	Plus	80430-81581
	404875	9801324	Plus	96588-96732,97722-97831
	404927	7342002	Plus	68690-69563
20	404977	3738341	Minus	43081-43229
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405033	7107731	Minus	142358-142546
	405064	7658416	Plus	81207-81416
	405494	8050952	Minus	70284-70518
25	405531	9665194	Plus	35602-35803
	405846	4914350	Plus	741-969
	405770	2735037	Plus	61057-62075
	405932	7767812	Minus	123525-123713
	406081	9123861	Minus	38115-38691
30	406117	9142932	Plus	54304-54584
	406360	9256107	Minus	7513-7673
	406467	9795551	Plus	182212-182958

35 TABLE 25A: 691 genes upregulated in head and neck cancer relative to normal body tissues

40 Table 25A lists about 691 genes upregulated in head and neck cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion transporter). Certain predicted protein domains are noted.

45 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Prod.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 50 R1 85th percentile of head and neck cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Prod.Domains; R1

55 422168; AA586894; Hs.112408; S100 calcium-binding protein A7 (psorias; ehand,S_100;TM=M;SS=N; 46.25
 408522; AJ541214; Hs.46320; Small proline-rich protein SPRK [human; none;Cornifin; 40.37
 417366; BE185289; Hs.1076; small proline-rich protein 1B (cornifin); Cornifin;TM=M;SS=N; 38.94
 401781; ; Target Exon; filament;TM=M;SS=N; 29.74
 422158; L10343; Hs.112341; protease inhibitor 3, skin-derived (SKAL; wap;TM=M;SS=Y; 29.54
 401780; ; NM_005557; Homo sapiens keratin 16 (foca; filament,filament; 28.58
 60 424098; AF077374; Hs.139322; small proline-rich protein 3; Cornifin;TM=M;SS=N; 28.55
 421948; L42583; Hs.334309; keratin 6A; filament,RhoGAP,DUF286,bZIP,Tropomyosin,tubulin,DUF164,TBCA,Collagen;TM=M;SS=N; 25.74
 428471; X57348; Hs.184510; stratifin; 14-3-3;TM=M;SS=N; 23.65
 417079; U65690; Hs.81134; Interleukin 1 receptor antagonist; IL1; 21.02
 421574; AJ000152; Hs.105924; defensin, beta 2; Defensin_beta;TM=M;SS=M; 20.83
 65 409601; AF237621; Hs.80828; keratin 1 (epidermolytic hyperkeratosis); filament,bZIP,UvrD-helicase,TBCA;TM=M;SS=N; 20.72
 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR_LY8,toxin,Activin_rec;TM=M;SS=Y; 19.63
 446292; AF081497; Hs.278682; Rh type C glycoprotein; Ammonium_transp,FacCD;TM=Y;SS=M; 19.53
 420783; AI659838; Hs.99923; lectin, galactoside-binding, soluble, 7; Gal-bind_lectin;TM=M;SS=N; 19.12
 70 407788; BE514982; Hs.38991; S100 calcium-binding protein A2; ehand,S_100,S_100,ehand; 17.93
 416091; AF295370; Hs.283082; defensin, beta 3; Defensin_beta;TM=M;SS=M; 17.63
 431211; M86849; Hs.323733; gap junction protein, beta 2, 25kD (conn; connexin;TM=Y;SS=M; 16.94
 429259; AA420450; Hs.380088; Plakophilin; none,none; 14.92
 417515; L24203; Hs.82237; ataxia-telangiectasia group D-associated; zf-B_box,zf-UBR1;TM=M;SS=N; 14.75
 75 423634; AW959908; Hs.1690; heparin-binding growth factor binding pr; none;TM=M;SS=M; 14.45
 418007; M13509; Hs.83169; matrix metalloproteinase 1 (interstitial; hemopexin,Peptidase_M10,Atsacin_PG_binding_1; 13.02
 409632; W74001; Hs.55279; serine (or cysteine) proteinase inhibitor; serpin; 12.82
 406621; X57809; Hs.181125; immunoglobulin lambda locus; Ig,HSP70,Ppx-GppA;TM=M;SS=N; 12.81
 431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placenta; cadherin,Cadherin_C_term;TM=Y;SS=M; 12.45
 446921; AB012113; Hs.16530; small inducible cytokine subfamily A (C); IL8; 11.71
 80 401760; ; Target Exon; none,bromodomain; 11.68
 407839; AA045144; Hs.161566; ESTs; cadherin,cadherin; 11.65
 454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member ; aldedh; 11.56
 444781; NM_014400; Hs.11950; GPI-anchored metastasis-associated protor; UPAR_LY6,lactamase_B; 11.31

- 453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1); none; TM=Y; SS=M; 11.03
 424012; AW368377; Hs.137569; tumor protein 63 kDa with strong homolog; SAM, P53; TM=M; SS=N; 10.75
 430630; AW269920; Hs.2621; cystatin A (slefin A); cystatin; TM=M; SS=N; 10.58
 419693; AA133749; Hs.301350; FXD domain-containing ion transport reg; ATP1G1_PLM_MAT8; TM=Y; SS=M; 10.30
 411274; NM_002776; Hs.69423; kallikrein 10; trypsin; TM=M; SS=N; 10.25
 441633; AW958544; Hs.112242; normal mucosa of esophagus specific 1; none; TM=M; SS=M; 9.84
 446989; AK001898; Hs.16740; hypothetical protein FLJ11038; none; TM=Y; SS=N; 9.74
 402075; ; ENSP00000251056; Plasma membrane calcium; none; 9.50
 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen; TM=M; SS=M; 9.50
 431009; BE149782; Hs.48956; gap junction protein, beta 6 (connexin 3; connexin; TM=Y; SS=M; 9.48
 439310; AF086120; Hs.102793; ESTs; casein_kappa, kinase, ig, none; 9.43
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2; TM=M; SS=N; 9.33
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member; aldedh; TM=M; SS=M; 9.14
 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (230/240kD); ehand, spectrin, GAS2, SH3, Plectin, RA, Xylose_isom, FlitD, bZIP, Tropomyosin, Myc-
 15 LZ, M, ldn_C, CH, AIP3; TM=M; SS=N; 9.12
 451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg; TM=M; SS=N; 9.11
 425650; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgaris antigen; cadherin; TM=M; SS=M; 8.66
 452240; AI591147; Hs.61232; ESTs; none, none; 8.57
 429228; AI553633; Hs.356828; ESTs; none, none; 8.46
 20 400289; X07820; Hs.2258; matrix metalloproteinase 10 (stromalysin; hemopexin, Peptidase_M10, Astacin; 8.44
 425071; NM_013989; Hs.154424; deiodinase, lodothyronine, type II; T4_deiodinase; TM=M; SS=Y; 8.15
 407242; M18728; ; gb:Human nonspecific crossreacting anti; ig; TM=M; SS=M; 8.05
 407944; R34008; Hs.239727; desmocollin 2; cadherin, Cadherin_C_term, Hanta_G2; TM=Y; SS=M; 7.90
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin; 7.82
 25 428330; L22524; Hs.2256; matrix metalloproteinase 7 (matrilysin; ; Peptidase_M10; 7.82
 417308; H60720; Hs.81892; KIAA0101 gene product; none; TM=M; SS=N; 7.77
 413753; U17760; Hs.75517; laminin, beta 3 (nicein (125kD), kalinin; laminin_EGF, laminin_Nterm; 7.76
 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolysis; Kunitz_BPT1, fn3, vwa, Collagen, beta-lactamase; TM=M; SS=M; 7.71
 430686; NM_001942; Hs.2633; desmoglein 1; cadherin, Cadherin_C_term; TM=Y; SS=M; 7.69
 30 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha, arf; TM=M; SS=N; 7.54
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino; ;
 aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, P13_P14_kinase, FAT, FATC, BolA, RUN; TM=M; SS=N; 7.53
 418663; AK001100; Hs.41690; desmocollin 3; cadherin, Cadherin_C_term, none; 7.30
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGFb_propeptide, TGF-beta, none; 7.28
 35 429211; AF052693; Hs.198249; gap junction protein, beta 5 (connexin 3; connexin; TM=Y; SS=M; 7.26
 412719; AW016610; Hs.816; ESTs; none, none; 7.17
 446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin; ; Osteopontin; 7.10
 423961; D13666; Hs.136348; periostin (OSF-2os); Fascidin; TM=M; SS=M; 7.09
 427668; AI791495; Hs.180142; calmodulin-like skin protein (CLSP); ehand; TM=M; SS=N; 7.08
 40 431846; BE019924; Hs.271580; uroplakin 1B; transmembrana4; TM=Y; SS=M; 7.06
 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage; hemopexin, Peptidase_M10; TM=M; SS=M; 7.03
 401747; ; ; Homo sapiens keratin 17 (KRT17); none, bromodomain; 7.01
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT, none; 6.98
 429002; AW248439; Hs.2340; junction plakoglobin; Armadillo_seg; TM=M; SS=N; 6.96
 432239; X81334; Hs.2936; matrix metalloproteinase 13 (collagenase; hemopexin, Peptidase_M10; 6.87
 417715; AW969587; Hs.86366; ESTs; none, none; 6.72
 422440; NM_004812; Hs.116724; aldo-keto reductase family 1, member B10; aldo_ket_red, ROK; TM=M; SS=N; 6.50
 429359; W00482; Hs.2399; matrix metalloproteinase 14 (membrane-In; hemopexin, Peptidase_M10; TM=M; SS=M; 6.39
 50 418844; M62982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase, PLAT; TM=M; SS=N; 6.38
 420039; NM_004605; Hs.376147; sulfotransferase family, cytosolic, 2B; ; Sulfotransfer; 6.38
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB, DNA_topoisolV, HATPase_c; 6.35
 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3, ank; TM=M; SS=N; 6.30
 409420; Z15008; Hs.54451; laminin, gamma 2 (nicein (100kD), kalini; laminin_B, laminin_EGF; 6.28
 424364; AW383226; Hs.163834; ESTs, Weakly similar to G01763 atrophin-; ras; TM=M; SS=N; 6.27
 55 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8; TM=M; SS=Y; 6.23
 424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2, hemopexin, Peptidase_M10; 6.22
 443428; AF098158; Hs.9329; chromosome 20 open reading frame 1; none; TM=M; SS=N; 6.21
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabq; 7tm_3; TM=Y; SS=M; 6.12
 423017; AW178761; Hs.227948; serine (or cysteine) proteinase inhibitor; serpin; 6.08
 60 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis, clone NT; none, none; 6.08
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_I; TM=Y; SS=M; 6.04
 439335; AA742697; Hs.62492; NM_052863; Homo sapiens secretoglobin, fa; none; 5.81
 439223; AW238299; Hs.250618; UL16 binding protein 2; ldl_recept_a, PKD, MHC, I; TM=M; SS=Y; 5.77
 65 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR, Lysyl_oxidase; TM=M; SS=M; 5.72
 454098; W27953; Hs.217493; Plakophilin; none, none; 5.71
 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevt; WD40; TM=M; SS=N; 5.70
 435505; AF200492; Hs.211238; Interleukin-1 homolog 1; IL1; TM=M; SS=N; 5.69
 406685; M18728; ; gb:Human nonspecific crossreacting anti; ig; TM=M; SS=M; 5.67
 430280; AA361258; Hs.237868; interleukin 7 receptor; fn3, none; 5.63
 70 430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none; TM=Y; SS=M; 5.61
 449722; BE280074; Hs.23960; cyclin B1; cyclin, cyclin_C; TM=M; SS=N; 5.61
 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1; TM=Y; SS=M; 5.60
 452862; AW378065; Hs.8687; ADAMTS2 (a disintegrin-like and metallo; Pep_M12B_propep, tsp_1, Reprolysin, none; 5.58
 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene family; ras, ABC, tran, arf; TM=M; SS=M; 5.57
 75 411296; BE207307; Hs.10114; growth suppressor 1; 2OG-Fell_Oxy; TM=M; SS=M; 5.55
 433848; AF095719; Hs.93764; carboxypeptidase A4; Zn_carbOpept, Propep_M14; 5.54
 416819; U77735; Hs.80205; pim-2 oncogene; pkinase; 5.48
 428368; BE440042; Hs.83326; matrix metalloproteinase 3 (stromelysin; hemopexin, Peptidase_M10, Astacin; 5.47
 452747; BE153955; Hs.61460; Ig superfamily receptor LNIR; ig, Rhabd_glycop; TM=Y; SS=M; 5.46
 80 444946; AW139205; Hs.156457; hypothetical protein FLJ22408; abhydrolase, abhydrolase_2; TM=Y; SS=M; 5.42
 413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cyr; IL8; 5.35
 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 5.28
 418462; BE001596; Hs.85266; integrin, beta 4; fn3, integrin_B, Catx-beta, EGF; TM=M; SS=M; 5.26

- 429554; NM_012275; Hs.207224; Interleukin 1, delta; IL1; TM=M; SS=N; 5.14
 421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN; HIN; TM=M; SS=N; 5.13
 439979; AW600291; Hs.6823; hypothetical protein FLJ10430; none; TM=M; SS=N; 5.11
 427099; AB032953; Hs.173560; odd Oz/ten-m homolog 2 (Drosophila, mous; NHL; TM=M; SS=N; 5.11
 426227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cy; IL8; TM=M; SS=Y; 5.08
 436396; AI683487; Hs.152213; wingless-type MMTV integration site famt; wnt; none; 5.07
 406690; M29540; Hs.220529; carcinoembryonic antigen-related cell ad; ig; TM=M; SS=M; 5.05
 453905; NM_002314; Hs.36566; LIM domain kinase 1; pkinase; LIM; PDZ; z1-PARP; TM=M; SS=N; 5.04
 414035; Y00630; Hs.75716; serine (or cysteine) proteinase inhibitor; serpin; 5.00
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fts, clone PL; HLJ1, death, TNFR_c6, Acyl-CoA_hydro; 4.96
 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK; TM=M; SS=N; 4.93
 412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like (rabkines; kinesin; Tropomyosin; TM=M; SS=N; 4.92
 445537; AJ245671; Hs.12844; EGF-like domain, multiple 6; EGF; MAM; 4.91
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfamily; 60s_ribosomal; Ribosomal_L10, TNFR_c6, DEAD; 4.90
 436553; AW407157; Hs.181125; immunoglobulin lambda locus; ig; HSP70, Ppx-GppA; TM=M; SS=N; 4.89
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none; none; 4.84
 430024; AI808780; Hs.227730; integrin, alpha 6; Integrin_A, FG-GAP; TM=Y; SS=M; 4.81
 439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_HUMAN DEATH; none; none; 4.80
 444371; BE540274; Hs.239; forkhead box M1; Fork_head; TM=M; SS=N; 4.75
 428582; BE336699; Hs.185055; BENE protein; none; TM=Y; SS=M; 4.74
 419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; DSPc; 4.69
 431630; NM_002204; Hs.265829; Integrin, alpha 3 (antigen CD49C, alpha; FG-GAP, Rhabd_glycop, Integrin_A; TM=Y; SS=M; 4.69
 422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypept; none; pkinase; fn3; ig; 4.68
 418067; AJ127958; Hs.83393; cystatin E/M; cystatin; 4.66
 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringla, trypsin, plasmin; 4.64
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; LIM; PDZ; pkinase; 4.62
 410418; D31382; Hs.63325; transmembrane protease, serine 4; k1_recept_a, trypsin; TM=Y; SS=M; 4.60
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen, COL1, TSPN, laminin, G, CorA; 4.60
 438113; AJ467908; Hs.8882; ESTs; 7tm_1; none; 4.60
 418140; BE613836; Hs.83551; microfibrillar-associated protein 2; none; TM=M; SS=M; 4.57
 408380; AF123050; Hs.44532; diubiquitin; ubiquitin; TM=M; SS=N; 4.55
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin, ABC_tran, ABC_membrane, GTP_EFTU; TM=M; SS=M; 4.50
 425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin; hemopexin, Peptidase_M10; 4.50
 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domain; death, DED; 4.49
 408482; NM_000676; Hs.45743; adenosine A2b receptor; 7tm_1; TM=Y; SS=M; 4.48
 414168; AW888941; Hs.75789; N-myc downstream regulated; DEAD, helicase C, rrm, Ndr, Cys_knot, TIL, vwa, vwc, vwd, IQ, RIIa, abhydrolase, TGF-beta, DUF139, TPR, DSPc, tsp_1, Ribosomal_S21, rvp; TM=M; SS=N; 4.47
 416178; AI808527; Hs.192822; serologically defined breast cancer anti; none; TM=M; SS=N; 4.47
 411789; AF245505; Hs.72157; Adican; ig, LRR, LRRNT, LRRCT; TM=M; SS=M; 4.47
 414561; AJ064613; Hs.195155; Homo sapiens amino acid transport system; Aa_trans; TM=Y; SS=N; 4.47
 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR; TM=M; SS=N; 4.45
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6, ET, PLA2_inh; 4.43
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase, DSPc; TM=M; SS=N; 4.42
 409041; AB033025; Hs.50081; Hypothetical protein, XP_051860 (KIAA119; none; TM=M; SS=M; 4.41
 406908; Z25437; ; gb: H.sapiens protein-tyrosine kinase gene; none; none; 4.40
 450701; H39960; Hs.288467; hypothetical protein XP_098151 (leucine; none; LRRCT, LRR; 4.40
 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2, SH3, pkinase; TM=M; SS=N; 4.38
 429500; X78565; Hs.289114; hexabrachion (tenascin C, cytotactin); EGF, fn3, fibrinogen_C, toxin_2, Keratin_B2; TM=M; SS=Y; 4.38
 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2, STAT, STAT_bind, STAT_prot; TM=M; SS=N; 4.32
 423725; AJ403108; Hs.132127; hypothetical protein LOC57822; none; TM=M; SS=N; 4.32
 411573; AB029000; Hs.70823; KIAA1077 protein; Sulfatase; TM=M; SS=N; 4.31
 408243; Y00787; Hs.624; Interleukin 8; HLJ, PAS, IL8; TM=M; SS=N; 4.31
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none; none; 4.30
 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC; none; 4.29
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys, ig, FAD_Synth, kdh, kdh_C, pkinase; 4.29
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig; TM=Y; SS=M; 4.29
 404996; ; Target Exon; Peptidase_C1; TM=M; SS=M; 4.29
 416539; Y07909; Hs.79368; epithelial membrane protein 1; PMP22_Claudin, oxidored_g5_N; TM=Y; SS=M; 4.28
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromosome; ABC_tran, M, SMC_N, SMC_C, DUF164; none; 4.25
 421532; AW138207; Hs.146170; hypothetical protein FLJ22969; Armadillo_seg, HEAT; TM=M; SS=N; 4.25
 424503; NM_002205; Hs.149609; Integrin, alpha 5 (fibronectin receptor; Integrin_A, FG-GAP; TM=Y; SS=N; 4.24
 414809; AA346699; Hs.77356; transferrin receptor (p90, CD71); PA; TM=Y; SS=N; 4.24
 439720; AJ935202; Hs.31181; Homo sapiens cDNA: FLJ23230 fts, clone C; none, SDF_sugar_tr; 4.23
 437044; AL035864; Hs.69517; differentially expressed in Fanconi's an; none; TM=M; SS=M; 4.23
 409956; AW103364; Hs.727; Inhibin, beta A (activin A, activin AB a; TGF-beta, TGFb_propeptide, Tub; 4.20
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA, ABC_tran, CoaE; TM=M; SS=N; 4.20
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK; TM=M; SS=Y; 4.19
 407137; T97307; ; gb: ye53h05.s1 Soares fetal liver spleen; GDA1_CD39; none; 4.18
 419235; AW470411; Hs.288433; neurotrimin; none; none; 4.18
 410290; AA402307; Hs.322844; hypothetical protein DKFZp664A176; Sema, PSI, TIG, Integrin_B; TM=Y; SS=M; 4.18
 456906; AF117646; Hs.156637; Cas-Br-M (murine) ectropic retroviral tr; zf-C3HC4, Cbl_N, Cbl_N2, Cbl_N3; TM=M; SS=N; 4.17
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked mot; NUDIX; TM=M; SS=M; 4.17
 400288; X06258; Hs.149609; Integrin, alpha 5 (fibronectin receptor; Integrin_A, FG-GAP; TM=Y; SS=N; 4.14
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase; TM=M; SS=N; 4.13
 455417; AK001058; Hs.12680; a disintegrin-like and metalloprotease w; tsp_1, Reprolysin, Pep_M12B_propep; none; 4.12
 433895; AJ287912; Hs.3628; mitogen-activated protein kinase kinase; pkinase, zf-CA, CNH, ERM; TM=M; SS=N; 4.12
 424490; AJ278016; Hs.55565; ankryrin repeat domain 3; ank, pkinase; TM=M; SS=N; 4.09
 419121; AA374372; Hs.89626; parathyroid hormone-like hormone; none; none; 4.08
 416602; NM_006159; Hs.367895; Protein kinase C-binding protein NELL2; EGF, vwc, TSPN; 4.07
 424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm_1; TM=Y; SS=N; 4.07
 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase; TM=M; SS=N; 4.06
 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase; TM=M; SS=N; 4.03
 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema, PSI, Integrin_B; TM=Y; SS=N; 4.02

- 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS; 4.02
 413186; AU077141; Hs.374548; solute carrier family 16 (monocarboxylic; sugar_tr; TM=Y; SS=M; 4.01
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 4.01
 406905; Z25424; ; gbr.H.sapiens protein-serine/threonine ki; none, none; 3.98
 450375; AA009647; Hs.352537; a disintegrin and metalloproteinase domain; Reprolysin, Pep_M12B_propep, disintegrin, Reprolysin, Pep_M12B_propep, disintegrin; 3.98
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase; 3.96
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, rec; ITAM; TM=Y; SS=M; 3.95
 425849; AJ000512; Hs.296323; serum/glucocorticoid regulated kinase; pkinase, pkinase_C; TM=M; SS=M; 3.95
 417433; BE270266; Hs.82128; ST4 oncofetal trophoblast glycoprotein; LRR, LRRNT, LRRCT; TM=Y; SS=M; 3.93
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily; SRP14, TNFR_c6; 3.93
 407792; AI077715; Hs.39384; putative secreted ligand homologous to f; none; TM=M; SS=Y; 3.91
 424441; X14850; Hs.147097; H2A histone family, member X; histone, CBFD_NFYB_HMF; 3.91
 415989; AI267700; Hs.351201; ESTs; none, none; 3.90
 423189; M59371; Hs.171596; EphA2; fn3, pkinase, SAM, EPH_1bd; TM=Y; SS=M; 3.90
 443859; NM_013409; Hs.9914; follistatin; kazal; 3.89
 429612; AF062649; Hs.252587; pituitary tumor-transforming 1; none; 3.89
 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death, ZU5; 3.88
 450684; AA872605; Hs.25333; interleukin 1 receptor, type II; ig; TM=Y; SS=M; 3.88
 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1, pkinase; TM=M; SS=N; 3.86
 413441; AI929374; Hs.75367; Src-like-adaptor; SH2, SH3; TM=M; SS=N; 3.84
 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1; TIMP, pkinase, DAG, PE-blind, RBD; 3.83
 436291; BE568452; Hs.344037; protein regulator of cytokinesis 1; none; TM=M; SS=N; 3.82
 417512; X76534; Hs.82226; glycoprotein (transmembrane) nmby; PKD; TM=Y; SS=M; 3.81
 427647; W19744; Hs.180059; Homo sapiens cDNA FLJ20653 fis, clone KA; none, pkinase; 3.80
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none; TM=M; SS=Y; 3.80
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HE; Nucleoside_tra2, none; 3.80
 430378; Z29572; Hs.2556; tumor necrosis factor receptor superfamily; IL2; 3.79
 428157; AI738719; Hs.198427; hexokinase 2; hexokinase, hexokinase2, none; 3.78
 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD, helicase_C, CARD; TM=M; SS=N; 3.78
 417720; AA205625; Hs.208067; ESTs; none, none; 3.77
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, pkinase, Recep_L_domain, YLP, none; 3.77
 449029; M28989; Hs.22891; solute carrier family 7 (cationic amino; aa_permeases; TM=Y; SS=M; 3.76
 413436; AF238083; Hs.58051; sphingosine kinase 1; DAGK; TM=M; SS=N; 3.75
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated; ig, ITAM, Zn_c1us; TM=Y; SS=M; 3.74
 413281; AA861271; Hs.222024; transcription factor BMAL2; HLH, PAS; 3.74
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-con; UQ_con; TM=M; SS=N; 3.74
 431890; X17033; Hs.271986; Integrin, alpha 2 (CD49B, alpha 2 subunit; vwa, integrin_A, FG-GAP; TM=Y; SS=M; 3.74
 424118; BE269041; Hs.140452; cargo selection protein (mannose 6 phosph; pentilin; 3.73
 426471; M22440; Hs.170009; transforming growth factor, alpha; EGF; TM=M; SS=M; 3.72
 422487; AJ010901; Hs.198267; mucin 4, tracheobronchial; EGF, vwd, AMOP; 3.72
 450125; AA005418; Hs.158186; ESTs; CIDE-N, 7tm_1, none; 3.71
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIIb, r; ig; TM=Y; SS=M; 3.70
 444006; BE395085; Hs.334762; type I transmembrane protein Fn14; Idl_recept_a, PKD, MHC; TM=M; SS=Y; 3.70
 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none, SDF, sugar_tr; 3.70
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3; TM=M; SS=N; 3.69
 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-t; fn3, Y_phosphatase, carb_anhydrase; TM=Y; SS=M; 3.68
 443759; BE390832; Hs.134729; FYXD domain-containing ion transport reg; ATP1G1_PLM_MATB; TM=Y; SS=M; 3.68
 452344; AI264357; Hs.55405; hypothetical protein MGC16212; Sulfate_transp, STAS; 3.68
 439625; AF066453; Hs.58611; ESTs; Fork_head, glycolytic_enzy, Na_sulph_symp; 3.66
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1; TM=Y; SS=M; 3.66
 452363; AI582743; Hs.94593; Homo sapiens, Similar to complement comp; SH3, PH, RhoGEF; TM=M; SS=N; 3.64
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (i; SH3, PH, RhoGEF; TM=M; SS=N; 3.64
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos; TM=M; SS=M; 3.64
 438707; U08239; Hs.5326; amino acid system N transporter 2; porcu; ACAT, MBOAT; TM=Y; SS=M; 3.64
 422596; AF063611; Hs.118633; 2'-5'-oligoadenylate synthetase-like; ubiquitin; 3.63
 449318; AW236021; Hs.78531; Homo sapiens, Similar to RIKEN cDNA 5730; none; TM=M; SS=N; 3.62
 438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin, Guanylate_kin, PDZ, SH3; 3.62
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT; TM=M; SS=Y; 3.62
 452699; AI826645; Hs.211534; ESTs; ArfGap, PH, ank, Guanylate_kin, PDZ, SH3; 3.60
 407634; AW016569; Hs.136414; UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc; Galactosyl_T; TM=M; SS=Y; 3.59
 423575; C18863; Hs.163443; intron of perostin (OSF-2os); Fasciclin, none; 3.59
 421391; AW304350; Hs.191958; immunoglobulin superfamily receptor tran; ig, none; 3.58
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig, pkinase; TM=Y; SS=M; 3.58
 419912; AF249745; Hs.6066; Rho guanine nucleotide exchange factor (i; SH3, PH, RhoGEF; TM=M; SS=N; 3.58
 431457; NM_012211; Hs.256297; Integrin, alpha 11; FG-GAP, vwa; TM=Y; SS=M; 3.57
 430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; ion_trans; TM=Y; SS=M; 3.55
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none; TM=Y; SS=M; 3.55
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog (E. coli Ra; none; 3.53
 426500; NM_014638; Hs.170156; KIAA0450 gene product; C2, PI-PLC-Y; TM=M; SS=N; 3.53
 429556; AW139399; Hs.314807; ESTs; none; TM=M; SS=N; 3.52
 449101; AA205847; Hs.23016; G protein-coupled receptor; 7tm_1; TM=Y; SS=M; 3.52
 432636; AA304864; Hs.278562; claudin 7; PMP22_Claudin; TM=Y; SS=M; 3.51
 433470; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none; TM=Y; SS=M; 3.51
 452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, sub; ABC_tran, ABC_membrane, SRP54, Thymidylate_kin; TM=Y; SS=M; 3.49
 425566; AW162943; Hs.250618; UL16 binding protein 2; Idl_recept_a, PKD, MHC; TM=M; SS=Y; 3.48
 402447; ; C1000201.gij204416[gb]AAA02527.1 (L0519; none; TM=Y; SS=M; 3.48
 431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept; TM=M; SS=M; 3.48
 448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A receptor, Neur_chan_LBD, Neur_chan_memb; TM=Y; SS=M; 3.48
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kd, chr; SH3, TPR; TM=M; SS=N; 3.48
 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease (APEX; Troponin, Exo_endo_phos, IQ; TM=M; SS=N; 3.47
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese; 3.44
 446051; BE048061; Hs.37054; ephrin-A3; Ephrin_A_deamin, dsrmz-alpha; 3.43
 418641; BE243136; Hs.86947; a disintegrin and metalloproteinase domain; disintegrin, Reprolysin, Pep_M12B_propep, EGF; TM=Y; SS=M; 3.42

- 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,Integrin_B; 3.42
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-assoc; kinesin; TM=M;SS=N; 3.42
 430044; AA464510; Hs.152812; ESTs; none,none; 3.42
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN; 3.39
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7m_1; TM=Y;SS=M; 3.39
 428293; BE250944; Hs.183556; solute carrier family 1 (neutral amino a; eIF6,SDF; TM=M;SS=N; 3.39
 443646; A085377; Hs.143610; ESTs; Fork_head,none; 3.39
 418869; AW516565; ; gb:xxq01d05.x1 Soares_NHCEC_cervical_tumo; none,RasGAP,WW,IQ; 3.38
 432179; X75208; Hs.2913; EphB3; EPH_lbd,fn3,pkinase,SAM; TM=Y;SS=M; 3.38
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell; lg; TM=Y;SS=M; 3.38
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE; 3.37
 408716; A1567839; Hs.151714; Homo sapiens mRNA for KIAA1769 protein; ; UvrD-helicase,RNB,Runt; TM=M;SS=N; 3.37
 457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metallothio_5; TM=M;SS=N; 3.37
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevis; CDC45; TM=M;SS=N; 3.37
 412817; AF146074; Hs.108660; ATP-binding cassette, sub-family C (CFTR; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU; TM=M;SS=M; 3.36
 400298; AA032279; Hs.61635; six transmembrane epithelial antigen of; none; TM=Y;SS=N; 3.35
 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3; 3.33
 400261; ; Hs.1802; Eos Control; Ig,MHC_II_beta; TM=Y;SS=M; 3.33
 410024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3; TM=M;SS=N; 3.32
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none,lactin_c; 3.32
 416065; BE267931; Hs.78996; proliferating cell nuclear antigen; PCNA,PCNA_C; TM=M;SS=N; 3.31
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg,UQ_con,none; 3.31
 426840; BE244217; Hs.172690; diacylglycerol kinase, alpha (80kD); eifhand,DAG_PE-bind,DAGKa,DAGKc,DC1; TM=M;SS=N; 3.31
 434419; AL040606; Hs.296938; dual specificity phosphatase 7; DSPc; TM=M;SS=N; 3.31
 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase,RIO1; TM=M;SS=N; 3.31
 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4; TM=Y;SS=M; 3.31
 421373; AF038461; Hs.136574; arachidonate 12-lipoxygenase, 12R type; lipoxygenase,PLAT; TM=M;SS=N; 3.30
 421733; AL119871; Hs.1420; fibroblast growth factor receptor 3 (act; lg,pkinase; TM=Y;SS=M; 3.30
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49,EGF,Ig,Neuregulin; TM=M;SS=N; 3.28
 423778; Y09267; Hs.132821; flavin containing monooxygenase 2; FMO-like,pyr_redox; TM=Y;SS=M; 3.28
 426457; AW894667; Hs.380138; chimerin (chimaerin) 1; DAG_PE-bind,RhoGAP,SH2; TM=M;SS=N; 3.28
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none; TM=Y;SS=M; 3.27
 431886; L77964; Hs.271980; mitogen-activated protein kinase 6; pkinase; TM=M;SS=N; 3.27
 430397; A1924533; Hs.105607; bicarbonate transporter related protein ; HCO3_cotransp; TM=Y;SS=N; 3.27
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic; PI3_P14_kinase,FAT,FATC; TM=M;SS=N; 3.26
 446006; NM_004403; Hs.13530; deafness, autosomal dominant 5; none; TM=M;SS=M; 3.26
 444783; AK001468; Hs.62180; anillin (Drosophila Scraps homolog), act; PH,none; 3.25
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7m_2; TM=Y;SS=M; 3.25
 405932; ; C15000305; g13806122[gb]AAC69198.1 (AF0; ras; TM=M;SS=N; 3.25
 400205; ; Hs.81848; NM_006265; Homo sapiens RAD21 (S. pombe); DUF173; 3.25
 432874; W94322; Hs.279651; melanoma inhibitory activity; SH3; TM=M;SS=Y; 3.24
 412942; AL120344; Hs.75074; mitogen-activated protein kinase-activat; pkinase; TM=M;SS=N; 3.23
 435472; AW972330; Hs.283022; triggering receptor expressed on myeloid; lg; TM=M;SS=M; 3.22
 439285; AL133916; Hs.47860; hypothetical protein FLJ20093; lg,pkinase,LRR,LRRNT,LRRCT,none; 3.22
 410434; AF051152; Hs.63868; toll-like receptor 2; LRR,LRRCT,TIR; TM=M;SS=M; 3.22
 427318; AF186081; Hs.175783; zinc transporter; Zip; TM=Y;SS=M; 3.22
 436075; BE090176; Hs.179902; transporter-like protein; none; TM=Y;SS=M; 3.22
 428698; AA852773; Hs.334838; KIAA1866 protein; none; NA;NA; 3.22
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M;SS=N; 3.22
 415149; X12451; Hs.78056; cathepsin L; Peptidase_C1; 3.21
 423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase,PBD; TM=M;SS=N; 3.21
 424518; L29472; Hs.1802; major histocompatibility complex, class ; lg,MHC_II_beta; TM=Y;SS=M; 3.20
 438564; AA381553; Hs.198253; major histocompatibility complex, class ; lg,MHC_II_alpha,none; 3.20
 456181; L36463; Hs.1030; ras inhibitor; RA,SH2,VPS9; TM=M;SS=N; 3.20
 418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase ; pkinase,CNH; TM=M;SS=N; 3.19
 440682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyc1in,bZIP; TM=M;SS=N; 3.18
 415010; NM_004203; Hs.77783; membrane-associated tyrosine- and threon; ank,pkinase,UPF0073; 3.16
 419216; AU076718; Hs.164021; small inducible cytokine subfamily B (Cy; IL8; 3.16
 450737; AW007152; Hs.63325; transmembrane protease, serine 4; trypsin_lid_recept_a,none; 3.16
 426395; BE151985; Hs.355669; hypothetical protein FLJ23316; pkinase,none; 3.15
 412939; AW411491; Hs.75069; eukaryotic translation elongation factor; none,none; 3.15
 433376; A1249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20; 3.15
 410668; BE379794; Hs.159651; hypothetical protein; death,TNFR_c6; TM=Y;SS=M; 3.15
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC; TM=Y;SS=N; 3.15
 432251; AW972983; Hs.232165; polycythemia rubra vera 1; cell surface ; none; TM=M;SS=M; 3.15
 407844; AW073716; Hs.8037; ESTs; transmembrane4,none; 3.14
 408634; AW407254; Hs.356216; calmodulin 2 (phosphorylase kinase, del; none,none; 3.14
 423061; A1290473; Hs.44807; ESTs; Integrin_B,Sema,PSI,TIG,none; 3.14
 438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ; 3.13
 431236; AV656840; Hs.285115; Interleukin 13 receptor, alpha 1; fn3; TM=Y;SS=M; 3.13
 425394; AA356730; Hs.323949; kangal 1 (suppression of tumorigenicity ; transmembrane4,none; 3.13
 429336; AB005038; Hs.199270; cytochrome P450, subfamily XXVIB (25-hy; p450; 3.13
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; lg,Isodh,Ribosomal_L6,F-box; TM=Y;SS=M; 3.13
 429305; AF095727; Hs.287832; myelin protein zero-like 1; lg,transmembrane4; TM=Y;SS=M; 3.12
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase; TM=M;SS=N; 3.12
 417386; AL037228; Hs.301957; D123 gene product; NUDIX_secY,E1_dehydrog,transket_pyr; TM=Y;SS=M; 3.11
 419138; UA8508; Hs.89631; ryanodine receptor 1 (skeletal); ion_trans,SPRY,RYDR_TPR,RyR,MIR; TM=Y;SS=N; 3.11
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-I; AAA,NB-ARC,PAAD_DAPIN;NA;NA; 3.10
 406467; ; Target Exon; eifhand,Acyltransferase,none; 3.10
 422956; BE545072; Hs.122579; ECT2 protein (Epithelial cell transform; BRCT,RhoGEF; TM=M;SS=N; 3.10
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazarot; none,none; 3.09
 437016; AU076916; Hs.5398; guanine monophosphate synthetase; PHD,SET,zf-COXC,EGF,ank,notch,WW,FCH,GATase,GMP_synth_C,Occludin,YEATS,metalothio,EB,heme_1,RCC1,ZZ,FeThRed_A,ENTH,Band_41,HECT; TM=M;SS=N; 3.09

- 441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3,none; 3.09
 416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic; none,none; 3.09
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans;TM=Y;SS=M; 3.09
 426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M;SS=N; 3.08
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; PSS;TM=Y;SS=M; 3.08
 402233; ; NM_030760; Homo sapiens endothelial diff; 7tm_1;TM=Y;SS=M; 3.07
 430066; AI929659; Hs.237825; signal recognition particle 72kD; TPR,AIRC,SAICAR_synth; 3.07
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 3.06
 434263; N34895; Hs.79187; ESTs; Ig,none; 3.06
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none;TM=M;SS=Y; 3.05
 408378; U42387; Hs.54426; pancreatic polypeptide receptor 1; 7tm_1;TM=Y;SS=M; 3.05
 410165; BE560228; Hs.71869; apoptosis-associated speck-like protein; PAAD,DAPIN,CARD;TM=M;SS=N; 3.05
 440270; NM_015986; Hs.7120; cytokine receptor-like molecule 9; fn3; 3.05
 449003; X76342; Hs.389; alcohol dehydrogenase 7 (class IV), mu alpha; adh_zinc;TM=M;SS=N; 3.05
 420189; AW296380; Hs.95821; osteoclast stimulating factor 1; SH3,ank; 3.05
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain; SH2; 3.05
 421541; NM_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C;TM=M;SS=N; 3.04
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4,LIM;TM=M;SS=N; 3.03
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb_DNA-binding,THF_DHG_CYH,THF_DHG_CYH_C,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,M,xan_ur_permease,HCO3_cotransp;TM=M;SS=N; 3.03
 449048; Z45051; Hs.22920; similar to S68401 (cattle) glucose induc; Lamp;TM=M;SS=M; 3.03
 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; none;TM=Y;SS=M; 3.02
 442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequ; K_tetra,DUF51,none; 3.02
 436576; AI458213; Hs.77542; ESTs; 7tm_1,DnaJ; 3.02
 446269; AW263155; Hs.14559; hypothetical protein FLJ10540; none;TM=M;SS=N; 3.02
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm_1,7tm_2;TM=Y;SS=M; 3.01
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cyr, IL8;TM=M;SS=Y; 3.00
 421267; BE314724; Hs.103081; ribosomal protein S6 kinase, 70kD, polyp; pkinase,pkinase_C;TM=M;SS=N; 3.00
 409705; M37762; Hs.56023; brain-derived neurotrophic factor; NGF; 2.99
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory su; CDK5_activator,none; 2.99
 430696; AA531276; Hs.59509; ESTs; pkinase,PP2C,none; 2.98
 418299; AA279530; Hs.83968; Integrin, beta 2 (antigen CD18 (p95), ly; integrin_B,EGF,PSI;TM=Y;SS=M; 2.97
 410026; AI912061; Hs.55016; hypothetical protein FLJ21935; none,none; 2.97
 448733; NM_005629; Hs.187958; solute carrier family 6 (neurotransmitte; SNF;TM=Y;SS=N; 2.97
 432562; BE531048; Hs.278422; DKFZP586G1122 protein; zf-C2H2;TM=M;SS=N; 2.97
 453035; AW581943; Hs.334; Rho guanine nucleotide exchange factor (none,none; 2.97
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none,spectrin,SH3,PH,CH; 2.97
 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 lis, clone CO; pkinase,Furin-like,Recep_L_domain,none; 2.96
 441389; AF134838; Hs.7835; endocytic receptor (macrophage mannose r; fn2,lectin_c;TM=Y;SS=M; 2.95
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (C; MIF,sugar_tr,none; 2.94
 427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 lis, clone L; 7tm_1,none; 2.94
 402558; ; C1000201.g12044161g1b|AA02627.1 (L0519; none;TM=Y;SS=M; 2.94
 425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member, death, TNFR_c6;TM=Y;SS=M; 2.94
 442080; AW444761; Hs.72901; ESTs; ank; 2.94
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;SS=N; 2.93
 444809; BE207568; Hs.208219; oculostanin; transmembrane4;TM=Y;SS=N; 2.93
 449843; R85337; Hs.24030; solute carrier family 31 (copper transpo; none;TM=Y;SS=M; 2.93
 416110; Z42262; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,Integrin_B;TM=Y;SS=M; 2.93
 453768; BE382670; Hs.198511; Homo sapiens mRNA; cDNA DKFZp7611177 (fr; arf,G-alpha,none; 2.92
 414825; X06370; Hs.77432; epidermal growth factor receptor (avian; Furin-like,pkinase,Recep_L_domain;TM=M;SS=M; 2.92
 421429; NM_014922; Hs.104305; death effector filament-forming Ced-4-like; LRR,PAAD,DAPIN,AAA,CARD,NB-ARC;NA;NA; 2.92
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 2.91
 451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M;SS=N; 2.91
 422127; AW504286; Hs.112049; SET binding factor 1; dDENN,DENN,GRAM,PH; 2.91
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=M; 2.90
 430451; AA836472; Hs.297939; cathepsin B; Peptidase_C1,pro_isomerase; 2.90
 424046; AF027866; Hs.138202; serine (or cysteine) proteinase inhibitor; serpin;TM=M;SS=N; 2.89
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal_L37ae,pkinase,POLO_box,IRNA-synt_1b,dynamin,dynamin_2,GED,bZIP,M; 2.89
 429619; AL120751; Hs.211568; eukaryotic translation initiation factor; none,none; 2.89
 413879; AA132961; Hs.212533; Homo sapiens cDNA: FLJ22572 lis, clone H; none,none; 2.89
 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related; SH2,SH3,pkinase;TM=M;SS=N; 2.89
 422610; AF153820; Hs.1547; potassium inwardly-rectifying channel, s; IRK;TM=Y;SS=N; 2.89
 405556; ; homeodomain-interacting protein kinase 3; trypsin;TM=M;SS=N; 2.89
 423804; AW403448; Hs.1706; interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M;SS=N; 2.89
 425262; D87119; Hs.155418; GS3955 protein; pkinase; 2.88
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A); NDK,PH,Oxysterol_BP; 2.88
 452888; AW955454; Hs.30942; ephrin-B2; Ephrin,fn2;TM=Y;SS=M; 2.88
 414703; BE243877; Hs.380063; ATPase, Na+ transporting, beta 3 polypep; Na_K-ATPase;TM=Y;SS=M; 2.87
 444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2,none; 2.86
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affi; SDF;TM=Y;SS=M; 2.86
 458039; AA835884; Hs.130685; leukotriene b4 receptor (chemokine recep; CIDE-N,none; 2.86
 434417; AL110157; Hs.3843; Homo sapiens mRNA; cDNA DKFZp586F2224 (f; DSPc,none; 2.86
 425802; Y14838; chemokine-like receptor 1; 7tm_1,none; 2.86
 403112; ; Target Exon; ehfand,C2,PH,PI-PLC-Y,PI-PLC-X; 2.86
 435563; AF210317; Hs.95497; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;SS=N; 2.85
 442117; AW664964; Hs.128899; ESTs; hypothetical protein for IMAGE; 447; none,none; 2.84
 457819; AA057484; Hs.35406; FLJ20522 Hypothetical protein FLJ20522; none,none; 2.84
 456629; AW891965; Hs.367942; histone deacetylase 3; HSP90,HATPase_c,zf-C2H2,PHD,none; 2.83
 408873; AL046017; Hs.356216; calmodulin 2 (phosphorylase kinase, delt; none,none; 2.83
 446947; AF146747; Hs.232165; polycythemia rubra vera 1; cell surface; none;TM=M;SS=M; 2.83
 448386; AB037750; Hs.21061; KIAA1329 protein; PKD,BNR;TM=Y;SS=M; 2.82
 427857; AL133017; Hs.288679; hypothetical protein FLJ22865; myosin_head,IQ,zf-MYND;TM=M;SS=M; 2.82
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC;TM=Y;SS=M; 2.82

- 459707; AA631362; Hs.120866; gb:np86b01.s1 NCI_CGAP_Thy1 Homo sapiens; 7tm_1:none; 2.82
- 422699; BE410590; Hs.119257; ems1 sequence (mammary tumor and squamous); SH3,HS1_rep;TM=M;SS=N; 2.82
- 438108; AA471795; Hs.287776; vanilloid receptor-related osmotically s; ank,lon,trans;TM=Y;SS=N; 2.82
- 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin,fn3,Y_phosphatase;TM=M;SS=N; 2.82
- 5 448595; AB014544; Hs.21572; KIAA0644 gene product; LRR,LRRCT;TM=Y;SS=M; 2.81
- 423596; BE247600; Hs.377966; ESTs; 7tm_1;TM=Y;SS=M; 2.81
- 412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanese,DSPT; 2.81
- 414198; AW505308; Hs.75812; phosphoenolpyruvate carboxykinase 2 (mit); PEPCK; 2.81
- 436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 2.81
- 10 432314; AA533447; Hs.285173; ESTs; Xlink:none; 2.81
- 416207; NM_014745; Hs.79077; Homo sapiens, clone MGC:2908, mRNA, comp; none;TM=Y;SS=M; 2.80
- 446985; AL038704; Hs.156827; ESTs, Weakly similar to ALU1_HUMAN ALU S; SAM,SH3,HS1_rep; 2.80
- 428023; AL038843; Hs.374530; Homo sapiens cDNA; FLJ23602 fis, clone L;
- 15 ea_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P14_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 2.80
- 432886; BE159028; Hs.279704; chromatin accessibility complex 1; none;TM=M;SS=N; 2.80
- 426006; RA9031; Hs.22627; ESTs; pkinase,TBC; 2.79
- 414217; AJ309298; Hs.279898; Homo sapiens cDNA; FLJ23165 fis, clone L; none;NA;NA; 2.79
- 411165; NM_000169; Hs.69089; galactosidase, alpha; Melibiose; 2.79
- 20 450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypothet; ABC_tran,ABC_membrane,Ig,MHC_I_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 2.78
- 424291; AL120051; Hs.144700; ephrin-B1; Ephrin;TM=Y;SS=M; 2.78
- 421448; AF033850; Hs.104519; phospholipase D2; PH,PLDc,PX;TM=M;SS=N; 2.78
- 410226; AJ831958; Hs.61053; hypothetical protein; SH3,TPR;TM=M;SS=N; 2.78
- 433535; AF111106; Hs.3382; protein phosphatase 4, regulatory subunit; HEAT;TM=M;SS=N; 2.78
- 25 442503; AF147078; Hs.375031; p53-responsive gene 5; K_tetra,lon,trans:none; 2.77
- 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/H; TPR,PDZ,WW,Guanylate_kin;TM=M;SS=N; 2.77
- 454294; AB000734; Hs.50640; JAK binding protein; SH2;TM=M;SS=N; 2.77
- 440188; AK001812; Hs.7036; N-Acetylglucosamine kinase; ROK;TM=M;SS=N; 2.77
- 449539; W80363; Hs.58446; ESTs; pkinase,Furin-like,Recep_L_domain:none; 2.76
- 30 422667; H25642; Hs.132821; ESTs; FMO-like,FMO-like; 2.76
- 415012; NM_004383; Hs.77793; c-src tyrosine kinase; SH2,SH3,pkinase;TM=M;SS=N; 2.76
- 402316; ; NM_013447;Homo sapiens egf-like module c; 7tm_2,GPS;TM=M;SS=M; 2.75
- 425465; L18964; Hs.1904; protein kinase C, Iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;SS=N; 2.75
- 447250; A1878909; Hs.17883; protein phosphatase 1G (formerly 2C), max; PP2C;TM=M;SS=N; 2.75
- 35 438629; A187380; Hs.257170; ESTs, Weakly similar to T12515 hypothet; TNFR,c6:none; 2.75
- 451144; AW956103; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme; HATPase_c:none; 2.74
- 408543; N78098; Hs.44289; ESTs; none;TM=M;SS=N; 2.74
- 429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 2.74
- 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinas; ptkB;TM=M;SS=N; 2.73
- 40602; AF060877; Hs.99236; regulator of G-protein signalling 20; RGS;TM=M;SS=N; 2.73
- 407217; AA477136; Hs.105584; ribosomal protein S6 kinase, 90kD, polyr; pkinase,pkinase_C;TM=M;SS=N; 2.73
- 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPT,Y_phosphatase;TM=M;SS=N; 2.73
- 410590; BE615216; Hs.64746; chloride intracellular channel 3; none;TM=M;SS=N; 2.73
- 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 2.73
- 438022; AW517524; Hs.135201; NOD2 protein; LRR,CARD,GTP_CDc,Viral_helicase1;TM=M;SS=N; 2.72
- 45 420929; A1694143; Hs.326248; programmed cell death 4; MA3;TM=M;SS=N; 2.72
- 421155; H87879; Hs.102267; lysyl oxidase; Lysyl_oxidase,Alkose_epim,Epimerase; 2.72
- 448564; AL044962; Hs.21453; inositol 1,4,5-trisphosphate 3-kinase C; IPK; 2.71
- 449961; AW265634; Hs.133100; ESTs; pkinase,Furin-like,Recep_L_domain:none; 2.71
- 444633; AF111713; Hs.12284; junctional adhesion molecule 1; Ig;TM=Y;SS=M; 2.71
- 50 412259; A1560292; Hs.279909; protein phosphatase 2 (formerly 2A), reg; WD40;TM=M;SS=N; 2.71
- 419569; A1971651; Hs.91143; jagged 1 (Alagille syndrome); DSL,EGF,laminin_EGF,ycw,metallo;TM=M;SS=M; 2.71
- 452401; NM_007115; Hs.29352; tumor necrosis factor, alpha-induced pro; Xlink,CUB; 2.71
- 458190; BE561793; Hs.21446; KIAA1716 protein; ASC,Galactosyl_T:none; 2.70
- 432126; AA865239; Hs.37196; ESTs; 7tm_1;TM=Y;SS=M; 2.70
- 55 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS,AIRS_C;TM=M;SS=N; 2.70
- 424717; H03754; Hs.152213; wingless-type MMTV integration site fam; wnt:none; 2.70
- 414108; A167592; Hs.75761; SFRS protein kinase 1; ank,PH,Oxysterol_BP,pkinase;TM=M;SS=N; 2.70
- 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrat; SH3,HS1_rep;TM=M;SS=N; 2.70
- 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none:none; 2.69
- 60 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG;TM=M;SS=N; 2.69
- 404891; ; Target Exon; none:none; 2.69
- 432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C;TM=M;SS=N; 2.69
- 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2,SH3,pkinase;TM=M;SS=N; 2.68
- 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; Ig,kringle,pkinase,Fz;TM=Y;SS=M; 2.68
- 65 414443; AU077268; Hs.76144; platelet-derived growth factor receptor.; Ig,pkinase;TM=Y;SS=N; 2.68
- 427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, fo; Ig,pkinase;TM=Y;SS=M; 2.68
- 436856; A1469355; Hs.127310; ESTs; pkinase,rm;TM=M;SS=N; 2.68
- 437429; H79981; Hs.6613; Homo sapiens mRNA; cDNA DKFZp564E2222 (f; SH2,SH3,BTB; 2.67
- 70 450590; AA296696; Hs.333418; FXD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 2.67
- 452069; AB028949; Hs.183994; KIAA1026 protein; Metallophos;TM=M;SS=N; 2.67
- 445330; R52658; Hs.21691; ESTs; 7tm_1:none; 2.67
- 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1;TM=Y;SS=M; 2.67
- 419754; H52299; Hs.308467; Homo sapiens mRNA; cDNA DKFZp586I0523 (f; none;TM=M;SS=N; 2.67
- 75 434237; AF119908; Hs.235516; hypothetical protein PRO2955; none; 2.67
- 445826; BE313754; Hs.13350; Homo sapiens mRNA; cDNA DKFZp586D0918 (f; Ig,isp_1,ZU5,Nucleoside_tran; 2.66
- 446696; AF279265; Hs.298476; solute carrier family 26, member 6; Sulfate_transp,STAS,xan_ur_permease;TM=Y;SS=N; 2.66
- 439750; A1359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C,IMPDH_N,CBS,integrin_B,Ricin_B_lactin; 2.66
- 80 413745; AW247252; Hs.75514; nucleoside phosphorylase; Mlap_PNP; 2.66
- 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 2.66
- 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 2.66
- 449030; A1365582; Hs.57100; Homo sapiens mRNA for FLJ00016 protein.; transmembrane4;TM=Y;SS=M; 2.66
- 434979; A1953054; Hs.89643; transketolase (Wernicke-Korsakoff syndro; ASC,transketolase,transket_pyr,transketolase_C,pkinase; 2.66
- 406137; ; NM_000179;Homo sapiens mutS (E. coli) h; MutS_C,PWWP,MutS_N;TM=M;SS=N; 2.66

- 412935; BE267045; Hs.75064; tubulin-specific chaperone c; none; 2.66
 408633; AW963372; Hs.222088; PRO2000 protein; bromodomain,AAA,Sigma54_activat; 2.66
 412817; AL037159; Hs.74619; proteasome (prosome, macropain) 26S subu; PC_rep;TM=M;SS=N; 2.65
 452682; AA456193; Hs.374574; progesterone membrane binding protein; homeobox;none; 2.65
 401752; ; RAN binding protein 3; SH2,STAT,STAT_bind,STAT_protIon_trans,PAC,PAS,Orexin; 2.65
 450747; AIO64821; Hs.129953; ESTs, Highly similar to 1818357A EWS gen; rrm,zf-RanBP,GAS2; 2.65
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm_2,HRM;TM=Y;SS=M; 2.64
 452701; NM_005110; Hs.30332; glutamine-fructose-6-phosphate transamin; GATase_2,SIS;TM=M;SS=N; 2.64
 433933; AJ754389; Hs.355397; Homo sapiens clone TCCIA00164 mRNA sequ; none;NA;NA; 2.64
 421677; H64092; Hs.38282; ESTs; A1pp,Armadillo_seg,IBB; 2.64
 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none; 2.64
 423198; M81933; Hs.1634; cell division cycle 25A; Rhodanese;none; 2.64
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3,RhoGAP,FCH;TM=M;SS=N; 2.64
 437712; X04588; Hs.85844; neurotrophic tyrosine kinase, receptor, ; Tropomyosin,pkinase,LRR,LRRCT,Hydantoinase_B,Hydantoinase_A;TM=M;SS=N; 2.63
 458946; AA009716; Hs.42311; ESTs; none,DSPc,Y_phosphatase; 2.63
 447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5_F8_type_C;TM=M;SS=M; 2.63
 445462; AA378776; Hs.288649; hypothetical protein MGC3077; none; 2.63
 425075; AA506324; Hs.1852; acid phosphatase, prostate; acid_phosphat;TM=Y;SS=M; 2.63
 405588; ; NM_000299; Homo sapiens plakophilin 1 (e; Armadillo_seg;TM=M;SS=N; 2.63
 438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH;none; 2.63
 448243; AW389771; Hs.367688; integrin, beta 8; integrin_B;none; 2.63
 452012; AA307703; Hs.279766; kinesin family member 4A; kinesin_DNA_topoisolV,K-box;TM=M;SS=N; 2.63
 412182; AA205588; Hs.73737; Splicing factor, arginine/serine-rich, 4; rrm,hormone_rec,zf-C4,sugar_tr; 2.63
 423887; AL080207; Hs.134585; DKFZP434G232 protein; ABC_tran;TM=Y;SS=N; 2.63
 417497; AW402482; Hs.82212; CD53 antigen; transmembrane4;TM=Y;SS=M; 2.62
 413407; AJ356293; Hs.75339; inositol polyphosphate phosphatase-like; SH2,SAM,Exo_endo_phos; 2.62
 414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin_c;TM=Y;SS=M; 2.62
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule; EGF,lectin_c,sushi;TM=M;SS=M; 2.62
 429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone;TM=M;SS=N; 2.62
 401812; ; sorting nexin 14; AAA,NB-ARC,APS_kinase,cdc48_N,cdc48_2;none; 2.61
 417886; AA214584; ; ESTs; SPRY,7tm_3,ANF_receptor;none; 2.61
 457670; AF119866; Hs.23449; insulin receptor tyrosine kinase substra; SH3;TM=M;SS=N; 2.61
 428512; AIO18187; Hs.375624; Human DNA sequence from clone RP11-243J1; none; 2.61
 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotat; Pribosyltran,OMPdecase;TM=M;SS=N; 2.61
 454042; H22570; Hs.47860; hypothetical protein FLJ20093; tp,pkinase,LRR,LRRNT,LRRCT;none; 2.61
 421077; AK000061; Hs.101590; hypothetical protein; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,DENN,uDENN;TM=M;SS=N; 2.60
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; pkinase;TM=M;SS=N; 2.60
 416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; KH-domain,rrm;TM=M;SS=N; 2.60
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofilin_ADF; 2.60
 411133; AW819204; ; gb:CM1-ST0283-071299-061-h03 ST0283 Homo; ANF_receptor;none; 2.60
 405602; ; Target Exon; pkinase; 2.60
 400440; X83957; Hs.83870; nebulin; SH3,Nebulin; 2.60
 424848; AJ263231; Hs.327090; EST; SH3,PDZ,Guanylate_kin;none; 2.59
 432258; BE311856; Hs.274230; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase,ATP-sulfurylase;TM=M;SS=N; 2.59
 452690; A1536070; Hs.15085; ESTs; pou,homeobox,lig_chan,ANF_receptor; 2.59
 422753; A1928995; Hs.1575; small nuclear ribonucleoprotein D3 poly; Sm; 2.59
 428028; U52112; Hs.182018; interleukin-1 receptor-associated kinase; death,pkinase;TM=M;SS=N; 2.58
 433573; AF234887; Hs.57652; cadherin, EGF LAG seven-pass G-type recs; 7tm_2,EGF,cadherin,laminin_EGF,laminin_G,Trypan_glycop,GPS,HRM;TM=Y;SS=M; 2.58
 422785; A1824114; Hs.289088; heat shock 90kD protein 1, alpha; zf-C2H2;none; 2.58
 418685; U76376; Hs.87247; harakiri, BCL2-interacting protein (cont; none;TM=M;SS=M; 2.58
 452329; N36626; Hs.29106; mitogen-activated protein kinase phosphat; DSPc;TM=M;SS=N; 2.58
 428405; Y00762; Hs.2266; cholinergic receptor, nicotinic, alpha p; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 2.58
 412251; Z28913; Hs.102948; enigma (LIM domain protein); LIM,PDZ; 2.57
 407245; X90568; Hs.172004; Ulin; fn3,jg,SGXXSG,pkinase;TM=M;SS=N; 2.57
 422309; U79745; Hs.114924; solute carrier family 16 (monocarboxylic; sugar_tr;TM=Y;SS=M; 2.57
 401751; ; RAN binding protein 3; Orexin,SH2,STAT,STAT_bind,STAT_protIon_trans,PAC,PAS;none; 2.57
 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M;SS=N; 2.57
 422282; AF019225; Hs.114309; apolipoprotein L; MotA_ExbB;TM=Y;SS=M; 2.57
 439863; BE547830; Hs.375208; paired immunoglobulin-like receptor beta; lipoxigenase,PLAT,lipoxygenase,PLAT; 2.57
 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 2.57
 401218; ; eukaryotic translation elongation factor; ion_trans;TM=Y;SS=N; 2.57
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L OR; PLDc;TM=M;SS=N; 2.57
 444743; AA045648; Hs.301957; nudix (nucleoside diphosphate linked moi; NUDIX,secY,E1_dehydro,transkel_Pyr;TM=Y;SS=M; 2.56
 429782; NM_005754; Hs.220689; Ras-GTPase-activating protein SH3-domain; rrm,NTF2;TM=M;SS=N; 2.56
 442994; AIO26718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal_S14; 2.56
 456602; AA411607; Hs.118964; ESTs, Weakly similar to KIAA1150 protein; none,pkinase; 2.56
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chr; SH3,PX;TM=M;SS=N; 2.56
 441699; AW511128; Hs.127572; ESTs; none,Aa_trans; 2.56
 447912; AW576549; Hs.165728; ESTs, Weakly similar to I38022 hypotheti; none,GSHPx,ABC_tran; 2.56
 442945; AIO24849; Hs.131853; ESTs; pkinase;none; 2.56
 453199; A1336266; Hs.32353; mitogen-activated protein kinase kinase ; pkinase;TM=M;SS=N; 2.56
 451477; AJ798425; Hs.42710; ESTs; SH3;none; 2.56
 415091; ALO48472; Hs.77910; 3-hydroxy-3-methylglutaryl-Coenzyme A sy; HMG_CoA_synt; 2.55
 413529; U11874; Hs.848; interleukin 8 receptor, beta; 7tm_1;TM=Y;SS=N; 2.55
 425345; AU077297; Hs.155894; protein tyrosine phosphatase, non-recept; Y_phosphatase,DSPc;TM=M;SS=M; 2.55
 401321; ; receptor tyrosine kinase-like orphan rec; none;TM=M;SS=N; 2.55
 446999; AA151520; Hs.351416; hypothetical protein MGC4485; none;none; 2.55
 410157; ; eukaryotic translation elongation factor; ion_trans,IQ;TM=Y;SS=N; 2.55
 414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antigen); transmembrane4;TM=Y;SS=M; 2.55
 408204; AA454501; Hs.43666; protein tyrosine phosphatase type IVA, m; Y_phosphatase;TM=M;SS=N; 2.54
 424539; L02911; Hs.150402; Activin A receptor, type I (ACVR1) (ALK; pkinase,Activin_rec;TM=M;SS=M; 2.54
 459060; H89244; Hs.303627; heterogeneous nuclear ribonucleoprotein ; rrm,pkinase;TM=M;SS=N; 2.54
 450167; AA446404; Hs.24563; NTF2-related export protein 1; NTF2;TM=M;SS=N; 2.54

- 425966; NM_001761; Hs.1973; cyclin F; cyclin_F-box; cyclin_C; TM=M; SS=N; 2.54
 446566; H95741; Hs.17914; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 2.54
 412834; R77123; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone L; 7tm_1; none; 2.54
 457255; AL133011; Hs.253920; Homo sapiens mRNA; cDNA DKFZp434P201 (fr, none, none; 2.54
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome; TM=M; SS=N; 2.53
 417331; AW411297; Hs.81972; SHC (Src homology 2 domain-containing) t; SH2, PID, zif-C2H2, SCAN, AMP-binding, KRAB; TM=M; SS=N; 2.53
 414570; Y00285; Hs.76473; Insulin-like growth factor 2 receptor; In2, CIMR; TM=M; SS=M; 2.53
 444838; AV651680; Hs.208558; ESTs; Integrin_A, FG-GAP; none; 2.53
 422609; Z46023; Hs.118721; sialidase 1 (lysosomal sialidase); BNR, SH2, SH3, pkinase; TM=Y; SS=M; 2.53
 450296; ALD41949; Hs.24756; hepatocyte growth factor-regulated tyros; none, none; 2.53
 400702; ; Target Exon; lig_chan, SBP_bac_3, ANF_receptor; TM=Y; SS=M; 2.53
 432336; NM_002759; Hs.274382; protein kinase, interferon-inducible dou; dsrm, pkinase; TM=M; SS=N; 2.53
 442643; U82756; Hs.374973; PRP4/STKWD splicing factor; WD40; 2.52
 452060; W26980; Hs.349089; ATP-binding cassette, sub-family F (GCN2; ABC_tran, IRK, SWIB; 2.52
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22, Claudin; none; 2.52
 428975; NM_004672; Hs.194694; mitogen-activated protein kinase kinase; pkinase; 2.52
 407608; AJ928218; Hs.380063; ATPase, Na⁺ transporting, beta 3 polypep; none, none; 2.51
 414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1; TM=Y; SS=M; 2.51
 410293; AK000047; Hs.61960; hypothetical protein; K_tetra; TM=M; SS=N; 2.51
 429663; M88874; Hs.211587; phosphatase A2, group IVA (cytosolic; C2, PLA2_B; TM=M; SS=N; 2.51
 425424; NM_004954; Hs.157199; ELK1 motif kinase; pkinase, UBA, KA1; TM=M; SS=N; 2.51
 457013; AA037145; Hs.172865; cleavage stimulation factor, 3' pre-RNA; WD40; TM=M; SS=N; 2.51
 439221; AA737106; Hs.32250; ESTs, Moderately similar to I78885 serin; adh_short, Bcl-2, BH4; none; 2.51
 405429; ; Target Exon; Y_phosphatase; none; 2.51
 443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible Ik; pkinase, RIO1; TM=M; SS=N; 2.51
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank; 2.50
 408056; AA312329; Hs.42331; ephrin-A4; Ephrin; TM=M; SS=M; 2.50
 414419; F06829; Hs.76090; tumor necrosis factor, alpha-induced pro; K_tetra; TM=M; SS=N; 2.50
 405369; ; NM_005569; Homo sapiens LIM domain kinase; pkinase, LIM, PDZ; 2.50
 418216; AA662240; Hs.263099; AF15q14 protein; Hemagglutinin, squash; TM=Y; SS=N; 2.50
 404321; ; C7001741; [gi]2499629[sp]Q63932[MPK2_MOUSE]; none, none; 2.50
 430900; U91939; Hs.248123; G protein-coupled receptor 25; 7tm_1; TM=Y; SS=M; 2.49
 440861; BE244115; Hs.7482; KIAA0682 gene product; rrm, Guanylate_kin; TM=M; SS=N; 2.49
 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity Iib, re; Ig; TM=Y; SS=N; 2.49
 418741; H83265; Hs.8881; ESTs, Weakly similar to S41044 chromosom; pkinase, Activin_rec, pkinase, Activin_rec; 2.49
 417034; NM_006183; Hs.80962; neurensin; none; 2.49
 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulated; none, none; 2.49
 408805; H69912; Hs.48269; vaccinia related kinase 1; pkinase; TM=M; SS=N; 2.49
 418255; AW135405; Hs.37251; ESTs; pkinase; none; 2.49
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase; TM=M; SS=N; 2.44
 417791; AW965339; Hs.44269; ESTs; none, fer2, FAD_binding_5, Ald_Xan_dh_C, fer2_2, Ald_Xan_dh_C2, CO_deh_flav_C; 2.44
 453941; U39817; Hs.36820; Bloom syndrome; DEAD, helicase_C, HRDC; TM=M; SS=N; 2.41
 417849; AW291587; Hs.82733; nidogen 2; EGF, Idl_recept_L, thyroglobulin_1; TM=M; SS=M; 2.39
 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase; 2.32
 428513; BE220806; Hs.184697; plexin C1; PSI; none; 2.31
 426761; A015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing me; none; TM=Y; SS=M; 2.31
 427585; D31152; Hs.179729; collagen, type X, alpha 1 (Schmid metaph; C1q, Collagen; 2.28
 412723; AA648459; Hs.335951; hypothetical protein AF301222; none; TM=M; SS=N; 2.28
 452461; N78223; Hs.108106; transcription factor; zif-C3HC4, ubiquitin, PHD, YDG_SRA; TM=M; SS=N; 2.26
 429547; AW009166; Hs.99376; FGENESH predicted novel secreted protein; none, none; 2.15
 429486; AF155827; Hs.203963; hypothetical protein FLJ10339; SNF2_N, helicase_C; TM=M; SS=N; 2.15
 401486; ; C4000647; [gi]4758508[ref]NP_004253.1; ai; none; TM=Y; SS=M; 2.15
 416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient, yeast; h; HORMA; TM=M; SS=N; 2.14
 424399; A1905687; Hs.348419; A1905687:IL-BT095-190199-019 BT095 Homo; none; TM=M; SS=M; 2.14
 423761; NM_006194; Hs.132576; paired box gene 9; PAX; TM=M; SS=N; 2.13
 439670; AF088076; Hs.59507; ESTs, Weakly similar to AC004858 3 U1 sm; none, none; 2.13
 439318; AW837046; Hs.6527; G protein-coupled receptor 58; 7tm_2, CytC_asm, GPS; TM=Y; SS=M; 2.03
 445019; A1205540; Hs.281295; ESTs; none, none; 2.00
 443211; A128388; Hs.143655; ESTs; none, none; 1.98
 449448; D60730; Hs.57471; ESTs; none, none; 1.92
 435243; AW292886; Hs.348932; hypothetical protein dJ434O14.3; IRF; none; 1.85
 406360; ; Target Exon; WD40; TM=M; SS=N; 1.84
 411388; X72925; Hs.69752; desmocollin 1; cadherin; TM=Y; SS=N; 1.84
 453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz, Frizzled, 7tm_2; TM=Y; SS=M; 1.79
 419183; U06669; Hs.89663; cytochrome P450, subfamily XXIV (vitamin; p450; 1.78
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5; TM=Y; SS=M; 1.77
 432842; AW674093; Hs.334822; hypothetical protein MGCA485; Ribosomal_L4; TM=M; SS=N; 1.76
 419743; AW408782; Hs.5957; Homo sapiens clone 24416 mRNA sequence; none, none; 1.73
 426427; M86699; Hs.169840; TTK protein kinase; pkinase; 1.62
 437915; A1637993; Hs.202312; Homo sapiens clone N11 NTera2D1 teratocarc; none, none; 1.58
 433336; AF017986; Hs.31386; secreted frizzled-related protein 2 (str; Fz, NTR; 1.50
 434377; AW137148; Hs.306593; intron of perlodin (OSF-2os); Fasciclin; none; 1.47
 451592; A1805416; Hs.213897; ESTs; none, none; 1.47
 404927; ; Target Exon; Galactosyl_T; TM=M; SS=Y; 1.28
 421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz, NTR; 1.27
 427335; AA448542; Hs.278444; G antigen 7B; none; 1.25
 431808; M30703; Hs.270833; amphiregulin (schwannoma-derived growth; EGF; TM=Y; SS=M; 1.24
 447993; AW139525; Hs.170362; ESTs; none, none; 1.21
 428182; BE386042; Hs.293317; ESTs, Weakly similar to GGC1_HUMAN G ANT; none; TM=M; SS=N; 1.18
 453637; NM_002589; Hs.34073; BH-protocadherin (brain-heart); cadherin; TM=Y; SS=M; 1.14
 438274; A1918906; Hs.55080; ESTs; PAX; none; 1.14
 453966; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin, Idl_recept_L; none; 1.10
 413268; AL039079; Hs.75256; regulator of G-protein signalling 1; RGS; TM=M; SS=N; 1.07

429921; AA526911; Hs.82772; collagen, type XI, alpha 1; Collagen, COL11, TSPN, Jaminin_G, CorA;; 1.00
452795; AW392555; Hs.18878; hypothetical protein FLJ21620; 2OG-Fell_Oxy; TM=M; SS=N; 1.00

TABLE 25B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
406685	0_0	M18728
418869	12789_14	AA229762 AA230035
425802	8884_3	AA122298 AA360788
417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572
411133	1070995_1	AW819203 AW819204 AW819197 AW819202 AW819211 BE158469 AW819221 BE158473 AW819235 AW819207 AW819220 AW819208 AW819238
AW819198	AW819234	

TABLE 25C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
401747	9789872	Minus	118596-118816,119119-119244,119609-11976
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
405932	7767812	Minus	123525-123713
406467	9795551	Plus	182212-182958
402233	7690102	Plus	90281-91477
402558	9863760	Plus	19047-19145,21133-21293,33968-34069
405556	1552511	Plus	163497-163623,164715-164968,165369-16550
403112	8980973	Minus	113051-113195
402316	7527774	Minus	10751-10919,18817-19052,22131-22328
404891	7329392	Plus	84974-85125
406137	9166422	Minus	30487-31058
401752	9828651	Plus	144600-144794
405588	5002511	Plus	46180-46366
401812	7407975	Minus	55084-55391
405602	4753260	Plus	44647-44778
401751	9828651	Plus	139165-139322
401218	9929301	Minus	40793-41031
401321	9863631	Minus	104278-104748
401057	8117645	Plus	158309-159238
400702	8118856	Minus	11457-11585,26311-26536,27902-28067,3204
405429	7321905	Minus	51577-51723
405369	2078469	Minus	34183-34357,35686-35751
404321	9665209	Minus	76594-77805
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,4401
406360	9256107	Minus	7513-7673
404927	7342002	Plus	68690-69563

TABLE 26A: 834 GENES UP-REGULATED IN EWING'S SARCOMA COMPARED TO NORMAL ADULT TISSUES

Table 26A lists about 834 genes up-regulated in Ewing's sarcoma compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" kidney cancer to "average" normal adult tissues was greater than or equal to 1.5. The "average" kidney cancer level was set to the 75th percentile amongst Ewing sarcomas. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 7.5th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of Ewing sarcoma to normal tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1
101447	M21305		gb:Human alpha satellite and satellite 3	38.4
115881	NM_005756	Hs.184942	G protein-coupled receptor 64	34.2
110278	AF061573	Hs.19492	protocadherin 8	32.2
121362	AF050147	Hs.97932	chondromodulin I precursor	30.3
101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	26.3

	121792	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	24.4
	121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidylseri	23.4
	104659	AW969769	Hs.105201	ESTs	20.2
	106533	AL134708	Hs.145998	ESTs	16.9
5	124006	AI147155	Hs.270016	ESTs	15.0
	110728	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	14.8
	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	14.6
	102836	U94320	Hs.158330	neuropeptide Y receptor Y5	14.5
	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	13.7
10	121231	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	12.3
	129526	S69681	Hs.177582	surfactant, pulmonary-associated protein	12.1
	119791	AA554907	Hs.58291	ESTs	11.7
	116301	AW969706	Hs.293332	ESTs	11.2
	123308	C14187	Hs.103538	ESTs	10.9
15	127742	AW293496	Hs.180138	ESTs	10.8
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	10.7
	127489	AA650250	Hs.272076	ESTs	10.6
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.6
20	101063	D54745	Hs.80247	cholecystokinin	10.6
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	10.5
	100299	D49493	Hs.2171	growth differentiation factor 10	10.1
	127987	AI022103	Hs.124511	ESTs	10.1
	131313	R96290	Hs.336629	ribosomal protein L44	9.2
25	126799	AW753865	Hs.74376	oligactomedin related ER localized protei	8.5
	125847	AW161885	Hs.249034	ESTs	7.0
	100380	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	6.9
	114837	BE244930	Hs.166895	ESTs	6.6
	123049	BE047680	Hs.211869	dickkopf (Xenopus laevis) homolog 2	6.6
30	129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	6.5
	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous r	6.5
	125186	AA610620	Hs.181244	major histocompatibility complex, class	6.4
	118644	AA443241	Hs.336629	ribosomal protein L44	6.3
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	6.3
35	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	6.1
	113003	AW292315	Hs.7215	ESTs	5.8
	126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.7
	101050	AU077324	Hs.1832	neuropeptide Y	5.7
	116790	AW161357	Hs.101174	microtubule-associated protein tau	5.5
40	119082	AF252297	Hs.91546	cytochrome P450 retnoid metabolizing pr	5.1
	132315	AF091086	Hs.44563	hypothetical protein	5.0
	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	4.9
	126077	M78772	Hs.210836	ESTs	4.7
	126426	AA125984		gb:zn27h06.r1 Stralagene neuroepithelium	4.6
45	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	4.5
	123619	AA602964		gb:nc097c02.s1 NCL_CGAP_Pr2 Homo sapiens	4.4
	128361	AW172570	Hs.130246	ESTs	4.3
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	4.3
	100020				4.2
50	125556	AB033064	Hs.334806	KIAA1238 protein	4.2
	105316	AI871245	Hs.24835	hypothetical protein FLJ14594	4.0
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	4.0
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (3.9
	128132	AA225632		gb:nc08a07.r1 NCL_CGAP_Pr1 Homo sapiens	3.9
55	129012	R81936	Hs.336629	ribosomal protein L44	3.9
	125447	AI582222	Hs.128686	ESTs	3.8
	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	3.6
	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	3.6
	128391	AW188326	Hs.170652	ESTs	3.5
60	123829	AF251237	Hs.112208	XAGE-1 protein	3.4
	123949	AA621665	Hs.208957	EST	3.4
	126872	AW450979		gb:U1-H-BI3-ata-e-12-0-U1.s1 NCL_CGAP_Su	3.4
	101266	L36645	Hs.73964	EphA4	3.3
	121309	AA293834	Hs.97312	ESTs	3.3
65	130637	AA356764	Hs.17109	integral membrane protein 2A	3.2
	125464	N71807		gb:yz29d09.r1 Soares_multiple_sclerosis_	3.2
	135175	M91463	Hs.95958	solute carrier family 2 (facilitated glu	3.2
	107599	AW664072	Hs.60136	ESTs	3.2
	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.2
70	131688	AI935413	Hs.30692	p21 (CDKN1A)-activated kinase 2	3.1
	120147	AI917116	Hs.155376	hemoglobin, beta	3.1
	110343	AW136703	Hs.17258	ESTs	3.1
	127664	AA806164	Hs.116502	ESTs	3.0
	103076	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	3.0
75	126127	N95428		gb:zb04d09.s1 Soares_senescent_fibroblas	3.0
	125558	R59305		gb:yh16c10.r1 Soares infant brain 1N1B H	3.0
	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.9
	133421	AF134160	Hs.7327	claudin 1	2.8
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.8
80	113577	AI300699	Hs.278937	PRO0470 protein	2.8
	118397	BE139479	Hs.161492	ESTs	2.8
	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	2.8
	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	2.8
	127262	AA828125		gb:zd71a09.s1 NCL_CGAP_Ov2 Homo sapiens	2.8

	106472	AI207162	Hs.3815	stathmin-like-protein RB3	2.7
	125032	T74884		gb:yc58d02.s1 Stratagene liver (937224)	2.7
	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	2.7
5	126600	AA699949	Hs.191385	ESTs	2.7
	120325	AA195651	Hs.104106	ESTs	2.7
	127256	AI738610	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN	2.7
	117357	N24829		gb:yx98h12.s1 Soares melanocyte 2NbHM Ho	2.7
	126735	M69113	Hs.226795	glutathione S-transferase pi	2.7
10	102745	AW753865	Hs.74376	olfactomedin related ER localized protei	2.6
	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (2.6
	129706	AA443241	Hs.336629	ribosomal protein L44	2.6
	107731	AA016086	Hs.272106	ESTs, Weakly similar to I38022 hypotheti	2.6
	128283	AI076570	Hs.134053	ESTs	2.6
15	125165	W45350		gb:zc81h08.s1 Pancreatic Islet Homo sapi	2.6
	111148	AB020690	Hs.7782	paraneoplastic antigen MA2	2.6
	105577	AW852257	Hs.171391	C-terminal binding protein 2	2.6
	128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	2.6
	130262	D63216	Hs.153684	frizzled-related protein	2.6
20	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.6
	102479	NM_001991	Hs.194669	enhancer of zeste (Drosophila) homolog 1	2.6
	128531	H03721	Hs.2953	ribosomal protein S15a	2.6
	126165	AI741816	Hs.125897	ESTs	2.5
25	126086	H75681		gb:yr77g01.r1 Soares fetal liver spleen	2.5
	118967	AI668670	Hs.216756	ESTs	2.5
	120830	AI568170	Hs.96888	ESTs	2.5
	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.5
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	2.5
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	2.5
30	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	2.5
	133761	AF041430	Hs.75922	brain protein I3	2.5
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.5
	126693	C05723		gb:C05723 Human pancreatic islet Homo sa	2.5
	126021	AA775894	Hs.187516	ESTs	2.5
35	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	2.5
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	2.5
	125743	H17151		gb:ym37a05.r1 Soares infant brain 1N1B H	2.5
	130580	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	2.4
40	113119	T47910		gb:yb18b11.s1 Stratagene fetal spleen (9	2.4
	123110	AA486256	Hs.193510	EST	2.4
	113283	T66813	Hs.12947	EST	2.4
	107711	W96141	Hs.220687	ESTs	2.4
	128992	H04150	Hs.107708	ESTs	2.4
	106111	AW875398	Hs.6451	PRO0659 protein	2.4
45	129948	AI537162	Hs.263988	ESTs	2.4
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	2.4
	116728	F13687	Hs.227976	EST	2.4
	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	2.4
50	124971	T23800	Hs.151001	hypothetical protein FLJ14728	2.4
	131019	W28614	Hs.306155	chorionic somatomammotropin hormone 1 (p	2.4
	128671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory s	2.4
	111795	AI435437	Hs.24567	ESTs, Weakly similar to KBF3_HUMAN NUCL	2.4
	119127	AA708035	Hs.12248	ESTs	2.4
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	2.4
55	111898	R38944	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.4
	131916	AA025976	Hs.34569	ESTs	2.4
	130850	AB040922	Hs.20237	DKFZP566C134 protein	2.4
	100571	L14561	Hs.78546	ATPase, Ca++ transporting, plasma membra	2.4
	126722	N66148	Hs.11125	HSPC033 protein	2.4
60	123720	AA609734	Hs.112755	EST	2.4
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retrovir	2.4
	131136	AB033099	Hs.23413	KIAA1273 protein	2.4
	129001	AA443323	Hs.107812	BPOZ protein	2.4
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	2.4
65	107593	AI093688	Hs.60051	ESTs	2.4
	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	2.4
	128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	2.4
	103080	AI077241	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	2.4
	128367	AW611791	Hs.150742	ESTs	2.4
70	123729	AI039779	Hs.278572	membrane component, chromosome 11, surfa	2.3
	112342	AW410273	Hs.92614	longevity assurance (LAG1, S. cerevisiae	2.3
	114721	D61939	Hs.103822	ESTs	2.3
	127768	AW085002	Hs.156187	ESTs	2.3
	127706	AI174238	Hs.186982	ESTs	2.3
75	126029	AA704253	Hs.169359	ESTs	2.3
	124250	AA350256	Hs.323875	EST, Weakly similar to 2109260A B cell	2.3
	117265	AA451966	Hs.43005	RAB9-like protein	2.3
	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	2.3
	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	2.3
80	127252	AI049545	Hs.94	DnaJ (Hsp40) homolog, subfamily A, membe	2.3
	129228	U40714	Hs.233307	tyrosyl-tRNA synthetase	2.3
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.3
	109252	BE440157	Hs.85944	ESTs	2.3
	127889	AI147408	Hs.144941	ESTs	2.3

	121292	AA401807		gbzv65f11.s1 Soares_total_fetus_Nb2HF8_	2.3
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	2.3
	132985	AL045579	Hs.62113	KIAA0717 protein	2.3
5	125174	W51835	Hs.231082	EST	2.3
	125401	AI204637	Hs.337585	ESTs, Highly similar to KIAA0350 [Hsapi	2.3
	135278	AA399542	Hs.229671	EST, Moderately similar to PEPTIDYL-PROL	2.3
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN	2.3
	123423	AA598484		gb:ae38f04.s1 Gessler Wilms tumor Homo s	2.3
10	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	2.3
	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	2.3
	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361.1 HSPC	2.3
	101086	AA382524	Hs.250959	histatin 1	2.3
	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	2.3
15	126879	D90391	Hs.1265	branched chain keto acid dehydrogenase E	2.3
	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	2.3
	124691	R05835	Hs.110153	ESTs	2.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	2.3
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	2.2
20	129052	BE275031	Hs.158210	hypothetical protein MGC2555	2.2
	129248	W04606	Hs.171637	hypothetical protein MGC2628	2.2
	100780	BE561958	Hs.302063	immunoglobulin heavy constant mu	2.2
	135416	BE281018	Hs.99969	fusion, derived from t(12;16) malignant	2.2
	129228	AJ388993	Hs.134535	ESTs	2.2
25	103319	X83492	Hs.82359	tumor necrosis factor receptor superfam	2.2
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	2.2
	120734	AA299948		gb:EST12544 Uterus tumor 1 Homo sapiens	2.2
	111777	AK001100	Hs.41690	desmocollin 3	2.2
	128963	J03890	Hs.1074	surfactant, pulmonary-associated protein	2.2
30	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	2.2
	134964	AI803516	Hs.272891	hippocalcin-like protein 4	2.2
	127248	AA364195		gb:EST75015 Pineal gland II Homo sapiens	2.2
	125761	R68351		gb:yh99b03.r1 Soares placenta Nb2HP Homo	2.2
	101358	M10058	Hs.12056	asiatriglycoprotein receptor 1	2.2
35	101613	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	2.2
	107121	AB015427	Hs.250493	zinc finger protein 219	2.2
	118751	N74210	Hs.50454	ESTs	2.2
	128952	ALD43463	Hs.6755	RaP2 interacting protein 8	2.2
	126581	W73306	Hs.306668	Homo sapiens cDNA FLJ14089 fis, clone MA	2.2
40	127634	AA633469	Hs.133283	ESTs, Weakly similar to unnamed protein	2.2
	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	2.2
	132867	AF226667	Hs.58553	CTP synthase II	2.2
	126323	N77584	Hs.68644	Homo sapiens microsomal signal peptidase	2.2
	111790	AW769683	Hs.6734	ESTs, Weakly similar to S26650 DNA-bind	2.2
45	125549	R20215		gb:yg18b09.r1 Soares infant brain 1N1B H	2.2
	128059	AA972446	Hs.145096	ESTs	2.2
	132342	AW162758	Hs.45232	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.2
	125722	H29796	Hs.269622	ESTs	2.2
	106383	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	2.2
50	127644	N88858	Hs.155101	ATP synthase, H+ transporting, mitochond	2.2
	128179	AW293689	Hs.127116	ESTs	2.2
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	2.2
	126962	R12014	Hs.20976	ESTs	2.2
	112369	AW966243	Hs.4243	hypothetical protein FLJ12650	2.2
55	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	2.2
	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypothet	2.2
	108743	AI580150	Hs.71074	ESTs	2.2
	133726	AI803188	Hs.252716	oxysterol-binding protein-related protei	2.2
	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	2.2
60	109929	AA773187	Hs.294027	ESTs	2.2
	129059	AW069534	Hs.279583	CGI-81 protein	2.2
	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	2.2
	116962	H79677		gb:yu76g10.s1 Soares fetal liver spleen	2.2
	118232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypotheti	2.2
65	106711	BE390125	Hs.143187	hypothetical protein	2.2
	135191	X16886	Hs.301086	cytochrome P450, subfamily IID (debrisoq	2.2
	125822	H03162	Hs.268768	ESTs	2.2
	130215	BE301883	Hs.152707	glioblastoma amplified sequence	2.2
	133363	AI866286	Hs.71962	ESTs, Weakly similar to B36298 protine-r	2.2
70	126250	AL050391	Hs.321247	Homo sapiens mRNA; cDNA DKFZp586A181 (fr	2.2
	103392	X94563		gb:Hsapiens dbi/acbp gene exon 1 & 2.	2.2
	129794	AF161399	Hs.23259	hypothetical protein FLJ13433	2.2
	100253	D38024	Hs.157425	double homeobox, 2	2.2
	130743	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.2
75	125466	R08234	Hs.180461	ESTs	2.2
	122682	AA984531	Hs.159293	ESTs	2.2
	133347	BE257758	Hs.71475	acid cluster protein 33	2.2
	104455	AL110261	Hs.157211	DKFZP586B0621 protein	2.2
	116332	AA491208	Hs.62620	chromosome 6 open reading frame 1	2.2
80	131163	AA099524	Hs.23754	ESTs	2.2
	109592	AI198059	Hs.26370	ESTs	2.2
	128721	AW403911	Hs.266175	phosphoprotein associated with GEMs	2.1
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	2.1
	128434	AI190914	Hs.143880	ESTs	2.1

5	103163	AU077018	Hs.3235	keratin 4	2.1
	112379	AK001713	Hs.17860	hypothetical protein FLJ10851	2.1
	127507	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	2.1
	133097	W03512	Hs.6479	hypothetical protein MGC13272	2.1
	126153	H85692	Hs.40730	ESTs	2.1
10	122110	AI123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	2.1
	100554	M95923		gb:Human 12-lipoxygenase mRNA, partial c	2.1
	104799	AA029703		gb:ze95h08.s1 Soares_fetal_heart_NbHH19W	2.1
	132664	AI740461	Hs.54542	ESTs	2.1
	114620	AA642974		gb:nr60h01.s1 NCI_CGAP_Lym3 Homo sapiens	2.1
15	115348	AA281562	Hs.292100	ESTs	2.1
	133231	AK000517	Hs.6844	hypothetical protein FLJ20510	2.1
	133160	N54968	Hs.66309	hypothetical protein MGC11061	2.1
	124656	AW297702	Hs.102915	ESTs	2.1
	133576	M19650	Hs.150741	Z,3'-cyclic nucleotide 3' phosphodiester	2.1
20	132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypothet	2.1
	126505	AA282881	Hs.190057	ESTs	2.1
	118865	AA736405	Hs.54530	ESTs	2.1
	134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	2.1
	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	2.1
25	133493	AW998046	Hs.194369	arginine-glutamic acid dipeptide (RE) re	2.1
	112853	T02843		gb:FB11H5 Fetal brain, Stratagene Homo s	2.1
	117457	N29582	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU	2.1
	112246	RS1321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MA	2.1
	134869	AL157518	Hs.90421	PRO2463 protein	2.1
30	128869	AA768242	Hs.80618	hypothetical protein	2.1
	129179	AW969025	Hs.109154	ESTs	2.1
	104857	AI920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	2.1
	101651	AL037111	Hs.75641	galactose-1-phosphate uridylyltransferas	2.1
	129726	H15474	Hs.132898	fatty acid desaturase 1	2.1
35	117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	126271	AI250773	Hs.270012	ESTs	2.1
	116925	H73110	Hs.260603	ESTs, Moderately similar to A47582 B-ce	2.1
	128468	T23625	Hs.150580	putative translation initiation factor	2.1
	116031	AA452239	Hs.103329	KIAA0970 protein	2.1
40	130724	AK001507	Hs.306084	Homo sapiens clone FLB6914 PRO1821 mRNA,	2.1
	121897	AA427419	Hs.229162	EST, Weakly similar to ZN91_HUMAN ZINC	2.1
	123808	AA620552		gb:ae58g11.s1 Stratagene lung carcinoma	2.1
	122333	AA625872	Hs.98977	ESTs, Moderately similar to T34561 hypot	2.1
	127841	AW136558	Hs.125246	ESTs	2.1
45	100023				2.1
	113002	BE243513	Hs.7212	hypothetical protein PP1044	2.1
	111567	F12628	Hs.334786	hypothetical protein MGC16040	2.1
	113697	T97183	Hs.17992	Homo sapiens mRNA; cDNA DKFZp434J1726 (f	2.1
	128033	AI248705	Hs.149321	ESTs	2.1
50	105225	AA211777		gb:zn57d02.s1 Stratagene muscle 937209 H	2.1
	112370	AF052095	Hs.167344	Homo sapiens clone Z3911 mRNA sequence	2.1
	132786	BE083422	Hs.56851	hypothetical protein MGC2668	2.1
	113226	AI821008	Hs.10697	ESTs	2.1
	117997	N52090	Hs.47420	EST	2.1
55	116996	H83935	Hs.40535	ESTs	2.1
	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	2.1
	122591	AI188219	Hs.99311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	2.1
	107279	S57296	Hs.323910	v-erb-b2 avian erythroblastic leukemia	2.1
	103898	AA248884		gb:k3517.seq.F Human fetal heart, Lambda	2.1
60	110312	BE256986	Hs.11896	hypothetical protein FLJ12089	2.1
	127447	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	2.1
	128352	AW137413	Hs.169942	ESTs	2.1
	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	2.0
	128275	AI218235	Hs.131240	ESTs	2.0
65	125976	AA347417		gb:zv67d11.r1 Soares_fetal_liver_Nb2HF8_	2.0
	120820	AA347417	Hs.96869	EST	2.0
	134937	AI251449	Hs.171939	ESTs	2.0
	129602	AI282193	Hs.198298	v-src avian sarcoma (Schmidt-Ruppin A-2)	2.0
	129535	AA397972	Hs.169965	chimerin (chimaerin) 1	2.0
70	106095	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.0
	128538	R44214	Hs.101189	ESTs	2.0
	105593	AA279341	Hs.174151	aldehyde oxidase 1	2.0
	105788	AB009598	Hs.23965	solute carrier family 22 (organic anion	2.0
	128148	AA918175	Hs.126637	ESTs	2.0
75	125982	R98091		gb:yr30e11.r1 Soares fetal liver spleen	2.0
	125746	AL137506	Hs.274256	hypothetical protein FLJ23563	2.0
	127835	AA748762	Hs.163113	ESTs, Weakly similar to I38022 hypotheti	2.0
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	2.0
	124282	AA018408	Hs.110287	ESTs	2.0
80	126926	AA179472	Hs.832	ESTs, Highly similar to A41029 Integrin	2.0
	100221	O28383		gb:Human mRNA for ATP synthase B chain,	2.0
	126053	H64450		gb:yu62d01.r1 Weizmann Olfactory Epithel	2.0
	100944	L07518	Hs.159593	mucin 6, gastric	2.0
	125581	AI272848	Hs.75309	eukaryotic translation elongation factor	2.0
	128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.0
	114612	AI124557	Hs.95456	ESTs	2.0
	130453	U80735	Hs.173854	PAX transcription activation domain inte	2.0

	135060	AK001887	Hs.259842	protein kinase, AMP-activated, gamma 2 n	2.0
	114419	AI248013	Hs.106532	ESTs, Weakly similar to I38588 reverse t	2.0
	126283	N40359	Hs.271896	ESTs	2.0
5	112003	AW978731	Hs.301824	hypothetical protein PRO1331	2.0
	127391	AW380893	Hs.11039	hypothetical protein MGC2722	2.0
	127717	F12209	Hs.173380	CK2 interacting protein 1; HQ0024c prote	2.0
	126893	AJ252060	Hs.26320	TRABID protein	2.0
	106798	BE252749	Hs.20558	hypothetical protein FLJ20345	2.0
10	103760	AA642973	Hs.183842	ubiquitin B	2.0
	118922	AW206193	Hs.91065	hypothetical protein DKFZp76182423	2.0
	133195	AI434760	Hs.279949	KIAA1007 protein	2.0
	133424	AA350994	Hs.20281	KIAA1700	2.0
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	2.0
15	132347	BE271016	Hs.169850	ESTs, Weakly similar to T21554 hypotheti	2.0
	125599	H13295	Hs.106135	ESTs	2.0
	114459	AW445217	Hs.103362	ESTs	2.0
	128478	AA708205	Hs.100343	ESTs	2.0
	127271	H96820		gb:yn99b03.r1 Soares melanocyte 2NbHM Ho	2.0
20	111122	N63753	Hs.16492	DKFZP564G2022 protein	2.0
	130695	T97205	Hs.17998	ESTs, Weakly similar to 2109260A B cell	2.0
	133571	BE515037	Hs.177556	melanoma antigen, family D, 1	2.0
	119244	AW407564	Hs.275865	ribosomal protein S18	2.0
	127603	AI015798	Hs.9925	hypothetical protein FLJ20772	2.0
25	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	2.0
	128115	AI435590	Hs.130168	ESTs	2.0
	117639	AA377165	Hs.44833	ESTs	2.0
	127033	AF169301	Hs.9098	sulfate transporter 1	2.0
	112411	R43090	Hs.271510	ESTs, Moderately similar to ALU1_HUMAN A	2.0
30	114601	AA075566		gb:zm88f06.s1 Stratagene ovarian cancer	2.0
	127573	AA594196	Hs.269464	ESTs, Weakly similar to S65657 alpha-1C-	2.0
	125500	AW952654	Hs.244624	ESTs	2.0
	119416	T97186		gb:ye50h09.s1 Soares fetal liver spleen	2.0
	115467	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	2.0
35	128902	AA036637	Hs.107052	ESTs	2.0
	127684	AA668831	Hs.32556	KIAA0379 protein	2.0
	126288	AW449560	Hs.89576	inner mitochondrial membrane peptidase 2	2.0
	122059	AA431737	Hs.98749	EST, Moderately similar to T42671 hypoth	2.0
	125486	AI023895	Hs.190587	ESTs	2.0
40	128895	AW467000	Hs.106985	ESTs	2.0
	105301	AW352357	Hs.7457	MAGE1 protein	2.0
	125536	F08266	Hs.77948	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
	121387	AA405854		gb:zu66g08.s1 Soares_testis_NHT Homo sap	2.0
	134126	NM_003747	Hs.131814	tankyrase, TRF1-interacting ankyrin-rela	2.0
45	126860	BE242814	Hs.323494	ESTs, Weakly similar to T27544 zinc resi	2.0
	102907	BE409861	Hs.202833	heme oxygenase (decycling) 1	2.0
	127804	AA740634	Hs.292084	ESTs	1.9
	130566	R85474	Hs.16073	ESTs	1.9
	113782	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	1.9
50	124119	AA040123	Hs.248953	solute carrier family 27 (fatty acid tra	1.9
	132490	NM_001290	Hs.4980	LIM domain binding 2	1.9
	125494	AJ077029	Hs.177543	antigen identified by monoclonal antibod	1.9
	100237	D30715	Hs.306333	Human PAP (pancreatitis-associated prot	1.9
	127687	AW772383	Hs.300635	ESTs	1.9
55	103136	AF087917	Hs.247936	olfactory receptor, family 1, subfamily	1.9
	125704	R55094	Hs.26239	Human DNA sequence from clone RP11-438B2	1.9
	126208	N22588	Hs.288548	Homo sapiens cDNA FLJ12368 fis, clone MA	1.9
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	1.9
	128660	AA011597	Hs.177398	ESTs	1.9
60	118049	N53145		gb:yy55f09.s1 Soares fetal liver spleen	1.9
	134624	AF035119	Hs.8700	deleted in liver cancer 1	1.9
	127432	AW067708	Hs.170311	heterogeneous nuclear ribonucleoprotein	1.9
	126414	AI363157	Hs.24756	hepatocyte growth factor-regulated tyros	1.9
	120861	AA350394	Hs.96952	ESTs	1.9
65	124669	AI571594	Hs.102943	hypothetical protein MGC12916	1.9
	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-li	1.9
	103891	NM_007212	Hs.124186	ring finger protein 2	1.9
	128727	AI223335	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	1.9
	126831	AI929107	Hs.79933	cyclin I	1.9
70	125360	AW898892	Hs.189741	ESTs	1.9
	124276	H83465		gb:ys91a11.s1 Soares retina N2b5HR Homo	1.9
	126524	Z45455	Hs.182447	heterogeneous nuclear ribonucleoprotein	1.9
	126647	AK000283	Hs.270502	hypothetical protein FLJ20276	1.9
	125957	H41694		gb:yo06b06.r1 Soares adult brain N2b5HB5	1.9
75	121782	AW452957	Hs.334698	Homo sapiens, clone MGC:15203, mRNA, com	1.9
	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	1.9
	130945	U20582	Hs.2149	actin like protein	1.9
	126348	T16243	Hs.6473	Homo sapiens cDNA FLJ13992 fis, clone Y7	1.9
	103558	BE616547	Hs.2785	keratin 17	1.9
80	126982	AA211419		gb:zn55g05.s1 Stratagene muscle 937209 H	1.9
	125613	AA765957	Hs.21077	KIAA0532 protein	1.9
	129601	AB032964	Hs.115726	KIAA1138 protein	1.9
	126007	H51097	Hs.143261	ESTs	1.9
	123627	AA909619	Hs.112668	ESTs	1.9

	111587	AI125867	Hs.20734	ESTs	1.9
	135231	BE613615	Hs.74280	hypothetical protein FLJ22237	1.9
	128897	AW979134	Hs.10700	hypothetical protein	1.9
	109891	H04757	Hs.323176	ESTs	1.9
5	127704	AA679809		gb:ag72c02.s1 Gessler Wilms tumor Homo s	1.9
	129340	H75334	Hs.11050	F-box only protein 9	1.9
	126502	T10077	Hs.13453	hypothetical protein FLJ14753	1.9
	129619	AA209534	Hs.284243	tetraspan NET-6 protein	1.9
10	127136	R36277	Hs.7773	Homo sapiens ubiquitin conjugating enzym	1.9
	110636	H72868	Hs.19110	ESTs	1.9
	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	1.9
	104689	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.9
	130829	BE262530	Hs.2006	glutathione S-transferase M3 (brain)	1.9
	125768	AI557486	Hs.119122	ribosomal protein L13a	1.9
15	123613	AA609158	Hs.291166	EST	1.9
	127506	T61039	Hs.252574	ribosomal protein L10a	1.9
	123546	AA608817	Hs.112597	EST	1.9
	126516	R95872	Hs.117572	chemokine binding protein 2	1.9
20	103973	AA305729	Hs.18272	amino acid transporter system A1	1.9
	127426	AA854756	Hs.124076	ESTs	1.9
	112339	R56570	Hs.50547	ESTs	1.9
	129101	NM_013403	Hs.108665	zinedin	1.9
	109442	AW296134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	1.9
25	118103	AA401733	Hs.184134	ESTs	1.9
	125752	AW136622	Hs.206673	ESTs	1.9
	102926	W28363	Hs.239752	nuclear receptor subfamily 2, group F, m	1.9
	133975	C18356	Hs.295944	tissue factor pathway inhibitor 2	1.9
	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.9
30	127329	AW160561	Hs.124021	soggy-1 gene	1.8
	126659	T16245		gb:NIB1005R Normalized infant brain, Ben	1.8
	127297	AW629485	Hs.140720	GSK-3 binding protein FRAT2	1.8
	127640	AI557486	Hs.119122	ribosomal protein L13a	1.8
	103409	NM_004454	Hs.43697	els variant gene 5 (els-related molecule	1.8
35	127964	F06298		gb:HSC13F081 normalized infant brain cDN	1.8
	122365	AA813546	Hs.99034	GTP-binding protein Rho7	1.8
	128193	AJ224442	Hs.155020	putative methyltransferase	1.8
	115173	BE612940	Hs.88252	ESTs	1.8
	125532	AJ734146	Hs.271800	ESTs, Weakly similar to alternatively sp	1.8
40	126541	AJ271671	Hs.7854	zinc/iron regulated transporter-like	1.8
	127309	AI669765	Hs.133184	ESTs	1.8
	129062	AA452970	Hs.155218	E1B-55kDa-associated protein 5	1.8
	126770	AI292320	Hs.81361	heterogeneous nuclear ribonucleoprotein	1.8
	127775	AA128808	Hs.179902	transporter-like protein	1.8
45	126994	AA455265	Hs.86686	ESTs, Moderately similar to I54374 gene	1.8
	130734	AW137091	Hs.18624	KIAA1052 protein	1.8
	114461	AA531187	Hs.126705	ESTs	1.8
	100842	U05597		gb:Human anion exchanger 3 cardiac isofo	1.8
	127389	T65126	Hs.12743	camitine O-octanoyltransferase	1.8
50	125394	BE178502	Hs.173772	ESTs, Weakly similar to I78885 serine/th	1.8
	107736	AA016239	Hs.60715	ESTs	1.8
	125669	R51308	Hs.333255	ESTs, Weakly similar to ALU8_HUMAN ALU	1.8
	100370	D79989	Hs.184884	KIAA0167 gene product	1.8
	113479	AI023133	Hs.10739	ESTs	1.8
55	105165	BE280787	Hs.16079	hypothetical protein FLJ10233	1.8
	120602	AA808018	Hs.109302	ESTs	1.8
	112399	R60920	Hs.296770	KIAA1719 protein	1.8
	123474	AA599209		gb:ag34b11.s1 Jia bone marrow stroma Hom	1.8
60	134212	AA654353	Hs.17719	EBP50-PDZ Interactor of 64 kD	1.8
	104204	AK001691	Hs.57655	hypothetical protein FLJ10829	1.8
	127464	AW971875	Hs.292071	ESTs	1.8
	116715	AL117440	Hs.170263	tumor protein p53-binding protein, 1	1.8
	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	1.8
65	132380	AW373665	Hs.46853	ESTs	1.8
	120087	AF186780	Hs.79219	RelGDS-like gene; KIAA0959 protein	1.8
	116356	AJ371223	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HE	1.8
	125499	H10543		gb:ym04c08.r1 Soares infant brain 1NIB H	1.8
	128846	AA730767	Hs.285753	SCG10-like-protein	1.8
70	123869	AA620924	Hs.112923	EST	1.8
	103889	AA135722	Hs.61481	ESTs	1.8
	126528	Z24895		gb:HSB67F122 STRATAGENE Human skeletal m	1.8
	127629	AA293279	Hs.29173	hypothetical protein FLJ20515	1.8
	130004	AA703684	Hs.245474	ESTs, Moderately similar to ALU5_HUMAN A	1.8
	130847	AJ672483	Hs.20220	lipase protein	1.8
75	111620	R14853	Hs.307478	EST, Weakly similar to I39058 hypotheti	1.8
	131971	BE567100	Hs.154938	hypothetical protein MDS025	1.8
	121360	AA405635	Hs.96854	ESTs, Weakly similar to DYXL_HUMAN CYTOP	1.8
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	1.8
80	124687	AA833902	Hs.270745	ESTs	1.8
	126698	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypotheti	1.8
	126730	AA442429		gb:zv70g02.r1 Soares_tetal_fetus_Nb2HF8_	1.8
	127916	AJ239950	Hs.294111	ESTs, Moderately similar to B34087 hypo	1.8
	128408	AI183407	Hs.143704	EST	1.8
	128440	AW090340	Hs.14337	Homo sapiens cDNA FLJ14407 fis, clone HE	1.8

	123783	AA610112		gb:af19g05.s1 Soares_tatal_fatus_Nb2HF8_	1.8
	109152	AW380723	Hs.73451	ESTs, Weakly similar to S55024 nebulin,	1.8
	107242	AB020672	Hs.175411	KIAA0865 protein	1.8
5	132804	AI805943	Hs.326067	hypothetical protein MGC5178	1.8
	125387	AJ243669	Hs.8127	KIAA0144 gene product	1.8
	121578	AA398791	Hs.178185	ESTs	1.8
	132944	T96641	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	1.8
	126295	AI281459	Hs.270114	ESTs	1.8
10	133335	BE251012	Hs.263812	nuclear distribution gene C (Ankikulans)	1.8
	129879	AK001696	Hs.13109	Ran binding protein 11	1.7
	125175	WS2355	Hs.303030	EST	1.7
	126919	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	1.7
	127773	AA725863	Hs.120508	ESTs	1.7
15	126495	AB029021	Hs.137732	KIAA1098 protein	1.7
	126948	AW968535	Hs.14328	hypothetical protein FLJ20071	1.7
	126671	C03105	Hs.285847	CGI-19 protein	1.7
	115428	AA284112	Hs.94680	ESTs, Weakly similar to I78885 serine/t	1.7
	128232	AI830319	Hs.334641	hypothetical protein DKFZp434I1916	1.7
20	126082	H81188	Hs.269571	ESTs	1.7
	120467	AW292562	Hs.187628	ESTs	1.7
	124041	AW590171	Hs.101413	ESTs	1.7
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	1.7
	123951	AB012822	Hs.173043	metastasis-associated 1-like 1	1.7
25	126449	AF223944	Hs.325443	breast cell glutaminase	1.7
	124554	N65961		gb:aa27d03.s1 Soares fetal liver spleen	1.7
	133651	AI301740	Hs.173381	dihydropyrimidinase-like 2	1.7
	126780	R12421	Hs.5811	chromosome 21 open reading frame 59	1.7
	125661	AA491830	Hs.25689	ESTs	1.7
30	125888	H18298		gb:yn48b09.r1 Soares adult brain N2b5HB5	1.7
	127245	AA323958		gb:EST26810 Cerebellum II Homo sapiens c	1.7
	111223	AA852773	Hs.334838	KIAA1866 protein	1.7
	115611	R44789	Hs.33191	Homo sapiens, Similar to transmembrane r	1.7
	124846	R59977	Hs.158196	transcriptional adaptor 3 (ADA3, yeast	1.7
35	100397	D84424	Hs.57697	hyaluronan synthase 1	1.7
	127180	T27097	Hs.22790	ESTs	1.7
	102598	BE250742	Hs.106673	eukaryotic translation initiation factor	1.7
	134076	AF086215		gb:Homo sapiens full length insert cDNA	1.7
	115659	W99382	Hs.283709	lipopolysaccharide specific response-7 p	1.7
40	125555	R19382	Hs.117869	ESTs	1.7
	128382	AI138886	Hs.143243	ESTs	1.7
	127710	AA682867	Hs.191901	ESTs	1.7
	125445	AI452722	Hs.7709	WW domain binding protein 1	1.7
	129951	AL110282	Hs.268024	Homo sapiens, clone IMAGE:3873720, mRNA	1.7
45	119898	R93325	Hs.58690	ESTs	1.7
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	1.7
	133531	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.7
	119726	AF086289	Hs.234766	skin-specific protein	1.7
	125198	W69474	Hs.323140	ESTs	1.7
50	121414	AW291477	Hs.188763	testis expressed sequence 13A	1.7
	112542	AI458867	Hs.24276	ESTs	1.7
	101368	M13058	Hs.73952	proline-rich protein HaellI subfamily 2	1.7
	125820	AA730136	Hs.75561	teratocarcinoma-derived growth factor 1	1.7
	129091	AA056483	Hs.301463	Human Chromosome 16 BAC clone CIT987SK-A	1.7
55	132609	U20165	Hs.53250	bone morphogenetic protein receptor, typ	1.7
	119447	W31714	Hs.122656	ESTs, Highly similar to formin 2-like pr	1.7
	113675	T81034	Hs.14841	ESTs	1.7
	113701	T97301	Hs.18026	ESTs	1.7
	116180	AA463902	Hs.13522	ESTs, Weakly similar to I38022 hypothet	1.7
60	127133	AA280740	Hs.292072	ESTs, Moderately similar to A46010 X-lin	1.7
	113316	T70318	Hs.268581	ESTs	1.7
	123316	AI290561	Hs.155361	ESTs	1.7
	122638	AL137476	Hs.123609	Homo sapiens mRNA; cDNA DKFZp434I0623 (f	1.7
	105053	AI884911	Hs.32989	receptor (calcitonin) activity modifying	1.7
65	103305	X82279		gb:Hsapiens Fas, Apo-1 gene (promoter a	1.7
	110384	H45282	Hs.268798	ESTs	1.7
	115626	AW630870	Hs.86674	ESTs, Weakly similar to hypothetical pro	1.7
	126905	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	1.7
	130820	AI353934	Hs.288798	hypothetical protein FLJ21012	1.7
70	112394	AK000373	Hs.8358	hypothetical protein FLJ20366	1.7
	129589	AW504292	Hs.11517	ESTs	1.7
	126446	NM_015670	Hs.118926	sentrin/SUMO-specific protease 3	1.7
	126547	U47732	Hs.84072	transmembrane 4 superfamily member 3	1.7
	120287	AF219946	Hs.102237	tubby super-family protein	1.7
75	129991	R28386	Hs.179925	ESTs, Weakly similar to ALU8_HUMAN ALU	1.7
	123912	AA621283	Hs.332855	EST	1.7
	102071	AL120051	Hs.144700	ephrin-B1	1.7
	121046	AB033083	Hs.97377	KIAA1257 protein	1.7
80	128403	AI908006	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	1.7
	104268	AL043864	Hs.70604	ATPase, Class II, type 9A	1.7
	111598	R11505	Hs.268912	ESTs	1.7
	128109	AW269421	Hs.128093	ESTs	1.7
	125435	R08480	Hs.272138	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.7
	133104	AI091195	Hs.65029	growth arrest-specific 1	1.7

	126826	AA099764		gb:zn61f12.r1 Stratagene muscle 937209 H	1.7
	106483	NM_006548	Hs.30299	IGF-II mRNA-binding protein 2	1.7
	129765	M86933	Hs.1238	amelogenin (Y chromosome)	1.7
5	115904	AI167560	Hs.61297	ESTs	1.7
	125514	AB040912	Hs.191098	hypothetical protein FLJ11598	1.7
	125797	H03117	Hs.111497	similar to mouse neuronal protein 15.6	1.7
	133179	U81599	Hs.66731	homeo box B13	1.7
	115167	AA749209	Hs.43728	hypothetical protein	1.7
10	118036	AI471862	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	1.7
	124540	N63232		gb:yz39a12.s1 Morton Fetal Cochlea Homo	1.7
	126183	BE018708	Hs.81972	SHC (Src homology 2 domain-containing) l	1.7
	127897	AA773881		gb:af77b12.r1 Soares_NhHMPu_S1 Homo sapi	1.7
	126680	F07097	Hs.133665	transmembrane 6 superfamily member 1	1.7
	126972	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	1.7
15	130605	BE514362	Hs.306024	FK506-binding protein 3 (25kD)	1.7
	127541	AA573449	Hs.171515	ESTs	1.7
	127392	AI816736	Hs.14896	DHHC1 protein	1.7
	106879	AI190785	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA,	1.7
20	128303	AI096444	Hs.7187	hypothetical protein FLJ10707	1.7
	126469	BE384361	Hs.182885	ESTs, Weakly similar to JC5024 UDP-galac	1.7
	125756	BE174587	Hs.289721	growth arrest specific transcript 5	1.7
	132332	AW978906	Hs.45005	hypothetical protein FLJ12960	1.6
	127142	AW452942	Hs.130393	ESTs	1.6
25	128416	F13165	Hs.12549	ESTs, Weakly similar to 2109260A B cell	1.6
	103790	AL122044	Hs.331633	hypothetical protein DKFZp566N034	1.6
	134578	AL110193	Hs.224137	hypothetical protein	1.6
	110023	AW294701	Hs.31040	ESTs	1.6
	125511	AJ271379	Hs.76194	ribosomal protein S5	1.6
30	111483	R06569	Hs.269534	ESTs	1.6
	127363	AF064104	Hs.221116	CDC14 (cell division cycle 14, S. cerevi	1.6
	126231	AA991766	Hs.300793	ESTs	1.6
	106181	AI803651	Hs.191608	ESTs	1.6
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S	1.6
35	119929	W86464	Hs.304825	ESTs	1.6
	132542	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434I0812 (f	1.6
	127155	AA284993		gb:z123a10.r1 Soares ovary tumor NbHOT H	1.6
	125956	AK000214	Hs.129014	hypothetical protein FLJ20207	1.6
	126854	AJ275986	Hs.71414	transcription factor (SMIF gene)	1.6
40	131330	D13969	Hs.184669	zinc finger protein 144 (Mel-18)	1.6
	129445	W52452	Hs.29797	ribosomal protein L10	1.6
	113427	T85105	Hs.15471	ESTs	1.6
	106124	H93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H	1.6
	128135	AA954381	Hs.269721	ESTs, Moderately similar to ALU1_HUMAN	1.6
45	111460	R02728	Hs.117331	ESTs	1.6
	125636	H12382	Hs.25119	ESTs, Weakly similar to YEX0_YEAST HYPOT	1.6
	134118	BE336680	Hs.182877	KIAA0116 protein	1.6
	111570	AF059203	Hs.20580	sterol O-acyltransferase 2	1.6
	113511	T89578	Hs.189740	ESTs	1.6
50	113296	AW449560	Hs.89576	inner mitochondrial membrane peptidase 2	1.6
	109875	H03260	Hs.30385	ESTs	1.6
	105930	AF016371	Hs.9880	peptidyl prolyl isomerase H (cyclophilin	1.6
	105564	BE616694	Hs.288042	hypothetical protein FLJ14299	1.6
	128063	AI377750	Hs.167177	ESTs	1.6
55	109779	AB029396	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucur	1.6
	125334	T86569	Hs.182118	ESTs	1.6
	127206	AW816490	Hs.337508	ESTs	1.6
	108845	AW362901	Hs.68864	ESTs, Weakly similar to phosphatidylseri	1.6
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	1.6
60	114062	AI560984	Hs.27283	ESTs	1.6
	122550	AA451859	Hs.99253	ESTs	1.6
	113413	R08672	Hs.186512	ESTs	1.6
	127019	AI929355	Hs.286128	hypothetical protein FLJ23329	1.6
	106251	R12607	Hs.35101	proline-rich Gla (G-carboxyglutamic acid	1.6
65	112670	AL138012	Hs.183840	ESTs, Moderately similar to ALU7_HUMAN A	1.6
	114913	AI435199	Hs.58940	ESTs, Weakly similar to I38022 hypotheti	1.6
	126604	AI023299	Hs.269806	ESTs	1.6
	125324	R07785		gb:yy15c06.r1 Soares fetal liver spleen	1.6
	121438	AW445024	Hs.139389	ESTs	1.6
70	127289	AI041014	Hs.220752	ESTs, Weakly similar to unnamed protein	1.6
	126935	AI198535	Hs.89463	potassium large conductance calcium-acti	1.6
	132430	AW973652	Hs.283105	ESTs	1.6
	133541	H75334	Hs.11050	F-box only protein 9	1.6
	102612	U85402	Hs.248124	G protein-coupled receptor 31	1.6
75	120228	AI192528	Hs.164537	ESTs	1.6
	122652	AA454641		gb:zx99d05.s1 Soares_NhHMPu_S1 Homo sapi	1.6
	103456	AA496425	Hs.9629	papillary renal cell carcinoma (transloc	1.6
	105355	AL031447	Hs.26938	Homo sapiens, clone IMAGE:4053044, mRNA,	1.6
	108043	AA042873	Hs.160412	ESTs	1.6
80	128695	NM_003478	Hs.101299	cullin 5	1.6
	127984	AA846377	Hs.193706	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.5
	124405	AA228137	Hs.25005	hypothetical protein MGC3329	1.6
	103934	BE278111	Hs.134200	DKFZP564C186 protein	1.6
	124195	H83034		gb:yy48e07.r1 Soares fetal liver spleen	1.6

5	110938	N48982	Hs.38034	Homo sapiens cDNA FLJ12924 fis, clone NT	1.6
	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.6
	121226	AA364109	Hs.177990	ESTs	1.6
	120415	AA235810		gb:zs41a03.s1 Soares_NhHMPu_S1 Homo sapi	1.6
	123864	AA620882		gb:af95g01.s1 Soares_testis_NHT Homo sap	1.6
10	125045	AI114630	Hs.208334	Homo sapiens cDNA: FLJ21874 fis, clone H	1.6
	133425	AA444390	Hs.155482	hydroxyacyl glutathione hydrolase	1.6
	126578	AF151861	Hs.107528	androgen induced protein	1.6
	102406	U43177		(NONE)	1.6
	114126	BE566962	Hs.7063	Homo sapiens cDNA: FLJ20913 fis, clone A	1.6
15	125233	W85713	Hs.110092	ESTs	1.6
	109635	F04296	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.6
	125675	BE294972	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL	1.6
	129707	AW572317	Hs.12082	Homo sapiens mRNA: cDNA DKFZp566L203 (fr	1.6
	127569	AI765107	Hs.274422	hypothetical protein FLJ20550	1.6
20	113302	T66919	Hs.268575	ESTs	1.6
	119705	AI984203	Hs.57874	ESTs	1.6
	127226	AL036559	Hs.3463	ribosomal protein S23	1.6
	123489	AA599708		gb:ag11a10.s1 Gessler Wilms tumor Homo s	1.6
	107468	AA740979	Hs.91389	ESTs	1.6
25	115916	AI052731	Hs.91910	ESTs	1.6
	127815	AA743490	Hs.255015	ESTs	1.6
	100364	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	1.6
	125568	AW615396	Hs.105613	ESTs	1.6
	105260	N81201	Hs.31755	ESTs	1.6
30	125659	T57693	Hs.87929	Homo sapiens cDNA FLJ13707 fis, clone PL	1.6
	111275	N70970	Hs.350006	ESTs	1.6
	106542	AA339541	Hs.24956	hypothetical protein FLJ22056	1.6
	133423	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	1.6
	124770	AA984414	Hs.120429	ESTs	1.6
35	117936	AI382904	Hs.47213	ESTs	1.6
	134385	M14660	Hs.169274	ESTs, Highly similar to IFT2_HUMAN INTER	1.6
	108367	AW410478	Hs.104019	transforming, acidic coiled-coil contain	1.6
	131143	NM_000312	Hs.2351	protein C (inactivator of coagulation fa	1.6
	105441	N28522	Hs.8935	quintilinate phosphoribosyltransferase (n	1.6
40	128215	AA973310		gb:op91e06.s1 Soares_NFL_T_GBC_S1 Homo s	1.6
	127344	AI003929	Hs.80624	hypothetical protein MGC2560	1.6
	126478	BE541249	Hs.109697	ESTs	1.6
	122053	AI637498	Hs.98745	ESTs	1.5
	111760	BE551929	Hs.268754	Homo sapiens cDNA FLJ11949 fis, clone HE	1.5
45	112401	R81279	Hs.237536	ESTs, Weakly similar to AF151067 1 HSPC2	1.5
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	1.5
	125575	H14983		gb:ym19h09.r1 Soares infant brain 1N1B H	1.5
	128765	AF073310	Hs.143648	insulin receptor substrate 2	1.5
	108935	AA147848	Hs.67991	hypothetical protein DKFZp434G0522	1.5
50	121221	AI140708	Hs.97461	ESTs	1.5
	120091	AW024672	Hs.59558	EST	1.5
	107375	BE011845	Hs.251064	high-mobility group (nonhistone chromoso	1.5
	125803	AW876115	Hs.29852	ESTs	1.5
	115132	AA811762	Hs.71433	ESTs	1.5
55	113346	AF143876	Hs.14318	Homo sapiens clone IMAGE:113399 mRNA seq	1.5
	107357	U63973	Hs.103501	rhodopsin kinase	1.5
	125443	BE251057	Hs.177592	ribosomal protein, large, P1	1.5
	133803	M24461	Hs.76305	surfactant, pulmonary-associated protein	1.5
	113378	T80738	Hs.14757	ESTs	1.5
60	105540	BE391690	Hs.9265	hypothetical protein FLJ20917	1.5
	127446	F13008		gb:HSC3HE011 normalized infant brain cDN	1.5
	134075	NM_012201	Hs.78979	Golgi apparatus protein 1	1.5
	127585	AA604144	Hs.190632	ESTs	1.5
	125824	Z45258	Hs.286013	short coiled-coil protein	1.5
65	127606	AA621135	Hs.136552	ESTs	1.5
	125585	AW298113	Hs.92909	SON DNA binding protein	1.5
	107757	BE621721	Hs.280792	hypothetical protein FLJ12387 similar to	1.5
	109978	H09356	Hs.22528	ESTs	1.5
	132297	BE272446	Hs.265317	hypothetical protein MGC2562	1.5
70	115784	AW402151	Hs.54673	tumor necrosis factor (ligand) superfam1	1.5
	127880	W39735	Hs.73818	ubiquinol-cytochrome c reductase hinge p	1.5
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	1.5
	102868	X02419	Hs.77274	plasminogen activator, urokinase	1.5
	133457	J04948	Hs.333509	alkaline phosphatase, placental-like 2	1.5
75	130339	AA435746		gb:zt79e03.s1 Soares_testis_NHT Homo sap	1.5
	125444	N28476	Hs.159161	Rho GDP dissociation inhibitor (GDI) alp	1.5
	123470	AW303285	Hs.303632	Human DNA sequence from clone RP11-110H4	1.5
	100025				1.5
	127063	AI276526	Hs.331564	Homo sapiens mRNA: cDNA DKFZp434H1215 (f	1.5
80	127945	AA815031	Hs.123598	ESTs	1.5
	111557	R09510	Hs.20373	EST	1.5
	116009	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	1.5
	119858	W01370	Hs.46824	ESTs	1.5
	106509	AI042309	Hs.64552	hypothetical protein MGC15563	1.5
	124124	AW294404	Hs.144515	Homo sapiens cDNA FLJ11672 fis, clone HE	1.5
	126713	AW249181	Hs.19954	ESTs, Weakly similar to T19873 hypotheti	1.5
	126475	AW959075	Hs.238797	ESTs, Moderately similar to I38022 hypot	1.5

	126851	R40611	Hs.137565	ESTs	1.5
	104820	AW162768	Hs.22620	ESTs	1.5
	127235	AI817309	Hs.225583	ESTs, Weakly similar to 2004399A chromos	1.5
	126552	AF168711	Hs.159397	x 010 protein	1.5
5	127523	AA617637		gbnp34h12.s1 NCI_CGAP_Lu1 Homo sapiens	1.5
	131692	BE559681	Hs.30736	KIAA0124 protein	1.5
	112974	AL353965	Hs.101174	microtubule-associated protein tau	1.5
	118921	N91914	Hs.54751	ESTs	1.5
	100676	X02761	Hs.287820	fibronectin 1	1.5
10	127721	T59578	Hs.188440	ESTs, Weakly similar to ALUF_HUMAN IIII	1.5
	115254	AA279024	Hs.269316	ESTs, Weakly similar to S65657 alpha-1C	1.5
	128173	AI457242	Hs.127024	ESTs	1.5
	126846	AA663527	Hs.116910	ESTs	1.5
	125294	R40025	Hs.106551	ESTs	1.5
15	127494	AW978730	Hs.291956	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.5
	134191	W26632	Hs.7979	KIAA0736 gene product	1.5
	107394	AAB64798	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	1.5
	131562	NM_003512	Hs.28777	H2A histone family, member L	1.5
	127310	AW450671	Hs.189284	ESTs	1.5
20	122359	AA523486		gb:ni67111.s1 NCI_CGAP_Pr12 Homo sapiens	1.5
	100524	M80902	Hs.183704	ubiquitin C	1.5
	128422	T77794		gb:yd20d09.r1 Soares fetal liver spleen	1.5
	129902	AA076278	Hs.13277	hypothetical protein FLJ22054	1.5
	126784	T81887	Hs.108854	HSPC163 protein	1.5
25	123343	AI761902	Hs.99597	ESTs	1.5
	106458	AW954377	Hs.26412	ring finger protein 26	1.5
	112266	AI652534	Hs.25934	ESTs, Weakly similar to HSHU11 histone H	1.5
	127622	AA628222	Hs.97883	ESTs	1.5
	113659	R06545	Hs.189781	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.5
30	116892	AI573283	Hs.38458	ESTs	1.5
	126995	NM_014351	Hs.189810	sulfotransferase family 4A, member 1	1.5
	111657	R07364	Hs.268667	ESTs, Weakly similar to ALU1_HUMAN ALU	1.5
	100243	AB028125	Hs.77854	regucalcin (senescence marker protein-30	1.5
	116153	AF107203	Hs.57937	ataxin 2-binding protein 1	1.5
35	108892	AK000002	Hs.56879	Homo sapiens mRNA; cDNA DKFZp434L0827 (f	1.5
	113294	AI037922	Hs.11000	leptin receptor overlapping transcript-1	1.5
	126691	W03046	Hs.283684	aspartate beta-hydroxylase	1.5
	106979	AW015227	Hs.289053	hypothetical protein FLJ14733	1.5
40	125546	H09950		gb:ym01d12.r1 Soares infant brain 1NIB H	1.5
	113990	AI497945	Hs.83097	hypothetical protein FLJ22955	1.5
	129295	U63127	Hs.110121	SEC7 homolog	1.5
	125431	AW851639	Hs.75584	polymyositis/scleroderma autoantigen 2 (1.5
	112558	AK001621	Hs.15921	hypothetical protein FLJ10759	1.5
45	122046	AI560456	Hs.107319	ESTs	1.5
	122472	AA448509	Hs.128652	ESTs	1.5
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (du	1.5
	131714	AA642831	Hs.31016	putative DNA binding protein	1.5
	101233	AL135173	Hs.878	sorbitol dehydrogenase	1.5
	109501	AF047437	Hs.90436	sperm associated antigen 7	1.5
50	126984	AA213820	Hs.256533	ESTs, Weakly similar to S11998 finger pr	1.5
	125765	BE243877	Hs.76941	ATPase, Na+/K+ transporting, beta 3 poly	1.5
	127693	AA676727		gb:zj68b11.s1 Soares_fetal_liver_spleen_	1.5
	128453	X02761	Hs.287820	fibronectin 1	1.5
55	119418	T97590	Hs.221711	ESTs, Weakly similar to ALU1_HUMAN ALU	1.5
	132669	W38586	Hs.293981	guanine nucleotide binding protein (G pr	1.5
	116708	F10528	Hs.70001	ESTs, Moderately similar to J06169 nucl	1.5
	122420	AA448971		gb:zw85f11.s1 Soares_total_fetus_Nb2HF8_	1.5
	100238	L24959	Hs.348	calcium/calmodulin-dependent protein kin	1.5
60	109710	D20044	Hs.12929	hypothetical protein FLJ20721	1.5
	105704	AI282341	Hs.75431	fibrinogen, gamma polypeptide	1.5
	112712	R91060	Hs.330761	ESTs	1.5
	100098	AF003743		gb:Homo sapiens delayed rectifier potass	1.5
	114122	R46128	Hs.12751	ESTs	1.5
65	132397	AA021160	Hs.4750	hypothetical protein DKFZp564K0822	1.5
	107881	AI568350	Hs.61273	hypothetical protein MGC2650	1.5
	106302	AA398859	Hs.18397	hypothetical protein FLJ23221	1.5
	125898	AK001823	Hs.92287	Homo sapiens mRNA; cDNA DKFZp564C2478 (f	1.5
	104957	AI359009	Hs.10026	mitochondrial ribosomal protein L17	1.5
70	102909	NM_005269	Hs.2693	glioma-associated oncogene homolog (zinc	1.5
	125559	BE297488	Hs.279877	cell division protein FtsJ	1.5
	109634	H17063	Hs.183646	ESTs	1.5
	116607	W05238	Hs.94316	ESTs, Weakly similar to T31613 hypotheti	1.5
	127175	R11937		gb:yf54b08.r1 Soares infant brain 1NIB H	1.5
75	110617	W93231	Hs.285901	Homo sapiens, clone IMAGE:3948563, mRNA,	1.5
	125988	W27648		gb:37e10 Human retina cDNA randomly prim	1.5
	115093	AI241932	Hs.3542	hypothetical protein FLJ11273	1.5
	121207	AA705799	Hs.183714	ESTs	1.5
	112652	BE269699	Hs.235782	solute carrier family 21 (organic anion	1.5
80	125213	AB014554	Hs.109299	protein tyrosine phosphatase, receptor t	1.5
	125912	AW867457	Hs.278712	eukaryotic translation initiation factor	1.5
	133046	R96881	Hs.53609	HpaI tiny fragments locus 9C	1.5
	122791	AL122055	Hs.129836	KIAA1026 protein	1.5

Table 268

5	Pkey:		Unique Eos probeset identifier number
	CAT number:		Gene cluster number
10	Accession:		Genbank accession numbers
	Pkey	CAT number	Accession
10	108451	13766_27	AA079195 AA084955 AA126308 AA084956
	124195	2606_3	H83034 H52379
	123619	371581_1	AA602964 AA609200
	125165	1852047_1	W45350 W45406
	125324	1692163_1	R07785 T85948 T86972
15	126053	1601238_1	H64450 H64464
	126086	1606216_1	H75681 H70975
	126098	1629789_1	M79088 N88221
	125464	168460_1	N71807 AA203399
	125499	1562851_1	H10543 R11878
20	126127	1205826_1	N95428 W24040 AW751366 H81987
	125546	356478_1	H09950 R18413 AA570553 AW973425
	125549	1702179_1	R20215 R18767
	125558	1703083_1	R59305 R19748
	125575	1566885_1	H14983 R21554
25	125743	5025_5	H17151 H11956
	125761	1744008_1	R68351 R68364
	126426	110687_1	AA125984 AA127189 AA065075 AA070377 AA100017
			AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512 AA085119 AA085208 AA085045
			AA284993 AA478122 AA477923
30	127155	200358_1	R11937 Z45532
	127175	1695805_1	Z24895 AW891336 R01294
	126528	1276201_1	H41694 H45213
	125957	1583542_1	AA436760 AW237453 BE327496 N47347 N56967
	125976	296453_1	R98091 W92898
35	125982	1766315_1	W27648 R99193 BE090398
	125988	1365728_1	AA323958 AA370268
	127245	226662_1	AA364195 AA325029 AW962050
	127248	227560_1	AA828125 AA834883 AA330555
	127262	231725_1	T16245 R19694 F13545 H10299 T66048 T65279 H18006
40	126659	1541209_1	C05723 AA018342
	126693	87363_1	AF116622 A1114507 AA640834 AA377999
	127315	37938_1	AA442429 T19477
	126730	297653_1	AA248884
	103898	187213_3	F13008 T75435
45	127446	16001_2	AA099764 AA112950
	126826	127356_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073, BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
	126872	142696_1	BE011368 BE011362 BE011215 BE011365 BE011363
			AA225632 A1820970 A1820952 AA226472 A1732140 A1732059 AA226307
	128132	177108_1	AA225500
50	127523	351071_1	AA617637 AA554963
	126982	171753_1	AA211419 AA211566
	128215	530345_1	AA973310
	127704	405690_1	AA679609 AA694592
	127705	966283_2	AJ003322 AJ003324
55	128422	1811283_1	T77794 T85681
	127897	446527_1	AA773681 AA773857
	120734	208882_1	AA299948 AA299949
	100098	25117_13	AF003743
	114620	32062_8	AA642974 AA084223
60	122652		26401_30 AA454641
	100842		figr_HT4398 U05597
	123783		genbank_AA610112
	125032		genbank_T74884
	123808		genbank_AA620552
65	123864		genbank_AA620882
	118049		genbank_N53145
	102406		entrez_U43177
	116962		genbank_H79677
	134076	40321_1	AF086215 W02702 AA284288 W25655
70	125888	266863_1	H18298 H46830
	127271	321389_1	H96820 H79463
	113119		genbank_T47910 T47910
	104799		genbank_AA029703 AA029703
	127693	790317_1	AA676727 AA704704
75	120415		genbank_AA235810 AA235810
	127964	135151_1	F06298 R18057
	122359		681003_1 AA523486 AW026780 A1821650 AA443898
	122420		genbank_AA446971
	124276		genbank_H83465
80	101447		entrez_M21305
	124540		genbank_N63232
	124554		genbank_N65961
	117357		genbank_N24829
	103305		entrez_X82279

103392	entrez_X94563
119416	genbank_T97186
105225	genbank_AA211777
121292	genbank_AA401807
112853	genbank_T02843
121387	genbank_AA405854
114601	genbank_AA075566
100221	entrez_D28383
130339	genbank_AA435746
100554	tigr_HT2241
123423	genbank_AA598484
123474	genbank_AA599209
123489	genbank_AA599708

TABLE 27A: ABOUT 895 GENES UP-REGULATED IN COMBINED LUNG FIBROSIS COMPARED TO NORMAL BODY

Table 27A lists about 895 genes that are upregulated in lung fibrosis (collection of IPF, HP, and NSIP) samples as compared with the normal "body map" samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" fibrosis sample expression level to "average" normal adult tissues was greater than or equal to about 2.0. The "average" fibrosis sample expression level was set to the 90th percentile amongst fibrosis samples. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of fibrosis to normal body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	56.0
424917	AI636208	Hs.96901	Homo sapiens cDNA: FLJ23049 fis, clone L	26.5
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitter)	25.5
457200	U33749	Hs.197764	thyroid transcription factor 1	22.2
414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	21.1
429272	W25140	Hs.110667	ESTs	19.4
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial)	19.1
442006	AW975183	Hs.292663	ESTs	18.8
445885	AI734009	Hs.127699	KIAA1603 protein	18.0
440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	17.8
422426	W79117	Hs.58569	ESTs, Weakly similar to rhoklein [M.musc]	17.4
444929	AI685841	Hs.161354	ESTs	16.5
440807	AV269421	Hs.128093	ESTs	16.3
408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	14.2
446967	AI699629	Hs.156781	ESTs	13.3
417801	AA417383	Hs.82582	Integrin, beta-like 1 (with EGF-like rep	12.3
437119	AI379921	Hs.177043	ESTs	12.3
451103	R52804	Hs.25956	DKFZP564D206 protein	11.5
443450	N66045	Hs.133529	ESTs	11.4
411880	AW872477	gb:hm30703.x1 NCL_CGAP_Thy4 Homo sapiens		11.3
432519	AI221311	Hs.130704	ESTs	11.0
414142	AW368397	Hs.150042	ESTs	10.1
433283	BE041135	Hs.175622	ESTs	10.1
441082	AW444804	Hs.202655	ESTs	10.0
452039	AI922988	Hs.172510	ESTs	9.9
417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	9.8
421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511.1 H	9.8
412372	R65998	Hs.118615	ESTs	9.7
426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfamily	9.4
431007	AF039564	Hs.248211	retinoblastoma-binding protein 9	9.3
443709	AI082692	Hs.134662	ESTs	9.2
446232	AI281848	Hs.165547	ESTs	9.2
448253	H25899	Hs.201591	ESTs	9.1
432133	AB033088	Hs.272587	KIAA1262 protein	9.0
409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp5564G112 (fr	8.8
431353	AA828032	Hs.189076	ESTs	8.8
450050	AI681268	Hs.257883	ESTs	8.8
458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	8.7
414968	C16096	Hs.297777	ESTs	8.7
425664	AJ006276	Hs.159003	transient receptor potential channel 6	8.6
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	8.5
453672	U73531	Hs.34526	G protein-coupled receptor	8.5
429420	AK001679	Hs.202289	hypothetical protein FLJ10376	8.4
421478	AI683243	Hs.97258	ESTs	8.4
404916				8.3
444396	T65213	Hs.4257	ESTs	8.3
442275	AW449467	Hs.54795	ESTs	8.2
437479	R61866	Hs.101277	ESTs	8.2
432203	AA305746	Hs.49	macrophage scavenger receptor 1	7.9
431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	7.9
406747	AI925153	Hs.217493	annexin A2	7.8

	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	7.7
	450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	7.6
	421798	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	7.5
	421155	H87879	Hs.102267	lysyl oxidase	7.5
5	446917	AI347863	Hs.156672	ESTs	7.5
	422798	R92347	Hs.34574	ESTs	7.4
	426830	AA385751	Hs.160392	ESTs	7.4
	437157	BE048860	Hs.120655	ESTs	7.4
10	433231	AB040826	Hs.143552	KIAA1493 protein	7.3
	451561	N52812	Hs.177403	ESTs	7.1
	430656	AA482900	Hs.162080	ESTs	7.1
	448206	BE522585	Hs.3731	ESTs	7.1
	420209	AA256444	Hs.32295	Homo sapiens cDNA FLJ12604 fis, clone NT	7.0
15	426803	AA362568	Hs.179747	ecotropic viral integration site 5	6.9
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	6.9
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	6.8
	443324	R44013	Hs.164225	ESTs	6.8
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	6.8
20	427356	AW023482	Hs.97849	ESTs	6.7
	418735	N48769	Hs.44609	ESTs	6.7
	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	6.6
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	6.6
	430099	AW194988	Hs.20537	Homo sapiens cDNA FLJ13942 fis, clone Y7	6.6
25	441835	AB036432	Hs.184	advanced glycosylation end product-speci	6.5
	428508	BE252383	Hs.184668	SBB131 protein	6.5
	438202	AW169287	Hs.22588	ESTs	6.5
	441233	AA972965	Hs.135568	ESTs	6.4
	433384	AI021992	Hs.124244	ESTs	6.3
	427043	AA397679	Hs.298460	ESTs	6.3
30	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	6.3
	438909	AF085839		gb:Homo sapiens full length insert cDNA	6.3
	433365	AF026944	Hs.293797	ESTs	6.3
	456964	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	6.2
35	445186	AW614544	Hs.123641	protein tyrosine phosphatase, receptor t	6.2
	431337	N48107	Hs.292593	ESTs	6.1
	434819	AA650099	Hs.291541	ESTs	6.0
	458219	H22195	Hs.31874	ESTs	6.0
	434377	AW137148	Hs.136348	osteoblast specific factor 2 (fascidin	5.9
40	435933	AA805520	Hs.192075	ESTs	5.9
	436954	AA740151	Hs.130425	ESTs	5.9
	445424	AB028945	Hs.12696	coractin SH3 domain-binding protein	5.8
	449108	AI140683	Hs.98328	ESTs	5.8
	410334	AW979261	Hs.291993	ESTs	5.7
	447112	H17800	Hs.7154	ESTs	5.7
45	447700	AA20183	Hs.171077	ESTs, Weakly similar to similar to serin	5.7
	449208	AW263635	Hs.48643	ESTs	5.7
	445657	AW612141	Hs.279575	ESTs	5.7
	421554	AW137676	Hs.97775	ESTs, Weakly similar to Testis-specific	5.7
	435299	AI745458	Hs.122614	ESTs, Weakly similar to apoptotic protea	5.6
50	416769	AI339257	Hs.115436	ESTs	5.6
	433527	AW235613	Hs.133020	ESTs	5.6
	452771	T05477		gb:EST03368 Fetal brain, Stratagene (cat	5.6
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	5.5
55	411514	AW850178	Hs.18995	KIAA1304 protein	5.5
	424084	AI940575	Hs.20914	Homo sapiens cDNA: FLJ23056 fis, clone L	5.5
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.4
	429710	AI337113	Hs.146025	Homo sapiens cDNA: FLJ23594 fis, clone L	5.4
	432113	AA935065	Hs.152385	ESTs	5.4
	447997	H00656	Hs.29792	ESTs	5.4
60	449328	AI962493	Hs.197647	ESTs	5.3
	416575	W02414	Hs.38383	ESTs	5.3
	432009	AL137424		gb:Homo sapiens mRNA; cDNA DKFZp761G2123	5.3
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	5.3
65	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	5.2
	414299	AA142989	Hs.71730	ESTs	5.2
	431041	AA490967	Hs.105276	ESTs	5.2
	448104	AI674818	Hs.178391	ribosomal protein L44	5.2
	445279	R41900	Hs.22245	ESTs	5.1
70	408978	AL133617	Hs.49421	Homo sapiens mRNA; cDNA DKFZp434M0728 (f	5.1
	415094	D59513		gb:HUM042H108 Clontech human fetal brain	5.1
	428244	AI564123	Hs.42500	ADP-ribosylation factor-like 5	5.1
	452784	BE463857	Hs.151258	Homo sapiens cDNA: FLJ21062 fis, clone C	5.1
	455431	AW938484	Hs.80738	sialophorin (gpL115, leukostatin, CD43)	5.1
	449416	AI651016	Hs.246311	ESTs	5.1
75	421659	NM_014459	Hs.106511	protocadherin 17	5.1
	407638	AJ404672	Hs.288693	Homo sapiens cDNA FLJ11667 fis, clone HE	5.0
	446164	AW273539	Hs.199329	Homo sapiens cDNA: FLJ23577 fis, clone L	5.0
	413048	M93221	Hs.75182	mannose receptor, C type 1	5.0
80	446608	N75217	Hs.257846	ESTs	4.9
	419807	R77402		gb:Y17511.1.1 Soares placenta NbZHP Homo	4.9
	447164	AF026941	Hs.17518	Homo sapiens c1g5 mRNA, partial sequence	4.9
	426552	AI005163	Hs.201378	ESTs, Weakly similar to KIAA0944 protein	4.9
	429496	AA453800	Hs.192793	ESTs	4.8

	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor I	4.8
	432824	AK001783	Hs.279012	hypothetical protein FLJ10921	4.8
	425509	AF079363	Hs.158213	sperm associated antigen 6	4.8
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	4.8
5	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	4.7
	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	4.7
	453382	AA709285	Hs.5997	Homo sapiens cDNA FLJ13078 fis, clone NT	4.7
	447033	AI357412	Hs.157601	ESTs	4.7
	417235	AA810278	Hs.24250	ESTs	4.7
10	418200	AW629751	Hs.206654	ESTs, Weakly similar to alternatively sp	4.7
	427652	AI673025	Hs.43874	ESTs	4.7
	431255	AA497043	Hs.115885	ESTs	4.7
	441143	AI027604	Hs.159650	ESTs	4.7
	452293	AI871833		gb:wm51h09.x1 NCI_CGAP_U12 Homo sapiens	4.7
15	443903	AI220547	Hs.135223	ESTs	4.7
	422352	AA766296	Hs.99200	ESTs	4.6
	424105	AI142336	Hs.43977	ESTs	4.6
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	4.6
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.6
20	430510	AW162916	Hs.241576	hypothetical protein PRO2577	4.6
	425804	BE501698	Hs.258189	ESTs	4.6
	435347	AW014873	Hs.116963	ESTs	4.6
	446002	AI346468	Hs.145789	ESTs	4.6
	452883	X80031	Hs.150318	ESTs	4.6
25	442176	AA983764	Hs.128910	ESTs	4.5
	443253	AI041212	Hs.132117	ESTs	4.5
	419556	U29515	Hs.91093	chitinase 1 (chitinotrioidase)	4.5
	439920	H05430	Hs.144455	ESTs	4.5
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	4.4
30	434424	AI811202	Hs.125365	Homo sapiens cDNA: FLJ23523 fis, clone L	4.4
	408625	AW243323	Hs.266785	ESTs	4.4
	449299	AA299919		gb:EST12592 Uterus tumor I Homo sapiens	4.4
	450656	AA010539	Hs.18912	ESTs	4.4
	433815	AI696602	Hs.112757	ESTs	4.3
35	416879	H98899	Hs.42599	ESTs	4.3
	432182	AW607789	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.3
	445386	AA22005	Hs.160380	ESTs	4.3
	450478	AW451709	Hs.271200	ESTs	4.3
	453080	AA23056	Hs.23921	Homo sapiens cDNA FLJ12482 fis, clone NT	4.3
40	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	4.3
	443257	AI334040	Hs.11614	Homo sapiens cDNA: FLJ23555 fis, clone L	4.3
	453921	AI824009	Hs.44577	ESTs	4.2
	419721	NM_001650	Hs.288650	aquaporin 4	4.2
	432316	AW973235	Hs.293697	ESTs	4.2
45	435202	AI971313	Hs.170204	KIAA0551 protein	4.2
	440320	AA879294		gb:wm86e09.s1 NCI_CGAP_Pr12 Homo sapiens	4.2
	438796	W67821	Hs.109590	genethonin 1	4.2
	400269				4.1
50	447724	AW298375	Hs.24477	ESTs	4.1
	446509	AF169693	Hs.132892	protocadherin 20	4.1
	451620	AW449888	Hs.257224	ESTs	4.1
	451963	AI825440	Hs.224952	ESTs	4.1
	456408	AI288348	Hs.23450	mRNA for FLJ00023 protein	4.1
55	425895	AI269484	Hs.161427	zinc finger protein 215	4.1
	447048	AW393080	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone L	4.0
	454024	AA993527	Hs.16281	hypothetical protein FLJ23403	4.0
	415929	AA724373	Hs.295306	ESTs, Highly similar to unnamed protein	4.0
	426625	T78300	Hs.171409	serologically defined colon cancer anti	4.0
60	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	4.0
	437138	AI935622	Hs.271245	ESTs	4.0
	455024	AW851309		gb:IL3-CT0220-170200-067-C11 CT0220 Homo	4.0
	436246	AW450963	Hs.119991	ESTs	4.0
	416030	H15261	Hs.21948	ESTs	3.9
65	459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA	3.9
	445122	AW241632	Hs.147377	Homo sapiens cDNA: FLJ23598 fis, clone L	3.9
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.9
	421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f	3.9
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	3.9
70	429208	AA447990	Hs.190478	ESTs	3.9
	442957	AI949952	Hs.49397	ESTs	3.9
	444050	AW138295	Hs.135024	ESTs	3.9
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	3.9
	451024	AA442176		gb:zw63b08.r1 Soares_t0tal_fetus_Nb2HF8_	3.9
75	442832	AW206560	Hs.253569	ESTs	3.9
	423377	AL049377		gb:Homo sapiens mRNA; cDNA DKFZp586H0718	3.9
	451895	T93573	Hs.16970	ESTs	3.8
	442353	BE379594	Hs.49136	ESTs	3.8
	421464	AA291553	Hs.190086	ESTs	3.8
80	404043				3.8
	407055	X89211		gb:H.sapiens DNA for endogenous retrovir	3.8
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (93720	3.8
	410247	AF181721	Hs.61345	RU2S	3.8
	417461	R38403	Hs.13305	ESTs	3.8

	423609	AA328348	Hs.218289	ESTs	3.8
	440444	AA885221	Hs.156984	ESTs	3.8
	446254	BE179829	Hs.179852	Homo sapiens cDNA FLJ12832 fis, clone NT	3.8
	447505	AL049266	Hs.18724	Homo sapiens mRNA: cDNA DKFZp564F093 (fr	3.8
5	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	3.8
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	3.8
	444271	AW452569	Hs.149804	ESTs	3.8
	434217	AW014795	Hs.23349	ESTs	3.8
	452571	W31518	Hs.34665	ESTs	3.7
10	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	3.7
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	3.7
	431322	AW970622		gb:EST382704 MAGE resequenes, MAGK Homo	3.7
	445034	AW293376	Hs.160323	ESTs	3.7
	438842	AA827176	Hs.124316	ESTs	3.7
15	424906	AI565086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7
	415025	AW207091	Hs.72307	ESTs	3.7
	420313	AB023230	Hs.96427	KIAA1013 protein	3.7
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone CO	3.7
20	433492	AW605849		gb:MR0-HT0241-200100-006-g02 HT0241 Homo	3.7
	434636	AA083764	Hs.241334	ESTs	3.7
	435747	AI079519	Hs.134398	ESTs	3.7
	458158	AW296778	Hs.300357	ESTs, Highly similar to dJ416F21.2 [H.sa	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration sila fami	3.7
25	410060	NM_001448	Hs.58367	glypican 4	3.7
	426116	AA868729	Hs.144694	ESTs	3.7
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	3.7
	414259	W44633	Hs.25044	Homo sapiens cDNA: FLJ23131 fis, clone L	3.7
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	3.6
30	431889	AA521277	Hs.124946	ESTs	3.6
	430414	AW365665	Hs.120388	ESTs	3.6
	433426	H69125	Hs.133525	ESTs	3.6
	421764	AI681535	Hs.99342	ESTs, Weakly similar to KCC1_HUMAN CALCI	3.6
	410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	3.6
35	455235	AW875951		gb:CM1-PT0013-131299-067-409 PT0013 Homo	3.6
	408399	NM_005426	Hs.44585	tumor protein p53-binding protein, 2	3.6
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	3.6
	436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular mat	3.6
	432231	AA339977	Hs.274127	CLST 11240 protein	3.6
40	432837	AA310693	Hs.279512	HSPC072 protein	3.6
	452166	AI948607	Hs.264680	ESTs	3.5
	458154	AW816379		gb:QV4-ST0234-181199-035-g01 ST0234 Homo	3.5
	420362	U79734	Hs.97206	huntingtin interacting protein 1	3.5
	424202	BE350295	Hs.15032	ESTs, Weakly similar to RAN binding prot	3.5
45	410658	AW105231	Hs.192035	ESTs	3.5
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	419503	AA243642	Hs.137422	ESTs	3.5
	439479	AI734258	Hs.245367	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	448404	BE089973		gb:RC6-BT0709-310300-021-G07 BT0709 Homo	3.5
50	424268	AA397653	Hs.144339	Human DNA sequence from clone 495O10 on	3.5
	420637	AW976153		gb:EST388262 MAGE resequenes, MAGN Homo	3.5
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.5
	428927	AA441837	Hs.90250	ESTs	3.5
	422544	AB018269	Hs.118140	KIAA0716 gene product	3.4
55	431207	AA495925	Hs.9394	ESTs	3.4
	424508	AL080103	Hs.149770	Homo sapiens cDNA FLJ13658 fis, clone PL	3.4
	441484	AA935481	Hs.58972	ESTs	3.4
	425916	NM_008786	Hs.162200	urotensin 2	3.4
	401793				3.4
60	431169	AW971240		gb:EST383329 MAGE resequenes, MAGL Homo	3.4
	438038	AI732629	Hs.194161	ESTs, Weakly similar to TA2R HUMAN, BETA	3.4
	439619	AW975998	Hs.58595	ESTs	3.4
	446577	AB040933	Hs.15420	KIAA1500 protein	3.4
	450445	AW974636	Hs.194563	ESTs	3.4
65	459482	AA625339	Hs.237052	EST, Weakly similar to ALU1_HUMAN ALU SU	3.4
	445495	BE622641	Hs.38489	ESTs	3.4
	428743	AL080060	Hs.301549	Homo sapiens mRNA: cDNA DKFZp564H172 (fr	3.4
	426320	W47695	Hs.169300	transforming growth factor, beta 2	3.4
	432869	AW974094		gb:EST386197 MAGE resequenes, MAGM Homo	3.3
70	419235	AW470411	Hs.288433	neurotrophin	3.3
	429703	T93154	Hs.28705	ESTs	3.3
	413499	BE144884		gb:CM0-HT0182-041099-065-e11 HT0182 Homo	3.3
	406182				3.3
	417307	N99673	Hs.3585	ESTs, Weakly similar to AF126743 1 DNAJ	3.3
75	430140	AW296771	Hs.221999	ESTs	3.3
	436111	AI803082	Hs.157212	ESTs	3.3
	449729	R72032	Hs.29235	ESTs	3.3
	457620	AA602711		gb:np03h06.s1 NCL_CGAP_Pr2 Homo sapiens	3.3
	428434	AW363590	Hs.65551	ESTs, Weakly similar to AF172993 1 PLUNC	3.3
80	406554				3.3
	451381	BE241831		gb:TCAAP2E0011 Pediatric acute myelogeno	3.3
	443113	AI040686	Hs.132908	ESTs	3.3
	421470	R27496	Hs.1378	annexin A3	3.3
	446428	AW082270	Hs.210617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3

	435031	AI632091	Hs.116877	ESTs	3.3
	413136	BE066941		gb:PMO-BT0340-091299-002-a11 BT0340 Homo	3.2
	429228	AI553633	Hs.104985	ESTs	3.2
	420252	AW270404	Hs.193161	ESTs	3.2
5	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.2
	444339	T96555	Hs.31562	ESTs	3.2
	434164	AW207019	Hs.148135	ESTs	3.2
	404599				3.2
	426920	AA393351	Hs.132121	ESTs	3.2
10	453736	AL118674	Hs.34871	KIAA0569 gene product	3.2
	408923	H73881	Hs.255436	ESTs	3.2
	430919	AA489041	Hs.295448	ESTs	3.2
	431622	AW979271	Hs.293184	ESTs	3.2
	433584	AW295399		gb:U1-H-BI2-ahv-h-03-0-UI.s1 NCL_CGAP_Su	3.2
15	437073	AI885608	Hs.94122	ESTs	3.2
	438394	BE379623	Hs.27693	CGI-124 protein	3.2
	446242	N66336	Hs.7360	ESTs	3.2
	452542	AW812256		gb:RCO-ST0174-191099-031-a07 ST0174 Homo	3.2
20	454009	AW015927	Hs.233071	ESTs	3.2
	449765	N92293	Hs.206832	EST, Moderately similar to ALU8_HUMAN AL	3.2
	415652	T79213	Hs.272073	ESTs	3.2
	453931	AL121278	Hs.25144	ESTs	3.2
	439382	BE247684	Hs.103070	ESTs	3.2
25	420077	AW512260	Hs.87767	ESTs	3.2
	430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	3.1
	446745	AW118189	Hs.156400	ESTs	3.1
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	3.1
	450320	AW291775	Hs.213793	ESTs	3.1
30	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.1
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.1
	451110	AI955040	Hs.301584	ESTs	3.1
	431745	AW972448	Hs.163425	ESTs	3.1
	410781	AI375672	Hs.165028	ESTs	3.1
35	419546	AA244199		gb:nc06c05.s1 NCL_CGAP_Pr1 Homo sapiens	3.1
	444330	AI597655	Hs.49265	ESTs	3.1
	408761	AA057264	Hs.238936	ESTs	3.1
	409026	AL137554	Hs.49927	Homo sapiens mRNA; cDNA DKFZp434H1720 (f	3.1
	432055	AW972359	Hs.293334	ESTs	3.1
40	432441	AW292425	Hs.163484	ESTs	3.1
	408045	AW138959	Hs.245123	ESTs	3.1
	427191	BE221825	Hs.97691	ESTs	3.1
	416965	N26223	Hs.160436	ESTs	3.1
	441594	AL041080	Hs.208765	ESTs	3.0
45	406992	S82472		gb:bela-pol=DNA polymerase beta (exon a	3.0
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	3.0
	438323	AI985394	Hs.123369	ESTs	3.0
	427698	AW972594	Hs.294140	ESTs	3.0
	424296	AI631874	Hs.169391	ESTs	3.0
50	450522	AI698839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.0
	407942	AA378608	Hs.5894	hypothetical protein FLJ10305	3.0
	417991	AA731452	Hs.190008	ESTs	3.0
	422589	AA312735	Hs.179725	ESTs	3.0
	437583	AA761190	Hs.244627	ESTs	3.0
55	452019	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.0
	449494	AW237014	Hs.288650	aquaporin 4	3.0
	444188	AI393165	Hs.19175	ESTs	3.0
	400297	AI127076	Hs.288381	hypothetical protein DKFZp564O1278	3.0
	410811	AW805687	Hs.300648	ESTs	3.0
60	450584	AA040403	Hs.60371	ESTs	3.0
	428043	T92248	Hs.2240	uteroglobin	3.0
	436120	AI248193	Hs.119860	ESTs	2.9
	442324	R63578	Hs.28426	ESTs	2.9
	448693	AW004854	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone L	2.9
65	425555	AA359291	Hs.130787	Homo sapiens cDNA: FLJ23553 fis, clone L	2.9
	431385	BE178536	Hs.11090	high affinity immunoglobulin epsilon rec	2.9
	408427	AW194270	Hs.177236	ESTs	2.9
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_Nbh	2.9
	438128	AA904430	Hs.122049	ESTs, Weakly similar to U4/U6 small nucl	2.9
70	408938	AA059013	Hs.22607	ESTs	2.9
	419276	BE165909	Hs.134682	Homo sapiens cDNA: FLJ23161 fis, clone L	2.9
	422022	AA302420	Hs.200442	ESTs	2.9
	426890	AA393167	Hs.41294	ESTs	2.9
	427374	AI150033	Hs.143686	ESTs	2.9
75	434208	T92641	Hs.127648	hypothetical protein PRO2176	2.9
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	2.9
	451229	AW967707	Hs.48473	ESTs	2.9
	415511	AI732617	Hs.182362	ESTs	2.9
	408776	AA057365	Hs.63356	ESTs	2.9
80	421110	AJ250717	Hs.1355	cathepsin E	2.9
	453636	R67837	Hs.169872	ESTs	2.9
	436578	AI091435	Hs.134859	ESTs	2.9
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	2.9
	419231	AL046294	Hs.136245	ESTs, Weakly similar to cJ202121.4 [H.sa	2.8

5	408171	AA301228	Hs.43299	Homo sapiens cDNA FLJ12890 fis, clone NT	2.8
	445189	AI936450	Hs.147482	ESTs	2.8
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	2.8
	427457	AW779105	Hs.164582	ESTs, Weakly similar to ORF2 consensus s	2.8
	435082	AA664273	Hs.186104	Homo sapiens cDNA FLJ13803 fis, clone TH	2.8
10	446932	AA961459	Hs.125644	ESTs	2.8
	439140	W85737	Hs.290830	ESTs	2.8
	405041				2.8
	421306	AA806207	Hs.125889	ESTs	2.8
	427514	AA640773	Hs.209224	ESTs	2.8
15	427939	T92459	Hs.16886	ESTs	2.8
	429127	AA749382	Hs.107233	ESTs	2.8
	429590	AI219490	Hs.44445	ESTs, Weakly similar to Kelch motif cont	2.8
	433163	R40468	Hs.163582	ESTs	2.8
	439635	AA477288	Hs.94891	Homo sapiens cDNA: FLJ22729 fis, clone H	2.8
20	448015	AI458065	Hs.23196	ESTs	2.8
	456761	D59899	Hs.127842	CGI-142	2.8
	457112	AW772449	Hs.268081	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
	449540	AA001713		gb:zh86e08.s1 Soares_fetal_liver_spleen_	2.8
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	2.8
25	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	2.8
	433515	AA595800	Hs.190246	ESTs	2.8
	424450	AL137526	Hs.147472	dynein intermediate chain 2	2.8
	438122	AI620270	Hs.129837	ESTs	2.8
	424086	AI351010	Hs.102267	lysyl oxidase	2.8
30	438885	AI886558	Hs.184987	ESTs	2.8
	412903	BE007967	Hs.155795	ESTs	2.8
	454111	AW081681	Hs.269064	ESTs	2.8
	439398	AA264267	Hs.221504	ESTs	2.8
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	2.8
35	434812	AA649860	Hs.189496	ESTs	2.8
	432583	AW023624	Hs.162282	ESTs	2.8
	428104	AA421350	Hs.191604	ESTs	2.8
	408217	AI433201	Hs.279860	hypothetical protein FLJ20030	2.8
	438016	AI949638	Hs.109150	SH3-domain binding protein 5 (BTK-assoc	2.8
40	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HE	2.7
	430887	N66801	Hs.260267	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
	446311	AW007294	Hs.149795	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	416185	AW975861	Hs.291995	ESTs	2.7
	408613	AW242086	Hs.253957	ESTs	2.7
45	442510	AF150179	Hs.249890	ESTs	2.7
	433293	AF007835	Hs.32417	ESTs	2.7
	413875	BE176776		gb:RC3-HT0586-110300-011-g09 HT0586 Homo	2.7
	404488				2.7
	408936	AL138043	Hs.293549	ESTs	2.7
50	431980	AA523696	Hs.222695	Homo sapiens cDNA: FLJ20986 fis, clone C	2.7
	436738	AW102613	Hs.152913	ESTs	2.7
	451797	AW663858	Hs.56120	ESTs	2.7
	452163	AI863140		gb:tz43h12x1 NCI_CGAP_Bm52 Homo sapien	2.7
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.7
55	459366	AA129703		gb:zn92b05.r1 Stratagene lung carcinoma	2.7
	431448	AL137517	Hs.288381	hypothetical protein DKFZp56401278	2.7
	430733	AW975920	Hs.283361	ESTs	2.7
	453652	AW009640	Hs.28368	ESTs	2.7
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	2.7
60	411905	BE265067		gb:601193893F1 NIH_MGC_7 Homo sapiens cD	2.7
	408729	AA195764	Hs.72639	ESTs	2.7
	450726	AW204600	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.7
	447720	AL038765	Hs.161304	ESTs	2.7
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	2.7
65	442074	C17511	Hs.128430	ESTs	2.7
	424115	AA335497	Hs.293965	ESTs	2.7
	417728	AW138437	Hs.24790	KIAA1573 protein	2.7
	433803	AI823593	Hs.27688	ESTs	2.7
	419247	S65791	Hs.89764	fragile X mental retardation 1	2.7
70	424310	AA338548	Hs.50334	ESTs	2.6
	438504	AW665281	Hs.224625	ESTs	2.6
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp58680220 (f	2.6
	430417	AA461045	Hs.50701	ESTs	2.6
	438297	AW515196	Hs.258238	ESTs, Moderately similar to ALU1_HUMAN A	2.6
75	422505	AL120862	Hs.124165	ESTs	2.6
	457285	AI038858	Hs.228780	ESTs, Highly similar to AF199597 1 A-tyr	2.6
	428667	AI375550	Hs.74407	nuclear protein p40; homolog of yeast	2.6
	431750	AA514986	Hs.283705	ESTs	2.6
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	2.6
80	413385	M34455	Hs.840	indoleamine-pyrole 2,3 dioxygenase	2.6
	403903				2.6
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.6
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	2.6
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	2.6
	436645	AW023424	Hs.156520	ESTs	2.6
	408380	AF123050	Hs.44532	diubiquitin	2.6
	402629				2.6

	406594				2.6
	415122	D60708	Hs.22245	ESTs	2.6
	416747	AW876523	Hs.15929	Homo sapiens cDNA FLJ12910 fis, clone NT	2.6
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.6
5	444361	W76027	Hs.23920	Homo sapiens cDNA FLJ13124 fis, clone NT	2.6
	446609	BE395090	Hs.15535	Human gene from PAC 886K2, chromosome 1	2.6
	449260	AA741180	Hs.29879	ESTs	2.6
	452311	AW304029	Hs.252744 ¹	ESTs	2.6
10	413802	AW964490	Hs.32241	ESTs	2.6
	417318	AW953937	Hs.12891	ESTs	2.6
	440028	AW473675	Hs.125843	ESTs	2.6
	437960	AI689586	Hs.222194	ESTs	2.6
	433687	AA743991		gb:ny57g01.s1 NCI_CGAP_Pr18 Homo sapiens	2.6
15	430573	AA744550	Hs.136345	ESTs	2.6
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	2.6
	453204	R10799	Hs.191990	ESTs	2.6
	436751	AA732217	Hs.294054	ESTs	2.6
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	2.5
20	431120	AA492588		gb:ng99c08.s1 NCI_CGAP_Thy1 Homo sapiens	2.5
	446638	AL133063	Hs.15783	Homo sapiens mRNA; cDNA DKFZp434P1115 (f	2.5
	438458	AW975186	Hs.162875	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5
	446063	AI720140	Hs.151079	ESTs	2.5
	430499	AW969408	Hs.231991	ESTs	2.5
25	450486	AW449251	Hs.257131	ESTs	2.5
	441330	AI692984	Hs.129354	ESTs	2.5
	424433	H04607	Hs.9218	ESTs	2.5
	434677	AW444575	Hs.130834	ESTs	2.5
	445779	AI253104	Hs.189267	ESTs	2.5
30	444649	AW207523	Hs.197628	ESTs	2.5
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	2.5
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.5
	404288				2.5
	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	2.5
35	408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513	2.5
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	2.5
	410095	AW589638	Hs.258947	ESTs	2.5
	410947	AK000305	Hs.67065	hypothetical protein FLJ20298	2.5
	418343	AA216372	Hs.159501	ESTs	2.5
40	423401	NM_001892	Hs.128087	coagulation factor II (thrombin) recepto	2.5
	428637	AW979268		gb:EST391378 MAGE resequences, MAGP Homo	2.5
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	2.5
	432507	BE391093		gb:601286042F1 NIH_MGC_44 Homo sapiens c	2.5
	433858	N69243	Hs.192974	Homo sapiens cDNA FLJ12735 fis, clone NT	2.5
45	438551	H64500	Hs.123846	ESTs	2.5
	443830	AI142095	Hs.143273	ESTs	2.5
	446800	AI341635	Hs.156486	ESTs	2.5
	450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMAN A	2.5
	451343	AW975057	Hs.293353	ESTs	2.5
50	451539	AA059467	Hs.218933	ESTs	2.5
	452412	AA029608	Hs.61373	ESTs	2.5
	454288	BE222648	Hs.279458	ESTs, Highly similar to c380A1.1b [H.sap	2.5
	445745	AB007924	Hs.13245	KIAA0455 gene product	2.5
	424943	AI077260	Hs.153924	death-associated protein kinase 1	2.5
55	440106	AA854968	Hs.127699	KIAA1603 protein	2.5
	458429	AV646559	Hs.12346	Homo sapiens cDNA: FLJ21399 fis, clone C	2.5
	415261	T40928	Hs.8346	ESTs	2.5
	420026	AI831190	Hs.166676	ESTs	2.5
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam	2.5
60	458722	AA741545	Hs.282832	ESTs	2.5
	419449	H18417	Hs.57483	Homo sapiens cDNA FLJ14294 fis, clone PL	2.5
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.5
	433644	AW342028	Hs.256112	ESTs	2.5
	419172	AW338625	Hs.22120	ESTs	2.5
65	437982	N93466	Hs.121764	ESTs, Weakly similar to testicular tek1	2.5
	443348	AW873596	Hs.57572	ESTs	2.5
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.5
	418236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	2.5
	448030	N30714	Hs.20161	HDCME31P protein	2.5
70	417203	AA406341	Hs.269908	Homo sapiens cDNA FLJ11991 fis, clone HE	2.4
	449275	AW450848	Hs.205457	KIAA1620 protein	2.4
	436198	AK001125	Hs.300922	Homo sapiens cDNA FLJ10263 fis, clone HE	2.4
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	2.4
	442191	W95186	Hs.8136	endothelial PAS domain protein 1	2.4
75	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease,	2.4
	453142	AA033648	Hs.7473	ESTs	2.4
	425657	T89839	Hs.119471	ESTs	2.4
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis, clone H	2.4
	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsulf	2.4
80	458332	AI000341	Hs.220491	ESTs	2.4
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	2.4
	459644				2.4
	429125	AA446854	Hs.271004	ESTs	2.4
	448337	AW206453	Hs.3782	ESTs	2.4

5	427778	AA412323	Hs.105323	ESTs	2.4
	425371	D49441	Hs.155981	mesothelin	2.4
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.4
	447610	AW296286	Hs.255534	ESTs	2.4
	409519	AA075368		gb:zmm86h10.r1 Stratagene ovarian cancer	2.4
	441006	AW605267	Hs.7627	CGI-60 protein	2.4
	440817	AI341423	Hs.270165	ESTs	2.4
	420020	BE295866	Hs.94382	adenosine kinase	2.4
10	435395	AA729235	Hs.117907	ESTs	2.4
	424144	AA454033	Hs.41644	Homo sapiens cDNA: FLJ23003 fis, clone L	2.4
	405494				2.4
	458145	AI239457	Hs.130794	ESTs	2.4
	408547	AA574291	Hs.57837	ESTs	2.4
15	408941	AI452469	Hs.165221	ESTs	2.4
	409457	AW818081		gb:CM4-ST0276-101299-059-b09 ST0276 Homo	2.4
	417137	U46265	Hs.81281	hypothetical protein	2.4
	418950	T78517	Hs.13941	ESTs	2.4
	420756	AA411800	Hs.189900	ESTs	2.4
20	428316	AI860775	Hs.98506	ESTs	2.4
	432896	NM_014097	Hs.279778	PRO1693 protein	2.4
	436148	BE005252		gb:CM1-BN0116-030400-171-g02 BN0116 Homo	2.4
	436284	AA708016	Hs.190389	ESTs	2.4
	437327	AL353942		gb:Homo sapiens mRNA; cDNA DKFZp761L2312	2.4
25	442611	BE077155	Hs.177537	ESTs	2.4
	456062	AI866286	Hs.71962	ESTs	2.4
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.4
	401335				2.4
	428771	AB028992	Hs.193143	KIAA1069 protein	2.4
30	419140	AI982647	Hs.215725	ESTs	2.4
	454693	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	2.4
	427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.4
	407339	AA777542	Hs.132670	ESTs	2.4
	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	2.4
35	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	2.4
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	2.4
	452561	AI692181	Hs.49169	KIAA1634 protein	2.4
	427878	C05766	Hs.181022	CGI-07 protein	2.4
	419752	AA249573	Hs.152618	ESTs	2.4
40	430073	U86136	Hs.232070	telomerase-associated protein 1	2.4
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	2.4
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	2.3
	407905	AW103655	Hs.252905	ESTs	2.3
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.3
45	422355	AW403724	Hs.140	immunoglobulin heavy constant gamma 3 (G	2.3
	453049	BE537217	Hs.30343	ESTs	2.3
	438568	R98865	Hs.11135	major histocompatibility complex, class	2.3
	453445	AL036532	Hs.91453	ESTs	2.3
	424711	NM_005795	Hs.152175	calcitonin receptor-like	2.3
50	446346	AI290205		gb:ql79g06.x1 Soares_NhHMPu_S1 Homo sapi	2.3
	441974	AI683782	Hs.128245	ESTs	2.3
	444805	AB007899	Hs.12017	KIAA0439 protein; homolog of yeast ubiqu	2.3
	424027	AW337575	Hs.201591	ESTs	2.3
	419606	AW294795	Hs.198529	ESTs, Weakly similar to similar to acyl-	2.3
55	428613	AB037749	Hs.186928	KIAA1328 protein	2.3
	434340	AI183043	Hs.128685	ESTs	2.3
	450297	AW901347	Hs.38592	Homo sapiens cDNA: FLJ23342 fis, clone H	2.3
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	2.3
60	433650	AA603472	Hs.28456	ESTs	2.3
	419086	NM_000216	Hs.89591	Kellmann syndrome 1 sequence	2.3
	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PL	2.3
	430153	AW968128		gb:EST380338 MAGE resequences, MAGJ Homo	2.3
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.3
	427669	AW461832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	2.3
65	400610				2.3
	402222				2.3
	407162	N63855	Hs.142634	zinc finger protein	2.3
	415250	F02614	Hs.27319	ESTs	2.3
70	421751	AW813731	Hs.159163	ESTs	2.3
	428552	AW274560	Hs.129520	ESTs	2.3
	432658	AW973769	Hs.162319	ESTs	2.3
	434742	AA648302	Hs.291695	ESTs	2.3
	436586	AI308862	Hs.167028	ESTs	2.3
	441675	AI914329	Hs.5461	ESTs	2.3
75	442039	AW276240	Hs.128352	ESTs, Weakly similar to p80 [R]nonvegicu	2.3
	443160	AI467915	Hs.36053	ESTs	2.3
	448764	AI568607	Hs.182112	ESTs	2.3
	449579	AW207260	Hs.134014	prostate cancer associated protein 6	2.3
	439810	AL109710	Hs.85568	EST	2.3
80	413714	AI560944	Hs.71428	ESTs	2.3
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	2.3
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	2.3
	438670	AI275803	Hs.123428	ESTs	2.3
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	2.3

	459702				2.3
	414888	AL039185	Hs.77558	thyroid hormone receptor Interactor 7	2.3
	438474	AW865818	Hs.6232	KIAA0764 gene product	2.3
	453037	AA045175	Hs.177552	ESTs	2.3
5	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	2.3
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	2.3
	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapie	2.3
	415083	AI632583	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	2.3
	417015	M83772	Hs.80876	flavin containing monooxygenase 3	2.3
10	406506				2.3
	448330	AL036449	Hs.207163	ESTs	2.3
	409719	AI769160	Hs.108681	ESTs	2.3
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	2.3
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	2.3
15	427961	AW293165	Hs.143134	ESTs	2.3
	447357	AI375922	Hs.159367	ESTs	2.3
	412642	BE244598	Hs.809	hepalcocyte growth factor (hepapoletin A;	2.3
	453716	AA037675	Hs.152675	ESTs	2.3
	437370	AI359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.2
20	407949	W21874	Hs.247057	ESTs	2.2
	427972	AA864870	Hs.181304	putative gene product	2.2
	453313	BE005771	Hs.153746	Homo sapiens cDNA: FLJ22490 fis, clone H	2.2
	426476	NM_003296	Hs.2042	testis specific protein 1 (probe H4-1 p3	2.2
	424238	AA337401	Hs.137635	ESTs	2.2
25	452930	AW195285	Hs.194097	ESTs	2.2
	424527	AW138558	Hs.267158	ESTs	2.2
	453095	AW295660	Hs.252756	ESTs	2.2
	449161	N53431	Hs.47647	ESTs, Weakly similar to KIAA0423 [H.sapi	2.2
	429586	T73510	Hs.209153	angiotensin-like 3	2.2
30	423782	AI472209	Hs.288369	ESTs	2.2
	458124	AW005548	Hs.124590	ESTs	2.2
	450109	AI539295	Hs.17957	ESTs	2.2
	421461	AW291023	Hs.97255	ESTs	2.2
	412222	AA528283	Hs.292737	ESTs	2.2
35	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.2
	441736	AW292779	Hs.169799	ESTs	2.2
	401049				2.2
	440727	AI073991	Hs.134268	ESTs	2.2
40	419751	AW195581	Hs.93121	KIAA0761 protein	2.2
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.2
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.2
	410282	AA843087	Hs.124194	ESTs	2.2
	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	2.2
45	449695	AA164569	Hs.34550	ESTs	2.2
	429399	AA452244	Hs.16727	ESTs	2.2
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	2.2
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.2
50	436772	AW975688	Hs.250867	zona pellucida glycoprotein 3A (sperm re	2.2
	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	2.2
	445268	AI218358	Hs.175048	ESTs	2.2
	402481				2.2
	412608	AA247995	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.2
55	416521	H60929	Hs.44197	hypothetical protein DKFZp564D0462	2.2
	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen	2.2
	419780	AA713522	Hs.87752	ESTs	2.2
	421211	AA284966	Hs.266308	ESTs, Weakly similar to AF216312 1 type	2.2
	427541	AI798983	Hs.97961	ESTs	2.2
60	432013	AI796879	Hs.162102	ESTs	2.2
	436461	AW511956	Hs.293261	ESTs	2.2
	438002	AI560246	Hs.201648	ESTs, Weakly similar to ZN42_HUMAN ZINC	2.2
	440312	AW614597	Hs.72475	ESTs	2.2
	440479	AA886461	Hs.208161	ESTs	2.2
65	441178	W90789	Hs.153976	ESTs	2.2
	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	2.2
	443314	AW771701	Hs.54646	ESTs	2.2
	422165	AL041199	Hs.1481	histidine decarboxylase	2.2
	450696	AI654223	Hs.16026	Homo sapiens cDNA: FLJ23191 fis, clone L	2.2
70	432974	BE348793		gb:ht70g02.x1 NCL_CGAP_Lu24 Homo sapiens	2.2
	404200				2.2
	435990	AI015862	Hs.131793	ESTs	2.2
	421309	AI222086	Hs.270449	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	451558	NM_001089	Hs.26530	ATP-binding cassette, sub-family A (ABC1	2.2
75	416642	T96118	Hs.226313	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	406672	M26041	Hs.198253	major histocompatibility complex, class	2.2
	417819	AI253112	Hs.133540	ESTs	2.2
	417355	D13168	Hs.82002	endothelin receptor type B	2.2
	459574	AI741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	2.2
80	404274				2.2
	415086	AI597963	Hs.118726	ESTs	2.2
	418210	R54575	Hs.13337	ESTs, Weakly similar to unnamed protein	2.2
	419220	AA811938	Hs.291759	ESTs	2.2
	444314	AI140497		gb:row6b09.s1 Soares_fetal_liver_spleen_	2.2

	451050	AW937420	Hs.69662	ESTs	2.2
	417412	X16896	Hs.82112	Interleukin 1 receptor, type I	2.2
	428414	AL049980	Hs.184216	DKFZP564C152 protein	2.2
5	412925	AI089319	Hs.179243	ESTs	2.2
	438192	AI859065	Hs.16808	ESTs, Weakly similar to paraplegin-like	2.2
	410976	R36207	Hs.25092	ESTs	2.2
	406673	M34996	Hs.198253	major histocompatibility complex, class	2.2
	449677	AA002071		gb:zh85d01.s1 Soares_fetal_liver_spleen_	2.2
10	449321	AA001150	Hs.132937	ESTs	2.2
	418557	BE140602	Hs.246645	ESTs	2.2
	416320	H47867	Hs.34024	ESTs	2.2
	426384	AI472078		gb:ij85h03.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.2
	414140	AA281279	Hs.23317	ESTs	2.2
15	419520	AB009303	Hs.297790	Human clone 23734 mRNA sequence	2.2
	469999	AA151520	Hs.279525	hypothetical protein PRO2605	2.2
	457447	X78261	Hs.272177	H.sapiens mRNA for TRE17 5' extremity an	2.2
	451099	R52795	Hs.25954	Interleukin 13 receptor, alpha 2	2.1
	407366	AF026942		gb:Homo sapiens clg33 mRNA, partial sequ	2.1
20	410048	W76467	Hs.274550	proline oxidase homolog	2.1
	400880				2.1
	418092	R45154	Hs.106604	ESTs	2.1
	428780	AI478578	Hs.50636	ESTs	2.1
	431067	AW574823	Hs.200413	ESTs	2.1
25	432803	AA565398		gb:nk41f01.s1 NCI_CGAP_GC2 Homo sapiens	2.1
	412104	AW205197	Hs.240951	ESTs	2.1
	422819	AL122084	Hs.121073	hypothetical protein FLJ10466	2.1
	454359	N71277		gb:za36e03.s1 Soares fetal liver spleen	2.1
	424806	AA382523	Hs.105689	ESTs	2.1
30	434445	AI349306	Hs.11782	ESTs	2.1
	442994	AI026718	Hs.16954	ESTs	2.1
	410371	AA084482	Hs.115850	ESTs	2.1
	450232	BE300815	Hs.201326	ESTs	2.1
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	2.1
35	430899	BE018217	Hs.183528	ESTs, Weakly similar to Bem46-like prote	2.1
	431814	BE256242	Hs.270847	delta-tubulin	2.1
	417543	AA203620	Hs.110153	ESTs, Weakly similar to BCGF_HUMAN B-CEL	2.1
	444542	AI161293	Hs.146862	ESTs, Weakly similar to KIAA0525 protein	2.1
	404593				2.1
40	434803	AW974640		gb:EST386744 MAGE resequences, MAGM Homo	2.1
	451623	H77818	Hs.268991	ESTs	2.1
	452466	N84635	Hs.29564	Human DNA sequence from clone 682J15 on	2.1
	402046				2.1
	434927	HA6612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.1
45	436192	W93847	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	2.1
	401987				2.1
	423119	AA322201	Hs.131976	EST	2.1
	427112	Z32887	Hs.290951	ESTs	2.1
	414464	AI870175	Hs.13957	ESTs	2.1
50	447829	AI433029	Hs.184104	ESTs	2.1
	449679	AI823951	Hs.296668	Homo sapiens cDNA FLJ11846 fis, clone HE	2.1
	405472				2.1
	413621	AI808648	Hs.184156	ESTs	2.1
	432212	AW137742	Hs.293451	ESTs	2.1
55	404289				2.1
	415362	F06735		gb:HSC1JB091 normalized Infant brain cDN	2.1
	427739	AW196755	Hs.98105	ESTs	2.1
	427772	AA412289	Hs.98123	ESTs	2.1
	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.1
60	434335	AA630107	Hs.213220	ESTs	2.1
	436052	AI021983	Hs.271432	ESTs	2.1
	442773	AB037722	Hs.8707	Homo sapiens mRNA; cDNA DKFZp434N1131 (f	2.1
	446799	AW978373	Hs.49221	ESTs, Weakly similar to zinc finger prot	2.1
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	2.1
65	455673	BE065939		gb:RC3-BT0319-100100-012-c11 BT0319 Homo	2.1
	458624	AI362790	Hs.181801	ESTs	2.1
	405095				2.1
	447207	AA442233	Hs.17731	hypothetical protein FLJ12692	2.1
	433589	AA886530	Hs.188912	ESTs	2.1
70	438398	AA806526	Hs.130277	ESTs	2.1
	447233	AW246333	Hs.17901	Homo sapiens cDNA: FLJ21974 fis, clone H	2.1
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.1
	431087	H12723	Hs.290791	ESTs	2.1
	409064	AA062954	Hs.141883	ESTs	2.1
75	427558	D49493	Hs.2171	growth differentiation factor 10	2.1
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	2.1
	438118	AW753311	Hs.259415	ESTs	2.1
	427621	BE621182	Hs.179882	Homo sapiens cDNA FLJ12437 fis, clone NT	2.1
	452114	N22687	Hs.8236	ESTs	2.1
80	448782	AL050285	Hs.301550	KIAA0758 protein	2.1
	403937				2.1
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	2.1
	452416	AA026115	Hs.114777	ESTs	2.1
	451609	AL046019	Hs.209276	ESTs	2.1

	435934	R19382	Hs.117869	ESTs	2.1
	445158	AJ992108	Hs.127206	ESTs	2.1
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	2.1
	439335	AA742697	Hs.62492	ESTs, Weakly similar to S59856 collagen	2.1
5	443949	AW827419	Hs.235070	ESTs	2.1
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.1
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	2.1
	438576	AA813745	Hs.123446	ESTs	2.1
	405848				2.1
10	416940	N75620	Hs.43157	ESTs	2.1
	442381	AI185136	Hs.48650	ESTs	2.1
	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp58611823 (f	2.1
	436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	2.1
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	2.1
15	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	2.1
	439425	AF086244	Hs.114659	ESTs	2.1
	421168	AF182277	Hs.1360	cytochrome P450, subfamily IIB (phenobar	2.1
	449611	AI970394	Hs.197075	ESTs	2.1
	404548				2.1
20	416734	H81213	Hs.14825	ESTs	2.1
	435865	AA883552	Hs.16810	ESTs	2.1
	439072	AF085930	Hs.269123	ESTs	2.1
	447482	AB033059	Hs.18705	KIAA1233 protein	2.1
	457292	AI921270	Hs.214178	Homo sapiens cDNA FLJ14251 fis, clone OV	2.1
25	444974	AI203500	Hs.151612	ESTs	2.1
	456034	AW450979		gb:U1-H-B13-ata-a-12-0-UI.s1 NCL.CGAP_Su	2.1
	430634	AI860651	Hs.26685	ESTs	2.0
	426782	R14614	Hs.191254	ESTs	2.0
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	2.0
30	445326	AJ220072	Hs.165893	ESTs	2.0
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.0
	409994	D86864	Hs.57735	acetyl LDL receptor; SREC	2.0
	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	2.0
	455226	AW902103		gb:QV0-NN1022-120500-220-c07 NN1022 Homo	2.0
35	417321	N68722	Hs.191368	ESTs	2.0
	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.0
	404323				2.0
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	2.0
40	421047	AW514772	Hs.104473	ESTs	2.0
	425497	AA524596	Hs.188844	ESTs	2.0
	444623	AI183829	Hs.202111	ESTs	2.0
	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.0
	433563	AI732637	Hs.277901	ESTs	2.0
	406485				2.0
45	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.0
	455807	BE141140		gb:MR0-HT0075-021299-006-d07 HT0075 Homo	2.0
	425465	L18964	Hs.1904	protein kinase C, iota	2.0
	449424	AW448937	Hs.197030	ESTs	2.0
50	427940	AA417812	Hs.38775	ESTs	2.0
	411502	AW946605	Hs.250154	Homo sapiens cDNA FLJ12973 fis, clone NT	2.0
	411365	M76477	Hs.278242	tubulin, alpha, ubiquitous	2.0
	412369	H80456	Hs.285243	Homo sapiens cDNA: FLJ22029 fis, clone H	2.0
	452959	AJ933416	Hs.189674	ESTs	2.0
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	2.0
55	428775	AA434579	Hs.143691	ESTs	2.0
	420000	AB036063	Hs.180726	Homo sapiens cDNA FLJ13543 fis, clone PL	2.0
	408321	AW405882	Hs.44205	cortistatin	2.0
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	2.0
60	411050	AW814902		gb:MR1-ST0206-120400-022-f08 ST0206 Homo	2.0
	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapien	2.0
	428978	AA442784	Hs.125445	ESTs	2.0
	458562	N34128	Hs.145268	ESTs	2.0
	425527	AL162032	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	2.0
	403760				2.0
65	424368	AB037766	Hs.146085	KIAA1345 protein	2.0
	421229	AI056590	Hs.7085	Homo sapiens cDNA: FLJ23000 fis, clone L	2.0
	436304	AA339622	Hs.108887	ESTs	2.0
	453498	BE181412	Hs.23245	Homo sapiens cDNA FLJ11767 fis, clone HE	2.0
	439018	AW300887	Hs.26638	ESTs, Weakly similar to unnamed protein	2.0
70	453280	AL157476	Hs.32913	Homo sapiens mRNA; cDNA DKFZp761C082 (fr	2.0
	420193	AI460080	Hs.202869	ESTs	2.0
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.0
	401575				2.0
75	419092	J05581	Hs.89603	mucin 1, transmembrane	2.0
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	2.0
	410763	AF279145	Hs.8966	tumor endothelial marker 8	2.0
	414783	AW069569	Hs.75839	zinc finger protein 6 (CMPX1)	2.0
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.0
	405963				2.0
80	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.0
	420831	AA280824	Hs.190035	ESTs	2.0
	424152	AL133591	Hs.301405	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.0
	424641	AB001106	Hs.151413	gila maturation factor, beta	2.0

5	427616	AI698684	Hs.98028	ESTs	2.0
	435115	AI821726	Hs.116603	ESTs	2.0
	437636	AA764781	Hs.291844	ESTs	2.0
	438295	AI394151	Hs.37932	ESTs	2.0
	439430	AF124250	Hs.6564	breast cancer anti-estrogen resistance 3	2.0
10	445388	AI925280	Hs.236842	EST	2.0
	447101	N72185	Hs.44189	ESTs	2.0
	448796	AA147829	Hs.33193	ESTs, Highly similar to AC007228 3 BC372	2.0
	449623	C00719	Hs.120440	ESTs	2.0
	450159	AI702416	Hs.200771	ESTs, Weakly similar to CAN2_HUMAN CALPA	2.0
15	456613	R19992	Hs.106620	Homo sapiens clone 23950 mRNA sequence	2.0
	457233	AI355009	Hs.221698	ESTs	2.0
	457384	AA501760	Hs.18075	chromosome 9 open reading frame 3	2.0
	457471	AW971364		gb:EST383453 MAGE resequences, MAGL Homo	2.0
					2.0

TABLE 27B

20	Pkey:	Unique Eos probeset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
25	Pkey	CAT number	Accession		
	409457	1132521_1	AW818081 AW392887 AW514700 AW392881		
	409519	113722_1	AA075368 AA075369		
	410008	116812_1	AA079552 BE142525 BE142527		
	410785	1221055_1	AW803341 AW803265 AW803403 AW803468 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355		
30	411050	1230330_1	AW814902 BE156658 BE156667 BE156590 BE156441 BE156447		
	411880	1263110_1	AW872477 BE088101 T05990		
	411905	1265181_1	BE265067 BE264978 AW875420		
	412303	1288130_1	AW936336 AW936339		
	413136	1350379_1	BE066941 BE066911 BE066979 BE066929 BE066925		
35	413499	1373910_1	BE144884 H97942		
	413875	1396766_1	BE176776 H85072		
	415094	1522103_1	D59513 D59515 D80174 D59514		
	415362	1534980_1	F06735 R55896 R12110 H08697		
	416624	1604694_1	H69044 T47567 H75691 T50292		
40	418378	174656_1	AW962081 AA218925 AA354237		
	419546	185766_1	AA244199 AA244272 H57440		
	419807	188252_1	R77402 AA262462 AA250988 R06794		
	420637	195241_1	AW976153 AA278945 AA747691		
	422429	216469_1	AA310527 AW962295 Z44865 H06641		
45	423377	22769_1	AL049377 AL079930 AL047223 AW885968 AA385235		
	426384	266211_1	AI472078 AA377209 AA865807		
	428637	293660_1	AW979268 AA878419 AA431342 AA431628		
	430153	313709_1	AW968128 AA468102 AA468165		
	430844	324570_1	T94960 AA487679 T95013		
50	431120	328264_1	AA492588 AA492498 AA492571		
	431169	328799_1	AW971240 AA453843 AA493723		
	431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188		
	432009	34025_1	AL137424 BE007148 T52277		
	432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528756		
55	432507	348711_1	BE391093 AA551334 BE389643		
	432779	354024_1	AW978241 AA565006 AA847102		
	432803	354267_1	AA565398 AW894072 H97930		
	432869	355475_1	AW974094 AA569074 AA602574		
	432974	356950_1	BE348793 AA573118 N79366		
60	433492	367934_1	AW605849 AW282898 N41060 AA594852		
	433584	370400_1	AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 AA778832		
	433687	373061_1	AA743991 AA604852 AW272737		
	434803	393471_1	AW974640 AA649516 N75626		
	436148	41500_1	BE005252 AK000786		
65	437327	43610_1	AL353942 AW994305		
	438909	46684_1	AF085839 R69137 AW188788 R69254		
	440320	491930_1	AA879294 N67538 AA74541		
	444314	600667_1	AI140497 AW749625 AW749626 AW749644		
	444610	612257_1	AI174783 R83569 R12271		
70	446346	673545_1	AI290205 AW235762 AI651268		
	447197	711623_1	R36075 AI366546 R36167		
	448404	761515_1	BE089973 AI498612 AW805032		
	449299	80436_1	AA299919 AW957012 AA001107 T83631 BE156389		
	449540	80945_2	AA001713 H63836		
75	449677	81270_1	AA002071 AA002232 T99209		
	450522	837264_1	AI698839 AI909260 AI909259		
	451024	85565_1	AA442176 AA259181		
	451381	867770_1	BE241831 AW249135 BE548847 AW250245		
	452163	902067_1	AI863140 W80703 R43474		
80	452293	909195_1	AI871833		
	452453	918300_1	AI902519 AI902518 AI902516		
	452542	921410_1	AW812256 AW812257 AI906423 AI906422		
	452771	930983_1	T05477 T07855 AI917711		
	454359	1130674_1	N71277 AW390764		

454693	1229132_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
455024	1249196_1	AW851309 AW850888 AW851419 AW851412 AW851299
455226	1262534_1	AW902103 AW859012 AW869139
455235	1266634_1	AW875951 AW875950 AW875936 AW875948 AW875939 AW875957
455673	1349656_1	BE065939 BE066079 BE065956
455807	1370914_1	BE141140 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108
	456034	142696_1 AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
		BE011368 BE011362 BE011215 BE011365 BE011363
457471	340916_1	AW971364 AA525021 AA570759
457620	371514_1	AA602711 BE078290
458154	491768_1	AW816379 AA888282 AA879046 AA879195
459267	966605_1	AJ003631 AJ003650 AJ003651

TABLE 27C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source: 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400610	9887671	Minus	117606-117928,124040-124147
400880	9931121	Plus	29235-29336,36363-36580
401049	7232177	Plus	149157-150692
401335	9884881	Plus	15736-16352
401575	7229804	Minus	76253-76364
401793	7263888	Minus	102945-103083
401987	4406829	Minus	72893-73021,76938-77049
402046	8072415	Plus	166394-166556,168167-168395
402222	9958106	Plus	3261-3834,3939-4269
402481	9797406	Plus	87891-88991
402629	9931216	Plus	33641-33775,34182-34372,36003-36084,40343-40612
403760	7712202	Minus	45910-46260,47563-47824
403903	7710671	Minus	101165-102597
403937	7711761	Minus	12609-12773
404043	9558573	Plus	29042-29135,46597-46699
404200	6010176	Minus	7066-7210
404274	9885189	Plus	104127-104318
404288	2769644	Plus	3512-3691
404289	2769644	Plus	15049-15286,30267-30457
404323	9719753	Minus	31913-32219
404488	8113286	Minus	64835-64994
404548	8570305	Minus	83896-84162
404593	9944086	Minus	74922-75788
404599	8705107	Plus	110443-110733
404916	7341826	Plus	91057-91188
405041	7547195	Plus	121230-121714
405095	8072599	Plus	138877-139066
405472	8439781	Plus	106297-106447,108462-108596
405494	8050952	Minus	70284-70518
405848	7651809	Minus	28135-28244
405963	8247786	Plus	4056-4699
406182	5923650	Minus	28256-28935
406485	7711305	Plus	125036-125422
406506	7711374	Minus	6843-8077
406554	7711566	Plus	106956-107121
406594	8248611	Minus	35543-35845

TABLE 28A: ABOUT 796 GENES DOWN-REGULATED IN LUNG FIBROSIS COMPARED TO NORMAL BODY

Table 28A lists of about 796 genes that are downregulated in lung fibrosis (collection of IPF, HP, and NSIP) samples as compared with normal "body map" samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" fibrosis sample expression level to "average" normal adult tissues sample expression was less than or equal to 0.1. The "average" normal lung tissue level was set to the 75th percentile amongst normal lung tissues. The "average" fibrosis expression level was set to the 95th percentile amongst fibrosis samples. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of normal lung to fibrosis

Pkey	ExAccn	Unigene ID	Unigene Title	R1
414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	18.18
421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	9.39
404518	AJ815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	8.30
404795				5.56

	403211				5.46
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	5.43
	400489				5.19
5	425571	AJ007292	Hs.158306	ephrin-A2	5.19
	406357				5.08
	407979	AA046306	Hs.62927	ESTs	5.08
	452378	AA025855	Hs.19597	ESTs	4.78
	408053	AW139474	Hs.246862	ESTs	4.62
10	421770	AA374192	Hs.108124	ribosomal protein L41	4.52
	425126	N32759	Hs.172944	chorionic gonadotropin, beta polypeptide	4.49
	402386				4.39
	402448				4.37
	448245	AI923551	Hs.170843	ESTs	4.31
15	413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	4.29
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	4.24
	447768	X86400	Hs.19520	FXFD domain-containing ion transport reg	4.21
	405163				4.19
	437120	AI356125	Hs.157767	ESTs, Weakly similar to human HOXA2 [Hs	4.19
	409020	AA062549	Hs.21162	ESTs	4.09
20	431073	BE254470	Hs.249186	cone-rod homeobox	4.07
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	4.05
	403716				3.99
	424969	AW950928	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	3.94
	404348				3.90
25	407070	Y10209		gb:H.sapiens mRNA for CD30L protein	3.82
	412919	AI368680	Hs.816	SRY (sex determining region Y)-box 2	3.81
	402409				3.80
	456150	Z42308		gb:HSC0FB121 normalized infant brain cDN	3.79
30	427030	AA397600	Hs.97531	ESTs	3.76
	426328	AW631296		gb:hh83c09.y1 NCI_CGAP_GU1 Homo sapiens	3.74
	429307	AU076592	Hs.198951	jun B proto-oncogene	3.71
	400172				3.70
	431227	X63755	Hs.2743	keratin, cuticle, ultrahigh sulphur 1	3.68
35	433883	AI925688	Hs.222312	ESTs, Weakly similar to B24264 proline-r	3.68
	446850	R71245	Hs.174303	ESTs	3.67
	405147				3.64
	406821	AA977896	Hs.128873	ESTs, Highly similar to ALFA_HUMAN FRUCT	3.57
	402762				3.55
	401496				3.50
40	421201	AW241940	Hs.102500	hypothetical protein FLJ20481	3.50
	402911				3.49
	425330	D25216	Hs.155650	KIAA0014 gene product	3.49
	438004	AA774984	Hs.220649	ESTs, Weakly similar to FCE2 MOUSE LOW A	3.46
	448185	AI633040	Hs.172730	ESTs	3.46
45	433367	AA584930	Hs.269451	ESTs, Weakly similar to XAP-5-like prote	3.43
	416596	H67669	Hs.38564	ESTs	3.41
	400545				3.39
	418464	R87580		gb:ym89h07.r1 Soares adult brain N2b4HB5	3.37
50	426507	AA380285		gb:EST93491 Supt cells Homo sapiens cDNA	3.35
	403479				3.34
	406082	S47833	Hs.82927	adenosine monophosphate deaminase 2 (iso	3.34
	401919				3.33
	449031	AI867502	Hs.271462	ESTs	3.33
55	400116				3.31
	401590				3.29
	401007				3.28
	404610	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PL	3.25
	408641	AW245207	Hs.5555	Homo sapiens cDNA FLJ13170 fis, clone NT	3.25
60	407196	D11747	Hs.177415	Finkel-Biskis-Reilly murine sarcoma viru	3.23
	410258	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-bi	3.23
	433232	AI658621	Hs.127769	ESTs	3.23
	457937	AW976930	Hs.128760	ESTs	3.23
	406101				3.18
65	407080	Z38133	Hs.113973	myosin, heavy polypeptide 6, skeletal mu	3.18
	419947	AW298744	Hs.118894	ESTs	3.16
	421905	AI660247	Hs.32659	ESTs, Weakly similar to LIV-1 protein [H	3.16
	454019	D31846	Hs.37025	aquaporin 2 (collecting duct)	3.16
	428674	AA431734	Hs.104915	ESTs	3.14
70	402056				3.06
	425182	AF041259	Hs.155040	zinc finger protein 217	3.06
	425393	NM_000218	Hs.156115	potassium voltage-gated channel, KQT-like	3.06
	433657	AI244368	Hs.8124	PH domain containing protein in retina 1	3.05
	402158				3.03
75	404938				3.02
	403376				3.01
	418828	AF020774	Hs.88844	Homo sapiens hair and skin epidermal-ty	3.00
	402423				2.99
	416253	BE250659	Hs.15463	ESTs	2.99
80	435265	AA779958	Hs.185932	ESTs	2.99
	425655	BE614551	Hs.158675	ribosomal protein L14	2.98
	428704	AA432007	Hs.249484	ESTs	2.98
	425439	D38024	Hs.157425	double homeobox, 2	2.97
	445613	BE550889	Hs.158491	ESTs	2.97

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	402714			2.96
	403526			2.96
	403605			2.95
	441852	AB028968	Hs.7989	KIAA1045 protein
5	417629	T76945	Hs.64211	ESTs, Weakly similar to similar to acyl-
	447744	AA313230	Hs.19413	S100 calcium-binding protein A12 (calgr
	419821	AW967486	Hs.189119	ESTs
	446993	AI570964	Hs.164257	ESTs
10	414580	BE386918		gb:601275386F1 NIH_MGC_20 Homo sapiens c
	423379	AI985349	Hs.157492	Homo sapiens cDNA FLJ14079 fis, clone HE
	440206	AI762232	Hs.46794	ESTs
	402212	AW502761	Hs.30909	KIAA0430 gene product
	406059			2.86
	423548	AF007194	Hs.129782	mucin 3A, intestinal
15	402051			2.85
	415196	AK000150	Hs.78185	MAX-like bHLHZIP protein
	455446	AW947749		gb:RCO-MT0005-130300-031-b01 MT0005 Homo
	442428	BE464988	Hs.298302	ESTs
20	403247			2.83
	404825			2.83
	459184	L35001	Hs.95669	ESTs
	402968			2.82
	417575	R00382	Hs.191199	ESTs
	404668			2.81
25	420619	AF130255	Hs.99430	testis zinc finger protein
	447241	BE382838	Hs.19322	ESTs
	448793	AI864581	Hs.215477	ESTs
	453014	AI937242	Hs.176590	ESTs
30	446775	AI792836	Hs.232273	ESTs
	455075	AW854850		gb:QV2-CT0261-201099-011-h03 CT0261 Homo
	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus
	457546	AA568484	Hs.153632	ESTs
	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy
35	433677	AI791912	Hs.190885	ESTs, Moderately similar to ALU1_HUMAN A
	405703			2.73
	408840	AW277132	Hs.254880	ESTs
	413958	BE277913	Hs.172364	Homo sapiens mRNA for FLJ00086 protein,
	454421	BE409759	Hs.59563	Homo sapiens mRNA for FLJ00007 protein,
40	406702	Z20656	Hs.278432	myosin, heavy polypeptide 6, cardiac mus
	408664	R56362		gb:yg93c07.r1 Soares infant brain 1N18 H
	402457			2.71
	403612			2.71
	407049	X72632		(NONE)
45	415423	AA164743	Hs.187617	Homo sapiens cDNA FLJ13941 fis, clone Y7
	402862			2.69
	403540			2.69
	431465	AW293178	Hs.180086	ESTs
	406563			2.68
50	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase
	426220	AI383475	Hs.171697	ESTs, Weakly similar to immunoglobulin s
	446707	AI591214	Hs.156336	ESTs
	447557	AW028809	Hs.229570	ESTs
	413529	U11874	Hs.846	Interleukin 8 receptor, beta
55	403997			2.66
	408704	AA066635	Hs.5366	Homo sapiens cDNA: FLJ21522 fis, clone C
	407005	U20230		gb:Human guanylyl cyclase C gene, partial
	405075			2.64
	430728	AW968522		gb:EST380598 MAGE resequences, MAGJ Homo
60	405327			2.63
	409419	BE207219	Hs.20474	ESTs, Highly similar to S17112 Interfero
	434300	AA740944	Hs.116295	ESTs
	405895			2.62
	431929	AW294163	Hs.146127	ESTs
65	405217			2.61
	437569	AA760849	Hs.294052	ESTs
	419822	AW966864	Hs.255780	ESTs
	445918	AW014139	Hs.145656	ESTs
	446149	BE242960	Hs.203181	ESTs
70	457829	AI742291	Hs.210843	ESTs, Weakly similar to dJ1039K5.2 [Hsa
	404282			2.53
	409778	AW499705		gb:UL-HF-BR0p-ajk-b-05-Q-ULr1 NIH_MGC_5
	445353	BE551465	Hs.175211	ESTs
	458764	BE619386		gb:601473204F1 NIH_MGC_68 Homo sapiens c
	402195			2.52
75	404247			2.52
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen
	402588			2.50
	432301	U34249	Hs.167075	ring finger protein 9
80	424958	AA984420	Hs.283659	ESTs
	442197	AW837912		gb:QV3-LT0048-260100-068-c02 LT0048 Homo
	415003	M11437	Hs.77741	kininogen
	420767	AF072711	Hs.99918	carboxyl ester lipase (bile salt-stimula
	422885	BE244068	Hs.121544	interleukin 12 receptor, beta 1
				2.47

5	440424	AJ991125	Hs.189109	Homo sapiens cDNA: FLJ21458 fis, clone C	2.47
	402153				2.46
	432152	AK000245	Hs.272790	Homo sapiens cDNA FLJ20238 fis, clone CO	2.46
	454414	R55574	Hs.164675	ESTs	2.45
	401603				2.44
10	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.44
	408513	AW206468	Hs.103118	ESTs	2.43
	409826	AW501112	Hs.34487	hypothetical protein FLJ23412	2.42
	400672				2.41
	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	2.41
15	449748	H23963	Hs.32043	ESTs	2.41
	453756	AW139415	Hs.61906	ESTs	2.41
	400624				2.40
	403125				2.40
	405118				2.39
20	402165				2.38
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	2.38
	425515	W26609		gb:35f12 Human retina cDNA randomly prim	2.38
	402951				2.37
	427886	AA417083	Hs.104789	ESTs	2.37
25	447173	AW449385	Hs.157294	ESTs	2.37
	448703	BE613942	Hs.170890	Homo sapiens cDNA: FLJ21129 fis, clone C	2.37
	426344	H41821	Hs.169393	transcriptional activator of the c-fos p	2.36
	401840				2.35
	403731				2.34
30	405378				2.34
	405555	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	2.34
	416559	AI039195	Hs.128060	ESTs, Weakly similar to cDNA EST yk481g5	2.34
	438216	Z83952	Hs.252815	ESTs	2.34
	448427	BE395260		gb:601311130F1 NIH_MGC_44 Homo sapiens c	2.34
35	451588	AW072057		gb:ws58g05.x1 NCI_CGAP_Bm25 Homo sapien	2.34
	423011	NM_000683	Hs.299847	ESTs, Highly similar to A2AD_HUMAN ALPHA	2.33
	451172	AW206465	Hs.207423	ESTs	2.33
	401015				2.32
	414705	BE464157	Hs.281455	ESTs	2.32
40	439894	AA853077		gb:NHTBCae03a05f1 Normal Human Trabecula	2.31
	446305	AW270149	Hs.254515	ESTs, Moderately similar to AF248953 1 g	2.31
	453512	AL040160	Hs.209542	ESTs, Weakly similar to B cell linker pr	2.29
	418556	T02850		gb:FB12A9 Fetal brain, Stratagene Homo s	2.28
	457197	AB016092	Hs.197114	RNA binding protein; AT-rich element bin	2.28
45	457275	AA463422	Hs.209431	ESTs	2.28
	458766	AW183618	Hs.188417	ESTs, Weakly similar to ZnT-3 [H.sapiens	2.27
	414075	U11862	Hs.75741	amide binding protein 1 (amine oxida	2.27
	430210	AL157426	Hs.235390	Homo sapiens mRNA; cDNA DKFZp761B101 (fr	2.27
	442614	AI269030		gb:qj73c12.x1 NCI_CGAP_Kid3 Homo sapiens	2.27
50	402538				2.26
	439891	AL389940	Hs.109968	ESTs	2.26
	440056	BE294828	Hs.13323	hypothetical protein FLJ22059	2.26
	406150				2.25
	426880	AA453482		gb:zx47a11.r1 Soares_testis_NHT Homo sap	2.25
55	447129	AW014123	Hs.161402	ESTs	2.25
	458893	BE161733	Hs.97283	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.25
	456778	AI458309	Hs.117406	ESTs	2.24
	401728				2.23
	404139				2.23
60	414095	BE293546		gb:601186671F1 NIH_MGC_15 Homo sapiens c	2.23
	432037	AW450592	Hs.300459	ESTs	2.23
	451965	AA021163	Hs.22287	ESTs	2.23
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	2.22
	427586	AA609661	Hs.190592	ESTs	2.22
65	454108	AA161071	Hs.71465	squalene epoxidase	2.22
	429749	AI685174	Hs.22293	ESTs	2.21
	434507	AW511138	Hs.256581	ESTs	2.21
	436652	AA724543	Hs.168824	ESTs	2.21
	437433	R74016	Hs.121581	ESTs	2.21
70	401688				2.20
	441748	R14439	Hs.209194	ESTs	2.19
	453072	BE251845	Hs.221516	ESTs, Weakly similar to tetraspan TM4SF	2.19
	400635				2.18
	417176	AW974475	Hs.143467	ESTs	2.18
75	427858	NM_001971	Hs.21	elastase 1, pancreatic	2.18
	454886	AW837063		gb:QV1-LT0037-150200-069-g08 LT0037 Homo	2.18
	458232	BE217872	Hs.279537	ESTs	2.18
	408922	R87388		gb:ym88g04.r1 Soares adult brain N2b4HB5	2.17
	423668	Y10148	Hs.131138	neurotensin receptor 2	2.17
80	440338	R62431	Hs.12758	ESTs	2.17
	403115				2.16
	409125	R17268	Hs.301560	ESTs	2.16
	426887	AI971975	Hs.212892	ESTs	2.16
	413811	BE168828		gb:QV1-HT0517-020400-145-004 HT0517 Homo	2.15
	442962	AI025315	Hs.131615	ESTs	2.15
	403921				2.14
	413140	T06507	Hs.6846	hypothetical protein FLJ13055	2.14

	421996	AW583807	Hs.1460	glucagon	2.14
	436130	AA341497	Hs.31408	ESTs	2.14
	407243	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	2.13
	407708	AF019968	Hs.37936	suppressor of variegation 3-9 (Drosophila)	2.13
5	442792	AI352340	Hs.131194	ESTs	2.12
	454406	AA213605	Hs.267861	ESTs	2.12
	424648	AA344576		gb:EST50478 Gall bladder I Homo sapiens	2.11
	433963	AI218808	Hs.187778	ESTs	2.11
	400736				2.10
10	406343				2.10
	409702	AI752244	Hs.285749	Human DNA from chromosome 19-specific co	2.10
	432092	AF135026		gb:Homo sapiens kallikrein-like protein	2.10
	441915	AI566116	Hs.207066	ESTs, Weakly similar to FOG [M.musculus]	2.10
	453147	AA733098	Hs.279909	CGI-05 protein	2.10
15	415604	Z44177	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	2.08
	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	2.08
	401211	AJ004832	Hs.5038	neuropathy target esterase	2.07
	413808	J00287	Hs.182183	caldesmon 1	2.07
20	414433	BE407755	Hs.169100	Homo sapiens cDNA FLJ12529 fis, clone NT	2.07
	421978	AJ243662	Hs.110196	NICE-1 protein	2.07
	431204	F28841	Hs.250760	cytochrome c oxidase subunit VIa polypep	2.07
	433605	AI378012	Hs.147953	ESTs	2.06
	449383	AW444712	Hs.196573	ESTs	2.06
	455652	BE064675		gb:RC1-BT0313-301299-012-h11 BT0313 Homo	2.05
25	402382				2.04
	407282	AI345597	Hs.254727	ESTs	2.04
	457273	AI167145	Hs.165538	ESTs	2.04
	459073	AW968616	Hs.296234	ESTs, Highly similar to mitogen-activate	2.04
	402394				2.03
30	428875	AW451624	Hs.178202	ESTs	2.03
	456634	AA609911	Hs.109012	ESTs	2.03
	434352	AF129505	Hs.86492	small muscle protein, X-linked	2.02
	439281	AA100768	Hs.48485	ESTs	2.02
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	2.02
35	401122				2.01
	444340	AI143198	Hs.143561	ESTs	2.01
	455104	BE064863		gb:RC1-BT0313-110300-015-406 BT0313 Homo	2.01
	415011	AW963085		gb:EST375158 MAGI resequences, MAGI Homo	2.00
40	440144	AW082297	Hs.88523	ESTs	2.00
	403183				1.99
	409802	AW500732		gb:UL-HF-BNO-akm-h-07-0-ULr1 NIH_MGC_50	1.98
	430144	AI732722	Hs.187694	ESTs	1.98
	444580	AI168365	Hs.268663	ESTs	1.98
	401704				1.97
45	401810				1.97
	424473	AK001405	Hs.148584	Homo sapiens cDNA FLJ10543 fis, clone NT	1.97
	438573	AW135084	Hs.299865	ESTs	1.97
	412921	BE008345	Hs.128942	ESTs	1.96
	422233	AB002058	Hs.113275	purinergic receptor P2X-like 1, orphan r	1.96
50	425352	NM_000939	Hs.1897	proopiomelanocortin (adrenocorticotropin	1.96
	410285	AA083609		gb:zm63d05.r1 Stratagene fibroblast (937	1.95
	414323	NM_014759	Hs.239500	KIAA0273 gene product	1.94
	428119	AW298211	Hs.256737	ESTs	1.94
	424510	AK001841	Hs.149797	hypothetical protein FLJ10979	1.92
55	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	1.92
	429785	H82114	Hs.301769	ESTs	1.92
	437344	R90921	Hs.6846	hypothetical protein FLJ13055	1.92
	451819	AI819096	Hs.249260	ESTs	1.92
	459060	H89244	Hs.79625	heterogeneous nuclear ribonucleoprotein	1.92
60	422664	AA315933	Hs.120879	ESTs	1.91
	432247	AA531287	Hs.105805	ESTs	1.91
	453820	R77494	Hs.75416	DAZ associated protein 2	1.91
	400675				1.90
65	405556	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	1.90
	407099	M94891	Hs.278423	pregnancy specific beta-1-glycoprotein 4	1.90
	440297	BE560553	Hs.205450	Homo sapiens cDNA: FLJ22570 fis, clone H	1.90
	443104	AA088470	Hs.83135	p53-responsive gene 6	1.90
	444329	W73753	Hs.58330	ESTs	1.89
	402690				1.89
70	432354	AW137262	Hs.192713	ESTs	1.88
	427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	1.88
	443322	AI825817	Hs.143272	ESTs	1.88
	458185	AI762757	Hs.129869	ESTs, Weakly similar to AF113685 1 PRO09	1.88
	459072	AI815978	Hs.160427	ESTs	1.88
75	402534				1.87
	409689	AA078492		gb:7P04D11 Chromosome 7 Placental cDNA L	1.87
	416931	D45371	Hs.80485	adipose most abundant gene transcript 1	1.87
	430176	AI161995	Hs.234775	neurturin	1.87
	430631	AJ003147	Hs.278464	olfactory receptor, family 1, subfamily	1.87
80	433114	AA121579		gb:zn77f02.r1 Stratagene NT2 neuronal pr	1.87
	439254	U57352	Hs.6517	amiloride-sensitive cation channel 1, ne	1.87
	448461	AW166358	Hs.124979	ESTs	1.87
	450675	AA010662	Hs.186639	ESTs	1.87

	401767				1.86
	449891	N64867	Hs.37848	ESTs	1.85
	400527				1.84
5	428581	AA430570	Hs.104881	ESTs	1.84
	443647	AV653846	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	1.84
	447785	AV651441	Hs.282475	ESTs	1.84
	449566	AA001778	Hs.288156	Homo sapiens cDNA: FLJ21819 fis, clone H	1.84
	436752	AW298529	Hs.255774	ESTs	1.83
10	437405	AA338837	Hs.42547	Homo sapiens cDNA FLJ13975 fis, clone Y7	1.83
	449174	T66136	Hs.12880	ESTs	1.83
	449887	AW080843	Hs.200275	ESTs	1.83
	453261	AA034116	Hs.118494	ESTs	1.83
	454243	AW241901	Hs.250683	ESTs	1.83
15	459188	AA216382	Hs.30002	SH3-containing protein SH3GLB2	1.83
	424334	AA393460		gb:z171e05.r1 Soares_testis_NHT Homo sap	1.82
	432150	AK000224	Hs.272789	hypothetical protein FLJ20217	1.82
	408123	AW163377		gb:au84e02.y1 Schnetder fetal brain 0000	1.81
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	1.80
20	442196	AI902646	Hs.31844	Homo sapiens cDNA FLJ12586 fis, clone NT	1.80
	421419	M99587	Hs.104134	homeo box (H6 family) 1	1.79
	405420				1.78
	405737				1.78
25	414016	AA134594	Hs.71528	ESTs	1.78
	415744	AW964850	Hs.279307	ESTs	1.78
	420375	AF182077	Hs.97244	glioma tumor suppressor candidate region	1.78
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	1.78
	421592	AF008801	Hs.105941	bagpipe homeobox (Drosophila) homolog 1	1.77
	401743				1.75
30	405187				1.75
	442763	AI017037	Hs.131121	ESTs	1.75
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	1.75
	413248	T64858	Hs.21433	ESTs	1.74
	423913	NM_016436	Hs.301055	hepatocellular carcinoma-associated anti	1.74
35	439999	AA115811	Hs.6838	ras homolog gene family, member E	1.74
	440185	AW104546	Hs.270929	ESTs	1.74
	450482	AI697844	Hs.221720	ESTs	1.74
	413972	BE278548	Hs.162717	ESTs, Weakly similar to HPPD_HUMAN 4-HYD	1.73
	420476	AW575863	Hs.136232	ESTs	1.73
40	428748	AW593206	Hs.98785	ESTs	1.73
	431148	AA502653	Hs.28621	ESTs	1.73
	447205	BE617015	Hs.11006	ESTs	1.73
	455994	BE179190		gb:RC0-HT0613-210300-032-07 HT0613 Homo	1.73
	401039				1.72
45	403251				1.72
	409762	AW498884	Hs.257970	ESTs	1.72
	440914	AA909552	Hs.143884	ESTs	1.72
	448507	AL133109	Hs.21333	Homo sapiens mRNA; cDNA DKFZp566N1047 (f	1.72
	409605	AW444477	Hs.258507	ESTs	1.71
50	441212	AW242447	Hs.146182	ESTs, Weakly similar to lactase phlorizl	1.71
	445624	AW140103	Hs.78880	livB (bacterial acetolactate synthase)-I	1.71
	458619	AA872064	Hs.301218	ESTs, Weakly similar to Unknown gene pro	1.71
	401969				1.70
	403327				1.70
55	407245	X90568	Hs.172004	Utin	1.70
	417361	NM_000275	Hs.82027	oculocutaneous albinism II (pink-eye dil	1.70
	436034	AF282693	Hs.150185	Inflammation-related G protein-coupled r	1.70
	442682	AI014545	Hs.231027	EST	1.70
	458494	AI380906	Hs.158436	ESTs	1.70
60	404682				1.69
	407402	AF035303		gb:Homo sapiens clone 23943 mRNA sequenc	1.69
	409368	AA071059		gb:zm66a10.r1 Stratagene neuroepithelium	1.69
	440362	AA883812	Hs.125508	ESTs	1.69
	448866	BE297743	Hs.284203	myogenic factor 3	1.69
65	402201				1.68
	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.68
	403186				1.67
	409543	AW410200		gb:th05b12.x1 NIH_MGC_17 Homo sapiens cD	1.67
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	1.67
70	450391	AI694522	Hs.202280	ESTs	1.67
	408919	AW295352	Hs.251836	ESTs	1.66
	416136	H45027	Hs.181770	ESTs	1.66
	416865	H97863	Hs.42455	ESTs	1.66
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	1.66
75	437237	BE513073		gb:601171435F1 NIH_MGC_15 Homo sapiens c	1.66
	429134	AA446953	Hs.99004	ESTs	1.65
	445041	T64183	Hs.11398	ESTs	1.65
	453240	AI969564	Hs.284249	Homo sapiens cDNA: FLJ22334 fis, clone H	1.65
	405243				1.64
80	426039	BE265133	Hs.217493	annexin A2	1.64
	430135	NM_000035	Hs.234234	aldolase B, fructose-bisphosphata	1.64
	435942	R06285	Hs.191215	ESTs	1.64
	448106	AI800470	Hs.171941	ESTs	1.64
	408591	AF015224	Hs.46452	mammaglobin 1	1.63

5	410881	AW809157		gb:RC0-ST0118-041099-031-c07_1 ST0118 Ho	1.63
	417743	R14738	Hs.8312	ESTs, Weakly similar to AF170723.1 prote	1.62
	430632	AC004597	Hs.248088	olfactory receptor, family 10, subfamily	1.62
	448651	BE246440	Hs.93728	pre-B-cell leukemia transcription factor	1.62
	453718	AL119317	Hs.120360	phospholipase A2, group VI (cytosolic, c	1.62
10	459499	AW402653	Hs.28355	Homo sapiens cDNA: FLJ22402 fis, clone H	1.61
	412374	X01388	Hs.73849	apolipoprotein C-III	1.61
	419113	AI446586	Hs.21835	ESTs	1.61
	426795	AI810474	Hs.196945	ESTs	1.61
	426998	BE274360		gb:601121068F1 NIH_MGC_20 Homo sapiens c	1.61
15	428407	NM_003963	Hs.184194	transmembrane 4 superfamily member 5	1.61
	444475	C75571		gb:C75571 Human pancreatic islet Homo sa	1.61
	453399	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	1.61
	456275	AW976183	Hs.88414	ESTs, Weakly similar to dJ512E2.1 [H.sap	1.61
	414060	BE246327		gb:TCBAP1E1957 Pediatric pre-B cell acut	1.60
20	418004	U37519	Hs.87539	aldehyde dehydrogenase 8	1.60
	428651	AF195478	Hs.188401	annexin A10	1.60
	443853	AI089054	Hs.250644	ESTs	1.59
	407007	U22961		gb:Human mRNA clone with similarity to L	1.59
	412067	N45697		gb:yy78d01.r1 Soares_multiple_sclerosis_	1.59
25	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	1.59
	448619	AI867182	Hs.202255	ESTs	1.58
	403665				1.58
	407524	X64985		gb:H.sapiens mRNA HTPCRX11 for olfactory	1.58
	424286	AA338285	Hs.90744	proteasome (prosome, macropain) 26S subu	1.57
30	412056	T28160	Hs.778	guanylate cyclase activator 1B (retina)	1.57
	430218	AW998865	Hs.186703	ESTs	1.57
	431882	NM_001426	Hs.271977	engrailed homolog 1	1.57
	450797	AI761930	Hs.205127	ESTs	1.57
	455366	AW947563		gb:RC0-MT0004-140300-031-g11 MT0004 Homo	1.56
35	408421	AW193734	Hs.253067	ESTs	1.56
	421907	BE018556	Hs.109358	ATPase, Class V, type 10B	1.56
	432742	AA564453	Hs.162339	ESTs	1.56
	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	1.56
	439543	W75935	Hs.146083	ESTs	1.56
40	443317	AI051601	Hs.200191	ESTs	1.56
	449097	BE271708	Hs.95110	ESTs, Weakly similar to PIP6_HUMAN 1-PHO	1.56
	457127	AA194554	Hs.183434	ATPase, H+-transporting, lysosomal (vacu	1.55
	407387	AB000895		gb:Homo sapiens mRNA for cadherin FIB1,	1.55
	418837	U48263	Hs.89040	preproenkephalin	1.55
45	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.55
	458475	AI650322	Hs.143249	ESTs	1.54
	402561				1.54
	411187	AW821291		gb:PM3-ST0307-241299-002-f03 ST0307 Homo	1.54
	419224	NM_012189	Hs.252716	fibrous sheathin II	1.53
50	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	1.53
	415426	Z41991	Hs.23197	ESTs	1.53
	421428	U26726	Hs.1376	hydroxysteroid (11-beta) dehydrogenase 2	1.53
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	1.53
	428489	AI807459	Hs.98582	ESTs	1.53
55	437728	AA766719		gb:oa39c09.a1 NCL_CGAP_GCB1 Homo sapiens	1.52
	407124	R08160	Hs.268857	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.52
	414932	C14577	Hs.194517	ESTs	1.52
	433500	AF064255	Hs.111401	very long-chain acyl-CoA synthetase homo	1.52
	439688	AW445181	Hs.209637	Homo sapiens cDNA FLJ12921 fis, clone NT	1.52
60	453391	AW600302	Hs.232655	ESTs	1.51
	424688	AA216287	Hs.1815	myosin, light polypeptide 3, alkali; ven	1.51
	436895	AF037335	Hs.5338	carbonic anhydrase XII	1.51
	443012	AI566813	Hs.132278	ESTs	1.50
	415824	D42039	Hs.78871	mesoderm development candidate 2	1.50
65	445152	AI214667	Hs.283597	ESTs	1.50
	455941	BE160011	Hs.129998	Homo sapiens cDNA FLJ14267 fis, clone PL	1.50
	457889	AL035864	Hs.69517	ESTs, Highly similar to differentially e	1.50
	458503	AL133933	Hs.64310	interleukin 11 receptor, alpha	1.49
	400694				1.49
70	420837	AW966719	Hs.1340	collipase, pancreatic	1.49
	426752	X69490	Hs.172004	titin	1.49
	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	1.49
	428874	W32133	Hs.194366	transferrin (prealbumin, amyloidosis t	1.49
	444287	AI033077	Hs.10755	dihydropyrimidinase	1.49
75	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.48
	425747	AI457620	Hs.205360	ESTs	1.48
	432378	AI493046	Hs.146133	ESTs	1.48
	447999	AW138840	Hs.201778	ESTs	1.48
	453888	AW450670	Hs.252819	ESTs	1.47
80	406667	M12523	Hs.75442	albumin	1.47
	418129	X52997	Hs.1144	glycoprotein IX (platelet)	1.47
	426309	AI912555	Hs.157195	peptide YY, 2 (seminaplasmin)	1.47
	426755	BE253469		gb:601108143F1 NIH_MGC_16 Homo sapiens c	1.46
	414258	AA203285	Hs.294141	ESTs, Weakly similar to dJ733D15.1 [H.s	1.46
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	1.46
	420562	AI345569	Hs.190046	ESTs	1.46
	425011	T51986	Hs.283108	hemoglobin, gamma G	1.46

5	443050	AI612788	Hs.132348	ESTs, Weakly similar to diaphanous 1 (H	1.46
	411074	XG0435	Hs.68137	adenylate cyclase activating polypeptide	1.45
	434680	T11738	Hs.127574	ESTs	1.45
	454771	AW819939	Hs.273629	ESTs	1.45
	415672	N53097	Hs.193579	ESTs	1.44
10	418141	AW845738	Hs.171118	Homo sapiens mRNA for FLJ00026 protein,	1.44
	406706	X03740	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	1.43
	418197	AA214253		gb:zn58g02.r1 Stratagene muscla 937209 H	1.43
	431821	AW452256	Hs.271221	hypothetical protein FLJ20064	1.43
	455433	AW939463		gb:QV1-DT0072-310100-056-g02 DT0072 Homo	1.43
15	407743	AW814118		gb:MR3-ST0203-151199-011-d09 ST0203 Homo	1.42
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	1.42
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	1.42
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.42
	452456	BE080763		gb:QV1-BT0631-150200-071-f09 BT0631 Homo	1.42
20	456535	AA305079	Hs.1342	cytochrome c oxidase subunit Vb	1.42
	408349	BE546947	Hs.44276	homeo box C10	1.41
	420391	AA456891	Hs.79123	KIAA0084 protein	1.41
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	1.41
	449329	AW752783		gb:IL3-CT0219-221199-029-F03 CT0219 Homo	1.41
25	453615	AA195712	Hs.132696	ESTs	1.41
	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	1.40
	420287	AA740907	Hs.88297	ESTs	1.40
	427583	M82962	Hs.179704	meprin A, alpha (PABA peptide hydrolase)	1.40
	418787	AW296134	Hs.86999	ESTs	1.39
30	422072	AB018255	Hs.111138	KIAA0712 gene product	1.39
	425988	BE045897	Hs.274454	ESTs	1.39
	428087	AA100573	Hs.182421	troponin C2, fast	1.39
	438136	NM_002290	Hs.6088	a disintegrin and metalloproteinase doma	1.39
	455579	BE011320		gb:PM3-BN0218-090500-002-d09 BN0218 Homo	1.39
35	402316				1.38
	417084	H08370	Hs.33067	ESTs	1.38
	423276	AC003034	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	1.38
	433787	AI472951	Hs.173688	ESTs	1.38
	413830	BE263439	Hs.13144	HSPC160 protein	1.37
40	423576	NM_000383	Hs.129829	autoimmune regulator (autoimmune polyen	1.37
	401886				1.36
	412688	AW583062	Hs.74502	chymotrypsinogen B1	1.36
	401238				1.34
	421511	AA488940	Hs.105216	hypothetical protein FLJ11125	1.34
45	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B11	1.34
	425450	U14755	Hs.157449	LIM homeobox protein 1	1.34
	427333	AF067797	Hs.176658	aquaporin 8	1.34
	430937	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	1.34
	445204	AW135523	Hs.245853	ESTs	1.34
50	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (f	1.34
	456379	W22206		gb:63E10 Human retina cDNA Tsp5091-cleav	1.34
	457416	BE142052		gb:CM3-HT0137-150999-011-b05 HT0137 Homo	1.34
	415741	AI902761	Hs.272087	ESTs	1.33
	422260	AA315993	Hs.105484	ESTs, Weakly similar to LITB_HUMAN LITB	1.33
55	429188	AB011171	Hs.198037	KIAA0599 protein	1.33
	442776	AW959498	Hs.8709	chymotrypsin C (caldecrin)	1.33
	454748	AW862014		gb:RC3-CT0347-160200-013-d09 CT0347 Homo	1.33
	437744	AW290905	Hs.300288	ESTs, Weakly similar to CGHU2E collagen	1.32
	451997	AA021351	Hs.158497	KIAA0724 gene product	1.32
60	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	1.32
	411879	BE145354	Hs.273758	Homo sapiens cDNA: FLJ23112 fis, clone L	1.31
	424304	NM_001395	Hs.144879	dual specificity phosphatase 9	1.31
	401442				1.30
	403942				1.30
65	443687	F13040	Hs.182937	peptidylprolyl isomerase A (cyclophilin	1.30
	401624				1.29
	411885	AA452636	Hs.131057	ESTs, Moderately similar to CRGD_HUMAN G	1.29
	418575	AA225313	Hs.222886	ESTs	1.29
	419818	AI657122	Hs.301931	ESTs	1.29
70	429845	AB020337	Hs.225943	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	1.29
	447586	AI081980	Hs.285829	solute carrier family 25 (mitochondrial	1.29
	407013	U35637		gb:Human nebulin mRNA, partial cds	1.28
	428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	1.28
	429780	AL137518	Hs.300388	ESTs	1.28
75	453539	AW731886	Hs.95196	ESTs, Weakly similar to T20B12.3 [C.eleg	1.28
	400846				1.27
	420257	AA257035	Hs.190042	ESTs	1.27
	429184	AF095735	Hs.198003	sarcosine dehydrogenase	1.27
	437389	AL359587	Hs.271586	hypothetical protein DKFZp762M115	1.27
80	444412	AI147652	Hs.216381	Homo sapiens clone HH409 unknown mRNA	1.27
	451139	AW293316	Hs.205558	ESTs	1.27
	431284	AA570148	Hs.126783	Homo sapiens cDNA: FLJ22610 fis, clone H	1.26
	431969	AA366217	Hs.2879	carboxypeptidase A1 (pancreatic)	1.26
	405158				1.25
	419648	T73661	Hs.91877	ESTs, Highly similar to THIH_HUMAN THYRO	1.25
	430681	AW969675	Hs.291232	ESTs	1.25
	434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.25

	436217	T53925	Hs.107	fibrinogen-like 1	1.25
	440089	AA864468	Hs.135646	ESTs	1.25
	446787	U67167	Hs.315	mucin 2, intestinal/tracheal	1.25
	448207	AJ475490	Hs.170577	ESTs	1.25
5	454869	AW836004		gb:PM0-LT0019-170200-001-d11 LT0019 Homo	1.25
	413271	AA127873	Hs.114949	ESTs	1.24
	422619	AA313322		gb:EST185218 Colon carcinoma (HCC) cell	1.24
	422796	AW897265		gb:CM0-NN0057-150400-335-a04 NN0057 Homo	1.24
	427530	AA405093	Hs.126519	ESTs	1.24
10	437727	AA766707	Hs.153039	ESTs	1.23
	426435	AJ827946	Hs.189118	ESTs	1.22
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	1.21
	407964	AW130334	Hs.281111	ESTs	1.21
	430828	AJ763257	Hs.86327	Homo sapiens cDNA: FLJ22431 fis, clone H	1.21
15	432029	D31628	Hs.2899	4-hydroxyphenylpyruvate dioxygenase	1.21
	457843	AW138211	Hs.128746	ESTs	1.20
	413242	BE074165		gb:PM3-BT0564-030300-002-e12 BT0564 Homo	1.20
	446057	AJ420227	Hs.149358	ESTs	1.20
	447198	D61523	Hs.283435	ESTs	1.20
20	449513	AJ653232	Hs.195059	EST	1.19
	415566	F12119		gb:HSC35H091 normalized infant brain cDN	1.19
	423315	R54109	Hs.26096	ESTs	1.19
	455817	BE142384		gb:CM2-HT0144-210999-011-d04 HT0144 Homo	1.19
25	459354	BE514778		gb:601317094F1 NIH_MGC_9 Homo sapiens cD	1.18
	408432	AW195262		gb:xn67b05.x1 NCL_CGAP_CML1 Homo sapiens	1.18
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.18
	419251	NM_001486	Hs.89771	glucokinase (hexokinase 4) regulatory pr	1.18
	456702	AJ684534		gb:wa72f10.x1 Soares_NFL_T_GBC_S1 Homo s	1.18
	458009	AJ221409	Hs.144983	ESTs	1.17
30	410193	AJ132592	Hs.59757	zinc finger protein 281	1.17
	417779	AA829526	Hs.124977	ESTs	1.17
	435101	AJ743156	Hs.131064	ESTs	1.17
	445360	AJ798776	Hs.156029	ESTs	1.15
	414160	BE257021		gb:601117426F1 NIH_MGC_16 Homo sapiens c	1.15
35	418078	AA521268	Hs.86508	ESTs	1.15
	425133	NM_002613	Hs.154729	3-phosphoinositide dependent protein kin	1.15
	437935	AW939591	Hs.5940	hypothetical protein FLJ20063	1.15
	446377	AW014022	Hs.170953	ESTs	1.13
	420097	AA700127	Hs.190504	ESTs	1.13
40	446591	H44186	Hs.15456	PDZ domain containing 1	1.13
	451477	AJ798425	Hs.42710	ESTs	1.13
	459197	BE244587		gb:TCBAP2E0851 Pediatric pre-B cell acut	1.12
	428934	AF039401	Hs.194659	chloride channel, calcium activated, fam	1.12
	431191	AW972118	Hs.100002	HSPC162 protein	1.11
45	424403	F05183	Hs.1799	CD1D antigen, d polypeptide	1.11
	433546	AJ075877	Hs.125461	Homo sapiens cDNA FLJ11539 fis, clone HE	1.11
	451179	W05469	Hs.31818	ESTs	1.10
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	1.10
	420774	AA280209	Hs.165270	ESTs	1.10
50	428887	AA437009	Hs.98984	ESTs	1.10
	430582	AJ215509	Hs.143964	ESTs	1.10
	453642	AJ370936	Hs.34074	dipeptidylpeptidase VI	1.09
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	1.09
55	417998	AW967420		gb:EST379495 MAGE resequences, MAGJ Homo	1.09
	456387	W28876		gb:52h7 Human retina cDNA randomly prime	1.08
	427965	D00306	Hs.183864	elastase 3B	1.08
	447388	AW630534	Hs.76277	ESTs, Weakly similar to TB2 [H.sapiens]	1.07
	413841	M34276	Hs.75576	plasminogen	1.07
60	429201	X03178	Hs.198246	group-specific component (vitamin D bind	1.07
	433313	W20128	Hs.296039	ESTs	1.07
	439450	R51613	Hs.125304	ESTs	1.07
	458963	AJ701393	Hs.278728	Rad and Gem-related 2 (rat homolog)	1.06
	405161				1.06
65	406741	AA058357	Hs.74486	carcinoembryonic antigen-related cell ad	1.06
	424294	BE299311		gb:601119256F1 NIH_MGC_17 Homo sapiens c	1.06
	424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.06
	444687	AW972109	Hs.135107	ESTs	1.06
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	1.05
70	421243	AW873803	Hs.102876	pancreatic lipase	1.05
	444290	AA262496	Hs.29280	ESTs	1.04
	407984	AW134708	Hs.243569	ESTs	1.04
	439706	AW872527	Hs.59761	ESTs	1.03
	402194				1.03
75	427506	AK000134	Hs.179100	hypothetical protein FLJ20127	1.03
	428819	AL135623	Hs.193914	KIAA0575 gene product	1.03
	434590	T47232		gb:yb64b08.s1 Stralagene ovary (937217)	1.02
	416378	AW044467	Hs.73708	ESTs, Weakly similar to A57291 cytokine	1.02
	431912	AJ660552	Hs.154903	ESTs, Weakly similar to A56154 Abi subst	1.02
80	443316	AJ478463	Hs.18443	ESTs	1.01
	428585	AB007863	Hs.185140	KIAA0403 protein	1.00
	400440	X83957	Hs.83870	nebulin	1.00
	404619	BE514535	Hs.77171	minichromosome maintenance deficient (S.	1.00
	407168	R45175		gb:yg40f01.s1 Soares infant brain 1NIB H	1.00

	408052	AW501117	Hs.283585	ESTs	1.00
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	1.00
5	410234	NM_003837	Hs.61255	fructose-1,6-bisphosphatase 2	1.00
	410319	R23413	Hs.71935	putative zinc finger protein from EUROM	1.00
	411000	N40449	Hs.201619	ESTs, Weakly similar to SEB4B [H.sapiens	1.00
	412098	AI493054	Hs.158968	ESTs	1.00
	412446	AI768015	Hs.92127	ESTs	1.00
	412637	AA115097	Hs.261313	ESTs	1.00
10	413147	BE067271		gb:PM2-BT0349-161299-001-b05 BT0349 Homo	1.00
	413597	AW302885	Hs.117183	ESTs	1.00
	414117	W88559	Hs.1787	proteolipid protein (Pelizaeus-Merzbache	1.00
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	1.00
15	417074	Z49878	Hs.81131	guanidinoacetate N-methyltransferase	1.00
	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myo	1.00
	419768	T72104	Hs.93194	apolipoprotein A-I	1.00
	420182	Z44245	Hs.22999	ESTs	1.00
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	1.00
20	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	1.00
	421204	AW081587	Hs.165051	ESTs	1.00
	422189	AF252292	Hs.112933	Tax interaction protein 40	1.00
	422792	AI951548	Hs.135163	ESTs	1.00
	423371	AU076819	Hs.1650	solute carrier family 26, member 3	1.00
25	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	1.00
	424922	BE368547	Hs.217112	ESTs, Weakly similar to Similarity to Ye	1.00
	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	1.00
	425545	N98529	Hs.158295	Human mRNA for myosin light chain 3 (MLC	1.00
	425983	AK000226	Hs.165619	mucin and cadherin-like	1.00
30	426004	AW600300	Hs.124123	ESTs, Weakly similar to synocollin [R.nor	1.00
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	1.00
	428848	NM_000230	Hs.194236	leptin (murine obesity homolog)	1.00
	429027	AL022314	Hs.194750	Human DNA sequence from clone 1170K4 on	1.00
	429231	AA813214		gb:af32e09.s1 Soares_testis_NHT Homo sap	1.00
35	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	1.00
	429930	AI580809	Hs.99569	ESTs	1.00
	429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	1.00
	430418	R98852	Hs.36029	heart and neural crest derivatives expre	1.00
	431845	AA516469	Hs.270554	ESTs	1.00
40	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	1.00
	433839	F35430	Hs.146070	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00
	434452	AA634333	Hs.116822	ESTs	1.00
	435499	R89344	Hs.14148	ESTs	1.00
	438433	AB018274	Hs.6214	KIAA0731 protein	1.00
45	442403	AW207724	Hs.129516	ESTs	1.00
	442803	AI675298	Hs.199917	ESTs	1.00
	443266	AI277101	Hs.25890	ESTs, Weakly similar to transducin [H.sa	1.00
	444656	AI277924	Hs.145199	ESTs	1.00
	445573	AI439646	Hs.157494	ESTs, Weakly similar to KIAA0676 protein	1.00
50	446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1.00
	447359	NM_012093	Hs.18268	adenylate kinase 5	1.00
	447551	BE066634	Hs.929	myosin, heavy polypeptide 7, cardiac mus	1.00
	448657	BE147857	Hs.293841	ESTs, Weakly similar to KIAA0672 protein	1.00
	449238	AA428229	Hs.85524	muscle-specific RING-finger protein homo	1.00
55	450085	AW293791	Hs.60162	Homo sapiens cDNA: FLJ21528 fis, clone C	1.00
	450390	N93227	Hs.98403	ESTs	1.00
	451681	Z28564	Hs.255950	ESTs, Weakly similar to AA64_HUMAN 64 KD	1.00
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	1.00
	452528	AA742457	Hs.291479	ESTs	1.00
60	452624	AU076606	Hs.30054	coagulation factor V (proaccelerin, labi	1.00
	453754	AW972580	Hs.172753	ESTs	1.00
	453991	AW014915	Hs.273741	ESTs	1.00
	454517	AW803340		gb:IL2-UM0079-090300-050-D02 UM0079 Homo	1.00
	459367	BE148877		gb:CM4-HT0244-111199-040-h12 HT0244 Homo	1.00
65	408021	AW137133	Hs.245867	ESTs	0.99
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	0.99
	437206	AW975934	Hs.283382	ESTs, Weakly similar to Protein sequence	0.99
	422890	Z43784	Hs.78713	solute carrier family 25 (mitochondrial	0.98
	425878	AW964806	Hs.38085	ESTs, Weakly similar to putative glycine	0.98
	441888	AI733306	Hs.128071	hypothetical protein FLJ21302	0.98
70	423068	M25629	Hs.123107	kallikrein 1, renal/pancreas/salivary	0.97
	453534	NM_014796	Hs.33187	KIAA0748 gene product	0.97
	457787	AA683268		gb:ae92b04.s1 Stratagene schizo brain S1	0.97
	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	0.96
75	422069	AJ010063	Hs.111110	titin-cap (teletthonin)	0.96
	425260	L47726	Hs.1870	phenylethanol hydroxylase	0.96
	418406	X73501	Hs.84905	cytokeratin 20	0.95
	425670	AW968536	Hs.190146	ESTs	0.95
	416373	AA195845	Hs.73680	ESTs, Weakly similar to AF198455 1 epith	0.94
80	452243	AL355715	Hs.28555	programmed cell death 9	0.94
	411908	L27943	Hs.72924	cytidine deaminase	0.93
	415067	AI264969	Hs.929	myosin, heavy polypeptide 7, cardiac mus	0.93
	437156	AI916600	Hs.121194	Homo sapiens cDNA: FLJ21569 fis, clone C	0.93
	450685	L15533	Hs.423	pancreatitis-associated protein	0.92

	427450	AB014526	Hs.178121	KIAA0626 gene product	0.91
	432440	X83597	Hs.2996	sucrase-isomaltase	0.91
	426651	AJ076646	Hs.171683	nuclear receptor subfamily 1, group H, m	0.90
	414910	X12662	Hs.29679	cofactor required for Sp1 transcription	0.89
5	423317	AJ272204	Hs.64616	chromosome 12 open reading frame 3	0.89
	424735	U31875	Hs.152677	Homo sapiens cDNA FLJ20338 fis, clone HE	0.89
	439751	AA196090	Hs.50794	Homo sapiens mRNA full length insert cDN	0.89
	452689	F33868	Hs.284176	transferrin	0.89
10	446240	AI535736	Hs.170165	ESTs	0.88
	449110	H56112	Hs.277053	ESTs	0.88
	453817	AW755253	Hs.61920	ESTs	0.88
	428221	U96781	Hs.183075	ESTs, Highly similar to Ca2+ ATPase off	0.87
	439461	AW075485	Hs.286049	phosphoserine aminotransferase	0.87
	446525	AW967069	Hs.211556	Homo sapiens cDNA: FLJ23378 fis, clone H	0.87
15	453341	AI758912	Hs.296341	adenylyl cyclase-associated protein 2	0.87
	403740				0.86
	420156	AW449258	Hs.6187	ESTs	0.86
	430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	0.86
	421142	AW503944	Hs.130822	ESTs	0.85
20	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	0.85
	419415	AW451692	Hs.192036	ESTs	0.84
	423321	AB013885	Hs.126926	beta-ureidopropionase	0.84
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	0.84
	433447	U29195	Hs.3281	neuronal pentraxin II	0.84
25	403047				0.83
	406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu	0.81
	407782	AA608956	Hs.112619	ESTs, Weakly similar to PQ0109 Purkinje	0.81
	405232				0.80
30	437776	AA768037	Hs.291671	ESTs	0.80
	415505	R39870	Hs.12548	ESTs	0.79
	444436	N25871	Hs.177337	ESTs	0.78
	409096	AA194412	Hs.50550	sarcomeric muscle protein	0.77
	432134	AI816782	Hs.122583	Homo sapiens cDNA: FLJ21934 fis, clone H	0.76
	437066	AA743570	Hs.200935	ESTs	0.76
35	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	0.75
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	0.73
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	0.71
	420567	AK000812	Hs.98874	similar to proline-rich protein 48	0.71
40	447145	AA761073	Hs.192943	ESTs	0.71
	452103	R42764	Hs.3248	muS (E. coli) homolog 6	0.70
	410929	H47233	Hs.30643	ESTs	0.70
	400301	X03635	Hs.1657	estrogen receptor 1	0.69
	415702	F28877		gb:HSPD18414 HM3 Homo sapiens cDNA clone	0.67
	411396	C04646	Hs.85428	ESTs	0.65
45	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	0.65

TABLE 28B

50	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
55	Pkey	CAT number
	407743	1012151_1
	408123	1040435_1
	408432	1058667_1
	408664	1073340_1
60	408922	109017_1
	409368	112377_1
	409543	1138723_1
	409689	114833_1
	409778	1154206_1
65	409802	1155179_1
	410285	119128_1
	410881	1225682_1
	411187	1235092_1
	412067	1275641_1
70	413147	1350637_1
	413242	135323_1
	413811	1391117_1
	414060	1413697_1
	414095	1416521_1
75	414160	1422273_1
	414580	1463848_1
	415011	151328_1
	415566	1539861_1
	415702	1547874_1
80	417998	171375_1
	418197	172864_1
	418464	1759038_-2
	418556	1767866_-1
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		AW814118 AW814257 AW072376
		AW163377 AW160398
		AW195262 R27868 AW811262
		R56362 AW248096 R07152 R07285
		R87388 R84328 AA058916
		AA071059 AA085201 AA085020
		AW410200 AW409705 AW411433 BE296786 BE270309
		AA078492 AA078333 AA077450 AA077745 AA076896
		AW499705 AW502537 AW503016
		AW500732 AW504061
		AA083609 AA083790 AA112048
		AW809157 AW812181 AW812175 AW812172 AW812161 AW812165
		AW821291 AW821264 AW821287 AW821290 AW821285 AW821280 AW821259
		N45697 N45540 AW890595
		BE067271 BE067266 BE067286 BE067278 BE067299 BE067285
		BE074165 BE075001 BE075009
		BE168828 BE168830 BE168823 BE168928 BE168820 BE168826
		BE246327 BE244704
		BE293546 BE249848
		BE257021 BE258316 BE257099
		BE386918 BE408833 BE385437
		AW963085 AA158005 AW963073
		F12119 Z45475 T64832
		F28877 F35687
		AW967420 AA210915 AA236951 AA210916
		AA214253 AA214259 Z28472 Z28881 Z17828
		R87580
		T02850

422619	218670_1	AA313322 BE408282 AA465612 BE073382
422796	221500_1	AW897265 AW897274 AL119504 AW897270 AW897312 AW897318 AW897317 AA317240 AW961361 T06241 AA326794 AL138130
		AW407975 AW999277
424294	237907_1	BE299311 AA338954 AA338468 AW960907
424334	238221_1	AA393460 AA338940 AW966277 AA419006
424648	241947_1	AA344576 AA732430 AA344601
425515	252721_1	W26609 W27360 AA358818
426328	254901_1	AW631296 AA375484
426507	268382_1	AA380285 AW934727 AW934914
426755	271382_1	BE253469 BE176417 BE176415 AA384133
426880	273277_2	AA453482 AF012388
426998	274259_1	BE274360
429231	301463_1	AA813214 AI936567 AI743529 AA448279 AA94476 AI807452 AI218180 AA972858
430728	322706_1	AW968522 AA485112 AA485162 AW968698
432092	34124_1	AF135026 AA583908
433114	35904_1	AA121579 AB005217
434590	38931_1	T47232 AF147365 T47231
437237	43506_2	BE513073
437728	441520_1	AA766719 AA767041 AW977440
439894	478738_1	AA853077 AA852175
442197	535550_1	AW837912 AW837934 AA984475 AW997490
442614	547073_1	AI269030 AI204085 AI004047
444475	607874_1	C75571 AI150469 T10778
448427	762970_1	BE395620 AW291036 AI500420
449329	80484_1	AW752783 H38266 AA001166
451588	87667_1	AW072057 AI225096 AA018702
452456	918391_1	BE080763 T96699 BE081135 AI902630 H49182 AI904021 AI902697
454517	1221063_1	AW803340 AW803280 AW803275 AW803415 AW803343 AW803422
454748	1233013_1	AW862014 AW858740 AW858735 AW818542 AW858765 AW862027 AW858775 AW858771 AW858763
454869	1238137_1	AW836004 AW836087 AW836163 AW836162 AW836085 AW836084 AW836079 AW836083 AW836082 AW836086 AW836088 AW836166 AW836164
		AW836002 AW836078 AW836161 AW862135 AW836165 AW836003
454886	1238987_1	AW837063 AW935882 AW935957
455075	1252389_1	AW854850 AW854848
455104	1253737_1	BE064863 BE153698 AW856751 BE153820 BE064737 BE153674 BE064730 BE065062 BE153536 AW856622 BE155079 BE064651 BE153655
		BE064650 BE064691
455366	1284685_1	AW947563 AW947543 AW947553 AW947549 AW947717 AW902859 AW902927 BE011032
455433	1290311_1	AW939463 AW939484 AW939480 AW939459 AW939546 AW939593 AW939548 AW939595 AW939106
455446	1291969_1	AW947749 AW947746 AW947754 AW946636 AW946674
455579	1333944_1	BE011320 BE006381 BE006361 BE011180 BE011328 BE011325 BE011157 BE006384 BE006387 BE006385 BE011160 BE011319 BE011346
		BE006370 BE006386 BE011173 BE006389 BE006378 BE006375 BE006364 BE011321 BE006379
455652	1348736_1	BE064675 BE064761 BE064809 BE064673 BE064672 BE064674
455817	1371986_1	BE142384 BE142387
455994	1398737_1	BE179190 BE179206 BE179182 BE179185 BE179186 BE179194
456150	1574395_1	Z42308 H23514
456379	1839113_2	W22206 W22498 W26922
456387	1842730_1	W28876 W26158
456702	219191_1	AI684534 BE262411 AA314031 AW752724
457416	334503_1	BE142052 AW265588 AA506741
457787	407235_1	AA683268 BE002903 BE002672
458764	73207_1	BE619386 AA300687
459197	924229_1	BE244587 AW938684 AW176490 AI940102 AW844995 AW938670 AI909850 AI909885 AI940079 AI909873

55 TABLE 28C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400489	8954013	Plus	131475-131652
400527	9796886	Plus	160750-161007
400545	9800107	Minus	124818-124881
400624	7228177	Minus	94097-94756
400635	8567750	Minus	102800-102932,107482-107689
400672	8118724	Minus	148067-148503
400675	8118750	Plus	11223-11816
400694	8118802	Plus	94288-94442
400738	8118985	Plus	143447-143851
400846	9188605	Plus	39310-39474
401007	8117333	Minus	140821-141050
401015	8117441	Plus	72260-72369
401039	7232177	Plus	6588-6884
401122	8570296	Plus	68256-68444
401238	9954455	Minus	49473-49544
401442	8346725	Minus	85674-85910
401496	7381769	Minus	82790-83002
401590	9966320	Minus	33547-33649
401603	7689963	Minus	116659-116780
401624	8575907	Plus	168318-168444,172964-173647

	401688	2347081	Plus	22016-22624
	401704	3097841	Plus	24712-25374
	401728	8134856	Minus	82117-82920
5	401743	2865207	Plus	115475-115640
	401767	9958312	Plus	156823-156921,157364-157554
	401810	7342191	Plus	129063-129476
	401840	7684597	Plus	56283-56439
	401886	7229913	Minus	79215-79393
10	401919	9502466	Plus	67536-67666
	401969	3126777	Plus	44863-45366
	402051	8082020	Minus	19346-19480,20041-20119
	402056	8084234	Plus	207002-207288
	402153	8247879	Minus	122580-122987
	402158	8516165	Minus	148298-148429,148566-148677
15	402165	8569830	Minus	65064-65979
	402194	8576113	Plus	70917-71191
	402195	7689778	Minus	147901-148884
	402201	8576119	Plus	655-951
20	402316	7527774	Minus	10751-10919,18817-19052,22131-22328
	402382	9690314	Minus	155331-155528
	402386	9799769	Plus	22069-22303
	402394	9929690	Plus	33308-33482
	402409	9796255	Minus	8571-10061
	402423	9796344	Minus	62487-62664
25	402448	9796640	Plus	112942-113069,114303-114521
	402457	9796782	Minus	16513-16577,16838-16926
	402534	9801061	Plus	58989-59457
	402538	9801137	Minus	96314-96539
	402561	9864675	Plus	72967-73163
30	402588	9908948	Minus	33027-33183,59060-59198
	402690	8348058	Plus	13368-13998
	402714	8969253	Minus	18811-18886,19105-19328,19525-19764
	402762	9230904	Minus	123298-124035
35	402862	2956660	Minus	18518-18656
	402911	7263904	Plus	142689-142979
	402951	9408717	Plus	73252-73329,73718-73877,76217-76299,78195-78401
	402968	9581763	Minus	58658-58924
	403047	3540153	Minus	59793-59968
40	403115	7331404	Minus	142952-143094,145474-145653,146269-146445,152816-152998
	403125	9180936	Minus	197548-197712
	403183	9838273	Plus	109930-110074
	403186	9838287	Minus	117513-117856
	403211	7630841	Minus	169211-169369
45	403247	7656833	Minus	76626-77140
	403251	7677983	Plus	100391-100652
	403327	8440025	Minus	174311-174451,174587-174705,175523-175592
	403376	9369545	Minus	108698-108830
	403479	7329292	Minus	148369-148533,150678-150809
50	403526	8017144	Plus	55367-55483
	403540	8077057	Minus	56315-56450
	403605	6862654	Plus	91614-91718
	403612	8469060	Minus	94723-94859
	403665	7249278	Plus	69027-69375
55	403716	7239669	Plus	86899-87122
	403731	7543752	Minus	144000-144618
	403740	7630882	Plus	86504-87227
	403921	7711590	Minus	3297-3536
	403942	7711825	Minus	99606-99757
60	403997	7708819	Plus	134427-134593
	404139	9838113	Plus	76707-76891
	404247	7406725	Minus	83949-84214,84312-84415,84499-84677,84878-85114
	404282	2276311	Plus	61503-62205
	404348	7630858	Minus	28895-29062
65	404668	9797204	Minus	11332-11546,12584-12718
	404682	9797231	Minus	40977-41150
	404795	4826439	Plus	147501-147780
	404825	6478944	Plus	210382-210494
	404938	7381808	Minus	165838-165950
70	405075	7770505	Minus	124680-125321
	405147	9438278	Minus	158996-159557
	405161	9966260	Plus	157607-157785
	405163	9966267	Minus	161171-161299
	405187	7229826	Plus	117025-117170,118567-118736
75	405217	7239551	Plus	32646-33138
	405232	7249042	Plus	125904-126063
	405243	7249201	Minus	22312-23197
	405327	6094661	Minus	120550-120750
	405378	6491714	Plus	91139-91440
80	405420	7211837	Minus	13428-13582
	405703	4240388	Minus	15850-16061
	405737	9943984	Minus	104275-104508,104755-104877
	405895	7677903	Minus	66990-67484
	406059	9103984	Minus	13856-14004

5	406101	9124019	Plus	125325-125831
	406118	9143818	Plus	53997-54629
	406150	9886026	Minus	59331-59701
	406158	7144874	Plus	62393-63016,65012-65578
	406343	9255974	Plus	17284-17440,18489-18646,18917-19004,19384-19538
	406357	9256093	Minus	77181-77415
	406563	7711604	Plus	34401-34538

10

TABLE 29A: 2286 GENES UP-REGULATED IN IDIOPATHIC PULMONARY FIBROSIS (IPF) COMPARED TO NORMAL BODY

15 Table 29A lists about 2286 genes that are up regulated in idiopathic pulmonary fibrosis samples as compared with normal "body map" samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" idiopathic pulmonary fibrosis expression level to "average" normal adult tissues sample expression was greater than or equal to about 2.0. The "average" fibrosis sample expression level was set to the 90th percentile amongst idiopathic pulmonary fibrosis samples. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

20 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of IPF to normal body tissue

25	Pkey	ExAccn	Unigene ID	Unigene Title	R1
30	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	211.8
	442275	AW449467	Hs.54795	ESTs	189.7
	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	134.1
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	130.4
	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	116.8
	421798	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	92.1
35	406964	M21305		gb:Human alpha satellite and satellite 3	80.7
	443709	AI082692	Hs.134662	ESTs	67.1
	431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	61.4
	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	57.4
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	54.6
	457200	U33749	Hs.197764	thyroid transcription factor 1	44.9
40	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	42.7
	443324	R44013	Hs.164225	ESTs	39.8
	414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	27.3
	442006	AW975183	Hs.292653	ESTs, Weakly similar to S72482 hypotheri	27.1
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	27.1
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	26.9
45	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	22.2
	421659	NM_014459	Hs.106511	protocadherin 17	21.0
	450478	AW451709	Hs.271200	ESTs	20.2
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	19.7
	447033	AJ357412	Hs.157601	ESTs	19.4
	445885	AJ734009	Hs.127699	KIAA1603 protein	18.9
50	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	17.9
	432437	W07088	Hs.293685	ESTs	17.8
	424105	AJ142336	Hs.43977	Human DNA sequence from clone RP11-196N1	17.3
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	17.2
	440807	AW269421	Hs.128093	ESTs	16.7
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	16.4
55	433365	AF026944	Hs.293797	ESTs	16.4
	445279	R41900	Hs.22245	ESTs	16.4
	417801	AA417383	Hs.82582	Integrin, beta-like 1 (with EGF-like rep	16.4
	405654				16.1
	449328	AI982493	Hs.197647	ESTs	16.1
	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	15.7
60	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	15.5
	417728	AW138437	Hs.24790	KIAA1573 protein	15.0
	440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	14.8
	452039	AI922988	Hs.172510	ESTs	14.4
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	14.3
	421464	AA291553	Hs.190086	ESTs	14.1
65	421554	AW137676	Hs.97775	ESTs	13.8
	431889	AA521277	Hs.124946	ESTs, Weakly similar to A46010 X-linked	13.2
	434424	AJ811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	13.2
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	12.9
	459702				12.7
	421110	AJ250717	Hs.1355	cathepsin E	12.6
70	407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	12.6
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	12.5
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	12.2
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	12.1
	436982	AB018305	Hs.5378	spodin 1, (I-spodin) extracellular mat	12.1
	451561	N52812	Hs.177403	ESTs	12.0
75	424086	AJ351010	Hs.102257	lysyl oxidase	12.0
	435299	AJ745458	Hs.122614	ESTs, Weakly similar to T20593 hypotheri	12.0
	429496	AA453800	Hs.192793	ESTs	11.9

	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
	403637				11.2
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21328 f1s, clone C	11.2
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	10.9
5	421470	R27496	Hs.1378	annexin A3	10.8
	440209	H05049	Hs.22269	neurexin 3	10.8
	428927	AA441837	Hs.90250	ESTs	10.7
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	10.5
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	10.4
10	416402	NM_000715	Hs.1012	complement component 4-binding protein,	10.4
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	10.4
	442176	AA983764	Hs.128910	ESTs	10.4
	439606	W79123	Hs.58561	G protein-coupled receptor 87	10.3
	452883	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture	10.3
15	417015	M83772	Hs.80876	flavin containing monooxygenase 3	10.3
	422022	AA302420	Hs.200442	ESTs	10.3
	447724	AW298375	Hs.24477	ESTs	10.2
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	10.0
	458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	9.9
20	446232	AI281848	Hs.194691	retinoic acid induced 3	9.9
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	9.9
	453392	AA709285	Hs.5997	hypothetical protein FLJ13078	9.8
	412372	R65998	Hs.285243	hypothetical protein FLJ22029	9.8
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H	9.8
25	407568	AA740964	Hs.62699	ESTs	9.6
	414259	W44633	Hs.301296	Homo sapiens cDNA: FLJ23131 f1s, clone L	9.5
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	9.5
	441484	AA935481	Hs.58972	ESTs	9.4
	422426	W79117	Hs.58559	ESTs	9.4
30	406747	AI925153	Hs.217493	annexin A2	9.4
	450050	AI681268	Hs.257883	ESTs	9.3
	431337	N48107	Hs.292593	ESTs	9.3
	408427	AW194270	Hs.177236	ESTs	9.3
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	9.3
35	453836	R67837	Hs.169872	ESTs	9.2
	443450	N66045	Hs.133529	ESTs	9.2
	418735	N48769	Hs.44609	ESTs	9.1
	421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f	9.1
40	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	9.1
	441233	AA972985	Hs.135568	ESTs	9.0
	459587	AA031956		gbzkl5e04.s1 Soares_pregnantUterus_NbH	9.0
	436246	AW450963	Hs.119991	ESTs	8.9
	445189	AI936450	Hs.147482	ESTs	8.9
	410781	AI375672	Hs.165028	ESTs	8.8
45	446868	AV660737	Hs.135100	ESTs	8.8
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	8.8
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	8.8
	414968	C16096	Hs.22826	tropomodulin 3 (ubiquitous)	8.8
	410334	AW979261	Hs.291993	ESTs	8.8
50	442510	AF150179	Hs.249890	ESTs	8.7
	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	8.7
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	8.7
	444929	AI685841	Hs.161354	ESTs	8.6
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	8.6
55	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	8.6
	412719	AW016610	Hs.129911	ESTs	8.5
	453445	AL036532	Hs.91453	ESTs	8.5
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	8.5
	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	8.3
60	433815	AI696602	Hs.112757	ESTs	8.3
	432203	AA305746	Hs.49	macrophage scavenger receptor 1	8.3
	451103	R52804	Hs.25956	DKFZP564D206 protein	8.3
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	8.3
	424989	AA985520	Hs.23575	ESTs	8.3
65	433231	AB040926	Hs.143552	KIAA1493 protein	8.2
	408217	AI433201	Hs.279860	tumor protein, translationally-controlled	8.1
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam	8.1
	435751	AA732217	Hs.294054	ESTs	8.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CLUA	8.0
70	413048	M93221	Hs.75182	mannose receptor, C type 1	8.0
	426803	AA362568	Hs.179747	ecotropic viral integration site 5	7.9
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	7.8
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	7.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.7
75	421013	M62397	Hs.1345	mutated in colorectal cancers	7.7
	437479	R61866	Hs.101277	ESTs	7.6
	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsulf	7.6
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	7.6
	444396	T65213	Hs.4257	ESTs	7.6
80	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 f1s, clone H	7.6
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	7.6
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	7.6
	446466	I38026	Hs.308	arrestin 3, retinal (X-arrestin)	7.6

	449108	AI140683	Hs.98328	hypothetical protein MGC13040	7.5
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.5
	416030	H15261	Hs.21948	ESTs	7.5
5	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	7.4
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	7.4
	448206	BE622585	Hs.3731	ESTs, Moderately similar to I38022 hypot	7.3
	432133	AB033088	Hs.272567	KIAA1262 protein	7.3
	447112	H17800	Hs.7154	ESTs	7.3
	446917	AI347863	Hs.156672	ESTs	7.3
10	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	7.3
	431761	AW002846	Hs.105468	hypothetical protein FLJ22690	7.3
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	7.2
	413499	BE144884		gb:CM0-HT0182-041099-065-e11 HT0182 Homo	7.2
	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	7.2
15	438122	AI620270	Hs.129837	ESTs, Weakly similar to Z263_HUMAN ZINC	7.2
	449511	AI970394	Hs.197075	ESTs	7.2
	453816	NM_003452	Hs.33846	dynein, axonemal, light intermediate pol	7.2
	410060	NM_001448	Hs.58367	glypican 4	7.2
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	7.2
20	452571	W31518	Hs.34665	ESTs	7.2
	453736	AL118674	Hs.34871	zinc finger homeobox 1B	7.2
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	7.2
	405494				7.2
	442832	AW206560	Hs.253569	ESTs	7.1
25	420193	AW60080	Hs.202869	ESTs	7.1
	434217	AW014795	Hs.23349	ESTs	7.0
	427356	AW023482	Hs.97849	ESTs	7.0
	436396	AI683487	Hs.152213	wingless-type MMTV integration site faml	6.9
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	6.9
30	442377	AA993807	Hs.167367	ESTs	6.9
	441143	AI027604	Hs.159650	ESTs	6.9
	445122	AW241632	Hs.147377	hypothetical protein FLJ23598	6.9
	431353	AA828032	Hs.189076	ESTs	6.9
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	6.8
35	426753	T89832	Hs.170278	ESTs	6.8
	445186	AW614544	Hs.123641	protein tyrosine phosphatase, receptor t	6.8
	451963	AI825440	Hs.224952	ESTs	6.8
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	6.8
	433426	H69125	Hs.133525	ESTs	6.8
40	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	6.8
	415236	R41400		gb:Y94b12.s1 Soares Infant brain 1N1B H	6.8
	409031	AA376836	Hs.76728	ESTs	6.7
	427558	D49493	Hs.2171	growth differentiation factor 10	6.7
	437259	AI377755	Hs.120695	ESTs	6.7
45	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	6.7
	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	6.7
	430099	AW194988	Hs.20537	hypothetical protein FLJ13942	6.7
	422475	AL359938	Hs.117313	Meis (mouse) homolog 3	6.7
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	6.7
50	424750	D29956	Hs.152818	ubiquitin specific protease 8	6.6
	403574				6.6
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	6.6
	415025	AW207091	Hs.72307	ESTs	6.5
55	448104	AI674818	Hs.316433	Homo sapiens cDNA FLJ11375 fis, clone HE	6.5
	444271	AW452569	Hs.149804	ESTs	6.5
	437157	BE048860	Hs.120655	ESTs	6.5
	444050	AW138295	Hs.135024	ESTs	6.5
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	6.5
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	6.5
60	424433	H04607	Hs.9218	ESTs	6.4
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	6.4
	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	6.4
	422544	AB018259	Hs.118140	KIAA0716 gene product	6.4
	449765	N92293	Hs.206832	ESTs, Moderately similar to ALL8_HUMAN A	6.3
65	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	6.3
	417246	AI760098	Hs.21411	ESTs	6.3
	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	6.3
	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	6.3
	438909	AF085839		gb:Homo sapiens full length insert cDNA	6.3
70	446002	AI346468	Hs.145789	ESTs	6.3
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	6.3
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	6.3
	424202	BE350295	Hs.15032	RAN binding protein 17	6.3
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	6.2
75	415511	AI732617	Hs.182362	ESTs	6.2
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	6.2
	416879	H98899	Hs.42599	ESTs	6.2
	432803	AA565398		gb:nk41f01.s1 NCI_CGAP_GC2 Homo sapiens	6.2
	442862	BE080429	Hs.15738	ESTs	6.2
80	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	6.2
	441082	AW444804	Hs.202655	ESTs	6.2
	404599				6.1
	453931	AL121278	Hs.25144	ESTs	6.1

	420252	AW270404	Hs.193161	ESTs	6.1
	431622	AW979271	Hs.293184	ESTs	6.1
	456964	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	6.1
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.0
5	424693	BE169810	Hs.47557	ESTs	6.0
	419172	AW338625	Hs.22120	ESTs	6.0
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	6.0
	453037	AA045175	Hs.177552	ESTs	6.0
10	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT gb:EST383329 MAGE resequences, MAGL Homo	6.0
	431169	AW971240	Hs.99200	ESTs	5.9
	422352	AA766296	Hs.133020	ESTs	5.9
	433527	AW235613	Hs.87767	ESTs	5.9
	420077	AW512260	Hs.28705	ESTs	5.9
15	429703	T93154	Hs.151143	ESTs	5.9
	433098	AW190593	Hs.25954	Interleukin 13 receptor, alpha 2	5.9
	451099	R52795	Hs.246311	ESTs	5.9
	449416	AI651016	Hs.60798	ESTs	5.9
	459023	AW968226	Hs.60371	ESTs	5.9
20	450584	AA040403	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	5.9
	427660	AI741320	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	5.9
	429125	AA446854	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	5.8
	450025	AK001875	Hs.245972	ESTs	5.8
	433479	AW511459	Hs.132908	ESTs	5.8
	443113	AI040686	Hs.120388	ESTs	5.8
25	430414	AW365665	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	5.8
	419752	AA249573	Hs.59203	ESTs	5.8
	435420	AI928513			5.8
	404916				5.8
30	424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.8
	448253	H25899	Hs.201591	ESTs	5.8
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	5.8
	446967	AI699629	Hs.156781	ESTs	5.7
	435082	AA664273	Hs.186104	Homo sapiens cDNA FLJ13803 fis, clone TH	5.7
35	438842	AA827176	Hs.124316	ESTs	5.7
	437260	AA747807	Hs.149500	ESTs	5.7
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	5.7
	428043	T92248	Hs.2240	uteroglobin	5.7
	408045	AW138959	Hs.245123	ESTs	5.7
40	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	5.7
	428508	BE252383	Hs.184668	SBB131 protein	5.6
	453393	AW956392	Hs.110376	ESTs	5.6
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	5.6
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.6
45	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	5.6
	433225	AW816515	Hs.173540	ATPase, Class V, type 10D	5.6
	416575	W02414	Hs.38383	ESTs	5.5
	404043				5.5
	415094	D69513	Hs.330778	ESTs	5.5
50	453049	BE537217	Hs.30343	ESTs	5.5
	430153	AW968128	Hs.336679	ESTs	5.5
	410811	AW805687	Hs.300648	ESTs	5.5
	443903	AI220547	Hs.135223	ESTs	5.5
	429420	AK001679	Hs.202289	hypothetical protein DKFZp434P1735	5.5
55	444471	AB020684	Hs.11217	KIAA0877 protein	5.5
	452542	AW812256		gb:RCO-ST0174-191099-031-a07 ST0174 Homo	5.5
	434088	AF116877	Hs.249270	hypothetical protein PRO1986	5.5
	432113	AA935085	Hs.152385	ESTs	5.5
	446608	N75217	Hs.257846	ESTs	5.5
60	419945	AW290975	Hs.118923	ESTs	5.4
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	5.4
	420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	5.4
	439382	BE247684	Hs.103070	ESTs	5.4
	428895	AA437124	Hs.187247	ESTs	5.4
65	446577	AB040933	Hs.15420	KIAA1500 protein	5.4
	419247	S65791	Hs.89764	fragile X mental retardation 1	5.4
	427778	AA412323	Hs.105323	ESTs	5.4
	437138	AI935622	Hs.271245	ESTs	5.4
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	5.4
70	430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	5.4
	435202	AI971313	Hs.170204	KIAA0551 protein	5.3
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	5.3
	434992	AA658501	Hs.283358	ESTs	5.3
	454039	AW079064	Hs.245540	ESTs	5.3
75	456408	AI288348	Hs.23450	mitochondrial ribosomal protein S25	5.3
	406554				5.3
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1048 (f	5.3
	416769	AI339257	Hs.115436	ESTs, Moderately similar to I54374 gene	5.3
	414299	AA142989	Hs.71730	ESTs	5.3
80	420362	U79734	Hs.97206	huntingtin interacting protein 1	5.3
	459664				5.3
	425509	AF079363	Hs.158213	sperm associated antigen 6	5.3
	401497				5.3
	440727	AI073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	5.2

5	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	5.2
	408776	AA057365	Hs.63356	ESTs, Weakly similar to I38022 hypothetical	5.2
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	5.2
	451050	AW937420	Hs.69662	ESTs	5.2
	400297	AJ127076	Hs.334473	hypothetical protein DKFZp554O1278	5.2
10	404957				5.2
	452771	T05477	Hs.333265	ESTs	5.2
	438885	AJ886558	Hs.184987	ESTs	5.2
	428244	AJ564123	Hs.42500	ADP-ribosylation factor-like 5	5.2
	420481	U50525	Hs.98201	Human BRCA2 region, mRNA sequence CG029	5.2
15	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	5.2
	408729	AA195764	Hs.72639	ESTs	5.1
	457100	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A	5.1
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.1
	417154	AJ674701	Hs.21388	ESTs	5.1
20	411869	W20027	Hs.23439	ESTs	5.1
	427043	AA397679	Hs.3991	ESTs	5.1
	445635	AJ769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.1
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	5.1
	422053	BE156476		gb:QV0-HT0368-040100-082-c05 HT0368 Homo	5.1
25	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	5.1
	408677	AJ279892	Hs.46801	sorting nexin 14	5.0
	404097				5.0
	437636	AA764781	Hs.291844	ESTs	5.0
	452822	X85689	Hs.288617	hypothetical protein FLJ22621	5.0
30	410733	D84284	Hs.66052	CD38 antigen (p45)	5.0
	439140	W85737	Hs.290830	ESTs	5.0
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	5.0
	405547				5.0
	423377	AL049377		gb:Homo sapiens mRNA; cDNA DKFZp586H0718	5.0
35	449168	NM_018206	Hs.23142	colon carcinoma related protein	5.0
	455431	AW938484		gb:CMO-DT0057-290200-253-d06 DT0057 Homo	5.0
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.0
	411149	N68715	Hs.269128	ESTs	5.0
	432441	AW292425	Hs.163484	ESTs	5.0
40	419807	R77402		gb:yl75f11.s1 Soares placenta Nb2HP Homo	5.0
	440815	AJ733055	Hs.130806	ESTs	5.0
	450109	AJ539295	Hs.115740	KIAA0210 gene product	5.0
	449695	AA164569	Hs.34550	ESTs	5.0
	421764	AJ681535	Hs.148135	serine/threonine kinase 33	4.9
45	404593				4.9
	423607	AA328329	Hs.6591	ESTs	4.9
	432009	AL137424	Hs.306458	Homo sapiens mRNA; cDNA DKFZp761G2123 (f	4.9
	419235	AW470411	Hs.288433	neurotrophin	4.9
	436304	AA339622	Hs.108887	ESTs	4.9
50	434613	AJ821826		gb:ns92b10.x5 NCL_CGAP_Pr3 Homo sapiens	4.9
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	4.9
	415245	N59650	Hs.27252	ESTs	4.9
	428780	AJ478578	Hs.50636	ESTs	4.9
	406333				4.9
55	445034	AW293376	Hs.143659	ESTs	4.8
	440202	AW516211	Hs.125300	ring finger protein 21, Interferon-respo	4.8
	424638	AJ472106	Hs.49303	Homo sapiens cDNA FLJ11663 fis, clone HE	4.8
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	4.8
	427652	AJ673025	Hs.43874	ESTs, Moderately similar to I54374 gene	4.8
60	458722	AA741545	Hs.282832	ESTs, Weakly similar to T24961 hypotheti	4.8
	407327	AA487182	Hs.269414	ESTs, Weakly similar to Z195_HUMAN ZINC	4.8
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	4.8
	415261	T40928	Hs.8346	ESTs	4.8
	453543	AA485425	Hs.48919	Homo sapiens cDNA FLJ11508 fis, clone HE	4.8
65	438014	N71183	Hs.121806	Homo sapiens cDNA FLJ11971 fis, clone HE	4.8
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	4.8
	441006	AW605267	Hs.7627	CGI-60 protein	4.8
	412222	AA528283	Hs.292737	ESTs	4.8
	424115	AA335497	Hs.293965	ESTs, Weakly similar to I38022 hypotheti	4.8
70	453197	AJ916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	4.8
	439398	AA284267	Hs.221504	ESTs	4.8
	436397	AA715013	Hs.169835	ESTs	4.8
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	4.8
	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
75	425916	NM_006786	Hs.162200	urotensin 2	4.8
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	4.8
	427457	AW779105	Hs.164682	ESTs	4.7
	451620	AW449888	Hs.257224	ESTs	4.7
	408938	AA059013	Hs.22607	ESTs	4.7
80	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586I1823 (f	4.7
	424508	AL080103	Hs.149770	Homo sapiens cDNA FLJ13658 fis, clone PL	4.7
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	4.7
	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	4.7
	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	435347	AW014873	Hs.116963	ESTs	4.7
	425458	H89317	Hs.182889	ESTs	4.7
	432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo	4.7

5	436594	AI419982	Hs.156189	ESTs	4.7
	421237	U25029	Hs.102761	Human glucocorticoid receptor alpha mRNA	4.7
	432731	R31178	Hs.287820	fibronectin 1	4.7
	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	4.7
	426320	W47595	Hs.169300	transforming growth factor, beta 2	4.6
	419751	AW195581	Hs.93121	KIAA0761 protein	4.6
	433515	AA595800	Hs.190246	ESTs	4.6
	451381	BE241831	Hs.172330	hypothetical protein MGC2705	4.6
10	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	4.6
	438297	AW515196	Hs.258238	ESTs, Moderately similar to ALU1_HUMAN A	4.6
	406992	S82472		gb:beta-pol=DNA polymerase beta (exon a	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	435933	AA805520	Hs.192075	ESTs	4.6
	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	4.6
15	445657	AW612141	Hs.279575	Homo sapiens G-protein coupled receptor	4.6
	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
	447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypotheti	4.6
	423735	AA330259		gb:EST33963 Embryo, 12 week II Homo sapi	4.6
20	424144	AA454033	Hs.41644	AKAP-associated sperm protein	4.6
	416258	N45661	Hs.90011	adenylosuccinate synthase	4.6
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	4.5
	454359	N71277		gb:za36e03.s1 Soares fetal liver spleen	4.5
	422977	AA631498		gb:np83h04.s1 NCI_CGAP_Thy1 Homo sapiens	4.5
25	433485	AA93076	Hs.201967	aldo-keto reductase family 1, member C2	4.5
	450192	AA263143	Hs.24596	RAD51-Interacting protein	4.5
	432015	AL157504	Hs.159115	Homo sapiens mRNA: cDNA DKFZp586O0724 (f	4.5
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	4.5
	409041	AB033025	Hs.50081	KIAA1199 protein	4.5
30	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	4.5
	452526	W38537	Hs.280740	hypothetical protein MGC3040	4.5
	403271			ESTs	4.5
	450656	AA010539	Hs.18912	gb:xq71a12.x1 Soares_NhHMPu_S1 Homo sapi	4.5
35	446096	AI276454		Homo sapiens mRNA for KIAA1771 protein,	4.5
	454036	AA374756	Hs.93560	ESTs	4.5
	437960	AI669586	Hs.222194	ESTs	4.5
	440862	H39048	Hs.127432	ESTs	4.5
	410615	AW772721		gb:hl95c01.x1 NCI_CGAP_Thy8 Homo sapiens	4.5
40	413583	AL120806	Hs.5888	ESTs	4.5
	419449	H18417	Hs.57483	Homo sapiens cDNA FLJ14294 fis, clone PL	4.4
	442324	R63578	Hs.28426	ESTs	4.4
	453080	AI423056	Hs.23921	hypothetical protein DKFZp547A023	4.4
	435747	AI079519	Hs.134398	ESTs	4.4
	446509	AF169693	Hs.132892	protocadherin 20	4.4
45	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	4.4
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	4.4
	448089	AI467945	Hs.173696	ESTs	4.4
	434367	AB020700	Hs.3830	KIAA0893 protein	4.4
	434757	AI038997	Hs.132921	ESTs	4.4
50	413453	AA129640	Hs.128065	ESTs	4.4
	454438	AA224053	Hs.172405	cell division cycle 27	4.4
	458154	AW816379	Hs.335018	ESTs	4.4
	430417	AA461045	Hs.50701	ESTs	4.4
	434819	AA650099	Hs.291541	ESTs, Weakly similar to ALUB_HUMAN IIII	4.4
55	438796	W67821	Hs.109590	genethonin 1	4.4
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.4
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.4
	414812	X72755	Hs.77367	monokine Induced by gamma Interferon	4.4
	451895	T93573	Hs.16970	ESTs	4.4
60	435434	AA680387	Hs.187850	ESTs	4.4
	449623	C00719	Hs.120440	EST	4.3
	433563	AI732637	Hs.277901	ESTs	4.3
	444649	AW207523	Hs.197628	ESTs	4.3
	441594	AL041080	Hs.208765	ESTs, Moderately similar to ALU7_HUMAN A	4.3
65	443314	AW771701	Hs.54646	ESTs	4.3
	400292	AA250737	Hs.72472	ESTs	4.3
	427972	AA864870	Hs.181304	putative gene product	4.3
	446932	AA961459	Hs.125644	ESTs	4.3
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 (H.sapi	4.3
70	452393	H87398	Hs.99858	ribosomal protein L7a	4.3
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	4.3
	400608			ESTs	4.3
	411156	AW819939	Hs.273629	ESTs	4.3
75	435772	AA700019	Hs.132992	ATP-binding cassette, sub-family G (WHIT	4.3
	439830	AA846666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEI	4.3
	455511	BE144762		gb:CMO-HT0180-041099-065-b04 HT0180 Homo	4.3
	443257	AI334040	Hs.11614	HSPC65 protein	4.3
	436033	H75391	Hs.255748	ESTs	4.3
	420214	AI146375	Hs.286073	ESTs, Moderately similar to ALU5_HUMAN A	4.3
80	410619	AW612264	Hs.131705	ESTs	4.3
	401189			hypothetical protein FLJ20069	4.3
	418852	BE537037	Hs.273294	Homo sapiens clone 23578 mRNA sequence	4.3
	425733	F13287	Hs.159388	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3
	447863	AL047611	Hs.288885		4.3

	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapie	4.3
	434677	AW444575	Hs.130834	ESTs	4.3
	403310				4.3
5	451830	H18433	Hs.21542	KIAA1035 protein	4.3
	422222	AI699372	Hs.193247	hypothetical protein DKFZp434A171	4.3
	435627	W88774	Hs.118370	ESTs	4.3
	436461	AW511956	Hs.293261	ESTs	4.3
	452166	AI948607	Hs.264680	ESTs	4.3
10	413998	AW103807	Hs.243933	ESTs	4.2
	416642	T96118	Hs.226313	ESTs	4.2
	452081	AW958859	Hs.7514	Homo sapiens cDNA FLJ12141 fis, clone MA	4.2
	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypothi	4.2
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.2
	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	4.2
15	424641	AB001106	Hs.151413	glia maturation factor, beta	4.2
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.2
	409629	AW449589	Hs.279724	ESTs	4.2
	458771	AW295151	Hs.163612	ESTs	4.2
	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	4.2
20	436645	AW023424	Hs.156520	ESTs	4.2
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	4.2
	445268	AI218358	Hs.175048	ESTs	4.2
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	4.2
25	431917	D16181	Hs.2868	peripheral myelin protein 2	4.2
	443348	AW873596	Hs.182278	calmodulin 2 (phosphorylase kinase, del	4.2
	443151	AI827193	Hs.132714	ESTs	4.2
	419255	AA235672	Hs.87491	ESTs	4.2
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	4.2
30	452561	AI692181	Hs.49169	KIAA1634 protein	4.2
	421106	AA877124	Hs.172844	ESTs	4.2
	424268	AA397653	Hs.307438	Human DNA sequence from clone 495010 on	4.2
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	4.2
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, l	4.2
35	423045	AW967472	Hs.183302	PCTAIRE protein kinase 2	4.2
	428771	AB028992	Hs.193143	KIAA1069 protein	4.1
	445745	AB007924	Hs.13245	KIAA0455 gene product	4.1
	417009	AA191719	Hs.314714	ESTs	4.1
	436517	BE080932	Hs.135225	ESTs	4.1
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	4.1
	414083	AL121282	Hs.257786	ESTs	4.1
	452728	AI915676	Hs.239708	ESTs	4.1
	409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	4.1
	441802	AA968636	Hs.127877	ESTs	4.1
45	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	4.1
	413875	BE176776		gb:RC3-HT0586-110300-011-g09 HT0586 Homo	4.1
	444009	AI380792	Hs.135104	ESTs	4.1
	410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	4.1
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	4.1
50	438993	AA828995		gb:cd77b08.s1 NCI_CGAP_Ov2 Homo sapiens	4.1
	435256	AF193768	Hs.13872	cytokine-like protein C17	4.1
	428104	AA421350	Hs.191604	ESTs	4.1
	439648	AW780192	Hs.267596	ESTs	4.1
	446194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	4.1
55	446364	AB006624	Hs.14912	KIAA0286 protein	4.1
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.0
	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
	408369	R38438	Hs.182575	solute carrier family 15 (H+)-peptide tra	4.0
	404561				4.0
60	401575				4.0
	419296	AA236115	Hs.120785	ESTs	4.0
	432055	AW972359	Hs.293334	ESTs	4.0
	439107	AL046134	Hs.13944	adrenergic, beta, receptor kinase 2	4.0
	450320	AW291775	Hs.213793	ESTs	4.0
65	447350	AI375572	Hs.172634	ESTs	4.0
	441974	AI683782	Hs.128245	ESTs	4.0
	453142	AA033648	Hs.7473	ESTs	4.0
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	4.0
	410292	AA843087	Hs.124194	ESTs	4.0
70	415811	AA450191	Hs.172963	hypothetical protein FLJ14624	4.0
	420218	AW958037	Hs.286	ribosomal protein L4	4.0
	426625	T78300	Hs.300642	serologically defined colon cancer anti	4.0
	417708	N74392	Hs.50495	ESTs	4.0
	451024	AA442176		gb:zw63b08.r1 Soares_total_fetus_Nb2HF8_	4.0
75	411745	AW867826		gb:MRO-SN0039-300300-001-c02 SN0039 Homo	4.0
	422058	AA862231	Hs.334443	ESTs	4.0
	439479	AI734258	Hs.245367	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
	409099	AK000725	Hs.50579	hypothetical protein FLJ20718	4.0
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	4.0
80	444188	AI393165	Hs.699	peptidylprolyl isomerase B (cyclophilin	4.0
	453096	AW294631	Hs.11325	ESTs	4.0
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	4.0
	421002	AF116030	Hs.100932	transcription factor 17	4.0
	445414	AV653692	Hs.146105	ESTs	4.0

	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	4.0
	451353	N21043	Hs.42932	ESTs	4.0
	437075	AA743748	Hs.40758	ESTs	3.9
	410505	AW752139	Hs.314323	ESTs	3.9
5	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	3.9
	426116	AA868729	Hs.144694	ESTs	3.9
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	3.9
	436298	AW293496	Hs.180138	ESTs	3.9
	417718	T86540	Hs.193981	ESTs	3.9
10	436772	AW975688	Hs.74170	metallothionein 1E (functional)	3.9
	401045				3.9
	408767	AA057279	Hs.211928	ESTs	3.9
	407303	AA016296	Hs.165200	ESTs, Weakly similar to A56194 thromboxa	3.9
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	3.9
15	451623	H77818	Hs.268991	ESTs	3.9
	450063	AI681509	Hs.277133	ESTs	3.9
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.9
	419276	BE165909	Hs.306881	MSTP043 protein	3.9
20	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.9
	436149	AI754308	Hs.159452	ESTs	3.9
	422667	H25642	Hs.133471	ESTs	3.9
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	3.9
	458219	H22195	Hs.31874	ESTs	3.9
25	443613	AI079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapi	3.9
	439810	AL109710	Hs.85568	EST	3.9
	436578	AI091435	Hs.134859	ESTs	3.9
	415598	AI433165	Hs.9856	ESTs	3.9
	425087	R62424	Hs.126059	ESTs	3.9
30	454111	AW081681	Hs.269064	ESTs, Weakly similar to T42689 hypotheti	3.9
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	3.9
	452466	N84635	Hs.29664	hypothetical protein DKFZp564B052	3.9
	424962	NM_012288	Hs.153954	TRAM-like protein	3.9
	435823	R07856	Hs.16355	ESTs	3.9
35	440633	AI140686	Hs.263320	ESTs	3.9
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	3.9
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked mol	3.9
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.9
	417461	R38403	Hs.13305	ESTs	3.9
40	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.8
	419140	AI982647	Hs.215725	ESTs	3.8
	415652	T79213	Hs.272073	ESTs	3.8
	430140	AW296771	Hs.221999	ESTs	3.8
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	3.8
45	422165	AL041199	Hs.1481	histidine decarboxylase	3.8
	417706	T90797	Hs.268623	ESTs	3.8
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.8
	450522	AI698839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.8
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.8
50	449729	R72032	Hs.29235	ESTs	3.8
	414700	H63202	Hs.38163	ESTs	3.8
	440899	AW449445	Hs.120021	DKFZP434I092 protein	3.8
	439335	AA742697	Hs.62492	ESTs, Weakly similar to B39066 proline-r	3.8
	408625	AW243323	Hs.266785	ESTs	3.8
55	421987	AI133161	Hs.286131	CGI-101 protein	3.8
	418915	AI474778	Hs.118977	ESTs	3.8
	410224	M55513	Hs.150208	potassium voltage-gated channel, shaker-	3.8
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	3.8
	442849	R10099	Hs.269805	ESTs	3.8
60	427191	BE221825	Hs.97691	ESTs	3.8
	407942	AA378608	Hs.5894	hypothetical protein FLJ10305	3.8
	437030	AA742577	Hs.303781	EST	3.8
	427940	AA417812	Hs.38775	ESTs	3.7
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	3.7
65	449679	AI823951	Hs.129700	toll-like 1	3.7
	425937	NM_013240	Hs.163846	putative N6-DNA-methyltransferase	3.7
	458663	AV658444	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	3.7
	458443	AW967500	Hs.133543	ESTs	3.7
	439957	AI453184	Hs.66357	ESTs	3.7
70	446999	AA151520	Hs.334822	hypothetical protein MGC4485	3.7
	428414	AL049980	Hs.184216	DKFZP564C152 protein	3.7
	455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	3.7
	418379	AA218940	Hs.137516	fidgetin-like 1	3.7
	419720	AA249131	Hs.337778	hypothetical protein FLJ11068	3.7
	443594	AI807036	Hs.267245	hypothetical protein FLJ14803	3.7
75	416185	AW975861	Hs.47367	KIAA1785 protein	3.7
	417235	AA810278	Hs.24250	ESTs	3.7
	441720	AI346487	Hs.28739	ESTs	3.7
80	451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.7
	417355	D13168	Hs.82002	endothelin receptor type B	3.7
	449321	AA001150	Hs.132937	ESTs	3.7
	424806	AA382523	Hs.105689	MSTP031 protein	3.7
	452338	AW608920	Hs.29159	zinc finger protein 75 (DBC6)	3.7
	409248	AB033035	Hs.51965	KIAA1209 protein	3.7

	421037	AI584808	Hs.197653	ESTs	3.7
	427088	AA398085	Hs.142390	ESTs	3.7
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	3.7
5	420026	AI831190	Hs.166676	ESTs	3.7
	429419	AB023226	Hs.202276	KIAA1009 protein	3.7
	447410	AI470235	Hs.172698	EST	3.7
	404274				3.7
	416320	H47867	Hs.34024	ESTs	3.7
10	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A;	3.7
	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.7
	446025	AW305075	Hs.180948	KIAA0729 protein	3.7
	450458	AA009926		gb:z07e05.r1 Soares_fetal_liver_spleen_	3.7
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor 1	3.6
	438257	AW474419	Hs.224794	ESTs	3.6
15	440887	AI799488	Hs.135905	ESTs	3.6
	454693	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	3.6
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	3.6
	408687	AL110280	Hs.301152	Homo sapiens mRNA; cDNA DKFZp434F053 (tr	3.6
20	407726	AA435679	Hs.88594	ESTs	3.6
	436026	AI349764	Hs.217081	ESTs	3.6
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	3.6
	452293	AI871833	Hs.304609	ESTs	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.6
	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	3.6
25	429208	AA447990	Hs.190478	ESTs	3.6
	458429	AV646559	Hs.12346	Homo sapiens cDNA: FLJ21399 fis, clone C	3.6
	404476				3.6
	405848				3.6
30	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transi	3.6
	403937				3.6
	437918	AI761449	Hs.121629	ESTs	3.6
	432408	N39127	Hs.332557	ESTs, Weakly similar to A46010 X-linked	3.6
	437641	AA811452	Hs.291911	ESTs	3.6
	439635	AA477288	Hs.94891	hypothetical protein FLJ22729	3.6
35	446102	AW168067	Hs.252956	ESTs	3.6
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	3.6
	425403	AL023753	Hs.156406	Human DNA sequence from clone 1198H6 on	3.6
	432030	AI908400	Hs.143789	ESTs	3.6
	446453	AV658469	Hs.188646	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
40	452055	AI377431	Hs.141693	hypothetical protein MGC10858	3.6
	440801	AA906366	Hs.190535	ESTs	3.6
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	3.6
	440886	AW511032	Hs.190516	ESTs	3.6
	401049				3.6
45	449424	AW448937	Hs.197030	ESTs	3.6
	418076	R61388	Hs.6724	ESTs	3.6
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
	435463	AA682507		gb:z18f08.s1 Soares_fetal_liver_spleen_	3.6
	438016	AI949638	Hs.336846	EST	3.6
50	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	3.6
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	3.5
	456536	AW135986	Hs.257859	ESTs	3.5
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	3.5
55	414400	X06948	Hs.897	Fc fragment of IgE, high affinity I, rec	3.5
	435344	AA700326	Hs.190599	ESTs	3.5
	445056	AB014530	Hs.12259	KIAA0630 protein	3.5
	449444	AW818438	Hs.23590	solute carrier family 16 (monocarboxylic	3.5
	442652	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	3.5
60	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
	449540	AA001713		gb:zh86e08.s1 Soares_fetal_liver_spleen_	3.5
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	3.5
	428409	AW117207	Hs.98523	ESTs	3.5
	431087	H12723	Hs.290791	ESTs	3.5
	426920	AA393351	Hs.132121	ESTs	3.5
65	427687	AW003867	Hs.1570	histamine receptor H1	3.5
	437583	AA761190	Hs.244627	ESTs	3.5
	421599	AA236555	Hs.97293	ESTs	3.5
	433687	AA743991		gb:ny57g01.s1 NCL_CGAP_Pr18 Homo sapiens	3.5
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (tr	3.5
70	430499	AW969408	Hs.231991	ESTs	3.5
	451531	AA018311	Hs.114762	ESTs	3.5
	457620	AA602711	Hs.336753	EST	3.5
	410658	AW105231	Hs.192035	ESTs	3.5
	427865	AA416931	Hs.126065	ESTs	3.5
75	453390	AA862496	Hs.28482	ESTs	3.5
	419583	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	3.5
	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	3.5
	427718	AI798680	Hs.25933	ESTs	3.5
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	3.5
80	420381	D50640	Hs.337616	phosphodiesterase 3B, cGMP-inhibited	3.5
	410908	AA121686	Hs.10692	ESTs	3.5
	442080	AW444761	Hs.44565	ESTs	3.5
	406685	M18728		gb:Human nonspecific crossreacting anti	3.5

	404200				3.5
	417976	BE565892	Hs.83077	Interleukin 18 (interferon-gamma-inducin	3.5
	433285	AW975944	Hs.237396	ESTs	3.5
	432868	AW974093	Hs.292775	ESTs	3.5
5	433492	AW605849		gb:MR0-HT0241-200100-006-g02 HT0241 Homo	3.5
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	3.4
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	3.4
	428775	AA434579	Hs.143691	ESTs	3.4
	410004	AJ298027	Hs.5057	carboxypeptidase D	3.4
10	422093	AF151852	Hs.111449	CGI-94 protein	3.4
	441736	AW292779	Hs.169799	ESTs	3.4
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	3.4
	405970				3.4
	431954	AK001974	Hs.272242	hypothetical protein FLJ11112	3.4
15	459482	AA625339	Hs.237052	EST, Weakly similar to I38022 hypothetic	3.4
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	3.4
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.4
	402230				3.4
	436120	AJ248193	Hs.119860	ESTs	3.4
20	405336				3.4
	434374	AA631439		gb:np85d02.s1 NCI_CGAP_Thy1 Homo sapiens	3.4
	428911	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (f	3.4
	437783	AJ683150	Hs.201550	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.4
	416057	AJ927382	Hs.29857	ESTs	3.4
25	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	3.4
	436088	AA704687	Hs.191294	ESTs	3.4
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	3.4
	454076	AW204712	Hs.61957	ESTs	3.4
	431733	AW298410	Hs.21475	ESTs	3.4
30	432974	BE348793	Hs.233331	ESTs	3.4
	412576	AA447718	Hs.107057	ESTs	3.4
	446142	AJ754693	Hs.145968	ESTs	3.4
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked mol	3.4
	433384	AJ021892	Hs.124244	ESTs	3.4
35	413621	AJ808648	Hs.184156	ESTs	3.4
	419546	AA244199		gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapiens	3.4
	436111	AJ803082	Hs.157212	ESTs	3.4
	421236	AJ287622	Hs.151956	ESTs	3.4
	433917	AJ809325	Hs.122814	Human DNA sequence from clone RP5-1028D1	3.4
40	403515				3.4
	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protei	3.4
	453375	AJ990114	Hs.240091	ESTs	3.4
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT	3.4
45	412209	AW901456		gb:RC0-NN1012-270300-031-c07 NN1012 Homo	3.4
	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi	3.4
	409642	AW450809	Hs.257347	ESTs	3.4
	420092	AA814043	Hs.88045	ESTs	3.3
	453365	AA035211	Hs.17404	ESTs	3.3
	437007	AA741300	Hs.202599	ESTs, Weakly similar to I38022 hypotheti	3.3
50	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	3.3
	439024	R96696	Hs.35698	ESTs	3.3
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	3.3
	417991	AA731452	Hs.190008	ESTs	3.3
	403356				3.3
55	433650	AA603472	Hs.28456	ESTs	3.3
	410318	AA084050	Hs.269269	ESTs, Weakly similar to S23650 retroviru	3.3
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	3.3
	413714	AJ560944	Hs.71428	ESTs	3.3
	430887	N66801	Hs.260287	KIAA1841 protein	3.3
60	413618	BE154078		gb:PMO-HT0339-200400-010-F04 HT0339 Homo	3.3
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	3.3
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE	3.3
	405692				3.3
65	432809	AA565509	Hs.131703	ESTs	3.3
	433805	AA706910	Hs.112742	ESTs	3.3
	436192	W93847	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	3.3
	435451	AF195420	Hs.303005	ESTs, Weakly similar to gamma-hergulin	3.3
	411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro	3.3
	448404	BE089973		gb:RC6-BT0709-310300-021-G07 BT0709 Homo	3.3
70	410434	AF051152	Hs.63668	toll-like receptor 2	3.3
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.3
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	3.3
	444301	AK000136	Hs.10760	asporin (LRR class 1)	3.3
	428795	R45503	Hs.97469	ESTs, Highly similar to A39769 N-acetyl	3.3
75	458924	BE242158	Hs.24427	DKFZP566O1646 protein	3.3
	435934	R19382	Hs.117869	ESTs	3.3
	400269				3.3
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	3.3
	412803	BE007967	Hs.155795	ESTs	3.3
80	400889				3.3
	449585	AJ655321	Hs.197693	ESTs	3.3
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	3.3
	418557	BE140602	Hs.246645	ESTs	3.3

	453204	R10799	Hs.191990	ESTs	3.3
	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	3.3
	427374	AI150033	Hs.143686	ESTs	3.3
5	443367	AW071349	Hs.215937	ESTs	3.3
	446645	AI336596	Hs.156294	ESTs	3.3
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypothet	3.3
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	3.3
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	3.3
10	403895				3.2
	414899	AW975433	Hs.36288	ESTs	3.2
	409044	AI129586	Hs.33033	hypothetical protein FLJ14623	3.2
	447233	AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	3.2
	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.2
15	427119	AW880562	Hs.114574	ESTs	3.2
	437073	AI885608	Hs.94122	ESTs	3.2
	443830	AI142095	Hs.143273	ESTs	3.2
	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	433644	AW342028		gb:hb75d03.x1 NCI_CGAP_U12 Homo sapiens	3.2
20	417561	AW974345		gb:EST386449 MAGE resequences, MAGM Homo	3.2
	446063	AI720140	Hs.151079	ESTs	3.2
	423609	AA328348	Hs.218289	ESTs	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.2
25	435808	AA702866	Hs.113150	ESTs	3.2
	424001	W67883	Hs.137476	paternally expressed 10	3.2
	415635	F13168		gb:HS3JF101 normalized infant brain cDN	3.2
	418946	AI798841	Hs.164526	ESTs	3.2
	431750	AA514986	Hs.283705	ESTs	3.2
30	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	3.2
	428268	AA424957	Hs.294132	ESTs	3.2
	418878	W20090	Hs.6616	ESTs	3.2
	416565	AW000960	Hs.44970	endoplasmic reticulum resident protein 5	3.2
	454288	BE222648	Hs.279458	ESTs, Highly similar to c380A1.1b [H.sap	3.2
35	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.2
	404588				3.2
	413087	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
	444910	AI201849		gb:qs76g04.x1 NCI_CGAP_Pr28 Homo sapiens	3.2
	407339	AA777542	Hs.132670	ESTs	3.2
40	414093	BE544867	Hs.283077	centrosomal P4.1-associated protein; unc	3.2
	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	3.2
	419340	AA236590	Hs.87530	ESTs	3.2
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone CO	3.2
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	3.2
45	421187	NM_014721	Hs.102471	KIAA0680 gene product	3.2
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	3.2
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	3.2
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	3.2
	438839	AW297945	Hs.128490	ESTs	3.2
50	410085	AA428482	Hs.55859	glycogenin 2	3.2
	427961	AW293165	Hs.143134	ESTs	3.2
	429228	AI553633	Hs.337139	ESTs	3.2
	431548	AI834273	Hs.9711	novel protein	3.1
	441839	AW975512	Hs.29160	ESTs	3.1
55	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.1
	441274	AW9593781	Hs.131357	ESTs	3.1
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
	436154	AA764950	Hs.119898	ESTs	3.1
	406752	AI285598		gb:qu49f06.x1 NCI_CGAP_Lym6 Homo sapiens	3.1
60	450689	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	3.1
	434164	AW207019	Hs.148135	serine/threonine kinase 33	3.1
	436739	BE208022	Hs.127685	KIAA1627 protein	3.1
	451674	AA019104	Hs.175483	Homo sapiens cDNA: FLJ22016 fis, clone H	3.1
	421166	AA305407	Hs.102308	potassium inwardly-rectifying channel, s	3.1
65	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.1
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.1
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	3.1
	424780	U39576	Hs.153058	butyrophilin, subfamily 1, member A1	3.1
70	456551	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	3.1
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	3.1
	431814	BE256242	Hs.270847	delta-tubulin	3.1
	440099	AL080058	Hs.6909	DKFZP564G202 protein	3.1
	436401	AI087958	Hs.29088	ESTs	3.1
75	437439	H29796	Hs.269622	ESTs	3.1
	403277				3.1
	408547	AA574291	Hs.57837	ESTs	3.1
	424131	AA335714	Hs.199665	ESTs	3.1
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN A	3.1
80	434636	AA083764	Hs.6101	hypothetical protein MGC3178	3.1
	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	3.1
	407905	AW103655	Hs.252905	ESTs	3.1
	452311	AW304029	Hs.252744	ESTs	3.1

	434849	AW292765	Hs.8053	ESTs	3.1
	446770	AV660309	Hs.154986	ESTs, Weakly similar to PLLP_HUMAN PLASM	3.1
	424238	AA337401	Hs.137635	ESTs	3.1
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	3.1
5	447829	AI433029	Hs.164104	ESTs	3.1
	406506				3.1
	428301	AW628666	Hs.98440	ESTs, Weakly similar to 138022 hypotheti	3.1
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	3.1
10	451229	AW967707	Hs.48473	ESTs	3.1
	401103				3.1
	433589	AA886530	Hs.188912	ESTs	3.1
	459370	AA889982	Hs.271826	ESTs, Weakly similar to 138022 hypotheti	3.1
	438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypotheti	3.1
	404288				3.1
15	406195				3.1
	438202	AW169287	Hs.22588	ESTs	3.1
	425516	BE000707	Hs.29567	ESTs	3.1
	425572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.1
	422692	AA332376	Hs.24135	transmembrane protein vezatin; hypotheti	3.1
20	435414	AW270550	Hs.116957	ESTs	3.1
	418950	T78517	Hs.13941	ESTs	3.1
	426890	AA393167	Hs.41294	ESTs	3.1
	457447	X78261	Hs.272177	H.sapiens mRNA for TRE17 5' extremity an	3.1
	443773	AV646452	Hs.30941	calcium channel, voltage-dependent, beta	3.1
25	459371	R20991		gb:yg06h01.r1 Soares infant brain 1N1B H	3.1
	421823	N40850	Hs.28625	ESTs	3.1
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.1
	452896	AA831508	Hs.32553	ESTs	3.1
	425895	AI269484	Hs.161427	zinc finger protein 215	3.1
30	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	3.1
	407340	AA810168	Hs.284289	vitiigo-associated protein VIT-1	3.1
	401862				3.1
	444325	AW152618	Hs.16757	ESTs	3.1
	408171	AA301228	Hs.43299	hypothetical protein FLJ12890	3.1
35	423949	AI014546	Hs.130912	ESTs	3.0
	419519	AI198719	Hs.176376	ESTs	3.0
	434683	AW298724	Hs.202639	ESTs	3.0
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
	415086	AI597963	Hs.118726	ESTs	3.0
40	419220	AA811938	Hs.291759	ESTs	3.0
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	3.0
	443634	H73972	Hs.134460	ESTs	3.0
	429682	NM_005306	Hs.211602	SMC1 (structural maintenance of chromoso	3.0
	405090				3.0
45	432267	AK000872	Hs.274227	Homo sapiens cDNA FLJ10010 fis, clone HE	3.0
	443253	AI041212	Hs.132117	ESTs	3.0
	444974	AI203500	Hs.151612	ESTs	3.0
	445717	AW684658	Hs.149332	ESTs	3.0
	449347	AV649748	Hs.295901	KIAA0493 protein	3.0
50	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.0
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.0
	424406	D54120	Hs.146409	cell division cycle 42 (GTP-binding prot	3.0
	410371	AA084482	Hs.115850	ESTs	3.0
	426384	AI472078	Hs.303662	ESTs	3.0
55	418200	AW629751	Hs.206654	ESTs, Weakly similar to alternatively sp	3.0
	427050	AA397789	Hs.161803	ESTs	3.0
	449579	AW207260	Hs.134014	ESTs, Weakly similar to T46425 hypotheti	3.0
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo	3.0
	454032	W31790	Hs.194293	ESTs, Weakly similar to 154374 gene NF2	3.0
60	455601	AI368660	Hs.816	SRY (sex determining region Y)-box 2	3.0
	447482	AB033059	Hs.18705	KIAA1233 protein	3.0
	439416	W58294	Hs.56254	ESTs	3.0
	436635	AW104325	Hs.272093	ESTs, Weakly similar to I78885 serine/th	3.0
65	419086	NM_000216	Hs.89591	Kellmann syndrome 1 sequence	3.0
	412566	AW862574		gb:EST374647 MAGE resequences, MAGG Homo	3.0
	415452	F09134	Hs.12839	ESTs	3.0
	427874	AA732367	Hs.98198	ESTs	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
70	454193	BE141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo	3.0
	454678	AW813089		gb:RC3-ST0186-240400-111-b05 ST0186 Homo	3.0
	415122	D60708	Hs.22245	ESTs	3.0
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.0
	400227				3.0
75	411905	BE265067		gb:601193893F1 NIH_MGC_7 Homo sapiens cD	3.0
	419503	AA243642	Hs.137422	ESTs	3.0
	446563	BE326588	Hs.141454	ESTs	3.0
	457285	AI038858	Hs.130522	Kv channel-interacting protein 1	3.0
	434998	AW975157	Hs.26037	ESTs	3.0
	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	3.0
80	424539	L02911	Hs.150402	activin A receptor, type I	3.0
	449856	AA203155	Hs.18200	ESTs	3.0
	427698	AW972594	Hs.294140	ESTs	3.0
	451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HUMAN A	3.0

	442994	AI026718	Hs.16954	ESTs	3.0
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	3.0
	421072	AI215069	Hs.89113	ESTs	3.0
	456273	AF154846	Hs.1148	zinc finger protein	3.0
5	404548				3.0
	428201	AA424158	Hs.206461	ESTs	3.0
	441519	AA972740	Hs.127092	ESTs	3.0
	445413	AA151342	Hs.12677	CGI-147 protein	3.0
	418717	AI334430	Hs.86984	ESTs	3.0
10	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fts, clone NT	3.0
	407758	D50915	Hs.38365	KIAA0125 gene product	3.0
	431906	AW328038	Hs.37486	ESTs	3.0
	424968	AA349086	Hs.259746	ESTs, Weakly similar to A46010 X-linked	3.0
	431023	AI283133	Hs.297420	ESTs	3.0
15	432596	AJ224741	Hs.278461	matrilin 3	3.0
	452412	AA029608	Hs.61373	ESTs	3.0
	421309	AI222086	Hs.270449	ESTs, Moderately similar to ALU1_HUMAN A	2.9
	438128	AA904430	Hs.122049	ESTs, Weakly similar to T2D4_HUMAN TRANS	2.9
	408321	AW405882	Hs.44205	cortistatin	2.9
20	439236	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN I	2.9
	400880				2.9
	417014	AA251720	Hs.104347	ESTs, Weakly similar to ALUC_HUMAN IIII	2.9
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.9
	405603				2.9
25	425573	AB005423	Hs.158308	serine (or cysteine) proteinase inhibitor	2.9
	427878	C05766	Hs.181022	CGI-07 protein	2.9
	451700	AI470262	Hs.29553	ESTs	2.9
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	2.9
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	2.9
30	422634	NM_016010	Hs.118821	CGI-62 protein	2.9
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.9
	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo	2.9
	408525	AW206972	Hs.253595	ESTs	2.9
	412248	BE176480		gb:RC3-HT0585-160300-022-c02 HT0585 Homo	2.9
35	432507	BE391093	Hs.324667	ESTs	2.9
	447290	AJ476732	Hs.263912	ESTs	2.9
	424188	AW954552	Hs.142634	zinc finger protein	2.9
	431448	AL137517	Hs.334473	hypothetical protein DKFZp56401278	2.9
	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
40	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	423119	AA322201	Hs.131976	ESTs	2.9
	423717	AA330036	Hs.152003	ESTs	2.9
	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
	431980	AA523696	Hs.324507	hypothetical protein FLJ20986	2.9
45	434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	2.9
	444339	T96555	Hs.31562	ESTs	2.9
	446745	AW118189	Hs.156400	ESTs	2.9
	459201	AW391177		gb:MR3-ST0203-221299-023-d05 ST0203 Homo	2.9
	430573	AA744550	Hs.136345	ESTs	2.9
50	451073	AI758905	Hs.206053	ESTs	2.9
	440575	AA889870	Hs.126006	ESTs	2.9
	402046				2.9
	426882	AA393108	Hs.97365	ESTs	2.9
	435738	AA699633	Hs.269543	ESTs, Weakly similar to A56194 thromboxa	2.9
55	420656	AA279098	Hs.187636	ESTs	2.9
	438323	AI985394	Hs.123369	ESTs	2.9
	453123	AI953718	Hs.221849	ESTs	2.9
	418343	AA216372	Hs.159501	ESTs	2.9
	431595	AA508196		gb:nh60f07.s1 NCI_CGAP_Pr8 Homo sapiens	2.9
60	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fts, clone HE	2.9
	459440	BE048054		gb:tz46c03.y1 NCI_CGAP_Bm52 Homo sapien	2.9
	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fts, clone PL	2.9
	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	2.9
	456034	AW450979		gb:U1-H-B13-ala-a-12-O-U1.s1 NCI_CGAP_Su	2.9
65	442118	AA976718	Hs.202242	ESTs	2.9
	420727	H75701	Hs.99886	complement component 4-binding protein,	2.9
	433849	BE465884	Hs.280728	ESTs	2.9
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.9
	429826	N93266	Hs.40747	ESTs	2.9
70	437913	AJ140825	Hs.121623	ESTs	2.9
	441330	AI692984	Hs.129354	ESTs	2.9
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fts, clone L	2.9
	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	2.9
75	444631	AW995395	Hs.84520	ESTs, Weakly similar to TRHY_HUMAN TRICH	2.9
	458186	AA904244	Hs.153205	ESTs	2.9
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fts, clone MA	2.9
	415757	AA830854	Hs.187810	ESTs	2.9
	449299	AA299919	Hs.84561	ESTs	2.9
80	457003	S78234	Hs.172405	cell division cycle 27	2.9
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	2.9
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	2.9
	426174	AA547959	Hs.115838	ESTs	2.9

	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	2.9
	429950	AW081608	Hs.105053	ESTs	2.9
	412733	AA984472	Hs.74554	KIAA0080 protein	2.9
5	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp43401214 (f	2.9
	442655	AW027457	Hs.30323	ESTs, Weakly similar to B34087 hypotheti	2.9
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	2.9
	430447	W17064	Hs.332848	SWI/SNF related, matrix associated, acti	2.9
	416871	H98716		gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	2.9
10	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	2.9
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	2.9
	401094				2.9
	401526				2.9
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	2.9
	417320	AA195567	Hs.86022	ESTs	2.9
15	418282	AA215535	Hs.98133	ESTs	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
	450006	AI241555	Hs.60171	ESTs	2.8
	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	2.8
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	2.8
20	403329				2.8
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	2.8
	419038	AW134924	Hs.190325	ESTs	2.8
	440106	AA864988	Hs.127699	KIAA1603 protein	2.8
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.8
25	431745	AW972448	Hs.163425	ESTs	2.8
	421426	AA291101	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA,	2.8
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.8
	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	2.8
	441790	AW294909	Hs.132208	ESTs	2.8
30	404443				2.8
	428129	AI244311	Hs.26912	ESTs	2.8
	435047	AA454985	Hs.54973	cadherin-like protein VR20	2.8
	423948	AW392342	Hs.283077	centrosomal P4.1-associated protein; unc	2.8
	449327	AI638743	Hs.224672	ESTs	2.8
35	400983				2.8
	415786	AW419198	Hs.257924	hypothetical protein FLJ13782	2.8
	411213	AA676939	Hs.69285	neuropilin 1	2.8
	420896	AW149342	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	2.8
	409994	D86864	Hs.57735	acetyl LDL receptor, SREC	2.8
40	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.8
	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.8
	455092	BE152428		gb:CMO-HT0323-151299-126-b04 HT0323 Homo	2.8
	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
	440192	AA872282	Hs.190596	ESTs	2.8
45	448466	AI522109	Hs.171066	ESTs	2.8
	414869	AA157291	Hs.21479	ubiquitin 1	2.8
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	2.8
	407594	AW057584	Hs.160681	ESTs	2.8
	439235	N45513	Hs.46608	ESTs	2.8
50	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	2.8
	434812	AA648860	Hs.189496	ESTs	2.8
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	2.8
	455512	AW983608		gb:RC3-HN0001-240400-012-c01 HN0001 Homo	2.8
	408380	AF123050	Hs.44532	diubiquitin	2.8
55	435990	AI015862	Hs.131793	ESTs	2.8
	410672	AW794600		gb:RC6-UM0014-170300-022-C05 UM0014 Homo	2.8
	432798	AA565309	Hs.194015	ESTs	2.8
	416288	H51299		gb:yp07c06.s1 Soares breast 3NbHBst Homo	2.8
60	438886	AA827728	Hs.128705	ESTs, Weakly similar to AF149422 2 unkno	2.8
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.8
	416940	N75620	Hs.43157	ESTs	2.8
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	2.8
	438398	AA806526	Hs.130277	ESTs	2.8
	435313	AI769400	Hs.189729	ESTs	2.8
65	414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens c	2.8
	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 plackstri	2.8
	413195	AA127382	Hs.22404	protease, serine, 12 (neurotrypsin, moto	2.8
	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	2.8
	401323				2.8
70	408296	AL117452	Hs.44155	DKFZP586G1517 protein	2.8
	428532	AF157326	Hs.184786	TBP-Interacting protein	2.8
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	2.8
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	2.8
	406970	M29994		gb:Human alpha-I spectrin gene, exon 12	2.8
75	426172	AA371307	Hs.125056	ESTs	2.8
	452114	N22687	Hs.8236	ESTs	2.8
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	430660	R11884	Hs.100826	ESTs	2.8
80	434133	AA625604		gb:zu86h01.s1 Soares_testis_NHT Homo sap	2.8
	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	2.8
	429881	T80112	Hs.192245	ESTs	2.8
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.8

	409435	AI810721	Hs.95424	ESTs	2.8
	442191	W95186	Hs.8136	endothelial PAS domain protein 1	2.8
	407305	AA715284		gb:uv3503.r1 NCI_CGAP_Br5 Homo sapiens	2.8
5	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	2.8
	412189	R60982	Hs.22581	ESTs	2.8
	420976	AI924940	Hs.108082	ESTs, Weakly similar to T31636 hypothe	2.8
	448330	AL036449	Hs.207163	ESTs	2.8
	418912	NM_000685	Hs.89472	angiotensin receptor 1	2.8
10	422505	AL120862	Hs.124165	ESTs	2.8
	427752	AA470687	Hs.104772	ESTs	2.8
	433513	AI566356	Hs.171437	ESTs	2.8
	433703	AA210863	Hs.3532	nemo-like kinase	2.8
	448912	D83781	Hs.22559	KIAA0197 protein	2.8
	405621				2.8
15	430687	BE274217	Hs.249247	heterogeneous nuclear protein similar to	2.8
	450400	AI694722	Hs.279744	ESTs	2.8
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.8
	418342	BE002723	Hs.226627	leptin receptor	2.8
20	420756	AA411800	Hs.189900	ESTs	2.8
	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
	440320	AA879294		gb:nw86e09.s1 NCI_CGAP_Pr12 Homo sapiens	2.8
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
	439831	AW136488	Hs.25545	ESTs	2.8
25	425661	AL133627	Hs.158923	Homo sapiens mRNA: cDNA DKFZp434K0722 (f	2.8
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	2.8
	418658	AW874263	Hs.32468	ESTs	2.8
	409978	D31897	Hs.57714	double C2-like domains, alpha	2.8
	421340	F07783	Hs.1369	decay accelerating factor for complement	2.8
30	449071	NM_005872	Hs.22960	breast carcinoma amplified sequence 2	2.8
	409241	AF070602	Hs.51649	Homo sapiens clone 24504 mRNA sequence	2.8
	448219	AA228092	Hs.42656	KIAA1681 protein	2.8
	408936	AL138043	Hs.293549	ESTs	2.8
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo	2.8
35	426471	M22440	Hs.170009	transforming growth factor, alpha	2.8
	454455	AW752710		gb:IL3-CT0219-281099-024-A03 CT0219 Homo	2.8
	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
	401335				2.7
	436577	W84774	Hs.17643	ESTs	2.7
40	409519	AA075368		gb:zm86h10.r1 Stratagene ovarian cancer	2.7
	421003	T72080	Hs.95667	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	2.7
	436007	AI247716	Hs.232168	ESTs	2.7
45	408874	AW818091	Hs.252730	ESTs	2.7
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	2.7
	435625	H50654	Hs.113999	ESTs	2.7
	435766	R11673	Hs.186498	ESTs	2.7
	410327	T33130	Hs.301746	RAP2A, member of RAS oncogene family	2.7
50	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
	417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain	2.7
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.7
	427134	AA398409	Hs.173561	EST	2.7
	428137	AA421792	Hs.170999	ESTs	2.7
55	429710	AI337113	Hs.146025	hypothetical protein FLJ23594	2.7
	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.7
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.7
	441928	AI370188	Hs.211454	ESTs	2.7
	409721	AW887732	Hs.257861	ESTs	2.7
60	427112	Z32887	Hs.290951	ESTs	2.7
	403776				2.7
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.7
	427839	AA608823	Hs.98244	ESTs	2.7
	432837	AA310693	Hs.87329	HSPC072 protein	2.7
65	438782	AA828380	Hs.126733	ESTs	2.7
	449396	BE169100	Hs.195029	ESTs	2.7
	458043	AW979009	Hs.328108	ESTs	2.7
	438171	AW976507	Hs.293515	ESTs	2.7
	452959	AI933416	Hs.189674	ESTs	2.7
70	439556	AI623752	Hs.163603	ESTs	2.7
	446152	AI292036	Hs.150028	ESTs	2.7
	434803	AW974640	Hs.303413	ESTs	2.7
	407771	AL138272	Hs.62713	ESTs	2.7
	411069	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	2.7
75	417543	AA203620	Hs.110153	ESTs	2.7
	401517				2.7
	403677				2.7
	416337	H48713		gb:yyq78d02.r1 Soares fetal liver spleen	2.7
80	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	2.7
	446800	AI341635	Hs.156486	ESTs	2.7
	457906	AW975939	Hs.153290	Homo sapiens cDNA FLJ14318 fis, clone PL	2.7
	452277	AL049013	Hs.28783	KIAA1223 protein	2.7
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.7
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypothe	2.7

5	408715	AA768873	Hs.112250	hypothetical protein FLJ23518	2.7
	410743	AA089474	Hs.272153	ESTs	2.7
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.7
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.7
	427565	AI287280	Hs.97933	ESTs, Weakly similar to T46370 hypotheti	2.7
10	406092				2.7
	410008	AA079552		gb:zm20h12.s1 Stralagene pancreas (93720	2.7
	438504	AW665281	Hs.224625	ESTs	2.7
	414783	AW069569	Hs.278270	inactive progesterone receptor, 23 kD	2.7
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	2.7
15	418686	Z36830	Hs.87268	annexin A8	2.7
	413795	AL040178	Hs.142003	ESTs	2.7
	457528	AW973791	Hs.292784	ESTs	2.7
	444230	H95537	Hs.146067	ESTs	2.7
	403760				2.7
20	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen	2.7
	428904	AI312526	Hs.46640	ESTs	2.7
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	2.7
	458638	N78553	Hs.282204	nucleosomal binding protein 1	2.7
	459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA	2.7
25	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	2.7
	433906	AI167816	Hs.43355	ESTs	2.7
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	2.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	2.7
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	2.7
30	421585	U85626	Hs.302043	chemokine (C-C motif) receptor-like 2	2.7
	445158	AI992108	Hs.127206	ESTs	2.7
	421175	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.7
	401793				2.7
	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
35	427038	NM_014633	Hs.173288	KIAA0155 gene product	2.7
	451343	AW975057	Hs.293353	ESTs	2.7
	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
	438475	W03856	Hs.13188	ESTs, Highly similar to Gene product wit	2.7
	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	2.7
40	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	2.7
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	2.7
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	2.7
	451487	AA018072		gb:ze51g02.r1 Soares retina N2b4HR Homo	2.7
	418269	AA806113	Hs.189025	ESTs	2.7
45	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	2.7
	459160	AI904723		gb:CM-BT066-120299-092 BT066 Homo sapien	2.7
	441963	AI733307	Hs.128002	ESTs	2.7
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.7
	426902	AI125334	Hs.97408	ESTs	2.7
50	414271	AK000275	Hs.75871	protein kinase C binding protein 1	2.7
	453313	BE005771	Hs.153746	hypothetical protein FLJ22490	2.7
	445265	AI218295	Hs.144942	ESTs	2.7
	422988	AW673847	Hs.97321	ESTs	2.7
	428613	AB037749	Hs.186928	KIAA1328 protein	2.7
55	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	2.7
	457300	AW297436	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	2.7
	402800				2.7
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.7
	414729	BE466928	Hs.281901	ESTs	2.7
60	453716	AA037675	Hs.152675	ESTs	2.7
	452693	T79153	Hs.48589	zinc finger protein 228	2.7
	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	2.7
	443305	AI050693	Hs.133318	ESTs	2.7
	416709	R99369	Hs.283108	hemoglobin, gamma G	2.7
65	419077	AA233885	Hs.164526	ESTs	2.7
	453878	AW964440	Hs.19025	DC32	2.7
	445660	AI702668	Hs.201955	ESTs	2.7
	446817	AI700584	Hs.134166	ESTs	2.7
	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	2.6
70	410406	AI969703	Hs.1466	glycerol kinase	2.6
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	2.6
	407830	NM_001086	Hs.587	arylacamide deacetylase (esterase)	2.6
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	2.6
	407055	X89211		gb:H.sapiens DNA for endogenous retrovir	2.6
75	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 integrin	2.6
	440310	AA878939	Hs.125406	ESTs	2.6
	425659	AK000590	Hs.158836	hypothetical protein FLJ20583	2.6
	418217	AI910647	Hs.13442	ESTs	2.6
	428667	AI375550	Hs.74407	nucleolar protein p40; homolog of yeast	2.6
80	414573	AI821846	Hs.71999	ESTs	2.6
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	2.6
	452821	AW471181	Hs.160874	ESTs	2.6
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	2.6
	428483	AI908539	Hs.321444	KIAA0344 gene product	2.6
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	2.6
	405059				2.6
	425178	H16097	Hs.161027	ESTs	2.6

	442952	AI743261	Hs.131860	ESTs	2.6
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	2.6
	456179	H75490	Hs.271930	ESTs	2.6
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	2.6
5	459456	AA486036	Hs.190124	ESTs	2.6
	425527	AL162032	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	2.6
	424711	NM_005795	Hs.152175	calcitonin receptor-like	2.6
	417956	AA210704	Hs.190465	ESTs	2.6
	420621	AA278808		gb:cs79c09.r1 NCI_CGAP_GCB1 Homo sapiens	2.6
10	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
	438295	AI394151	Hs.37932	ESTs	2.6
	445550	AI242754	Hs.137306	ESTs	2.6
	450469	AI955049	Hs.281326	ESTs	2.6
	458804	AL157625		gb:DKFZp761L2016_r1 761 (synonym: hamy2)	2.6
15	443657	R14973		gb:yf42f10.s1 Soares fetal liver spleen	2.6
	429250	H56585	Hs.198308	tryptophan rich basic protein	2.6
	437906	AA771704	Hs.194626	ESTs	2.6
	426775	AA384564	Hs.108829	ESTs	2.6
	443372	AI792557	Hs.133107	ESTs	2.6
20	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.6
	425465	L18964	Hs.1904	protein kinase C, Iota	2.6
	422746	NM_004484	Hs.119651	glypican 3	2.6
	413450	Z99716	Hs.75372	N-acetylglucosaminidase, alpha-	2.6
25	424527	AW138558	Hs.267158	ESTs, Weakly similar to I54374 gene NF2	2.6
	414180	AI863304	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	2.6
	411402	BE297855	Hs.69855	NRAS-related gene	2.6
	445264	AI218263	Hs.323472	EST	2.6
	458861	AI630223		gb:ad06g08.r1 Proliferating Erythroid Ce	2.6
30	415227	AW821113	Hs.72402	ESTs	2.6
	435429	AW592035	Hs.254414	ESTs, Weakly similar to 1805195B RNA-bin	2.6
	434445	AI349306	Hs.11782	ESTs	2.6
	448570	AI923944	Hs.30913	ESTs	2.6
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
35	422879	AI241409	Hs.188092	ESTs	2.6
	409026	AL137554	Hs.49927	protein kinase NYD-SP15	2.6
	425717	X07282	Hs.171495	retinoic acid receptor, beta	2.6
	429127	AA749382	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homo	2.6
	438298	H23542	Hs.181788	ESTs	2.6
40	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.6
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.6
	444517	AI939339	Hs.146883	ESTs	2.6
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.6
	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapien	2.6
45	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6
	437939	AW298600	Hs.141840	ESTs, Weakly similar to S59501 Interfero	2.6
	430719	AA488988	Hs.293796	ESTs	2.6
	452864	AA033714	Hs.287629	hypothetical protein FLJ14260	2.6
	432095	AW022273	Hs.105769	ESTs	2.6
50	431086	AI829692	Hs.211561	ESTs	2.6
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	2.6
	423952	AW877787	Hs.136102	KIAA0853 protein	2.6
	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	2.6
	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.6
55	430933	AW863635		gb:MR3-SN0010-270300-103-h02 SN0010 Homo	2.6
	420691	AA829433	Hs.275343	ESTs	2.6
	429761	AI276780	Hs.135173	ESTs	2.6
	437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 feml	2.6
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
60	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.6
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	2.6
	438647	AA813118	Hs.163230	ESTs	2.6
	438192	AI859065	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	2.6
65	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.6
	440460	H92571	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
	414612	BE274552	Hs.76578	protein inhibitor of activated STAT3	2.6
	428170	H05530	Hs.12565	ESTs	2.6
	457343	NM_013936	Hs.247862	olfactory receptor, family 12, subfamily	2.6
70	424020	R76946	Hs.39738	ESTs	2.6
	455226	AW902103		gb:QV0-NN1022-120500-220-c07 NN1022 Homo	2.6
	411965	BE467339	Hs.280115	ESTs	2.6
	432656	NM_000246	Hs.3076	MHC class II transactivator	2.6
	455488	AA102322		gb:z190f03.r1 StrataGene colon (937204)	2.6
75	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.6
	404285				2.6
	418744	AI887288	Hs.195379	ESTs, Weakly similar to putative p150 [H	2.6
	454714	AW815088		gb:QV4-ST0212-091199-023-f10 ST0212 Homo	2.6
80	429828	AB019494	Hs.225767	IDN3 protein	2.6
	436387	AA714760	Hs.240075	Homo sapiens cDNA FLJ13234 fis, clone OV	2.6
	448587	AI539652	Hs.28338	KIAA1546 protein	2.6
	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	2.6
	440479	AA886461	Hs.208161	ESTs	2.6
	443160	AI467915	Hs.36053	ESTs	2.6

	428978	AA442784	Hs.125445	ESTs	2.5
	444670	H58373	Hs.332938	hypothetical protein MGC5370	2.5
	453459	BE047032	Hs.257789	ESTs	2.5
5	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32105, mRNA seq	2.5
	442875	BE623003	Hs.23625	Homo sapiens clone TCCTA00142 mRNA sequ	2.5
	414373	AW162907	Hs.75969	proline-rich protein with nuclear target	2.5
	458760	AI498631	Hs.111334	ferritin, light polypeptide	2.5
	434131	AI858275	Hs.143659	ESTs	2.5
10	441805	AA285136	Hs.301914	neuronal specific transcription factor D	2.5
	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	2.5
	417351	T90278	Hs.15049	ESTs	2.5
	409695	AA296961		gb:EST112514 Adrenal gland tumor Homo sa	2.5
	432824	AK001783	Hs.279012	hypothetical protein FLJ10921	2.5
15	438038	AI732629	Hs.194161	ESTs, Weakly similar to TA2R HUMAN, BETA	2.5
	454836	AW833711		gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
	453919	AW959912	Hs.7076	KIAA1705 protein	2.5
	422487	AJ010901	Hs.198267	much 4, tracheobronchial	2.5
	408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513	2.5
20	427491	R43279	Hs.22574	ESTs, Weakly similar to I38022 hypotheti	2.5
	435102	AW899053	Hs.76917	F-box only protein 8	2.5
	409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	2.5
	455866	BE149024		gb:CMO-HT0249-291099-084-c04 HT0249 Homo	2.5
	432887	AI926047	Hs.162859	ESTs	2.5
25	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5
	401078				2.5
	410365	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	2.5
	425201	AA352111		gb:EST60061 Activated T-cells XX Homo sa	2.5
30	457112	AW772449	Hs.268081	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5
	455252	AW876627		gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
	444542	AI161293	Hs.280380	aminopeptidase	2.5
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	2.5
	428497	BE010877	Hs.98584	ESTs	2.5
	457336	AW969657	Hs.291029	ESTs	2.5
35	427621	BE621182	Hs.179882	hypothetical protein FLJ12443	2.5
	423782	AJ472209	Hs.323117	ESTs	2.5
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	2.5
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	2.5
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	2.5
40	417137	U46265	Hs.81281	mitochondrial ribosomal protein S21	2.5
	436787	AA908554	Hs.192756	ESTs	2.5
	440331	AL048412	Hs.202151	ESTs	2.5
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.5
	417169	R13550	Hs.246773	ESTs	2.5
45	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	2.5
	455286	BE144384		gb:MR0-HT0166-191199-004-c11 HT0166 Homo	2.5
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5
	400432	AX015809	Hs.287767	Sequence 8 from Patent WO9950285	2.5
	415747	AA381209		gb:EST94257 Activated T-cells I Homo sap	2.5
50	446346	AI290205	Hs.309940	ESTs	2.5
	450209	AW008921	Hs.13138	Homo sapiens, clone IMAGE:3448343, mRNA,	2.5
	453202	AW085781	Hs.26270	hypothetical protein FLJ11588	2.5
	425523	AB007948	Hs.158244	KIAA0479 protein	2.5
	433124	U51712	Hs.13775	hypothetical protein SMAP31	2.5
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.5
55	425657	T89839	Hs.119471	ESTs	2.5
	401254				2.5
	426604	H53354	Hs.97141	ESTs, Weakly similar to hypothetical pro	2.5
	449535	W15267	Hs.23672	low density lipoprotein receptor-related	2.5
60	433138	AB029496	Hs.59729	semaphorin sem2	2.5
	425804	BE501698	Hs.258189	ESTs	2.5
	429515	AL031228	Hs.204370	DNA segment on chromosome 6 (unique, pse	2.5
	437267	AW511443	Hs.258110	ESTs	2.5
	454305	BE062633	Hs.28338	KIAA1546 protein	2.5
	455631	BE063031		gb:MR0-BT0265-231199-002-e09 BT0265 Homo	2.5
65	401878				2.5
	450350	T97817	Hs.174880	ESTs	2.5
	436532	AA721522		gb:nv54h12.r1 NCL_CGAP_Ew1 Homo sapiens	2.5
	457460	AI143312	Hs.129206	casein kinase 1, gamma 3	2.5
70	427304	AA761526	Hs.163853	ESTs	2.5
	419721	NM_001650	Hs.288650	aquaporin 4	2.5
	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	2.5
	446252	AI283125	Hs.150009	ESTs	2.5
	421229	AI056590	Hs.7086	hypothetical protein MGC12435	2.5
75	434273	AA913143	Hs.26303	ESTs	2.5
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	2.5
	434353	AA630863	Hs.131375	ESTs, Moderately similar to ALUB_HUMAN I	2.5
	436198	AK001125	Hs.300922	Homo sapiens cDNA FLJ10263 fis, clone HE	2.5
	452232	AW020603	Hs.158423	radial spoke protein 3	2.5
80	433764	AW753676	Hs.39982	ESTs	2.5
	412050	H96503	Hs.109087	Homo sapiens cDNA: FLJ22845 fis, clone K	2.5
	422342	AA309272		gb:EST180209 Liver, hepatocellular carci	2.5
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	2.5
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.5

	408813	AI580090	Hs.48295	RNA helicase family	2.5
	414109	BE250744		gb:600943376F1 NIH_MGC_17 Homo sapiens c	2.5
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.5
	419985	H66373	Hs.15973	ESTs, Highly similar to bA393J16.3 [Hsa	2.5
5	417859	T26453		gb:AB214F6R Infant brain, LLNL array of	2.5
	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	2.5
	448015	AI458065	Hs.23196	ESTs	2.5
	454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	2.5
10	445865	AI262584	Hs.145575	ESTs	2.5
	451800	AW977435	Hs.323867	ESTs	2.5
	456987	AI557290	Hs.173536	ESTs	2.5
	403568				2.5
	435209	AW027809	Hs.187698	Homo sapiens cytomegalovirus partial fus	2.5
	430371	D87466	Hs.240112	KIAA0276 protein	2.5
15	418033	W68180	Hs.259855	elongation factor-2 kinase	2.5
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.5
	453619	H87648	Hs.33922	Homo sapiens, clone MGC:9084, mRNA, comp	2.5
	431071	AA491379		gb:aa65f05.r1 NCI_CGAP_GCB1 Homo sapiens	2.5
20	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	2.5
	409045	AA635062	Hs.50094	Homo sapiens mRNA: cDNA DKFZp434C00515 (f	2.5
	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	2.5
	408420	NM_006915	Hs.44766	refinitis pigmentosa 2 (X-linked recessi	2.4
	417318	AW953937	Hs.12891	ESTs	2.4
25	413382	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.4
	405748	AW339105	Hs.217493	annexin A2	2.4
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	2.4
	441817	AW969706	Hs.293332	ESTs	2.4
	450551	AJ010046	Hs.25155	neuroepithelial cell transforming gene 1	2.4
30	457940	AL360169	Hs.306517	Homo sapiens TRIPartite motif protein ps	2.4
	446135	AW130288	Hs.170318	hypothetical protein FLJ10147	2.4
	436907	AA737171	Hs.131809	ESTs	2.4
	429399	AA452244	Hs.16727	ESTs	2.4
	446782	AL050295	Hs.22039	KIAA0758 protein	2.4
35	434404	AW445034	Hs.256578	ESTs	2.4
	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease,	2.4
	440164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	2.4
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	2.4
	450705	U90304	Hs.25351	iroquois homeobox protein 5	2.4
40	425506	NM_003666	Hs.158205	basic leucine zipper nuclear factor 1 (J	2.4
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fascilin	2.4
	458986	AI802772	Hs.208655	ESTs	2.4
	443861	AW449462	Hs.134743	ESTs	2.4
	412879	BE092219		gb:IL2-BT0734-240400-071-804 BT0734 Homo	2.4
45	415250	F02614	Hs.27319	ESTs	2.4
	434627	AI221894	Hs.39311	ESTs	2.4
	443919	AI091284	Hs.135224	ESTs, Weakly similar to A47582 B-cell gr	2.4
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	2.4
	400385	NM_020389	Hs.283104	putative capacitative calcium channel	2.4
50	411322	AW887330	Hs.172405	cell division cycle 27	2.4
	434638	H50758		gb:cyp85e06.r1 Soares fetal liver spleen	2.4
	435559	AF209198	Hs.42636	zinc finger protein 277	2.4
	447849	AI538147	Hs.164277	ESTs	2.4
	448005	AW207437	Hs.170378	ESTs	2.4
55	454201	AB023191	Hs.44131	KIAA0974 protein	2.4
	456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.4
	449486	AI652715	Hs.270811	ESTs	2.4
	421516	AI362418	Hs.105379	FT005 protein	2.4
	412167	AW897230		gb:CMO-NN0057-150400-335-a11 NN0057 Homo	2.4
60	426910	AA470023	Hs.190089	ESTs, Moderately similar to ALU1_HUMAN A	2.4
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	2.4
	400641				2.4
	430576	AA767125	Hs.293574	ESTs	2.4
	434423	NM_006769	Hs.3844	LIM domain only 4	2.4
65	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	2.4
	441499	AW298235	Hs.101689	ESTs	2.4
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.4
	417819	AI253112	Hs.133540	ESTs	2.4
	431728	NM_007351	Hs.268107	multimerin	2.4
70	425025	AW953168	Hs.12407	ESTs	2.4
	421168	AF182277	Hs.330780	cytochrome P450, subfamily 11B (phenobar	2.4
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.4
	408867	AA437199	Hs.656	cell division cycle 25C	2.4
	439446	AI927629	Hs.57873	ESTs	2.4
	445038	AI635444	Hs.143917	dJ467N11.1 protein	2.4
75	450682	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	2.4
	455107	BE154113		gb:PM1-HT0340-151299-003-a08 HT0340 Homo	2.4
	458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	2.4
80	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	2.4
	453864	AW021407	Hs.21068	hypothetical protein	2.4
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	2.4
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.4
	426603	AA382291		gb:EST95683 Testis I Homo sapiens cDNA 5	2.4

	447357	AI375922	Hs.159367	ESTs	2.4
	452631	AI188658	Hs.87496	ESTs	2.4
	405041				2.4
	405472				2.4
5	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	2.4
	433868	AA612960	Hs.337300	ESTs	2.4
	437119	AI379921	Hs.177043	ESTs	2.4
	455114	AW857121		gb:RC1-CT0302-040400-017-a12 CT0302 Homo	2.4
10	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.4
	434936	AI285970	Hs.183817	ESTs	2.4
	408918	BE218603	Hs.279708	ESTs	2.4
	444106	AI123922	Hs.138215	Homo sapiens cDNA FLJ11400 fis, clone HE	2.4
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	2.4
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	2.4
15	446659	AI335361	Hs.226376	ESTs	2.4
	418636	AW749855		gb:QV4-BT0534-281299-053-c05 BT0534 Homo	2.4
	434995	AW974995		gb:EST387100 MAGE resequences, MAGN Homo	2.4
	438005	BE151746		gb:PM1-HT0305-061299-003-a06 HT0305 Homo	2.4
	444755	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	2.4
20	427131	AA448460	Hs.112017	GE36 gene	2.4
	442039	AW276240	Hs.128352	ESTs	2.4
	448595	AB014544	Hs.21572	KIAA0644 gene product	2.4
	432949	AA570749	Hs.298866	ESTs	2.4
	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	2.4
25	417420	T85150	Hs.268814	ESTs	2.4
	427551	T96203		gb:ye48b07.r1 Soares fetal liver spleen	2.4
	420057	AA806899	Hs.184387	ESTs	2.4
	434950	AW974892		gb:EST386997 MAGE resequences, MAGN Homo	2.4
30	425497	AA524596		gb:nh34b02.s1 NCI_CGAP_Pr3 Homo sapiens	2.4
	438214	H06076	Hs.26320	TRABID protein	2.4
	416100	H18700	Hs.268799	ESTs	2.4
	419637	W27493		gb:31h10 Human retina cDNA randomly prim	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
	454403	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	2.4
35	419179	AW275291	Hs.113009	hypothetical protein FLJ22527	2.4
	436391	AJ227892	Hs.146274	ESTs	2.4
	449511	AI436187	Hs.296261	guanine nucleotide binding protein (G pr	2.4
	447499	AW262580	Hs.147674	protocadherin beta 16	2.4
40	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.4
	412877	BE011168		gb:PM3-BN0218-100500-003-d08 BN0218 Homo	2.4
	435985	AA703154	Hs.191934	ESTs	2.4
	440674	BE581546		gb:601347208F1 NIH_MGC_8 Homo sapiens cD	2.4
	446476	AW294072	Hs.141376	ESTs	2.4
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.4
45	435731	AA699581	Hs.186811	ESTs	2.4
	437105	AA744554	Hs.222127	ESTs	2.4
	406091				2.4
	457024	AA397546	Hs.119151	ESTs	2.4
	404249				2.4
50	419556	U29615	Hs.91093	chitinase 1 (chitobiosidase)	2.4
	424943	AU077260	Hs.153924	death-associated protein kinase 1	2.4
	444229	AV648613	Hs.282397	ESTs	2.4
	404860				2.4
	432223	AA333283	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	2.4
55	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.4
	420843	H96982	Hs.42321	ESTs	2.4
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.4
	413642	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo	2.4
	436998	AA745625	Hs.291414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
60	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	2.4
	445748	U80766	Hs.13252	Human EST clone 22453 mariner transposon	2.4
	451018	AW865599	Hs.247324	mitochondrial ribosomal protein S14	2.3
	409073	AA063458		gb:zf71a07.s1 Soares_pineal_gland_N3HPG	2.3
	418782	AI792648	Hs.14665	ESTs	2.3
65	447870	BE139479	Hs.161492	ESTs	2.3
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.3
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	2.3
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypothi	2.3
	424049	AB014524	Hs.138380	KIAA0624 protein	2.3
70	425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	2.3
	430702	U56979	Hs.250651	H factor 1 (complement)	2.3
	409620	AA076278	Hs.13277	hypothetical protein FLJ22054	2.3
	441675	AI914329	Hs.5461	ESTs	2.3
	430884	AF053748	Hs.248114	glial cell derived neurotrophic factor	2.3
75	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	2.3
	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	2.3
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	2.3
	417583	AA668782	Hs.191284	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	2.3
80	404513				2.3
	410999	AW813004		gb:RC3-ST0186-230300-019-h02 ST0186 Homo	2.3
	448506	AI524673	Hs.38170	ESTs	2.3
	434811	AW971205	Hs.114280	ESTs	2.3

	457065	AI476318	Hs.192480	ESTs	2.3
	407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha polypep	2.3
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	2.3
	423596	AA328195	Hs.234101	ESTs, Weakly similar to CTL1 protein [H]	2.3
5	455807	BE141140		gb:MR0-HT0075-021299-006-c07 HT0075 Homo	2.3
	435867	AA954229	Hs.114052	ESTs	2.3
	440196	N72847	Hs.125221	ESTs	2.3
	401213				2.3
	407291	AA001464		gb:ze45b01.r1 Soares retina N2b4HR Homo	2.3
10	442490	AW965078	Hs.30212	thyroid receptor interacting protein 15	2.3
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	2.3
	438138	R98299	Hs.177502	ESTs	2.3
	440283	AI732892	Hs.190489	ESTs	2.3
	447039	AV661798	Hs.282915	ESTs	2.3
15	412777	AI335773	Hs.270123	ESTs	2.3
	421424	AW452690	Hs.258776	ESTs	2.3
	406673	M34996	Hs.198253	major histocompatibility complex, class	2.3
	440555	D31292	Hs.6853	hypothetical protein FLJ22167	2.3
	451516	AI800515	Hs.12024	ESTs	2.3
20	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	2.3
	421046	AA810854	Hs.89081	ESTs	2.3
	423604	AA486585	Hs.258901	ESTs	2.3
	409029	BE087807		gb:QV1-BT0681-290400-181-g02 BT0681 Homo	2.3
	444206	AW301017	Hs.146492	ESTs	2.3
25	451836	T63673	Hs.173220	ESTs	2.3
	454784	AW820626		gb:RC0-ST0299-190100-012-e10 ST0299 Homo	2.3
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.3
	436671	AW137159	Hs.146151	ESTs	2.3
	434988	AI418055	Hs.161160	ESTs	2.3
30	452862	AW378065	Hs.8687	ESTs	2.3
	439480	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	2.3
	410606	AW418779	Hs.114889	ESTs	2.3
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	2.3
	423239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	2.3
35	430217	N47863	Hs.336901	ribosomal protein S24	2.3
	417479	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC	2.3
	421253	AI188102	Hs.31028	ESTs	2.3
	438180	AA808189	Hs.272151	ESTs	2.3
	439715	AA524504	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
40	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypothei	2.3
	443055	AV653742	Hs.15536	hypothetical protein DKFZp761J139	2.3
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	2.3
	448831	AL080123	Hs.22182	zinc finger protein 23 (KOX 16)	2.3
	412953	Z45784	Hs.238809	ESTs	2.3
45	430789	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	2.3
	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.3
	423003	AL120077	Hs.122957	ketch (Drosophila)-like 2 (Mayven)	2.3
	428595	AB037795	Hs.186547	KIAA1374 protein	2.3
	437887	AA811524	Hs.29263	hypothetical protein FLJ11896	2.3
50	447720	AL038765	Hs.161304	ESTs	2.3
	452355	N54926	Hs.29202	G protein-coupled receptor 34	2.3
	408374	AW025430	Hs.155591	forhead box F1	2.3
	440381	AA917808	Hs.190495	ESTs	2.3
	425478	AB007953	Hs.268840	ESTs	2.3
55	432231	AA339977	Hs.274127	CLST 11240 protein	2.3
	431757	AA196930	Hs.268526	Homo sapiens chromosome 21q22.1 anonymou	2.3
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	2.3
	452837	AL121053	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	2.3
	417428	NM_002291	Hs.82124	laminin, beta 1	2.3
60	423739	AA398155	Hs.97600	ESTs	2.3
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	2.3
	425876	AW005887	Hs.234058	ESTs	2.3
	457411	AW085961	Hs.130093	ESTs	2.3
	413136	BE066941		gb:PM0-BT0340-091299-002-a11 BT0340 Homo	2.3
65	420313	AB023230	Hs.96427	KIAA1013 protein	2.3
	421751	AW813731	Hs.159153	ESTs, Moderately similar to S65657 alpha	2.3
	424827	AI057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fis, clone L	2.3
	436331	AI239495	Hs.120189	ESTs	2.3
	439275	AF086093	Hs.141566	ESTs	2.3
70	449272	AW137656	Hs.197645	ESTs	2.3
	454352	AW389668		gb:RC2-ST0168-071299-013-f08 ST0168 Homo	2.3
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	2.3
	407242	M18728		gb:Human nonspecific crossreacting antiq	2.3
	445326	AI220072	Hs.165893	ESTs	2.3
75	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.3
	452607	AI160029	Hs.61438	ESTs	2.3
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	2.3
	418851	AI417828	Hs.192435	ESTs	2.3
	458332	AI000341	Hs.220491	ESTs	2.3
80	432565	AA553477	Hs.152428	ESTs	2.3
	437511	AI807500	Hs.125247	ESTs	2.3
	430957	AI937072	Hs.55043	Homo sapiens cDNA FLJ13277 fis, clone OV	2.3
	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	2.3

	448225	AI476429	Hs.19238	ESTs	2.3
	408955	BE315170	Hs.8087	NAG-5 protein	2.3
	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypotheti	2.3
5	428976	AL037824	Hs.194695	ras homolog gene family, member I	2.3
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.3
	440348	AW015802	Hs.47023	ESTs	2.3
	436340	R42246	Hs.21606	ESTs	2.3
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	2.3
10	438462	AI624122	Hs.89578	general transcription factor IIH, polype	2.3
	411124	AW196937	Hs.53929	ESTs, Weakly similar to ALUB_HUMAN IIII	2.3
	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	2.3
	412505	AA974491	Hs.21734	ESTs	2.3
	418236	AW994005	Hs.337534	ESTs	2.3
15	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	2.3
	453901	BE065902		gb:RC2-BT0318-150200-011-b09 BT0318 Homo	2.3
	418565	AK001529	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.3
	433404	T32982	Hs.102720	ESTs	2.3
	408517	X90780	Hs.120036	troponin I, cardiac	2.3
20	439871	R88518	Hs.46736	hypothetical protein FLJ23476	2.3
	445641	AI245987	Hs.149442	ESTs	2.3
	449276	AW241510	Hs.252713	ESTs	2.3
	436547	AI297351	Hs.30824	leucine zipper transcription factor-like	2.3
	437770	AA767881	Hs.122897	ESTs	2.3
25	409064	AA052954	Hs.141883	ESTs	2.3
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	2.3
	449869	W57990	Hs.60059	Homo sapiens cDNA FLJ11478 fis, clone HE	2.3
	422108	AA297914	Hs.111749	postmeiotic segregation increased (S. ce	2.3
	418251	AA832123	Hs.177723	ESTs	2.3
30	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA P	2.3
	413638	H71252		gb:ys12h12.s1 Soares fetal liver spleen	2.3
	415980	R52414		gb:yg80b05.r1 Soares infant brain 1NIB H	2.3
	449232	AW192780	Hs.196080	ESTs	2.3
	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	2.3
35	454389	AW752571		gb:IL3-CT0213-170100-055-F02 CT0213 Homo	2.3
	438089	W05391	Hs.83623	nuclear receptor subfamily 1, group I, m	2.3
	400238				2.3
	404488				2.3
40	407809	AW082279	Hs.244106	ESTs	2.3
	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.3
	420478	AA521259	Hs.193796	ESTs	2.3
	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp586I1518 (f	2.3
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	2.3
45	426567	AA381579	Hs.182962	ESTs	2.3
	435708	AI362949	Hs.75169	ESTs	2.3
	441417	AI733297	Hs.144474	ESTs	2.3
	445117	AI208754	Hs.147369	ESTs	2.3
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.2
50	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	2.2
	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	2.2
	445280	AW055063	Hs.306088	v-erk avian sarcoma virus CT10 oncogene	2.2
	420653	AI224532	Hs.88550	ESTs	2.2
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	2.2
55	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	2.2
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	2.2
	411893	R82845	Hs.273789	ESTs	2.2
	428192	AA424051	Hs.304742	ESTs	2.2
	435634	T82384		gb:yc14f05.r1 Stratagene lung (937210) H	2.2
60	437637	AJ003029	Hs.65792	synaptophysin, gamma 2	2.2
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
	446164	AW273539	Hs.288750	hypothetical protein FLJ23577	2.2
	450232	BE300815	Hs.201326	ESTs	2.2
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	402745				2.2
65	434008	AA740878	Hs.112982	ESTs	2.2
	439492	AF086310	Hs.103159	ESTs	2.2
	436853	BE328074	Hs.148661	ESTs	2.2
	417648	R06552		gb:y09e12r1 Soares fetal liver spleen	2.2
	427690	AI253134	Hs.283410	ESTs	2.2
70	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.2
	450229	R18717	Hs.8929	hypothetical protein FLJ11362	2.2
	400756				2.2
	408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fis, clone PL	2.2
	403388				2.2
75	433643	AI821787	Hs.179586	ESTs	2.2
	442078	AW268583	Hs.262629	ESTs	2.2
	455685	BE066976		gb:PM0-BT0340-211299-003-c12 BT0340 Homo	2.2
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.2
	439920	H05430	Hs.288433	neurotrophin	2.2
80	432436	AW300248	Hs.181693	ESTs	2.2
	429493	AI134708	Hs.145998	ESTs	2.2
	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	2.2
	450101	AV649989	Hs.24385	Human hbc547 mRNA sequence	2.2

	442757	AI739528	Hs.28345	ESTs	2.2
	430212	AA469153		gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	2.2
	437146	AA730977		gb:mw55f05.s1 NCI_CGAP_Ew1 Homo sapiens	2.2
5	432101	AJ918950	Hs.123642	EphA3	2.2
	459644				2.2
	453887	BE564037	Hs.36237	hypothetical protein	2.2
	431170	AW971246	Hs.291022	ESTs	2.2
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	2.2
10	443682	AJ383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	2.2
	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	2.2
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.2
	425810	AJ923627	Hs.31903	ESTs	2.2
	433037	NM_014158	Hs.279938	HSPC067 protein	2.2
15	407162	N63855	Hs.142634	zinc finger protein	2.2
	441826	AW503603	Hs.129915	phosphotriesterase related	2.2
	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	2.2
	454766	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	414221	AW450979		gb:U1-H-BI3-ata-a-12-0-U1.s1 NCI_CGAP_Su	2.2
20	459608	AL119471		gb:DKFZp761M141_r1 761 (synonym: hamy2)	2.2
	400639				2.2
	406149				2.2
	424027	AW337575	Hs.201591	ESTs	2.2
	427531	AA405097	Hs.97957	ESTs	2.2
25	448353	BE407125	Hs.231510	ESTs	2.2
	417669	T99898		gb:ye68g01.r1 Soares fetal liver spleen	2.2
	449650	AF055575	Hs.23838	calcium channel, voltage-dependent, L ty	2.2
	452335	AW188944	Hs.61272	ESTs	2.2
	419216	AJ076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.2
30	447748	AI422023	Hs.161338	ESTs	2.2
	403534				2.2
	410594	AW770778	Hs.281238	ESTs	2.2
	438550	AW976002	Hs.258402	ESTs	2.2
	439626	N22415	Hs.189080	ESTs	2.2
35	444540	AI693927	Hs.265165	ESTs	2.2
	450024	AA005129		gb:zh90h08.r1 Soares fetal liver spleen	2.2
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	2.2
	439443	AF086261	Hs.127892	ESTs	2.2
	418824	AW751661	Hs.53542	choreoacanthocytosis gene; KIAA0986 prot	2.2
40	451273	NM_014811	Hs.26163	KIAA0649 gene product	2.2
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.2
	432702	AW973953	Hs.293744	ESTs	2.2
	414195	BE263293	Hs.89605	cholinergic receptor, nicotinic, alpha p	2.2
	425570	AA359558		gb:EST68590 Fetal lung II Homo sapiens c	2.2
45	414935	C15671		gb:C15671 Clontech human aorta polyA+ mR	2.2
	453153	N53893	Hs.24360	ESTs	2.2
	430832	AJ073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	2.2
	439867	AA847510	Hs.161292	ESTs	2.2
	419780	AA713522	Hs.87752	ESTs	2.2
50	433420	AI674093	Hs.293961	ESTs, Moderately similar to putative DNA	2.2
	434690	AI887679	Hs.148410	ESTs	2.2
	436572	AA723274	Hs.279596	ESTs	2.2
	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	431688	AA513906		gb:ng67c08.s1 NCI_CGAP_Lip2 Homo sapiens	2.2
55	403133				2.2
	414885	AA157531	Hs.269276	ESTs, Moderately similar to S65657 alpha	2.2
	432111	AW972777		gb:EST384871 MAGE resequences, MAGL Homo	2.2
	410073	AW408163	Hs.58488	catenin (cadherin-associated protein), a	2.2
	448869	AI792798	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.2
60	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	2.2
	446565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	2.2
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfat	2.2
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	2.2
	403378				2.2
65	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (2.2
	438580	AA811262	Hs.299202	ESTs	2.2
	409191	AW818390	Hs.175613	homolog of Xenopus Claspilin	2.2
	412282	BE160188		gb:QV1-HT0413-010200-059-g05 HT0413 Homo	2.2
	411966	AA099113	Hs.118609	ESTs	2.2
70	443915	Z40763	Hs.135292	ESTs	2.2
	427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.2
	446094	AK001760	Hs.13801	KIAA1685 protein	2.2
	436486	AA742221	Hs.120633	ESTs	2.2
	411139	AW819461		gb:RCS-ST0293-061299-031-C03 ST0293 Homo	2.2
75	409070	AA063003	Hs.224560	ESTs	2.2
	432713	AL118623	Hs.29494	PRO1912 protein	2.2
	419384	AA490866	Hs.39429	ESTs	2.2
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	2.2
	408444	AW661839	Hs.253204	ESTs	2.2
	432128	AA127221	Hs.117037	ESTs	2.2
80	418027	AB037807	Hs.83293	hypothetical protein	2.2
	446060	Z42061	Hs.27004	ESTs	2.2
	436198	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, clone HE	2.2
	411987	AA375975	Hs.183380	ESTs, Moderately similar to ALU8_HUMAN A	2.2

	443401	AI394067	Hs.160159	ESTs	2.2
	424665	AW368576	Hs.139851	caveolin 2	2.2
	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	2.2
	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	2.2
5	414564	AA164803	Hs.71994	ESTs, Weakly similar to I38022 hypothe	2.2
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	2.2
	419160	AA911342	Hs.35524	KIAA1559 protein	2.2
	420111	AA255652		gb:zs21h11.1 r1 NCJ_CGAP_GCB1 Homo sapiens	2.2
	442879	AF032922	Hs.8813	syntaxin binding protein 3	2.2
10	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.2
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	2.2
	432074	AA525248	Hs.149723	ESTs	2.2
	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	2.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	2.2
15	409723	AW885757	Hs.257862	ESTs	2.2
	425627	AF019612	Hs.297007	membrane-bound transcription factor prot	2.2
	435090	BE217923	Hs.149595	ESTs	2.2
	449369	AA001256	Hs.27260	ESTs	2.2
	425514	AF112345	Hs.158237	integrin, alpha 10	2.2
20	455821	BE143341		gb:MR0-HT0162-191099-002-d04 HT0162 Homo	2.2
	427224	AL135554	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.2
	432284	AA532807	Hs.105822	ESTs	2.2
	403467				2.2
25	436032	AA150797	Hs.109276	latexin protein	2.2
	404356				2.2
	434205	AF119861	Hs.283032	hypothetical protein PRO2015	2.2
	405257				2.2
	402103				2.2
30	456649	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	2.2
	432985	T92383	Hs.178703	ESTs	2.2
	417649	AW239285	Hs.82359	tumor necrosis factor receptor superfam	2.2
	431277	AA501806	Hs.249965	ESTs	2.2
	454056	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypothe	2.2
	401694				2.2
35	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	431364	AW971382	Hs.294016	ESTs, Moderately similar to B34087 hypot	2.2
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
	448390	AL035414	Hs.21068	hypothetical protein	2.2
	449939	T86420	Hs.272139	ESTs	2.2
40	455678	BE066007		gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.2
	404555				2.2
	418186	BE541042	Hs.23240	Homo sapiens cDNA: FLJ21848 fis, clone H	2.2
	419981	AA897581	Hs.128773	ESTs	2.2
45	449581	AI989517	Hs.181605	ESTs	2.2
	419229	AI827237	Hs.282884	ESTs	2.2
	403891				2.2
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	2.2
	443479	AF027219	Hs.9443	zinc finger protein 202	2.2
50	425329	AI961644	Hs.145444	Homo sapiens cDNA FLJ11494 fis, clone HE	2.2
	453345	AA302862	Hs.90063	neurocalcin delta	2.2
	424335	AW021508	Hs.28170	ESTs	2.2
	451072	AA013451	Hs.117929	ESTs	2.2
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	2.2
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	2.2
55	438035	AA938198	Hs.146123	poly(A) polymerase gamma	2.2
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	2.2
	400241				2.2
	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
60	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	2.2
	411151	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	446009	AI989885	Hs.231926	ESTs	2.1
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	2.1
	416441	BE407197		gb:601301552F1 NIH_MGC_21 Homo sapiens c	2.1
	414891	R27124	Hs.268754	Homo sapiens cDNA FLJ11949 fis, clone HE	2.1
65	430172	AA468591	Hs.161889	ESTs	2.1
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.1
	422985	AU076411	Hs.1602	dihydropyrimidine dehydrogenase	2.1
	448552	AW973553	Hs.20104	hypothetical protein FLJ00052	2.1
	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fis, clone L	2.1
70	450726	AW204600	Hs.250505	retinoic acid receptor, alpha	2.1
	438379	N23018	Hs.171391	C-terminal binding protein 2	2.1
	412608	AA247995	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.1
	451270	AW341392	Hs.235795	ESTs	2.1
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	2.1
75	415992	C05837	Hs.145807	hypothetical protein FLJ13593	2.1
	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.1
	437132	AL049353	Hs.297268	ESTs	2.1
	415304	T66079	Hs.12799	ESTs	2.1
	450152	AI138635	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	2.1
80	421147	AW592167	Hs.293299	ESTs	2.1
	421413	AI826128	Hs.57637	ESTs, Weakly similar to A49364 59 protei	2.1
	451750	AA280851	Hs.226930	ESTs	2.1
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	2.1

	406945	K01383	Hs.173451	metallothionein 1A (functional)	2.1
	452449	AW068658	Hs.20943	ESTs	2.1
	436009	H57130	Hs.120925	ESTs	2.1
	418637	T86737	Hs.193536	ESTs	2.1
5	420495	AJ338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	2.1
	449203	AJ634578	Hs.282121	ESTs	2.1
	437751	AA767373	Hs.35669	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	428412	AA428240	Hs.126083	ESTs	2.1
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.1
10	441967	AA972742	Hs.209786	ESTs	2.1
	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
	406018				2.1
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	2.1
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	2.1
15	431229	AA496479	Hs.259929	ESTs	2.1
	435148	AJ918049	Hs.124961	ESTs	2.1
	436349	AI445255	Hs.115315	ESTs	2.1
	446895	AA166655	Hs.282803	ESTs	2.1
	448582	AI538880	Hs.94812	ESTs	2.1
20	442762	AF035119	Hs.8700	deleted in liver cancer 1	2.1
	442738	AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	2.1
	451874	AW963137	Hs.194233	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	448076	AJ133123	Hs.20196	adenylate cyclase 9	2.1
	443484	AI091458	Hs.134559	ESTs	2.1
25	430686	NM_001942	Hs.2633	desmoglein 1	2.1
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	2.1
	407624	AW157431	Hs.248941	ESTs	2.1
	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.1
30	428923	BE047698	Hs.188785	ESTs	2.1
	422496	AA311301	Hs.278827	ESTs	2.1
	413385	M34455	Hs.840	indoleamine-pyrole 2,3 dioxygenase	2.1
	408418	AW963897	Hs.44743	KIAA1435 protein	2.1
	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega	2.1
	427434	BE538374	Hs.301732	hypothetical protein MGC5306	2.1
35	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
	459325	AW088369	Hs.282184	ESTs	2.1
	416996	W91892	Hs.59609	ESTs	2.1
	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	2.1
40	408000	L11690	Hs.620	bulbous pemphigoid antigen 1 (230/240kD)	2.1
	418894	W73921	Hs.50743	ESTs	2.1
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.1
	437378	AI198823	Hs.160473	ESTs	2.1
	454100	AI693231	Hs.126043	chromosome 21 open reading frame 51	2.1
45	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	2.1
	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	2.1
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.1
	440028	AW473675	Hs.125843	ESTs, Weakly similar to T17227 hypotheti	2.1
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	2.1
50	424103	NM_001918	Hs.139410	dihydrolipoamide branched chain transacy	2.1
	407995	AJ094748	Hs.100134	hypothetical protein FLJ12787	2.1
	449911	AI262106	Hs.12653	ESTs	2.1
	449509	AA001615	Hs.84561	ESTs	2.1
	452762	AW501435	Hs.278582	v-akt murine thymoma viral oncogene homo	2.1
55	422839	AI674784	Hs.298908	ESTs	2.1
	435040	AI932350	Hs.152825	ESTs	2.1
	401200				2.1
	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	2.1
	442262	BE170651	Hs.8700	deleted in liver cancer 1	2.1
60	449754	H00820	Hs.30977	ESTs, Weakly similar to B34087 hypotheti	2.1
	453908	AW613920	Hs.282178	ESTs	2.1
	446965	BE242873	Hs.16577	WD repeat domain 15	2.1
	412798	AW998657	Hs.119120	E3 ubiquitin ligase SMURF1	2.1
	416085	H18072	Hs.92576	ESTs	2.1
65	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.1
	455995	BE179408		gb:IL3-HT0618-060500-125-807 HT0618 Homo	2.1
	422411	AW749443	Hs.22511	ESTs	2.1
	410888	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo	2.1
	446893	AJ610818	Hs.7110	ESTs	2.1
	442992	AJ914699	Hs.13297	ESTs	2.1
70	407021	U52077		gb:Human mariner1 transposase gene, comp	2.1
	436938	AW139680	Hs.161393	ESTs	2.1
	433194	AB040883	Hs.83243	KIAA1450 protein	2.1
	454790	AW820852		gb:RC2-ST0301-120200-011-112 ST0301 Homo	2.1
75	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein	2.1
	434739	AA804487	Hs.144130	ESTs	2.1
	406468				2.1
	457023	AA001732	Hs.173233	hypothetical protein FLJ10970	2.1
	416226	N55342	Hs.34372	ESTs	2.1
80	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	2.1
	432810	AA863400	Hs.23054	ESTs	2.1
	412894	R09778	Hs.186510	ESTs	2.1
	430602	D13752	Hs.184927	cytochrome P450, subfamily XB (steroid	2.1
	436981	AA740891	Hs.293316	ESTs	2.1

	452501	AB037791	Hs.29716	hypothetical protein FLJ10980	2.1
	449838	AB020653	Hs.24024	KIAA0846 protein	2.1
	447160	AA330310	Hs.24181	ESTs	2.1
	422156	N34524		gb:yy56d10.s1 Soares_multiple_sclerosis_	2.1
5	440137	AA866199	Hs.171397	ESTs	2.1
	423998	H29138	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	2.1
	436471	AA719813	Hs.117662	ESTs	2.1
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	2.1
10	426782	R14614	Hs.191254	ESTs	2.1
	430027	AB023197	Hs.227743	KIAA0980 protein	2.1
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.1
	413252	BE074910		gb:RCS-BT0580-170300-021-F12 BT0580 Homo	2.1
	427115	AW972853	Hs.112237	ESTs	2.1
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.1
15	400451				2.1
	435255	W87434	Hs.106015	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	2.1
	418375	NM_003081	Hs.84389	synaplosomal-associated protein, 25kD	2.1
20	442835	AI021989	Hs.131903	ESTs	2.1
	400196				2.1
	415734	NM_014747	Hs.78748	KIAA0237 gene product	2.1
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	2.1
	438940	AF075045	Hs.271609	ESTs	2.1
25	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	2.1
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	2.1
	410557	AA085803	Hs.192997	ESTs, Moderately similar to I78885 serin	2.1
	442562	BE379584	Hs.34789	dolichyl-diphosphooligosaccharide-prote	2.1
	413488	BE144017		gb:MR0-HT0165-191199-004-d09 HT0165 Homo	2.1
30	419088	AI538323	Hs.52620	integrin, beta 8	2.1
	447373	AI381922	Hs.158781	ESTs	2.1
	457465	AW301344	Hs.122908	DNA replication factor	2.1
	413918	AW015898	Hs.71245	ESTs	2.1
	402820				2.1
35	424872	AA347923		gb:EST54302 Fetal heart II Homo sapiens	2.1
	428552	AW274560	Hs.129520	ESTs	2.1
	435464	BE548300	Hs.192999	ESTs, Moderately similar to KIAA0961 pro	2.1
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	2.1
	420838	AW118210	Hs.5244	ESTs	2.1
40	428231	U17989	Hs.183105	nuclear autoantigen	2.1
	434933	R91095	Hs.4276	KIAA1701 protein	2.1
	444870	AI200621	Hs.148504	ESTs	2.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	2.1
45	429183	AB014604	Hs.197955	KIAA0704 protein	2.1
	439155	H81076	Hs.269001	ESTs	2.1
	442787	W93048	Hs.250723	hypothetical protein MGC2747	2.1
	429864	AA460039	Hs.286	ribosomal protein L4	2.1
	438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	2.1
	437140	AA312799	Hs.283689	activator of CREM in testis	2.1
50	421991	NM_014918	Hs.110488	KIAA0990 protein	2.1
	446534	AI307356	Hs.176225	ESTs	2.1
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	2.1
	444838	AV651680	Hs.208558	ESTs	2.1
	402318				2.1
55	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
	414494	AA768491	Hs.6783	hypothetical protein FLJ22724	2.1
	421306	AA806207	Hs.125889	ESTs	2.1
	427027	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
	429088	D81542	Hs.227716	KIAA0934 protein	2.1
60	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	2.1
	428060	AA420616	Hs.249483	ESTs	2.1
	419553	BE267154	Hs.125752	ESTs	2.1
	443718	AI083580	Hs.221373	ESTs	2.1
	444187	AW138466	Hs.151274	ESTs	2.1
65	428048	AA705745		gb:zf41b11.s1 Soares_fetal_heart_NbHH19W	2.1
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	2.1
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.1
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.1
	430335	D80007	Hs.239499	KIAA0185 protein	2.1
70	414618	AI204600	Hs.96978	hypothetical protein MGC10764	2.1
	434029	AA621763	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	2.1
	410945	AW811552		gb:QV2-ST0145-071299-017-h10 ST0145 Homo	2.1
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.1
	433374	AI821409	Hs.332789	EST	2.1
75	445644	R77766	Hs.271593	ESTs, Moderately similar to A47582 B-cel	2.1
	450271	AI693900	Hs.200920	ESTs	2.1
	448084	AI457800	Hs.271000	ESTs, Weakly similar to I38022 hypotheti	2.1
	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	2.1
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	2.1
80	435542	AA687376	Hs.269533	ESTs	2.1
	443544	AI076315	Hs.16359	ESTs	2.1
	421103	AI625835	Hs.27104	Homo sapiens mRNA; cDNA DKFZp667D226 (fr	2.1
	405759				2.1
	446242	N66336	Hs.7360	ESTs	2.1

	457938	AI373638	Hs.133900	ESTs	2.1
	433017	Y15067	Hs.279914	zinc finger protein 232	2.1
	436729	BE621807	Hs.3337	transmembrane 4 superfamily member 1	2.1
5	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	2.1
	439224	AW471088	Hs.145950	ESTs, Highly similar to T08692 hypotheti	2.1
	410976	R36207	Hs.25092	hypothetical protein MGC10744	2.1
	454574	AW809109		gb:MR4-ST0117-070100-027-a04 ST0117 Homo	2.1
	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	2.1
10	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	2.1
	446891	AL036877	Hs.282878	ESTs	2.1
	434294	AJ271379	Hs.76194	ribosomal protein S5	2.1
	449057	AB037784	Hs.22941	KIAA1363 protein	2.1
	432769	AA620814	Hs.144959	ESTs	2.1
15	441224	AU076964	Hs.7753	calumenin	2.1
	407891	AA486620	Hs.41135	endomucin-2	2.1
	429017	AA463605	Hs.66295	multi-PDZ-domain-containing protein	2.1
	406817	AI936028		gb:wo47a09.x1 NCL_CGAP_Gas4 Homo sapiens	2.1
	430566	AA481282	Hs.190149	ESTs	2.1
20	449208	AW263635	Hs.48643	ESTs	2.1
	451397	AA017432	Hs.84529	ESTs, Weakly similar to Z202_HUMAN ZINC	2.1
	452042	H38857	Hs.243901	Homo sapiens cDNA FLJ20738 fls, clone HE	2.1
	444779	AI192105	Hs.147170	ESTs	2.0
	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	2.0
25	415954	AA171850	Hs.42251	ESTs	2.0
	420273	AI652864	Hs.197257	ESTs	2.0
	411354	AW992424	Hs.288141	hypothetical protein MGC3156	2.0
	422389	AF240635	Hs.115897	protocadherin 12	2.0
	446994	AV650435	Hs.16755	MBIP protein	2.0
30	417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypept	2.0
	422654	AA314316	Hs.163725	ESTs	2.0
	425999	AW513051	Hs.332981	ESTs, Weakly similar to I38022 hypotheti	2.0
	405634				2.0
	451562	H04150	Hs.107708	ESTs	2.0
35	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	2.0
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	2.0
	442010	AI032680	Hs.132213	ESTs	2.0
	442891	BE281238	Hs.8686	hypothetical protein FLJ20424	2.0
	425312	AA354940	Hs.145958	ESTs	2.0
40	415191	AA190381	Hs.120810	ESTs	2.0
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	2.0
	425316	AA354977	Hs.191565	ESTs, Moderately similar to T14342 NSD1	2.0
	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin	2.0
	452241	AL050204	Hs.28540	Homo sapiens mRNA; cDNA DKFZp586F1223 (f	2.0
45	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	2.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	2.0
	409190	AU076536	Hs.50984	sercoma amplified sequence	2.0
	413783	AA314337	Hs.301547	ribosomal protein S7	2.0
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.0
50	429418	AI381028	Hs.118769	ESTs	2.0
	445829	AA52457	Hs.145526	ESTs	2.0
	452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	2.0
	446593	W79572	Hs.13277	hypothetical protein FLJ22054	2.0
	400462				2.0
55	422003	AA361760	Hs.296326	ESTs	2.0
	444585	AW170015	Hs.6594	ESTs	2.0
	444898	AI201548	Hs.308338	ESTs	2.0
	403525				2.0
60	443031	AW134696	Hs.49418	ESTs	2.0
	430818	AI311928		gb:qo89h04.x1 NCL_CGAP_Kid5 Homo sapiens	2.0
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	2.0
	440941	BE268362	Hs.7535	COBW-like protein	2.0
	409627	AW997628	Hs.313637	ESTs	2.0
65	433268	AI806626	Hs.207300	ESTs, Weakly similar to ALUB_HUMAN IIII	2.0
	412863	AA121673	Hs.59757	zinc finger protein 281	2.0
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.0
	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	2.0
	417280	AW173116	Hs.262206	ESTs	2.0
70	423528	AB011137	Hs.300938	KIAA0565 gene product	2.0
	424800	AL035588	Hs.153203	MyoD family inhibitor	2.0
	446019	AJ362520	Hs.279789	histone deacetylase 3	2.0
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	2.0
	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	2.0
75	430473	AW130690	Hs.59962	ESTs	2.0
	431363	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	2.0
	438118	AW753311	Hs.259415	ESTs	2.0
	400859				2.0
	405829				2.0
80	415258	AW752247	Hs.293853	ESTs	2.0
	420314	H81671	Hs.320921	ESTs, Weakly similar to T22688 hypotheti	2.0
	437733	AI792574	Hs.122876	ESTs	2.0
	452019	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	2.0
	453118	AW195849	Hs.252757	ESTs	2.0

	430706	NM_003540	Hs.247816	H4 histone family, member C	2.0
	420568	F09247	Hs.247735	protocadherin alpha 10	2.0
	452759	AW590773	Hs.258996	ESTs	2.0
5	408496	AI683802	Hs.136182	ESTs	2.0
	420674	NM_000055	Hs.1327	butyrylcholinesterase	2.0
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein	2.0
	450086	AW016343	Hs.233301	ESTs	2.0
	410853	H04588	Hs.30469	ESTs	2.0
	438607	AW080237	Hs.252884	ESTs	2.0
10	422232	D43945	Hs.113274	transcription factor EC	2.0
	432801	NM_016260	Hs.278963	zinc finger DNA binding protein Helios	2.0
	402490				2.0
	446551	AI308176	Hs.65636	ESTs	2.0
	438315	R56795	Hs.82419	ESTs	2.0
15	445261	T79759	Hs.282939	ESTs, Weakly similar to I38022 hypothe	2.0
	401986				2.0
	420335	AA258771	Hs.43616	Homo sapiens mRNA for FLJ00029 protein,	2.0
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	2.0
	435413	AI267476	Hs.46669	ESTs	2.0
20	458175	AW296024	Hs.150434	ESTs	2.0
	458433	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypothe	2.0
	417494	AI369494	Hs.222137	ESTs	2.0
	416045	H15990	Hs.31403	ESTs	2.0
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	2.0
25	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	2.0
	411578	AW238524		gb:xp27c05.x1 NCL_CGAP_HN10 Homo sapiens	2.0
	453116	AI276680	Hs.146086	ESTs	2.0
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.0
	435608	AW183971	Hs.250896	ESTs	2.0
30	402102				2.0
	458308	AI828155	Hs.211055	ESTs	2.0
	438177	BE327015	Hs.281391	ESTs	2.0
	415205	H71616	Hs.135233	ESTs	2.0
	427244	AA402400	Hs.178045	ESTs	2.0
35	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	2.0
	438979	AW976218	Hs.32565	ESTs	2.0
	400285				2.0
	405966				2.0
40	407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
	427739	AW198755	Hs.98105	NYD-SP14 protein	2.0
	433584	AW295399		gb:U1-H-B12-ahv-h-03-0-UIs1 NCL_CGAP_Su	2.0
	448956	AK001674	Hs.22630	cofactor required for Sp1 transcription	2.0
	439474	AI824060	Hs.211501	ESTs	2.0
	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.0
45	454566	AW807605		gb:MR4-ST0098-120100-001-b06 ST0098 Homo	2.0
	418836	AI655499	Hs.161712	ESTs	2.0
	453108	AI311457	Hs.99472	ESTs	2.0
	447101	N72185	Hs.44189	ESTs	2.0
	408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	2.0
50	426226	AA769045		gb:oa80h07.s1 NCL_CGAP_GCB1 Homo sapiens	2.0
	401157				2.0
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	2.0
	425646	AW157044	Hs.158512	cyclin-dependent kinase-like 2 (CDC2-rel	2.0
	408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	2.0
55	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	2.0
	402855				2.0
	443644	AI080491	Hs.93270	ESTs, Moderately similar to S65657 alpha	2.0
	445672	AI907438	Hs.282862	ESTs	2.0
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.0
60	411941	AW876909	Hs.25201	ESTs, Weakly similar to FAT DROME CADHER	2.0
	430664	AW969834	Hs.303303	ESTs	2.0
	402812				2.0
	457434	AW628192	Hs.18851	hypothetical protein FLJ10875	2.0
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	2.0
65	402048				2.0
	423347	AI660412	Hs.234557	ESTs	2.0
	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	2.0
	433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
	437373	H67505	Hs.191979	KIAA1733 protein	2.0
70	439217	AF086041	Hs.42975	ESTs	2.0
	446609	BE395090	Hs.15535	Homo sapiens clone 24582 mRNA sequence	2.0

75 TABLE 3B: List of accession numbers for primekeys lacking unigenelD's for Table 3A. For each such probe set is listed a gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

80 Pkey: Unique Eos probe set identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT number Accession

408690	107490_1	AW864542 AA056567 AW882724
409029	1095422_1	BE087807 AW301579
409073	109851_1	AA063458 AA063018 AA444822
409519	113722_1	AA075368 AA075369
409695	114876_1	AA296961 AA296889 AA076945 AA077528 AA077497
410008	116812_1	AA079552 BE142525 BE142527
410615	1212203_1	AW772721 AW873372 H89212
410672	1214882_1	AW794600 AW794730
410784	1221005_1	AW803201 BE079700 BE062940
410785	1221055_1	AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355
410888	1225955_1	AW861207 AW809508
410901	1226077_1	AW810001 AW810092 AW810170 AW809884 AW809664 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786
410934	1227240_1	AW810006 AW809872 AW809694 AW810552 AW810345 AW810432 AW809960
410945	1227561_1	AW811114 AW811095 AW811087 AW811124 AW811054 AW811094 AW811157
410999	1228809_1	AW811552 AW811470 AW811523 AW811482 AW811514 AW811456 AW811525
411004	1228975_1	AW813004 AW812962 AW812961
411018	1229132_1	AW813242 BE146089 AW813195 AW813173 AW813206 BE145953 BE146212 AW813196 AW854582 AW813241 BE061582
411139	1233781_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
411151	1234022_1	AW819461 AW819478 AW819479 AW819559 AW819505
411479	1247077_1	AW866497 AW819775 AW819868 AW866602 AW865561
411514	1248638_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069
411578	125013_1	AW848905 AW848214
411745	1256160_1	AW850178 AW850233 AW850445 AW850446
411880	1263110_1	AW238524 AA094059 R59022
411905	1265181_1	AW867826 AW859896
412167	1280605_1	AW872477 BE088101 T05990
412209	1283610_1	BE265067 BE264978 AW875420
412248	1285000_1	AW897230 AW897252 AW897244 AW897231 AW897263
412282	1287679_1	AW901456 AW901450 AW901441
412303	1288130_1	BE176480 AW903298 AW903313
412566	1306469_1	BE160188 AW935785 BE160401 BE160319 BE160313 BE160395
412877	1333953_1	AW936336 AW936339
412879	1334272_1	AW962574 BE073261
413087	1348720_1	BE011168 BE006371 BE011172 BE011313 BE011166
413136	1350379_1	BE092219 BE092361 BE006789
413252	1355877_1	BE064655 BE153953
413382	1365954_1	BE066941 BE066979 BE066929 BE066925
413488	1373234_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
413499	1373910_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698 BE090686
413618	1380384_1	BE144017 BE185527 BE144023
413638	1381238_1	BE144884 H97942
413642	1381386_1	BE154078 BE154006 BE153891 BE153523 BE153983
413875	1396766_1	H71252 BE154668 BE154642
414109	1417307_1	BE154837 BE154879 BE154850 BE154877 BE154835 BE154849 BE154902 BE154905 BE154867 BE154901 BE154904 BE154899
414221	142696_1	BE176776 H85072
414605	1465790_1	BE250744 BE294770
414935	1509157_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368
415236	1531080_1	BE011362 BE011215 BE011365 BE011363
415635	1540853_1	BE390440
415747	155189_1	C15671 C15333 C15833 D81433 C14657 C14811
415980	1564218_1	R41400 H06659 Z38637 F02023 T16516
416288	1585983_1	F13168 R21289 T77628
416337	1589299_1	AA381209 AA381245 AA167683
416441	159480_1	R52414 R61681 H12009 T74429
416548	1600181_1	H51299 H44619 H46391 R86024 H51892 T72744
416624	1604694_1	H48713 H83057 H48694 H65247
416871	1626761_1	BE407197 AA182474 AA180369 BE275628 BE276131
416913	163001_1	H62953 N76608 N72413
416972	163668_1	H69044 T47567 H75691 T50292
417561	168747_2	H98716 N90792 N24283
417648	1691070_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
417669	1692157_1	BE019570 AA191284 AA191255
417859	1703724_1	AW974345 BE145400 T97088 AA639076
418378	174656_1	R06552 T98985 R08656
418636	177402_1	T99898 T92080 T91447 R07806 R07779
419546	185766_1	T26453 Z44226 R20425
419637	186639_1	AW962081 AA218925 AA354237
419807	188252_1	AW749855 AA225995 AW750208 AW750206
420111	190755_1	AA244199 AA244272 H57440
420621	195113_1	V27493 AA248063 AA249685 AA429679
420637	195241_1	R77402 AA262462 AA250988 R06794
421065	198936_1	AA255652 AA280911 AW967920 AA262684
422063	210852_1	AA278808 BE082076 BE081812 BE081581
422156	212379_1	AW976153 AA278945 AA747691
422342	215498_1	AA329711 AA287436 AA283148
422429	216469_1	BE156476 BE156473 BE156474 BE156475 AA302839
422977	223410_1	N34524 AA305071 AW954803 AA502335 A1433430 A1203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512
423121	225175_1	A1334966 W32951 H62656 H53902 R88904 AW835732
		AA309272 AA309312 AW961837
		AA310527 AW962295 Z44865 H06641
		AA631498 A1017191 AA491211 AA761823 AA714555 AA768099 AA808286 A1934069 AA570223 AA574389 AA582438 A1745346 AW954510
		AA319642 AW853758 H56414
		AW864848 AA322213 AA322209 AW961624

5	423377	22769_1	AL049377 AL079930 AL047223 AW885968 AA385235
	423532	229362_1	BE090503 BE090490 BE090483 BE090501 BE090500 BE090365 BE090505 BE090509 BE090499 BE090502 BE090504 BE090497 AA327285
	423735	231498_1	AA330259 AA661806 AA502431 AW974633 AA649496
	423841	232507_1	AW753967 AA370795 AA331630 AW962550
	423867	232732_1	AA331886 AW962559 AW962655 T89841
10	424872	244505_1	AA347923 AA347928 AW961769
	425201	247933_1	AA352111 AW962247 AA429695
	425497	252499_1	AA524596 AA358494 AA513507
	425570	253248_1	AA359558 AA359819 AW963122
	426226	262918_1	AA769045 AA372590 AW963633
15	426497	268121_1	AA379913 AA379981 AW963523
	426603	269825_1	AA382291 AA994657
	427551	280163_1	T96203 AA405343 T96121
	428048	286394_1	AA705745 AA420850 AA420433
	428679	294049_1	AA431765 AA432015
20	430212	314437_1	AA469153 AI718503 AA469225
	430818	324239_1	AJ311928 AA936030 T51931 AA609816 AA487195 AA664207
	430844	324570_1	T94960 AA487679 T95013
	430933	325757_1	AW863635 BE179901 BE179402 AW863789 AA489179 BE010747 BE010748
	431071	327550_1	AA491379 H86020 AW969148
25	431169	328799_1	AW971240 AA493843 AA493723
	431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
	431595	335512_1	AA508196 BE142920 AI280311 AI205616 D61709
	431688	336609_1	AA513906 AA847734 AI357044
	432111	341618_1	AW972777 AA526795 AA526305
30	432189	342819_1	AA527941 AI810608 AI620190 AA635286
	432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528756
	432779	354024_1	AW979241 AA565006 AA847102
	432803	354287_1	AA565398 AW894072 H97930
	432869	355475_1	AW974094 AA569074 AA602574
35	433347	36388_1	AF023130 AF181250 AA984703 AA694303 AA351792
	433492	367934_1	AW605849 AW262898 N41060 AA594852
	433584	370400_1	AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 AA778832
	433644	371919_1	AW342028 AA641080 AA603282
	433687	373061_1	AA743991 AA604852 AW272737
40	434138	380572_1	AA625804 AW418787 AW074833 AI675642 AI393368
	434374	384889_1	AA631439 AI086355 AI082577
	434613	389550_1	AJ821826 AA640657 AA658836 AA650055 AI821079
	434638	38990_1	H50758 AF147434 H50666
	434950	396061_1	AW974892 AA654375
45	434995	397210_1	AW974995 AI821880 AI821932 AI791196 AA659617 AI821137 AA658925
	435079	399783_1	AA664192 H60250 T71388
	435463	406582_1	AA682507 AW851124
	435634	409239_1	T82384 R05307 AA693714
	436532	421802_1	AA721522 AW975443 T93070
50	437146	43371_1	AA730977 AI261584 AA334473 Z43283 AW875861 AW938044 BE150701 AW936262 AA306862 BE565575 BE567380 AA728920 AA167612
	438005	447553_1	AI239729 AI251752 AA485791 BE568425 AW962958
	438458	457837_1	BE151746 BE336853 D63271 T94955 AA774994
	438909	46684_1	AW975186 AA807807 D29548
	438993	467651_1	AF085839 R69137 AW188788 R69254
55	440320	491930_1	AA828955 AA834879 AI926361
	440674	49997_1	AA879294 N67538 AI474541
	443613	575391_1	BE561546 Z25124 AI307139 Z28800
	443657	576685_1	AI079356 W23287
	444314	600667_1	R14973 R14967 AI081006
60	444610	612257_1	AI140497 AW749625 AW749626 AW749644
	444910	624951_1	AI174783 R83569 R12271
	446096	661959_1	AI201849 BE069007 AW946544
	446901	697809_1	AI276454 AI633717 AI275116
	447197	711623_1	AJ347274 AW844024
65	448404	761515_1	R36075 AI366546 R36167
	449540	80945_2	BE089973 AI498612 AW805032
	450024	82296_1	AA001713 H63836
	450458	83586_1	AA005129 AA678084 AA694399
	450522	837264_1	AA009926 BE149301
70	451024	85565_1	AJ698839 AI909260 AI909259
	451487	87131_1	AA442176 AA259181
	452453	918300_1	AA018072 N46370 R84847
	452542	921410_1	AJ902519 AI902518 AI902516
	453823	982526_1	AW812256 AW812257 AI906423 AI906422
75	453901	986414_1	AL137957 BE064160 BE064186
	454190	1049996_1	BE065902 AW749032 AW003637
	454193	1050256_1	AW177821 AW177896 AW177867
			BE141183 AW178167 AW178162 AW178166 AW178172 AW845893 AW178159 AW178222 AW178213 AW178215 AW178090 AW178091
			AW178161 AW178207 AW178210 AW178214 AW178212 BE140918 BE140917 AW178135 AW178205 AW178209 AW178223 AW178220
80	454352	1129667_1	AW178206 AW178203 AW178165 AW178168 AW178160 AW178136 AW845878 AW178131 AW178138 AW178105 AW845894 AW178129
	454359	1130674_1	AW845810 AW845828 AW178216 AW178112 AW178211 AW178224 BE140915 AW178221 AW178130 AW178134 AW178096 AW178108
	454389	115682_1	AW178133 AW178164 AW178218 AW178171 AW178157 AW178158 AW178103 BE141189 AW178170 AW845816 BE141586 AW178156
	454403	1170435_1	AW178104 AW178163 AW178093 AW178208 AW178137 AW178140 AW178219 BE141592 AW845901 BE141580 AW178155 BE141598 BE140957
			AW389668 AW389657 AW609198 AW389649
			N71277 AW390764
			AW752571 AW847602 AA077979
			BE065985 BE065944 BE066008 BE066083 BE066093

5	454455	1206965_1	AW572710 BE180336 BE180186
	454566	1224432_1	AW807605 AW807690 AW807839 AW807752 AW807673 AW807667 AW807955 AW807760 AW807615 AW807898 AW807849 AW807821 AW807832 AW807842 AW807827 AW807822 AW807829 AW807830 AW807825 AW807603 AW807612 AW807908 AW807595 AW807617 AW807678 AW807687 AW807918 AW807921 AW807596 AW807602 AW807688 AW807609 AW807684 AW807770 AW807593 AW807754 AW807679 AW807957 AW807683 AW807763 AW807902 AW807840 AW807819 AW807836 AW807769 AW807685 AW807847 AW807674 AW807686 AW807670 AW807917 AW807677 AW807680 AW807900 AW807669 AW807952 AW807907 AW807846 AW807756 AW807835 AW807608 AW807753 AW807601 AW807956 AW809109 AW809112 AW809122 AW809126 AW809128 AW809133 AW809131 AW809113 AW809111 AW809132 AW810001 AW810092 AW810170 AW809884 AW809564 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786 AW810006 AW809672 AW809694 AW810552 AW810345 AW810432 AW809960 AW813089 W28102 AW813428 AW813444 AW813367 AW813368 AW813429 AW813424 AW815098 BE154843 BE154831 AW866497 AW819775 AW819868 AW866602 AW866561 AW820626 AW820621 AW820608 AW820852 AW820773 AW821088 AW833711 AW833620 AW833699 AW847645 AW847791 AW854083 AW853945 AW852530 AW852527 AW852526 BE152428 AW855572 AW855607 BE160198 AW935898 T11520 AW935930 AW856073 AW861034 BE154113 AW856797 AW856847 AW861128 AW856817 AW857121 AW857123 AW881238 AW860972 AW862598 AW862599 AW860988 AW860983 AW860989 AW860925 AW860922 AW860986 AW860984 AW860989 AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878 AW902103 AW869012 AW869139 AW876627 AW876630 AW876631 AW876625 BE144384 AW887474 AW887403 BE144386 AW893961 AW893998 AW894034 AW894019 AW938484 BE001245 BE001190 AA102322 BE144762 AW979091 AW983608 AW983628 AW983610 AW983688 AW983601 AW983645 AW983607 AW983640 AW983625 AW983612 AW983642 AW983687 AW983602 AW983624 AW983634 AW983637 AW983632 AW983617 AW983635 AW983630 AW983636 AW983639 AW983616 AW983689 AW983641 AW983621 AW983603 AW983609 AW983623 AW983644 AW983618 AW983615 AW983611 AW983604 AW983686 AW983622 AW983619 AW983633 AW983589 AW983605 AW983626 AW983643 AW983631 AW983627 AW983613 AW983614 AW983685 AW983593 AW983590 AW983594 AW983620 AW983638 AW983592 AW983588 BE003714 BE003721 BE003720 BE003716 BE063031 BE063002 BE063008 BE063024 BE063040 BE063006 BE063072 BE066007 BE066017 BE066074 BE066976 BE066928 BE066927 BE141140 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108 BE143341 BE143344 BE143378 BE143358 BE149024 BE149056 BE152826 BE149025 BE149057 BE152819 BE149030 BE149062 BE149023 BE149055 BE179015 BE178965 BE179010 BE179002 BE178961 BE179005 BE178964 BE179012 BE179011 BE178963 BE178997 BE179408 BE179798 BE179980 AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363 AL157625 N72696 BE622492 AI630223 AI630470 AI904723 AI904725 AI904729 AI904722 AI904758 AI904736 AW391177 W45021 AJ003631 AJ003650 AJ003651
10	454574	1225636_1	
	454600	1226077_1	
15	454678	1228915_1	
	454693	1229132_1	
	454714	1230493_1	
	454766	1234022_1	
	454784	1234630_1	
	454790	1234752_1	
	454836	1236509_1	
	454962	1246750_1	
20	455047	1250536_1	
	455092	1252971_1	
	455100	1253334_1	
	455107	1253874_1	
	455114	1254106_1	
25	455170	1256906_1	
	455201	1259748_1	
	455226	1262534_1	
	455252	1266222_1	
	455286	1273576_1	
	455310	1278158_1	
30	455431	1289854_1	
	455488	129372_1	
	455511	1321229_1	
	455512	1321443_1	
35			
40	455571	1331885_1	
	455631	1347545_1	
	455678	1349716_1	
	455685	1350393_1	
	455807	1370914_1	
	455821	1372714_1	
	455866	1377119_1	
45	455992	1398552_1	
	455995	1398903_1	
	456034	142696_1	
50	458804	75803_1	
	458861	798085_1	
	459160	920051_1	
	459201	925883_1	
	459267	966605_1	
55			

TABLE 29C

60	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
65	Pkey	Ref	Strand	Nt_position
	400451	8113550	Minus	82189-82320
	400462	9929659	Minus	197610-197785
70	400608	9887666	Minus	96756-97558
	400639	9887597	Plus	23150-23580
	400641	8117693	Plus	4786-4992
	400756	8119084	Minus	38734-38857
	400859	9757499	Minus	91888-92018,98131-98294,99474-99570
75	400880	9931121	Plus	29235-29336,36363-36580
	400889	9958234	Minus	169782-170036
	400983	8081198	Plus	107903-108832
	401045	8117619	Plus	90044-90184,91111-91345
	401049	7232177	Plus	149157-150692
80	401078	3687273	Plus	105052-105171
	401094	9965511	Plus	137130-137302,139283-139506
	401103	8568122	Minus	98330-98449
	401157	9438289	Minus	114133-114247,114567-114645
	401189	9690246	Minus	90815-90929

	401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
	401213	9858408	Plus	98243-98380,98489-98619
	401254	9796309	Plus	152209-152383
	401323	9212516	Plus	213509-214450
5	401335	9884881	Plus	15736-16352
	401497	7381770	Plus	92807-92813
	401517	7677912	Plus	29278-29770
	401526	7770561	Plus	91570-93177
	401575	7229804	Minus	76253-76364
10	401694	3540172	Minus	64056-64168
	401793	7263888	Minus	102945-103083
	401862	7770606	Minus	55839-55993,59145-59293
	401878	8099802	Minus	162268-162474,163089-163195
	401986	4406829	Minus	31137-31293
15	402046	8072415	Plus	166394-166556,168167-168395
	402048	8072512	Plus	43936-44078
	402102	8117771	Minus	174566-174740
	402103	7249203	Plus	14453-15414
20	402230	9966312	Minus	29782-29932
	402318	7582559	Minus	12843-13403
	402490	9797648	Plus	149982-150929
	402745	9212200	Minus	76516-76690
	402800	6010175	Plus	43921-44049,46181-46273
	402812	6010110	Plus	25026-25091,25844-25920
25	402820	6456853	Minus	82274-82443
	402855	9662953	Minus	59763-59909
	403133	7331427	Plus	38314-38634
	403271	7230852	Plus	134283-134485
30	403277	8072597	Minus	27494-27642
	403310	8139936	Minus	183883-184026
	403329	8516120	Plus	96450-96598
	403356	8569930	Plus	92839-93036
	403378	9438244	Minus	44264-44443
35	403388	9438331	Plus	112733-113001,114599-114735
	403467	9929556	Minus	73431-73602
	403515	7656757	Minus	173358-179553
	403525	7960440	Plus	152431-153243
	403534	8076917	Minus	46652-47332
40	403568	8101145	Minus	85509-85658
	403574	8101156	Plus	5542-8176
	403637	8671936	Minus	142647-142771,145531-145762
	403677	7331517	Minus	55008-55083,62860-63051
	403691	7387384	Minus	88280-88463
45	403760	7712202	Minus	45910-46260,47563-47824
	403776	7770611	Minus	1414-1513,1624-1756
	403895	7381715	Minus	3502-4002,4070-4308
	403937	7711761	Minus	12609-12773
	404043	9558573	Plus	28042-29135,46597-46699
50	404097	7770701	Plus	55512-55781
	404200	6010176	Minus	7066-7210
	404249	8655533	Plus	64270-64633
	404274	9885189	Plus	104127-104318
	404285	2326514	Plus	32282-32416
55	404288	2769644	Plus	3512-3691
	404356	7630858	Minus	126433-126623
	404443	7579073	Minus	87198-87441
	404476	8080699	Plus	101841-102043
	404488	8113286	Minus	64835-64994
60	404513	8151941	Minus	112837-113339
	404548	8570305	Minus	83896-84162
	404555	7243881	Minus	63963-64157
	404561	9795980	Minus	69039-70100
	404588	6456726	Minus	40059-40210
65	404593	9944086	Minus	74922-75788
	404599	8705107	Plus	110443-110733
	404860	8979555	Plus	65852-66081
	404916	7341826	Plus	91057-91188
	404957	7407827	Plus	147512-148011
70	405041	7547195	Plus	121230-121714
	405059	7656683	Plus	349-822
	405090	8072525	Minus	38552-39202
	405267	7329310	Plus	73121-73273
	405336	6094635	Plus	33267-33563
75	405472	8439781	Plus	106297-106447,108462-108596
	405494	8050952	Minus	70284-70518
	405547	1054740	Plus	124361-124520,124914-125050
	405621	5523811	Plus	59362-59607
	405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
80	405654	4895155	Minus	53624-53759
	405692	4314424	Plus	61379-62562
	405759	3288022	Minus	18283-18399
	405829	7109593	Minus	15628-16127
	405848	7651809	Minus	28135-28244

5	405966	8247788	Minus	51762-51978
	405970	8247789	Minus	45795-46295
	406018	6758904	Minus	37795-38168
	406091	9123919	Minus	197370-197935
	406092	9123919	Plus	251370-251797,252168-252882
10	406149	7144791	Minus	44464-45164
	406195	7289992	Minus	36293-36827
	406333	9213235	Plus	64689-64798
	406468	9795553	Plus	4373-4616,8870-9046,11366-11509,11625-11880
	406506	7711374	Minus	6843-8077
15	406554	7711566	Plus	106956-107121
	406603	8272659	Minus	39506-39694

TABLE 30A: ABOUT 1840 GENES UP-REGULATED IN IDIOPATHIC PULMONARY FIBROSIS (IPF) COMPARED TO HYPERSENSITIVITY PNEUMONITIS (HP)

Table 30A lists about 1840 genes that are up regulated in idiopathic pulmonary fibrosis (IPF) samples as compared with hypersensitivity pneumonitis (HP) samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 Gene Chip array such that the ratio of "average" idiopathic pulmonary fibrosis sample expression level to "average" hypersensitivity pneumonitis sample expression was greater than or equal to about 2.0. The "average" idiopathic pulmonary fibrosis level was set to the 90th percentile amongst idiopathic pulmonary fibrosis samples. The "average" hypersensitivity pneumonitis level was set to the 90th percentile amongst hypersensitivity pneumonitis samples.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of IPF (idiopathic pulmonary fibrosis) to HP (hypersensitivity pneumonitis)

Pkey	ExAccn	Unigene ID	Unigene Title	R1
450478	AW451709	Hs.271200	ESTs	20.2
432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
405654				11.8
440209	H05049	Hs.22269	neurexin 3	10.8
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	10.4
439606	W79123	Hs.58561	G protein-coupled receptor 87	10.3
425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	10.2
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	9.5
416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.3
420481	U50525	Hs.98201	Human BRCA2 region, mRNA sequence CG029	9.2
403574				9.1
415817	U88967	Hs.78887	protein tyrosine phosphatase, receptor-4	8.8
419519	AI198719	Hs.176376	ESTs	8.2
435256	AF193766	Hs.13872	cytokine-like protein C17	8.1
423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	8.1
429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	8.0
405443				7.8
428766	AA477989	Hs.98800	ESTs	7.7
441802	AA968636	Hs.127877	ESTs	7.6
453649	Y07494	Hs.34114	ATPase, Na+/K+ transporting, alpha 2 (+)	7.5
447410	AI470235	Hs.172698	EST	7.2
442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	7.2
405494				6.9
442377	AA993807	Hs.167367	ESTs	6.9
409928	AL137163	Hs.57549	hypothetical protein dJ47384	6.8
420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-II	6.8
415236	R41400		gb:Y94b12.s1 Soares Infant brain 1NIB H	6.8
451562	H04150	Hs.107708	ESTs	6.8
403310				6.7
445189	AI936450	Hs.147482	ESTs	6.7
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	6.7
439780	AL109688		gb:Homo sapiens mRNA full length insert	6.6
402076				6.6
415025	AW207091	Hs.72307	ESTs	6.5
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	6.5
438557	AW364104	Hs.143509	hypothetical protein FLJ21924	6.5
428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	6.4
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	6.4
409545	BE296182	Hs.19002	hypothetical protein MGC4675	6.4
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.4
411966	AA099113	Hs.118609	ESTs	6.4
440274	R24595	Hs.7122	scrapie responsive protein 1	6.3
442879	AF032922	Hs.8813	syntactin binding protein 3	6.3
419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	6.3
420185	AL044056	Hs.158047	ESTs	6.3
415672	N53097	Hs.193579	ESTs	6.2
455488	AA102322		gb:Z90R03.r1 Stratagene colon (937204)	6.2
420026	AI831190	Hs.166876	ESTs	6.1
446868	AV660737	Hs.135100	ESTs	6.1
431622	AW979271	Hs.293184	ESTs	6.1
407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	6.1
421300	AW297398	Hs.96617	ESTs	6.0
416045	H15990	Hs.31403	ESTs	6.0

5	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	6.0
	424693	BE169810	Hs.47557	ESTs	6.0
	436397	AA715013	Hs.169835	ESTs	6.0
	440504	AI948966	Hs.130017	ESTs, Weakly similar to JN0908 H+-transp	6.0
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	6.0
10	403625				5.9
	418986	AI123555	Hs.81796	ESTs	5.9
	416035	H42314		gb:yo09a02.s1 Soares adult brain N2b5HB5	5.9
	400292	AA250737	Hs.72472	ESTs	5.9
	442849	R10099	Hs.269805	ESTs	5.8
15	440887	AI799488	Hs.135905	ESTs	5.7
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	5.7
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	5.7
	431374	BE258532	Hs.251871	CTP synthase	5.7
	444963	AI916973	Hs.213603	ESTs	5.6
20	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	5.6
	444992	R37658	Hs.21375	ESTs	5.5
	416575	W02414	Hs.38383	ESTs	5.5
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	5.5
	451830	H18433	Hs.21542	KIAA1035 protein	5.5
25	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	5.5
	404043				5.5
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	5.5
	455540	BE080231		gb:RC4-ST0629-120200-012-111 BT0629 Homo	5.5
	434683	AW298724	Hs.202639	ESTs	5.5
30	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	5.5
	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	5.4
	428895	AA437124	Hs.187247	ESTs	5.4
	450018	AA421642	Hs.24309	hypothetical protein FLJ11106	5.4
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	5.4
35	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	5.3
	454039	AW079064	Hs.245540	ESTs	5.3
	403637				5.3
	414725	AA769791	Hs.125300	ring finger protein 21, interferon-respo	5.3
	409073	AA063458		gb:zf71a07.s1 Soares_pineal_gland_N3HPG	5.3
40	403329				5.3
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	5.3
	459664				5.3
	401497				5.2
	410797	AW857191		gb:RC2-CT0304-080100-011-b12 CT0304 Homo	5.2
45	411402	BE297855	Hs.69855	NRAS-related gene	5.2
	448844	AI581519	Hs.177164	ESTs	5.1
	435202	AI871313	Hs.170204	KIAA0551 protein	5.1
	439418	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	5.1
	443584	AI807036	Hs.267245	hypothetical protein FLJ14803	5.1
50	434352	AF129505	Hs.86492	small muscle protein, X-linked	5.1
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	5.1
	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	5.0
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.0
	437636	AA764781	Hs.291844	ESTs	5.0
55	455747	BE074910		gb:RC6-BT0580-170300-021-F12 BT0580 Homo	5.0
	455464	AW983901		gb:RC1-HN0003-220300-011-f10 HN0003 Homo	5.0
	418771	AA807881	Hs.25329	ESTs	5.0
	434820	AI821863		gb:ns90f05.x5 NCL_CGAP_Pr3 Homo sapiens	5.0
	440615	AI733055	Hs.130806	ESTs	4.9
60	454482	BE147919		gb:RC3-HT0230-160200-016-a08 HT0230 Homo	4.9
	400432	AX015809	Hs.287767	Sequence 8 from Patent WO9950285	4.9
	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	4.9
	423607	AA328329	Hs.6591	ESTs	4.9
	407415	AF073328		gb:Homo sapiens tetracycline transporter-	4.9
65	401878				4.9
	443162	T49951	Hs.9029	DKFZP434G032 protein	4.9
	451325	AA021283	Hs.59788	ESTs	4.9
	440515	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	4.9
	406333				4.8
70	409105	AW467539	Hs.255877	ESTs	4.8
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	4.8
	421482	AL135462	Hs.104715	Inversin	4.8
	442757	AI739528	Hs.28345	ESTs	4.8
	459717				4.8
75	436637	AI783629	Hs.26766	ESTs	4.8
	412222	AA528283	Hs.292737	ESTs	4.8
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	4.8
	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
	426217	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	4.8
80	441640	AI733345	Hs.144104	ESTs	4.8
	422977	AA631498		gb:np83h04.s1 NCL_CGAP_Thy1 Homo sapiens	4.8
	425361	AA355933	Hs.132221	hypothetical protein FLJ12401	4.8
	414955	C15506		gb:C15506 Clontech human aorta polyA+ mR	4.7
	411965	BE467339	Hs.280115	ESTs	4.7
	403341				4.7
	411726	AW858612		gb:CM3-CT0341-190400-152-h12 CT0341 Homo	4.7
	443271	BE568568	Hs.195704	ESTs	4.7

	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	426097	BE327369	Hs.112238	ESTs	4.7
	439199	R40373	Hs.26299	ESTs	4.7
5	440728	AW086077	Hs.153272	Homo sapiens cDNA: FLJ22715 fis, clone H	4.6
	434381	AA631834		gb:np77h05.s1 NCL_CGAP_Pr2 Homo sapiens	4.6
	417428	N87579		gb:LL2030F Human fetal heart, Lambda ZAP	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	431242	AA987742	Hs.251278	KIAA1201 protein	4.6
10	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
	442360	AJ374621	Hs.29055	ESTs	4.6
	452171	AJ863302	Hs.211930	EST	4.6
	440801	AA906366	Hs.190535	ESTs	4.5
	411738	AW859353		gb:MR1-CT0353-150300-102-a12 CT0353 Homo	4.5
15	431447	AA505138	Hs.291341	ESTs	4.5
	433485	AA93076	Hs.201967	aldo-keto reductase family 1, member C2	4.5
	401365				4.5
	408281	BE141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo	4.5
	411657	AW855583		gb:CM4-CT0278-221099-027-07 CT0278 Homo	4.5
20	423085	R96158	Hs.267130	Homo sapiens, clone MGC:5406, mRNA, comp	4.5
	428528	AJ004034	Hs.98638	ESTs	4.5
	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.5
	417252	AA195014	Hs.85971	ESTs	4.5
	417135	AA422067	Hs.50547	ESTs	4.5
	403089				4.4
25	420691	AA829433	Hs.275343	ESTs	4.4
	412147	AW895984		gb:QV4-NN0039-040500-197-e08 NN0039 Homo	4.4
	425578	U65652	Hs.158313	chromosome 17 open reading frame 1A	4.4
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfamily	4.4
30	454438	AA224053	Hs.172405	cell division cycle 27	4.4
	435434	AA680387	Hs.187850	ESTs	4.4
	420828	AA280778	Hs.186878	ESTs	4.3
	435586	AJ279137	Hs.151498	ESTs	4.3
	452393	H87398	Hs.99858	ribosomal protein L7a	4.3
35	416170	H42454	Hs.220645	ESTs	4.3
	408891	AW250525		gb:2821626.5prime NIH_MGC_7 Homo sapiens	4.3
	428912	AW103117	Hs.98949	ESTs, Weakly similar to MEA6 [H.sapiens]	4.3
	455511	BE144762		gb:CM0-HT0180-041099-065-b04 HT0180 Homo	4.3
	413849	BE173561	Hs.15384	AP1 gamma subunit binding protein 1	4.3
40	401189				4.3
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	4.3
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3
	422654	AA314316	Hs.163725	ESTs	4.3
	435463	AA682507		gb:zj18f08.s1 Soares_fetal_liver_spleen_	4.3
45	417919	AJ928203	Hs.86379	ESTs	4.3
	405784				4.3
	431853	AA521034	Hs.70834	ESTs	4.3
	409629	AW449589	Hs.279724	ESTs	4.2
	403281				4.2
50	427173	BE255017	Hs.97540	ESTs	4.2
	433717	AF063536		gb:AF063536 Homo sapiens library (Yu Y)	4.2
	406777	T23625	Hs.150580	putative translation initiation factor	4.2
	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	4.2
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.2
55	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae)	4.2
	449762	N93057	Hs.54888	ESTs	4.2
	421106	AA877124	Hs.172844	ESTs	4.2
	439382	BE247684	Hs.103070	ESTs	4.1
	404957				4.1
60	436332	AL049679	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	4.1
	446393	AW014174	Hs.301956	zinc finger protein	4.1
	452728	AJ915676	Hs.239708	ESTs	4.1
	456386	W28481		gb:47e1 Human retina cDNA randomly prime	4.1
	406288	AW068311	Hs.311054	Homo sapiens mRNA full length insert cDN	4.1
65	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	4.1
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.1
	403344				4.1
	438993	AA828995		gb:od77b08.s1 NCL_CGAP_Ov2 Homo sapiens	4.1
	444922	AJ921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.1
70	401596	AA172106	Hs.110950	Rag C protein	4.1
	418693	AJ750878	Hs.87409	thrombospondin 1	4.1
	414299	AA142989	Hs.71730	ESTs	4.1
	452744	AJ267652	Hs.30504	Homo sapiens mRNA; cDNA DKFp434E082 (fr	4.0
	458552	AW136139	Hs.245856	ESTs	4.0
75	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi	4.0
	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
	441201	AW118822	Hs.128757	ESTs	4.0
	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	4.0
	440472	AA886169	Hs.169071	ESTs	4.0
80	418379	AA218940	Hs.137516	fidgetin-like 1	4.0
	435878	R08330	Hs.20152	ESTs	4.0
	437263	AA747822		gb:bx97a04.s1 NCL_CGAP_GCB1 Homo sapiens	4.0
	444087	AV647899	Hs.282375	ESTs	4.0
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	4.0

	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	4.0
	405521				4.0
	411597	AW852925		gb:PMO-CT0248-131099-001-f10 CT0248 Homo	4.0
	415655	W05433	Hs.49890	ESTs	4.0
5	404822				4.0
	441107	AA917075	Hs.190520	ESTs	4.0
	404834				4.0
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	4.0
	428102	AA968441	Hs.126866	ESTs	4.0
10	436511	AA721252	Hs.291502	ESTs	4.0
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoietin	3.9
	453098	Z25935	Hs.86379	ESTs	3.9
	410811	AW805687	Hs.300648	ESTs	3.9
	425048	H05468	Hs.164502	ESTs	3.9
15	431071	AA491379		gb:aa65f06.r1 NCL_CGAP_GCB1 Homo sapiens	3.9
	436298	AW293496	Hs.180138	ESTs	3.9
	440356	AI933184	Hs.127922	ESTs, Moderately similar to S65657 alpha	3.9
	452768	AW069459	Hs.61539	ESTs	3.9
	455241	AW876249		gb:PM4-PT0019-131299-006-B05 PT0019 Homo	3.9
20	409070	AA063003	Hs.224560	ESTs	3.9
	409044	AI129586	Hs.33033	hypothetical protein FLJ14623	3.9
	419091	T85332	Hs.178294	ESTs	3.9
	422591	L07648	Hs.118530	MAX-interacting protein 1	3.9
	403188				3.9
25	418857	D10216	Hs.89394	POU domain, class 1, transcription factor	3.9
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	3.9
	436149	AI754308	Hs.159452	ESTs	3.9
	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.9
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.9
30	439818	AL360137	Hs.19934	Homo sapiens mRNA full length Insert cDN	3.9
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	3.9
	451221	AI949701	Hs.210589	ESTs	3.9
	455475	AW948126		gb:RCO-MT0013-280300-031-a12 MT0013 Homo	3.9
	433197	AB040889	Hs.281022	KIAA1456 protein	3.9
35	429881	T80112	Hs.192245	ESTs	3.9
	415598	AI433165	Hs.9856	ESTs	3.9
	431220	N52937	Hs.102679	ESTs	3.9
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.9
	424029	AB014594	Hs.137579	KIAA0694 gene product	3.9
40	404443				3.9
	407340	AA810168	Hs.284289	villig-associated protein VIT-1	3.9
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retrovirus	3.9
	412400	AW948066		gb:RCO-MT0012-290300-031-h10 MT0012 Homo	3.9
	427167	AI239607	Hs.99196	hypothetical protein MGC11324	3.8
45	438090	AA777534	Hs.191992	ESTs	3.8
	407938	AA905097	Hs.85050	phospholamban	3.8
	440454	AI733037	Hs.129990	ESTs	3.8
	417706	T90797	Hs.268823	ESTs	3.8
50	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	3.8
	407762	AW235638	Hs.29475	ESTs	3.8
	420727	H75701	Hs.99886	complement component 4-binding protein,	3.8
	417508	BE163512	Hs.180877	H3 histone, family 3B (H3.3B)	3.8
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	3.8
	425798	AA364002		gb:EST74529 Pineal gland II Homo sapiens	3.8
55	459429	AA278779	Hs.335696	EST	3.8
	430205	AB025904	Hs.235168	carbonic anhydrase XIV	3.8
	437458	AL390131	Hs.128751	Homo sapiens cDNA FLJ12235 fis, clone MA	3.8
	451073	AI758905	Hs.206063	ESTs	3.8
	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	3.8
60	429846	AB023021	Hs.226945	fucosyltransferase 9 (alpha (1,3) fucosyl	3.8
	444414	AW293214	Hs.8752	transmembrane protein 4	3.7
	402615				3.7
	410585	AW770523	Hs.337501	ESTs	3.7
	425168	R96366		gb:yq37d04.s1 Soares fetal liver spleen	3.7
65	449729	R72032	Hs.29235	ESTs	3.7
	459359	N99545		gb:za40a05.r1 Soares fetal liver spleen	3.7
	456443	AW967500	Hs.133543	ESTs	3.7
	439001	AF075068		gb:Homo sapiens full length Insert cDNA	3.7
	443657	R14973		gb:y42f10.s1 Soares fetal liver spleen	3.7
70	404193				3.7
	416379	N38857	Hs.203933	ESTs	3.7
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	3.7
	426603	AA382291		gb:EST95683 Testis I Homo sapiens cDNA 5	3.7
	412589	R28660	Hs.24305	ESTs	3.7
75	421037	AI684808	Hs.197653	ESTs	3.7
	427088	AA398085	Hs.142390	ESTs	3.7
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	3.7
	453375	AI990114	Hs.240091	ESTs	3.7
	435451	AF195420	Hs.303006	ESTs, Weakly similar to gamma-heregulin	3.7
80	451882	AI821324	Hs.100445	ESTs	3.7
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	3.7
	405001	U58196	Hs.296281	interleukin enhancer binding factor 1	3.7
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	3.7

5	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	3.7
	432781	NM_014133	Hs.278940	PRO0618 protein	3.7
	443773	AV646452	Hs.30941	calcium channel, voltage-dependent, beta	3.7
	406964	M21305		gb:human alpha satellite and satellite 3	3.7
	430682	AW971949	Hs.291252	ESTs, Weakly similar to ZN91_HUMAN ZINC	3.7
10	449804	AI535663	Hs.39379	ESTs	3.7
	411505	AF155659	Hs.70565	molybdenum cofactor synthesis 2	3.7
	430503	AA533574	Hs.152274	ESTs	3.7
	443305	AI050893	Hs.133318	ESTs	3.7
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	3.7
15	452280	AI911410	Hs.167224	ESTs	3.6
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	3.6
	406992	S82472		gb:bela -pol=DNA polymerase beta (exon a	3.6
	441416	AI990139	Hs.148809	ESTs	3.6
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	3.6
20	413998	AW103807	Hs.243933	ESTs	3.6
	440385	AA884283	Hs.192136	ESTs	3.6
	431673	AW971302	Hs.293233	ESTs	3.6
	401887				3.6
	404793				3.6
25	422054	AA322506		gb:EST25146 Cerebellum II Homo sapiens c	3.6
	432030	AI908400	Hs.143789	ESTs	3.6
	449645	AI961092	Hs.196155	ESTs	3.6
	404476				3.6
	449336	AL119995	Hs.15260	ESTs, Highly similar to AC007228 2 BC372	3.6
30	401200				3.6
	403937				3.6
	437918	AI761449	Hs.121629	ESTs	3.6
	443394	AI055865	Hs.133485	ESTs	3.6
	439107	AL046134	Hs.13944	adrenergic, beta, receptor kinase 2	3.6
35	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.6
	425403	AL023753	Hs.156406	Human DNA sequence from clone 1198H6 on	3.6
	436269	AA707472	Hs.190760	ESTs	3.6
	453823	AL137967		gb:DKFZp781D2315_r1 761 (synonym: hamy2)	3.6
	416394	H64111		gb:yr5703.r1 Soares fetal liver spleen	3.6
40	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	3.6
	439326	W07140	Hs.54721	ESTs	3.6
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
	435766	R11673	Hs.186498	ESTs	3.6
	448067	R68568	Hs.183373	src homology 3 domain-containing protein	3.6
45	441605	AA984647	Hs.128801	ESTs	3.5
	414400	X06948	Hs.897	Fc fragment of IgE, high affinity I, rec	3.5
	418405	AI868282	Hs.11898	ESTs, Highly similar to KIAA1370 protein	3.5
	437642	AL079309		gb:Homo sapiens mRNA full length insert	3.5
	450350	T97817	Hs.174880	ESTs	3.5
50	451704	AI755209	Hs.205616	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	459037	AW439497	Hs.290656	EST	3.5
	419247	S65791	Hs.89764	fragile X mental retardation 1	3.5
	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
	426724	AA383623	Hs.293616	ESTs	3.5
55	434273	AA913143	Hs.26303	ESTs	3.5
	438042	AW296971	Hs.255593	ESTs	3.5
	410500	R09442		gb:yr26c09.r1 Soares fetal liver spleen	3.5
	416154	Z46122		gb:HSC0V8031 normalized infant brain cDN	3.5
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomed)	3.5
60	454447	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	3.5
	458067	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.5
	444338	AI937026	Hs.146642	ESTs	3.5
	427687	AW003887	Hs.1570	histamine receptor H1	3.5
	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	3.5
65	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.5
	421515	Y11339	Hs.105352	GaINac alpha-2, 6-sialyltransferase I, I	3.5
	403515				3.5
	435793	AB037734	Hs.4993	KIAA1313 protein	3.5
	439953	AA918129	Hs.124638	ESTs	3.5
70	457620	AA602711	Hs.336753	EST	3.5
	442006	AW975183	Hs.292663	ESTs, Weakly similar to S72482 hypotheti	3.5
	453931	AL121278	Hs.25144	ESTs	3.5
	453128	AWD26516	Hs.31791	acylphosphatase 2, muscle type	3.5
	413468	BE504766		gb:hz40g01.x1 NCL_CGAP_GC6 Homo sapiens	3.5
75	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	3.5
	451065	AW295132	Hs.222231	ESTs, Weakly similar to granule cell mar	3.5
	444493	R59410	Hs.282094	ESTs, Moderately similar to I38022 hypot	3.5
	426447	AV655843	Hs.169919	electron-transfer-flavoprotein, alpha po	3.5
	410908	AA121686	Hs.10592	ESTs	3.5
80	440364	AA910460	Hs.128626	ESTs	3.5
	406190				3.5
	430762	AJ343652	Hs.105867	ESTs	3.5
	451182	D52562	Hs.296317	KIAA1789 protein	3.4
	432437	W07088	Hs.293685	ESTs	3.4
	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	3.4
	405970				3.4
	407676	AW064111	Hs.279823	ESTs	3.4

5	413141	BE166323		gb:QV4-HT0492-270100-086-e12 HT0492 Homo	3.4
	431418	X68242	Hs.252722	Hin-1	3.4
	431954	AK001974	Hs.272242	hypothetical protein FLJ11112	3.4
	459371	R20991		gb:yg06h01.r1 Soares infant brain 1NIB H	3.4
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	3.4
10	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	3.4
	420430	AI703192		gb:wd92h04.x1 NCL_CGAP_Lu24 Homo sapiens	3.4
	443921	AJ091310	Hs.134848	ESTs	3.4
	444453	AW379394	Hs.145126	ESTs	3.4
	443475	AJ066470	Hs.134482	ESTs	3.4
15	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.4
	453263	R91778	Hs.99369	ESTs	3.4
	410888	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo	3.4
	456303	AA224872	Hs.115088	ESTs	3.4
	431474	AL133990	Hs.190642	ESTs	3.4
20	439702	AW085525	Hs.134182	ESTs	3.4
	458797	AW001835	Hs.13323	hypothetical protein FLJ22059	3.4
	430140	AW296771	Hs.221999	ESTs	3.4
	423871	AA331906		gb:EST35805 Embryo, 8 week 1 Homo sapien	3.4
	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	3.4
25	449572	T05514		gb:EST03403 Fetal brain, Stratagene (cat	3.4
	431548	AI834273	Hs.9711	novel protein	3.4
	416182	NM_004354	Hs.79069	cyclin G2	3.4
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.4
	417663	R07483	Hs.180461	ESTs	3.3
30	405455			ESTs	3.3
	426235	AI631964	Hs.34447	ESTs	3.3
	439567	AI056618	Hs.134314	ESTs	3.3
	444848	AW451176	Hs.195954	ESTs	3.3
	451426	AW205003	Hs.208063	ESTs	3.3
35	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	3.3
	401626				3.3
	405780				3.3
	417991	AA731452	Hs.190008	ESTs	3.3
	443212	AW269515	Hs.102500	hypothetical protein FLJ20481	3.3
40	403356				3.3
	404518	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, l	3.3
	413581	BE150618		gb:RC3-HT0272-110100-013-c06 HT0272 Homo	3.3
	426701	AI968103	Hs.209461	Homo sapiens cDNA FLJ12836 fis, clone NT	3.3
	445510	AA946676	Hs.282824	ESTs	3.3
45	418663	AK001100	Hs.41690	desmocollin 3	3.3
	447617	AI400762	Hs.176675	ESTs	3.3
	448150	AI472167	Hs.302739	ESTs	3.3
	410140	AL134435	Hs.22269	neurexin 3	3.3
	443283	BE568610		gb:601342622F1 NIH_MGC_53 Homo sapiens c	3.3
50	454777	AW820027		gb:QV0-ST0294-240300-173-g04 ST0294 Homo	3.3
	410767	AJ001873	Hs.66185	Homo Sapiens mRNA, partial cDNA sequence	3.3
	433183	AF231338	Hs.222024	transcription factor BMAL2	3.3
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE	3.3
	438456	AA913381	Hs.190513	ESTs	3.3
55	411186	AW821257		gb:PM3-ST0307-231299-001-b11 ST0307 Homo	3.3
	411880	AW872477		gb:hm30103.x1 NCL_CGAP_Thy4 Homo sapiens	3.3
	433567	AF073299	Hs.103132	solute carter family 9 (sodium/hydrogen	3.3
	433805	AA706910	Hs.112742	ESTs	3.3
	409434	AF278761	Hs.131581	Homo sapiens testis transcript Y 7 (TTY7	3.3
60	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	3.3
	456555	AW592167	Hs.293299	ESTs	3.3
	419189	T95862	Hs.112318	6.2 kd protein	3.3
	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfam	3.3
	407995	AJ094748	Hs.100134	hypothetical protein FLJ12787	3.3
65	413200	AA127395	Hs.222414	ESTs	3.3
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.3
	416737	AF154335	Hs.79691	LIM domain protein	3.3
	428356	AL046991	Hs.10338	ESTs	3.3
	429216	AI369472	Hs.66407	ESTs	3.3
70	432488	AA551010	Hs.216640	ESTs	3.3
	433386	AW360833		gb:PM1-CT0243-201099-004-d08 CT0243 Homo	3.3
	400889				3.3
	416294	D86980	Hs.79170	KIAA0227 protein	3.3
	446190	AI279299	Hs.256584	ESTs	3.3
75	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	3.3
	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	3.3
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kd	3.3
	443357	AW071349	Hs.215937	ESTs	3.3
	446645	AI336596	Hs.156294	ESTs	3.3
80	434294	AJ271379	Hs.76194	ribosomal protein S5	3.3
	452372	AI885742	Hs.228474	ESTs	3.2
	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	3.2
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	3.2
	430548	AW450575	Hs.163203	ESTs, Weakly similar to B34087 hypothi	3.2
	427119	AW880562	Hs.114574	ESTs	3.2
	437073	AI885608	Hs.94122	ESTs	3.2
	437845	AA769578	Hs.90488	ESTs	3.2

	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	414394	A1904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.2
	417175	R44558	Hs.94002	ESTs	3.2
	456536	AW135986	Hs.257859	ESTs	3.2
5	401132				3.2
	407764	BE008347		gb:CM0-BN0154-080400-325-h04 BN0154 Homo	3.2
	426004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	450947	A1745400	Hs.204662	ESTs	3.2
	456605	A1827786	Hs.259044	ESTs	3.2
10	452879	AW905328	Hs.180842	ribosomal protein L13	3.2
	454754	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	3.2
	429479	AA453468	Hs.99333	ESTs	3.2
	448090	A1608821	Hs.270289	ESTs	3.2
	401324				3.2
15	404731				3.2
	419936	A1792788		gb:ol91d05.y5 NCI_CGAP_Kid5 Homo sapiens	3.2
	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	3.2
	433990	AA889328	Hs.112950	ESTs	3.2
	415239	R42608	Hs.139270	ESTs	3.2
20	418878	W20090	Hs.6616	ESTs	3.2
	438079	R09664	Hs.191223	ESTs	3.2
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	3.2
	457460	A1143312	Hs.129206	casein kinase 1, gamma 3	3.2
	454145	AA046872	Hs.62798	ESTs	3.2
25	446577	AB040933	Hs.15420	KIAA1500 protein	3.2
	430664	AW969834	Hs.303303	ESTs	3.2
	404588				3.2
	407834	AW084991	Hs.26100	ESTs	3.2
30	413087	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
	440790	AW593050	Hs.128580	ESTs	3.2
	452081	AW958859	Hs.7514	Homo sapiens cDNA FLJ12141 fis, clone MA	3.2
	421916	R34441	Hs.101007	Homo sapiens cDNA: FLJ23546 fis, clone L	3.2
	419261	X07876	Hs.89791	wingless-type MMTV integration site fam1	3.2
	419340	AA236590	Hs.87530	ESTs	3.2
35	444771	AB023201	Hs.11912	KIAA0984 protein	3.2
	445233	AV653034	Hs.297559	ESTs	3.2
	457030	A1301740	Hs.173381	dihydropyrimidinase-like 2	3.2
	408334	AW514652	Hs.321637	ESTs	3.2
40	410085	AA428482	Hs.58589	glycogenin 2	3.2
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	3.2
	403623				3.2
	432223	AA333283	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	3.2
	444050	AW138295	Hs.135024	ESTs	3.2
45	421036	AA810560	Hs.303577	ESTs	3.2
	401459				3.1
	404404				3.1
	450438	A1696071	Hs.253800	ESTs	3.1
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibitor	3.1
50	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypothel	3.1
	441274	AW593781	Hs.131357	ESTs	3.1
	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	3.1
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
	400816				3.1
55	410307	AF022913	Hs.62187	phosphatidylinositol glycan, class K	3.1
	431906	AW328038	Hs.37486	ESTs	3.1
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
	450271	A1693900	Hs.200920	ESTs	3.1
	415811	AA450191	Hs.172963	hypothetical protein FLJ14624	3.1
	415273	Z39840	Hs.22229	ESTs	3.1
60	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
	451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.1
	446364	AB006624	Hs.14912	KIAA0286 protein	3.1
	436638	A1271945	Hs.134984	ESTs	3.1
	418079	R40058	Hs.6911	ESTs	3.1
65	448466	A1522109	Hs.171066	ESTs	3.1
	448835	BE277929	Hs.11081	UBX domain-containing 2	3.1
	415046	R40018	Hs.56400	ESTs	3.1
	448134	A1470790	Hs.34494	ESTs	3.1
	456027	BE327387	Hs.13913	KIAA1577 protein	3.1
70	458023	AW978161	Hs.268555	5'-3' exonuclease 2	3.1
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.1
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	3.1
	414884	R54418	Hs.183745	hypothetical protein FLJ13456	3.1
	449138	AW294215	Hs.195631	ESTs	3.1
75	455756	BE079307		gb:RC1-BT0623-120200-011-g09 BT0623 Homo	3.1
	428170	H05530	Hs.12565	ESTs	3.1
	429878	AA460188	Hs.127263	ESTs	3.1
	455000	AW850283	Hs.324429	Homo sapiens cDNA FLJ14015 fis, clone HE	3.1
	438369	T77886	Hs.83428	nuclear factor of kappa light polypeptid	3.1
80	415840	R15955	Hs.21758	ESTs	3.1
	444955	AW002844	Hs.148641	ESTs	3.1
	436020	AA778177	Hs.121724	ESTs	3.1
	453051	AW196690	Hs.224269	ESTs	3.1

	425178	H16097	Hs.161027	ESTs	3.1
	402145				3.1
	410685	AA497117	Hs.129600	ESTs, Moderately similar to ALU1_HUMAN A	3.1
	449238	AA428229	Hs.331561	muscle-specific RING-finger protein 3	3.1
5	456737	BE247203	Hs.124831	CGI-57 protein	3.1
	438214	H06076	Hs.26320	TRABID protein	3.1
	436250	AY004867	Hs.85844	neurotrophic tyrosine kinase, receptor,	3.1
	411622	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp5648176 (fr	3.0
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
10	449357	AI076363	Hs.288806	Homo sapiens cDNA FLJ11778 fis, clone HE	3.0
	418950	T78517	Hs.13941	ESTs	3.0
	431508	NM_012481	Hs.182979	ribosomal protein L12	3.0
	405090				3.0
	445409	AI949081	Hs.147862	ESTs	3.0
15	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.0
	455577	BE006341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	3.0
	408235	AA053381	Hs.75969	proline-rich protein with nuclear target	3.0
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	3.0
	452073	AA625150	Hs.82098	ESTs	3.0
20	427050	AA397789	Hs.161803	ESTs	3.0
	427244	AA402400	Hs.178045	ESTs	3.0
	448405	AW207634	Hs.170849	ESTs	3.0
	433767	AA609245		gb:af13a11.s1 Soares_testis_NHT Homo sap	3.0
	421376	AA287948	Hs.134110	ESTs	3.0
25	441519	AA972740	Hs.127092	ESTs	3.0
	404367				3.0
	453502	AL039786	Hs.21273	transcription factor NYD-sp10	3.0
	421948	L42583	Hs.334309	keratin 6A	3.0
	438165	AA779344	Hs.138136	ESTs, Weakly similar to 1510254A L1 repe	3.0
30	400608				3.0
	404042				3.0
	405229				3.0
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	3.0
	415452	F09134	Hs.12839	ESTs	3.0
35	430371	D87466	Hs.240112	KIAA0276 protein	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
	455851	BE146879		gb:QV4-HT0222-261099-014-c11 HT0222 Homo	3.0
	429014	AI800518	Hs.118158	ESTs	3.0
	405605				3.0
40	400227				3.0
	439037	AF075084		gb:Homo sapiens full length insert cDNA	3.0
	439593	AI741816	Hs.125897	ESTs	3.0
	427533	R36022	Hs.179566	hypothetical protein FLJ22624	3.0
45	418355	L42563	Hs.11165	ATPase, H+K+ transporting, nongastric,	3.0
	433536	AI732163	Hs.188909	ESTs, Weakly similar to alternatively sp	3.0
	448446	AI521251	Hs.171030	ESTs	3.0
	449623	C00719	Hs.120440	EST	3.0
	445568	H00918	Hs.268744	KIAA1796 protein	3.0
	440448	AA885428	Hs.125646	ESTs	3.0
50	428201	AA424158	Hs.206461	ESTs	3.0
	444148	AW003204	Hs.151167	ESTs	3.0
	447972	AL137275	Hs.20137	hypothetical protein DKFZp434P0116	3.0
	432584	AA928829	Hs.47099	hypothetical protein FLJ21212	3.0
	440925	AW511090	Hs.130419	ESTs	3.0
55	428398	AI249368	Hs.98558	ESTs	3.0
	415913	H70302		gb:yr95f07.r1 Soares fetal liver spleen	3.0
	418145	AF121260	Hs.83577	cysteine and glycine-rich protein 3 (car	3.0
	413252	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	3.0
	400335	Y13187	Hs.248067	Homo sapiens dmd gene, intron 11	3.0
60	426132	AA370501		gb:EST82261 Prostate gland I Homo sapien	3.0
	436938	AW139680	Hs.161393	ESTs	3.0
	437980	R50393	Hs.278436	KIAA1474 protein	3.0
	455955	BE162394		gb:PM2-HT0451-170100-004-a08 HT0451 Homo	3.0
	414899	AW975433	Hs.36288	ESTs	2.9
65	403786				2.9
	430187	AI799909	Hs.158989	ESTs	2.9
	451700	AI470262	Hs.29553	ESTs	2.9
	455866	BE149024		gb:CM0-HT0249-291099-084-c04 HT0249 Homo	2.9
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	2.9
70	457041	AA399018	Hs.250835	ESTs	2.9
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	2.9
	422336	AI761322	Hs.115285	dihydrolipoamide S-acetyltransferase (E2	2.9
	451664	AA889081	Hs.153952	5' nucleotidase (CD73)	2.9
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.9
75	455249	AW876538		gb:RC3-PT0028-190100-012-b06 PT0028 Homo	2.9
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	2.9
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (fr	2.9
	405302				2.9
	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
80	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	423119	AA322201	Hs.131976	ESTs	2.9
	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
	431980	AA523696	Hs.324507	hypothetical protein FLJ20986	2.9

	425793	AA363946	Hs.20969	ESTs	2.9
	401462				2.9
	458817	AI522129	Hs.173119	ESTs	2.9
5	422163	AF027208	Hs.112360	prominin (mouse)-like 1	2.9
	419875	AA853410	Hs.93557	proenkephalin	2.9
	423047	NM_005323	Hs.123064	H1 histone family, member T (testis-spec	2.9
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	2.9
	401368				2.9
10	418531	R96760	Hs.183758	ESTs	2.9
	447290	AJ476732	Hs.263912	ESTs	2.9
	441143	AI027604	Hs.159650	ESTs	2.9
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	2.9
	405783				2.9
15	444459	AI680624	Hs.148676	ESTs	2.9
	402112	R58624	Hs.2186	eukaryotic translation elongation factor	2.9
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.9
	444827	R09764	Hs.20416	ESTs	2.9
	451195	U10492	Hs.438	mesenchyme homeo box 1	2.9
20	411417	AW845481		gb:MR1-CT0056-201199-008-b04 CT0056 Homo	2.9
	418343	AA216372	Hs.159501	ESTs	2.9
	431595	AA508196		gb:nh6007.s1 NCL_CGAP_Pr8 Homo sapiens	2.9
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	2.9
	455699	BE068121		gb:CM1-BT0368-051299-060-a02 BT0368 Homo	2.9
	459440	BE048054		gb:tz46c03.y1 NCL_CGAP_Brn52 Homo sapien	2.9
25	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
	423492	AF020761	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homo	2.9
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.9
	437913	AI140825	Hs.121623	ESTs	2.9
30	443185	NM_006134	Hs.284142	chromosome 21 open reading frame 4	2.9
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
	426803	AA362568	Hs.179747	ecotropic viral integration site 5	2.9
	437183	AI928184	Hs.122011	ESTs	2.9
	420879	N31165	Hs.238837	ESTs, Weakly similar to S43603 RNA bindi	2.9
35	442726	AW136066	Hs.19145	ESTs	2.9
	456189	H91010	Hs.44940	ESTs	2.9
	441115	R69910	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	2.9
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2.9
40	415628	F13080		gb:HSC3ID041 normalized infant brain cDN	2.9
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (f	2.9
	443246	T75157	Hs.337603	ESTs, Weakly similar to T08580 hypotheti	2.9
	450877	AJ799608	Hs.29178	ESTs	2.9
	439063	AF085922	Hs.113968	ESTs	2.9
	401526				2.9
45	408751	N91553	Hs.258343	ESTs	2.9
	417320	AA195667	Hs.86022	ESTs	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
	444125	AI124882	Hs.118121	ESTs	2.9
	452148	AF007143	Hs.28205	Homo sapiens clone 23738 mRNA sequence	2.9
50	453901	BE065902		gb:RC2-BT0318-150200-011-b09 BT0318 Homo	2.9
	452589	BE159915	Hs.61406	ESTs, Weakly similar to 2004399A chromos	2.8
	403011				2.8
	436154	AA764950	Hs.119898	ESTs	2.8
	408221	AA912183	Hs.47447	ESTs	2.8
55	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	2.8
	415399	T26994	Hs.177198	ESTs	2.8
	441817	AW969706	Hs.293332	ESTs	2.8
	443556	AA256769	Hs.94949	methylmalonyl-CoA epimerase	2.8
	455092	BE152428		gb:CAM0-HT0323-151299-126-b04 HT0323 Homo	2.8
60	439703	AF086538	Hs.196245	ESTs	2.8
	411024	BE062590		gb:QV1-BT0260-261099-023-f05 BT0260 Homo	2.8
	414546	BE379492		gb:601236215F1 NIH_MGC_44 Homo sapiens c	2.8
	434715	BE005346	Hs.116410	ESTs	2.8
	407594	AW057584	Hs.160681	ESTs	2.8
	439235	N45513	Hs.46608	ESTs	2.8
65	453736	AL118674	Hs.34871	zinc finger homeobox 1B	2.8
	404967				2.8
	437783	AI683150	Hs.201550	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
	412887	BE007420		gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.8
70	426942	AA393551	Hs.97450	ESTs	2.8
	403513				2.8
	419077	AA233885	Hs.164526	ESTs	2.8
	421823	N40850	Hs.28625	ESTs	2.8
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	2.8
	451007	H38108	Hs.32759	ESTs	2.8
75	407803	AW081681	Hs.269064	ESTs, Weakly similar to T42689 hypotheti	2.8
	409642	AW450809	Hs.257347	ESTs	2.8
	439492	AF086310	Hs.103159	ESTs	2.8
	420814	AA721156	Hs.190440	ESTs	2.8
80	449508	AK001566	Hs.23618	hypothetical protein FLJ10704	2.8
	428350	AW873520	Hs.112017	GE36 gene	2.8
	405456				2.8
	442459	AJ264628	Hs.125428	ESTs	2.8
	415763	Z42285	Hs.5181	proliferation-associated 2G4, 38kD	2.8

5	428532	AF157326	Hs.184786	TBP-interacting protein	2.8
	436720	AW975902		gb:EST388011 MAGE resequences, MAGN Homo	2.8
	449539	W80363	Hs.58446	ESTs	2.8
	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.8
	408749	H65489	Hs.250659	ESTs	2.8
10	404652				2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	424960	BE245380	Hs.153952	5' nucleotidase (CD73)	2.8
	402131				2.8
	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.8
15	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
	444217	AV648751	Hs.282395	ESTs	2.8
	449579	AW207260	Hs.134014	ESTs, Weakly similar to T46425 hypotheti	2.8
	412323	AW937143		gb:PM1-DT0041-281299-001-R01 DT0041 Homo	2.8
	418912	NM_000685	Hs.89472	angiotensin receptor 1	2.8
20	433513	AI566356	Hs.171437	ESTs	2.8
	448912	D83781	Hs.22559	KIAA0197 protein	2.8
	451496	AW503407		gb:UI-HF-BN0-akw-d-11-Q-ULr1 NIH_MGC_50	2.8
	420273	AI652864	Hs.197257	ESTs	2.8
	451949	U03884	Hs.463	potassium inwardly-rectifying channel, s	2.8
25	420756	AA411800	Hs.189900	ESTs	2.8
	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
	425012	T77666	Hs.92414	Homo sapiens cDNA: FLJ22030 fis, clone H	2.8
	441609	AA946764	Hs.133460	ESTs	2.8
	448870	BE181783	Hs.175358	ESTs, Weakly similar to A47582 B-cell gr	2.8
30	451206	H86228	Hs.271780	ESTs, Weakly similar to I38022 hypotheti	2.8
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J11119	2.8
	416192	NM_005036	Hs.998	peroxisome proliferative activated recep	2.8
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	2.8
	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
35	459450	AA426429	Hs.98463	EST	2.7
	424188	AW954552	Hs.142634	zinc finger protein	2.7
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	2.7
	427443	AA402713	Hs.97872	ESTs	2.7
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.7
40	413091	BE065063		gb:RC1-BT0313-110500-017-e02 BT0313 Homo	2.7
	421003	T72080	Hs.95667	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
	445611	AW418497	Hs.145583	ESTs	2.7
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	2.7
45	408243	Y00787	Hs.624	interleukin 8	2.7
	407308	H67394	Hs.331325	ESTs, Weakly similar to I38022 hypotheti	2.7
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	2.7
	404587	M99587	Hs.104134	homeo box (H6 family) 1	2.7
	410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.7
50	416431	AW384459	Hs.172004	titin	2.7
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
	417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain	2.7
	427134	AA398409	Hs.173561	EST	2.7
	428137	AA421792	Hs.170999	ESTs	2.7
55	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.7
	441218	BE327561	Hs.202345	ESTs	2.7
	440911	AA909536	Hs.143562	ESTs	2.7
	411131	AW819212		gb:CM1-ST0283-071299-061-c07 ST0283 Homo	2.7
	438802	AI167149	Hs.123374	ESTs, Weakly similar to mariner transpos	2.7
60	441191	AI693930	Hs.148816	ESTs	2.7
	403776				2.7
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.7
	427839	AA608823	Hs.98244	ESTs	2.7
	429905	AL080128	Hs.225998	DKFZP434C153 protein	2.7
65	449396	BE169100	Hs.195029	ESTs	2.7
	450777	AA255646	Hs.60478	ESTs, Moderately similar to S47073 finge	2.7
	458043	AW979009	Hs.326108	ESTs	2.7
	405523				2.7
	434849	AW292765	Hs.8053	ESTs	2.7
70	452755	AW138937	Hs.213436	ESTs, Weakly similar to A34087 hypotheti	2.7
	438055	AA776655	Hs.270942	ESTs	2.7
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	2.7
	405738				2.7
	417806	AI867277	Hs.183733	ESTs	2.7
75	430698	AA492071		gb:ne97b04.s1 NCL_CGAP_Kd1 Homo sapiens	2.7
	441969	AI733386	Hs.129194	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	446092	N33522	Hs.145894	ESTs	2.7
	456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.7
	413617	BE155373	Hs.279518	amyloid beta (A4) precursor-like protein	2.7
80	444931	AV652066	Hs.75113	general transcription factor IIIA	2.7
	412236	AW902583		gb:QV3-NN1024-260400-171-f10 NN1024 Homo	2.7
	453264	AA034137	Hs.271955	ESTs	2.7
	438370	AA843242	Hs.48523	ESTs	2.7
	406092				2.7
	454874	AW836407	Hs.270143	extracellular glycoprotein EMILIN-2 prec	2.7
	455880	BE153208		gb:PM0-HT0335-050400-007-F10 HT0335 Homo	2.7
	459275	AI808913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.7

	411987	AA375975	Hs.183380	ESTs, Moderately similar to ALLU8_HUMAN A	2.7
	441884	AW172630	Hs.144884	ESTs	2.7
	416211	R14625		gb:yg45c03.r1 Soares infant brain 1N1B H	2.7
5	433128	AB021923	Hs.23367	EST-YD1 protein	2.7
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	2.7
	453696	AI989482	Hs.146286	kinesin family member 13A	2.7
	456208	AW299698	Hs.334625	Homo sapiens cDNA FLJ14890 fis, clone PL	2.7
	425876	AW005887	Hs.234058	ESTs	2.7
10	450458	AA009926		gb:z107e05.r1 Soares_fetal_liver_spleen_	2.7
	406603				2.7
	410181	AA468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
	410871	D78367	Hs.66739	keratin 12 (Meesmann corneal dystrophy)	2.7
	412706	R97106	Hs.167546	ESTs	2.7
	422897	AA679784	Hs.4290	ESTs	2.7
15	436329	AI798750	Hs.163960	Homo sapiens heat shock transcription fa	2.7
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	2.7
	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	2.7
	419296	AA236115	Hs.120785	ESTs	2.7
20	454747	AW818535		gb:RC1-ST0278-140300-016-f05 ST0278 Homo	2.7
	455791	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.7
	411409	AW844803		gb:RC3-CN0056-170300-015-f08 CN0056 Homo	2.7
	426662	AA879474	Hs.122710	ESTs	2.7
	400268				2.7
25	438782	AA828380	Hs.126733	ESTs	2.7
	443764	F23283		gb:HSPD22980 HM3 Homo sapiens cDNA clone	2.7
	412486	AF210650	Hs.150858	NAG19 protein	2.7
	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	2.7
	457900	AW976692	Hs.291665	ESTs	2.7
30	417376	AA253314	Hs.154103	LIM protein (similar to rat protein kina	2.7
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.7
	435608	AW183971	Hs.250896	ESTs	2.7
	413627	BE182082	Hs.246973	ESTs	2.7
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	2.7
35	445660	AI702668	Hs.201955	ESTs	2.7
	441396	AW293677	Hs.186890	ESTs	2.6
	452046	AB018345	Hs.27657	KIAA0802 protein	2.6
	454936	AW846082		gb:MR3-CT0176-081099-002-d01 CT0176 Homo	2.6
40	454434	AA083558	Hs.261286	ESTs	2.6
	436888	AI942357	Hs.187870	ESTs	2.6
	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.6
	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 Integrin	2.6
	416890	H84078	Hs.108551	ESTs	2.6
	436471	AA719813	Hs.117662	ESTs	2.6
45	425659	AK000590	Hs.158836	hypothetical protein FLJ20583	2.6
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	2.6
	458257	U48351	Hs.201219	ESTs, Weakly similar to S18946 ultra hig	2.6
	455544	AW993880		gb:RC3-BN0034-240400-017-d09 BN0034 Homo	2.6
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
50	452821	AW471181	Hs.160874	ESTs	2.6
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	2.6
	429864	AA460039	Hs.286	ribosomal protein L4	2.6
	456273	AF154846	Hs.1148	zinc finger protein	2.6
	402603				2.6
55	411162	AW819944		gb:QV0-ST0294-240300-172-e03 ST0294 Homo	2.6
	420621	AA278808		gb:z79c09.r1 NCL_CGAP_GC81 Homo sapiens	2.6
	435113	AA665469	Hs.117136	ESTs	2.6
	438188	AA779975	Hs.128859	ESTs	2.6
	438295	AI394151	Hs.37932	ESTs	2.6
60	450181	H05254	Hs.201198	ESTs	2.6
	433764	AW753676	Hs.39982	ESTs	2.6
	433229	AB040925	Hs.91625	KIAA1492 protein	2.6
	443718	AI083580	Hs.221373	ESTs	2.6
	418246	AI472179	Hs.121276	ESTs, Weakly similar to R5HU7A ribosomal	2.6
65	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	2.6
	400365	Y10259	Hs.274501	H.sapiens ACTH receptor mRNA 3'UTR	2.6
	419318	AW969742	Hs.291005	ESTs	2.6
	428527	AI902398	Hs.34492	Cyt19 protein	2.6
	404414				2.6
70	446444	AI743737	Hs.24370	ESTs	2.6
	411354	AW992424	Hs.288141	hypothetical protein MGC3156	2.6
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	2.6
	418310	AA814100	Hs.86693	ESTs	2.6
	454481	AW794878	Hs.314230	ESTs, Highly similar to clock (H.sapiens	2.6
75	441216	BE299830	Hs.192908	ESTs	2.6
	438257	AW474419	Hs.224794	ESTs	2.6
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	419505	AA243660	Hs.143061	ESTs	2.6
	417595	R07343	Hs.226823	ESTs, Moderately similar to I54374 gene	2.6
80	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.6
	444517	AI939339	Hs.146883	ESTs	2.6
	454887	AW835924		gb:PM1-LT0018-250200-002-e09 LT0018 Homo	2.6
	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6

5	457630	AI680803	Hs.112627	ESTs	2.6
	424210	T71397	Hs.222707	KIAA1718 protein	2.6
	447748	AA22023	Hs.161338	ESTs	2.6
	411970	AA099142	Hs.13804	hypothetical protein dJ462023.2	2.6
	441233	AA972965	Hs.135568	ESTs	2.6
10	400706				2.6
	436033	H75391	Hs.255748	ESTs	2.6
	440836	AW370882	Hs.222080	ESTs	2.6
	431086	AI829692	Hs.211561	ESTs	2.6
	455110	BE154505		gb:PM0-HT0343-281299-003-e06 HT0343 Homo	2.6
15	455678	BE066007		gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.6
	413088	BE064962		gb:RC1-BT0313-130400-016-c02 BT0313 Homo	2.6
	436196	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, clone HE	2.6
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.6
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	2.6
20	442690	AI014727	Hs.160047	ESTs, Weakly similar to B28096 line-1 pr	2.6
	441700	AA233556	Hs.126908	hypothetical protein FLJ12994	2.6
	410286	AI739159	Hs.61898	DKFZP586N2124 protein	2.6
	403271				2.6
	429761	AI276780	Hs.135173	ESTs	2.6
25	437085	AA743935	Hs.202329	ESTs	2.6
	450822	AW771860	Hs.205130	ESTs	2.6
	457506	AF131757	Hs.274533	Homo sapiens clone 24926 mRNA sequence	2.6
	416585	X54162	Hs.79386	leiomodrin 1 (smooth muscle)	2.6
	430357	AW975789	Hs.165607	ESTs	2.6
30	417249	NS8198	Hs.182898	ESTs	2.6
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	2.6
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	2.6
	440460	H92571	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
	446302	AI285848	Hs.149757	ESTs	2.6
35	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.6
	428944	AA780181	Hs.41182	Homo sapiens DC47 mRNA, complete cds	2.6
	419647	AA348947	Hs.91816	hypothetical protein	2.6
	455500	AW963582		gb:EST375655 MAGE resequences, MAGH Homo	2.6
	419435	AI200540	Hs.14877	ESTs, Weakly similar to (define not ava	2.6
40	452450	AW854891	Hs.194720	ATP-binding cassette, sub-family G (WHIT	2.6
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	2.6
	436421	AI678031	Hs.122813	ESTs, Weakly similar to ZN22_HUMAN ZINC	2.6
	447505	AL049266	Hs.18724	Homo sapiens mRNA: cDNA DKFZp564F093 (fr	2.6
	419758	U31973	Hs.93173	phosphodiesterase 6C, cGMP-specific, con	2.6
45	426698	AA394104	Hs.97489	ESTs	2.6
	446861	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.5
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	2.5
	447624	AI640326	Hs.62713	ESTs	2.5
	411736	AW859089		gb:MR1-CT0350-150200-002-d02 CT0350 Homo	2.5
50	416334	H53139	Hs.36271	ESTs	2.5
	446818	AI342668	Hs.279765	ESTs	2.5
	454836	AW833711		gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
	442278	AI733477	Hs.166313	ESTs	2.5
	453393	AW956392	Hs.110376	ESTs	2.5
55	420854	AW296927		gb:UL-H-BW0-ajc-c-07-0-ULs1 NCI_CGAP_Su	2.5
	408729	AA195764	Hs.72639	ESTs	2.5
	455675	BE065984		gb:RC3-BT0319-120200-014-a06 BT0319 Homo	2.5
	411660	AW855718		gb:RC1-CT0279-070100-021-a06 CT0279 Homo	2.5
	455252	AW876627		gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
60	409156	N76186	Hs.173518	M-phase phosphoprotein homolog	2.5
	423175	W27595	Hs.18653	hypothetical protein FLJ14627	2.5
	430291	AV660345	Hs.238126	CGI-49 protein	2.5
	401785				2.5
	402369				2.5
65	439079	AF085937	Hs.38348	ESTs	2.5
	412566	AW962574		gb:EST374647 MAGE resequences, MAGG Homo	2.5
	411463	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	2.5
	413758	BE162391		gb:PM2-HT0451-090100-002-f04 HT0451 Homo	2.5
	404988				2.5
70	409446	AI561173	Hs.67688	ESTs	2.5
	412613	AA853507	Hs.285711	hypothetical protein FLJ13089	2.5
	417909	R35614		gb:yg66e08.r1 Soares infant brain 1NIB H	2.5
	454743	AW818456	Hs.79347	KIAA0211 gene product	2.5
	406364				2.5
75	404108				2.5
	411934	AW876538		gb:RC3-PT0028-190100-012-b06 PT0028 Homo	2.5
	415747	AA381209		gb:EST94257 Activated T-cells I Homo sap	2.5
	443526	AW792804	Hs.134002	ESTs	2.5
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	2.5
80	454864	AW835775		gb:QV4-LT0016-240200-110-d04 LT0016 Homo	2.5
	458771	AW295151	Hs.163612	ESTs	2.5
	414349	BE512968		gb:601172296F1 NIH_MGC_15 Homo sapiens c	2.5
	426589	AW954460		gb:EST366530 MAGE resequences, MAGC Homo	2.5
	429515	AL031228	Hs.204370	DNA segment on chromosome 6 (unique, pse	2.5
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	2.5
	411772	BE170301		gb:QV4-HT0536-040500-193-f05 HT0536 Homo	2.5
	434784	AA649051	Hs.164007	ESTs	2.5

5	429322	D85984	Hs.199243	KIAA0231 protein	2.5
	446252	AI283125	Hs.150009	ESTs	2.5
	453361	AA035197	Hs.107375	ESTs	2.5
	455275	AW977806		gb:EST389810 MAGE resequences, MAGO Homo	2.5
	449410	AA001356	Hs.18159	ESTs	2.5
10	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	2.5
	458861	AI630223		gb:ad06g08.r1 Proliferating Erythroid Ce	2.5
	416944	NZ2809		gb:yw41e07.s1 Weizmann Olfactory Epithel	2.5
	423010	W25436	Hs.90725	ESTs, Moderately similar to I38022 hypot	2.5
	412505	AA974491	Hs.21734	ESTs	2.5
15	446399	AI298405	Hs.150080	ESTs	2.5
	412139	BE044976		gb:hn25b10.x1 NCL_CGAP_Thy7 Homo sapiens	2.5
	403691				2.5
	424025	AI701852	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, clone L	2.5
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	2.5
20	422342	AA309272		gb:EST180209 Liver, hepatocellular card	2.5
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.5
	457770	BE065030	Hs.124179	ESTs	2.5
	427731	AA411750	Hs.20943	ESTs	2.5
	426920	AA393351	Hs.132121	ESTs	2.5
25	427794	AA709186	Hs.282963	ESTs	2.5
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	2.5
	454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	2.5
	414550	BE379808		gb:601159567T1 NIH_MGC_53 Homo sapiens c	2.5
	436391	AJ227892	Hs.146274	ESTs	2.5
30	401989				2.5
	423346	AI267677	Hs.127416	synaptotagmin 1	2.5
	444905	AW135863	Hs.209228	ESTs	2.5
	424539	L02911	Hs.150402	activin A receptor, type I	2.5
	400861				2.5
35	458426	AI084514	Hs.249587	ESTs	2.5
	429520	AA160142	Hs.205058	hypothetical protein FLJ20075	2.5
	403568				2.5
	430692	X80240		gb:H.sapiens endogenous retrovirus HERV-	2.5
	451078	AI927694	Hs.204470	ESTs	2.5
40	424560	AA158727	Hs.150555	protein predicted by clone 23733	2.5
	427888	AA417088	Hs.137598	ESTs	2.5
	425541	AA359119		gb:EST68172 Fetal lung II Homo sapiens c	2.5
	422840	U44059	Hs.121481	thyrotrophic embryonic factor	2.5
	404708				2.5
45	405008				2.5
	453772	BE281431	Hs.16323	Homo sapiens, Similar to G antigen 8, cl	2.5
	411036	AA857218	Hs.297007	membrane-bound transcription factor prot	2.5
	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	2.5
	449311	AI657014		gb:tt49a12.x1 NCL_CGAP_GC8 Homo sapiens	2.5
50	454277	AW295069	Hs.31743	ESTs, Weakly similar to Z157_HUMAN ZINC	2.5
	454566	AW807605		gb:MR4-ST0098-120100-001-b05 ST0098 Homo	2.5
	454597	AW809648		gb:MR4-ST0124-261099-015-d01 ST0124 Homo	2.5
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	2.4
	407851	NM_014496	Hs.40434	ribosomal protein S6 kinase, 90kD, polyp	2.4
55	446554	AA151730	Hs.301789	nrd1x (nucleoside diphosphate linked moi	2.4
	452850	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-in	2.4
	406468				2.4
	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	2.4
	408617	R61736	Hs.124128	ESTs	2.4
60	409627	AW997628	Hs.313637	ESTs	2.4
	416665	H72974		gb:yu28a10.s1 Soares fetal liver spleen	2.4
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.4
	418994	AA296620	Hs.89546	selectin E (endothelial adhesion molecu	2.4
	428709	BE268717	Hs.104916	hypothetical protein FLJ21940	2.4
65	429654	AI435046	Hs.164318	ESTs	2.4
	432253	AW090822	Hs.274174	transcription elongation factor (SIII) a	2.4
	439786	AV652707	Hs.33756	Homo sapiens mRNA full length insert cDN	2.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	2.4
	453052	R63050	Hs.223813	ESTs	2.4
70	454137	AW500340	Hs.313876	ESTs, Weakly similar to I38022 hypotheti	2.4
	459608	AL119471		gb:DKFZp761M141_r1 761 (synonym: hamy2)	2.4
	452843	AI796769	Hs.208320	ESTs	2.4
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN A	2.4
	449695	AA164569	Hs.34550	ESTs	2.4
75	431532	AI537817	Hs.270311	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4
	425967	NM_007159	Hs.4007	Sarcolemmal-associated protein	2.4
	400641				2.4
	430982	R17432	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	2.4
	432808	NM_015985	Hs.278973	angiotensin-3	2.4
80	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	2.4
	411561	H81164	Hs.285017	hypothetical protein FLJ21799	2.4
	421083	AA283628	Hs.298016	ESTs, Weakly similar to I38022 hypotheti	2.4
	423513	AF035960	Hs.129719	transglutaminase 5	2.4
	434627	AI221894	Hs.39311	ESTs	2.4
80	435663	AI023707	Hs.134273	ESTs	2.4
	455879	BE153275		gb:PMO-HT0335-180400-008-e11 HT0335 Homo	2.4
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	2.4

	409041	AB033025	Hs.50081	KIAA1199 protein	2.4
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	2.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.4
5	448889	BE140902		gb:IL1-HT0028-240699-001-C11 HT0028 Homo	2.4
	439481	AF086294	Hs.125844	ESTs	2.4
	412074	S74683	Hs.73139	ADP-ribosyltransferase 1	2.4
	403053	R58624	Hs.2186	eukaryotic translation elongation factor	2.4
	409298	AA070211		gb:zm68c04.s1 Stratagene neuroepithelium	2.4
10	411322	AW887330	Hs.172405	cell division cycle 27	2.4
	447640	AI417187		gb:lg75g11.x1 Soares_NhHMPu_S1 Homo sapi	2.4
	447849	AI538147	Hs.164277	ESTs	2.4
	458763	AI693417	Hs.293309	ESTs	2.4
	404538				2.4
	413986	Z43567		gb:HSC1FC021 normalized infant brain cDN	2.4
15	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	2.4
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	2.4
	408238	W95901		gb:ze43d11.r1 Soares retina N2b4HR Homo	2.4
	436747	AW977192	Hs.291343	ESTs	2.4
	437048	AA743240	Hs.91582	ESTs	2.4
20	413143	BE067232		gb:PM3-BT0347-170200-001-b05 BT0347 Homo	2.4
	404561				2.4
	444009	AI380792	Hs.135104	ESTs	2.4
	400250				2.4
	403891				2.4
25	417002	T79613	Hs.14613	ESTs	2.4
	439446	AI927629	Hs.57873	ESTs	2.4
	441227	AW295407	Hs.128893	ESTs	2.4
	445038	AI635444	Hs.143917	dJ467N11.1 protein	2.4
	455107	BE154113		gb:PM1-HT0340-151299-003-e08 HT0340 Homo	2.4
30	458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
	459344	AW499533	Hs.257976	ESTs	2.4
	452605	AW968557	Hs.90012	hypothetical protein FLJ23441	2.4
	457652	AF116658	Hs.273809	Homo sapiens PRO1167 mRNA, complete cds	2.4
	450068	AW207212	Hs.280925	ESTs	2.4
35	444750	AW242684	Hs.243623	ESTs	2.4
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	407264	L34727		gb:Homo sapiens T-cell receptor beta (TC	2.4
	443169	AI038687	Hs.133338	ESTs	2.4
	426536	AI949749	Hs.44441	ESTs	2.4
40	449752	AI668626	Hs.61773	Homo sapiens cDNA FLJ11648 fis, clone HE	2.4
	459592	AL037421	Hs.208746	ESTs, Moderately similar to pot. ORF 1 [2.4
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	2.4
	429063	AW363845	Hs.122142	ESTs, Weakly similar to A46010 X-linked	2.4
	430484	D82880	Hs.241548	RAS p21 protein activator 2	2.4
45	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.4
	447375	AI376660	Hs.257822	ESTs	2.4
	444230	H95537	Hs.146067	ESTs	2.4
	439911	AA854024	Hs.189110	ESTs	2.4
50	421296	NM_002666	Hs.103253	perilipin	2.4
	449385	AI650471	Hs.270370	ESTs	2.4
	430044	AA464510	Hs.152812	ESTs	2.4
	427131	AA448460	Hs.112017	GE36 gene	2.4
	409103	AF251237	Hs.112208	XAGE-1 protein	2.4
	421354	AA766485	Hs.269664	ESTs	2.4
55	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	2.4
	440048	AA897461	Hs.328737	ESTs, Weakly similar to envelope protein	2.4
	441358	AW173212	Hs.129041	ESTs	2.4
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	2.4
	414290	AI568801	Hs.71721	ESTs	2.4
60	427342	AL110150	Hs.176680	Homo sapiens mRNA; cDNA DKFZp586D0724 (f	2.4
	459459	AA460445		gb:zx66h11.r1 Soares_tetal_fetus_Nb2HF8_	2.4
	434638	H50758		gb:yp86a06.r1 Soares fetal liver spleen	2.4
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.4
65	419637	W27493		gb:31h10 Human retina cDNA randomly prim	2.4
	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
	458734	AI554946	Hs.158794	ESTs	2.4
	449529	AI990559	Hs.232033	ESTs	2.4
70	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	2.4
	420195	NA4348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	2.4
	418105	AW937488	Hs.178000	ESTs, Weakly similar to FV1 MOUSE FRIEND	2.4
	430957	AI937072	Hs.55043	Homo sapiens cDNA FLJ13277 fis, clone OV	2.4
	418188	AW139413	Hs.151880	ESTs	2.4
75	424103	NM_001918	Hs.139410	dihydroilpoamide branched chain transacy	2.4
	454324	AW608930	Hs.52184	hypothetical protein FLJ20618	2.4
	437369	AA765230	Hs.121742	ESTs	2.4
	453211	W84829		gb:zh53f04.r1 Soares_fetal_liver_spleen_	2.4
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.4
	400462				2.4
80	413697	AA131315	Hs.47144	DKFZP586N0819 protein	2.4
	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.4
	424195	U50536	Hs.142907	Human BRCA2 region, mRNA sequence CG011	2.4
	434163	AW974720	Hs.25206	group XII secreted phospholipase A2	2.4

	435985	AA703154	Hs.191934	ESTs	2.4
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	2.4
	458661	AI299789	Hs.166999	ESTs, Moderately similar to I38344 tfin	2.4
5	459023	AW968226	Hs.60798	ESTs	2.4
	406005				2.4
	456561	AI868634	Hs.246358	ESTs, Weakly similar to T32250 hypotheti	2.4
	452161	R43077	Hs.221747	ESTs	2.4
	436590	AI393115	Hs.127655	ESTs	2.4
10	430151	AW968203		gb:EST380398 MAGE resequences, MAGJ Homo	2.4
	445635	AI769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4
	433479	AW511459	Hs.249972	ESTs	2.4
	441676	BE564206	Hs.49889	ESTs	2.4
	407965	W21483	Hs.41707	heat shock 27kD protein 3	2.4
	450682	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	2.4
15	452958	AA883929	Hs.40527	ESTs	2.4
	454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	2.4
	405347				2.4
	440577	AA889945	Hs.326381	EST	2.4
20	455780	BE088828		gb:CM2-BT0693-230300-129-g09 BT0693 Homo	2.4
	457024	AA397546	Hs.119151	ESTs	2.4
	404249				2.4
	437511	AI807500	Hs.125247	ESTs	2.4
	421338	AA287443		gb:zs52c10.r1 NCL_CGAP_GCB1 Homo sapiens	2.4
	425146	AW954627		gb:EST366697 MAGE resequences, MAGC Homo	2.4
25	428277	AA425220	Hs.179203	ESTs	2.4
	444870	AI200621	Hs.148504	ESTs	2.4
	402090				2.4
	458507	AI185703	Hs.206957	ESTs	2.4
30	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	2.4
	446534	AI307356	Hs.175225	ESTs	2.4
	453111	AB014598	Hs.31720	hephaestin	2.4
	405230				2.4
	405935				2.4
35	413642	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo	2.4
	420724	AA279694	Hs.191540	ESTs	2.4
	436998	AA745625	Hs.291414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	445748	U80766	Hs.13252	Human EST clone 22453 mariner transposon	2.4
	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	2.3
40	407404	AF040257		gb:Homo sapiens TNF receptor homolog mRNA	2.3
	440621	AW296024	Hs.150434	ESTs	2.3
	423417	AP000365	Hs.128342	potassium large conductance calcium-acti	2.3
	424131	AA335714	Hs.199665	ESTs	2.3
	450737	AW007152	Hs.203330	ESTs	2.3
45	453687	T56674	Hs.283108	hemoglobin, gamma G	2.3
	442704	AI015463	Hs.130987	ESTs	2.3
	457756	AA126136	Hs.38125	Interferon-induced protein 75, 52kD	2.3
	412732	AW993300		gb:RC2-BN0033-180200-015-g06 BN0033 Homo	2.3
	418998	F13215	Hs.287849	ESTs, Weakly similar to T22074 hypotheti	2.3
50	419751	AW195581	Hs.93121	KIAA0761 protein	2.3
	429485	AW197086	Hs.99338	ESTs	2.3
	433377	AI752713	Hs.43845	ESTs	2.3
	434896	AW022054	Hs.136591	ESTs	2.3
	441675	AI914329	Hs.5461	ESTs	2.3
55	444711	AI188739	Hs.148488	ESTs	2.3
	445621	AI733818	Hs.145549	ESTs	2.3
	449182	AW292381	Hs.224150	ESTs	2.3
	430987	Y08564	Hs.248190	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.3
	404068				2.3
60	414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sapiens c	2.3
	438315	R56795	Hs.82419	ESTs	2.3
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	2.3
	447998	AI768289	Hs.304389	ESTs	2.3
	410150	AW382942	Hs.6774	ESTs	2.3
65	432792	AA448114	Hs.278950	protocadherin beta 1.	2.3
	443363	AI792629	Hs.133293	ESTs	2.3
	440729	AA904739	Hs.128204	ESTs	2.3
	411045	AW854691	Hs.115325	RAB7, member RAS oncogene family-like 1	2.3
	459207	AW138410	Hs.45051	ESTs	2.3
	459124	AW301478	Hs.184592	protein kinase, lysine deficient 1	2.3
70	458684	BE281115	Hs.98855	hypothetical protein FLJ20909	2.3
	427962	AA946582	Hs.8700	deleted in liver cancer 1	2.3
	401899				2.3
	432116	AA902953	Hs.308538	ESTs	2.3
	404196				2.3
75	410999	AW813004		gb:RC3-ST0186-230300-019-h02 ST0186 Homo	2.3
	413308	W28131		gb:427 Human retina cDNA randomly prime	2.3
	430264	AA470519		gb:nc71f10.s1 NCL_CGAP_Pr1 Homo sapiens	2.3
	443482	AW188093	Hs.250385	ESTs	2.3
80	453305	R39224	Hs.267997	EHM2 gene	2.3
	451963	AI825440	Hs.224952	ESTs	2.3
	453043	AW136440	Hs.224277	ESTs	2.3
	435559	AF209198	Hs.42636	zinc finger protein 277	2.3
	440727	AI073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	2.3

	434120	AI436050	Hs.143937	ESTs	2.3
	429768	AA805719	Hs.192154	ESTs	2.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	2.3
5	455841	BE145836		gb:MR0-HT0208-101299-202-b08 HT0208 Homo	2.3
	411093	BE067650		gb:MR4-BT0358-090300-003-e01 BT0358 Homo	2.3
	430706	NM_003540	Hs.247816	H4 histone family, member C	2.3
	428268	AA424957	Hs.294132	ESTs	2.3
	458833	AW236702	Hs.171431	ESTs, Weakly similar to A46010 X-linked	2.3
10	452215	AK002043	Hs.28472	hypothetical protein FLJ11181	2.3
	444109	AI124553	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.3
	428411	AW291464	Hs.10338	ESTs	2.3
	433098	AW190593	Hs.151143	ESTs	2.3
	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	2.3
	453178	AA496086	Hs.61648	ESTs	2.3
15	404569				2.3
	413841	M34276	Hs.75576	plasminogen	2.3
	424068	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	2.3
	433532	AW975367		gb:EST387475 MAGE resequences, MAGN Homo	2.3
20	442710	AI015631	Hs.23210	ESTs	2.3
	444206	AW301017	Hs.146492	ESTs	2.3
	451264	AI768235		gb:wg82g08.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.3
	454784	AW820626		gb:RCO-ST0299-190100-012-e10 ST0299 Homo	2.3
	429080	AA446228	Hs.99057	ESTs	2.3
	404166				2.3
25	416327	R99822	Hs.36172	ESTs	2.3
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.3
	438504	AW665281	Hs.224625	ESTs	2.3
	435325	AI038388	Hs.119309	ESTs	2.3
30	421253	AI188102	Hs.31028	ESTs	2.3
	427046	BE246180	Hs.121385	ESTs	2.3
	432711	AA563785	Hs.152465	ESTs, Weakly similar to I38022 hypotheti	2.3
	439715	AA524504	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypotheti	2.3
	448458	AW614367	Hs.171054	ESTs	2.3
35	452542	AW812256		gb:RCO-ST0174-191099-031-a07 ST0174 Homo	2.3
	417768	R24732	Hs.175139	ESTs	2.3
	427374	AI160033	Hs.143686	ESTs	2.3
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.3
40	423600	AI633559	Hs.310359	ESTs	2.3
	413006	W03857	Hs.34298	ESTs	2.3
	434698	BE044674		gb:hm46f02.x1 NCL_CGAP_RDF1 Homo sapiens	2.3
	407639	AW205369	Hs.312830	ESTs	2.3
	455121	BE156459		gb:QV0-HT0368-040100-082-f06 HT0368 Homo	2.3
45	448117	H49129	Hs.172982	ESTs	2.3
	443931	H23213	Hs.22857	ESTs	2.3
	450795	AW173371	Hs.60435	ESTs	2.3
	418632	AW118745	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	2.3
	419441	AW023731	Hs.274368	MSTP032 protein	2.3
50	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	2.3
	418291	BE300369	Hs.289038	hypothetical protein MGC4126	2.3
	455964	BE168924		gb:CM4-HT0501-240300-519-f01 HT0501 Homo	2.3
	445944	H06336	Hs.13480	Homo sapiens clone 24875 mRNA sequence	2.3
	424827	AI057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fis, clone L	2.3
55	449272	AW137656	Hs.197645	ESTs	2.3
	445292	AV653264	Hs.13982	Homo sapiens cDNA FLJ14666 fis, clone NT	2.3
	416131	D61119		gb:HUM158C11B Clontech human fetal brain	2.3
	444715	AV650947	Hs.282464	ESTs	2.3
	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	2.3
60	444140	AV648089	Hs.282383	ESTs	2.3
	423949	AI014546	Hs.130912	ESTs	2.3
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.3
	445711	T79611	Hs.193691	ESTs	2.3
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	2.3
65	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.3
	429180	AA806287	Hs.58893	ESTs	2.3
	418849	AW474547	Hs.53665	Homo sapiens PIG-M mRNA for mannosyltran	2.3
	425523	AB007948	Hs.158244	KIAA0479 protein	2.3
	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
70	419337	AW291112	Hs.209978	ESTs	2.3
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypotheti	2.3
	428976	AL037824	Hs.194695	ras homolog gene family, member I	2.3
	436294	AA708310		gb:zg07b07.s1 Soares_pineal_gland_N3HPG	2.3
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.3
75	433939	AL133887	Hs.254122	hypothetical protein	2.3
	450048	AI693269	Hs.202273	ESTs	2.3
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	2.3
	416677	T83470	Hs.334840	ESTs, Moderately similar to I78885 serin	2.3
	405920				2.3
80	405747				2.3
	412105	H07971	Hs.94319	VPS10 domain receptor protein	2.3
	420457	AA482280	Hs.191656	ESTs	2.3
	407726	AA435579	Hs.88594	ESTs	2.3
	423720	AL044191	Hs.23388	hypothetical protein DKFZp434F0318	2.3

5	409517	X90780	Hs.120036	troponin I, cardiac	2.3
	435352	AI056599	Hs.120893	ESTs	2.3
	439871	R88518	Hs.46736	hypothetical protein FLJ23476	2.3
	444098	AV647969	Hs.109694	KIAA1451 protein	2.3
	449276	AW241510	Hs.252713	ESTs	2.3
10	417712	AA205569	Hs.194193	ESTs, Moderately similar to ALU1_HUMAN A	2.3
	449015	AL038958	Hs.22868	protein tyrosine phosphatase, non-recept	2.3
	411377	AW841462		gb:RC6-CN0014-080300-012-809 CN0014 Homo	2.3
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	2.3
	411816	AW864609		gb:PM3-SN0017-240300-001-h03 SN0017 Homo	2.3
15	455280	AW886156		gb:RCS-OT0078-150300-021-E08 OT0078 Homo	2.3
	407809	AW082279	Hs.244106	ESTs	2.3
	420478	AA521259	Hs.193796	ESTs	2.3
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	2.3
	445117	AI208754	Hs.147369	ESTs	2.3
20	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	2.2
	420230	AL034344	Hs.284186	forkhead box C1	2.2
	411517	AW850267		gb:IL3-CT0219-161199-031-A09 CT0219 Homo	2.2
	403678				2.2
	457003	S78234	Hs.172405	cell division cycle 27	2.2
25	404531	Z25884	Hs.121483	chloride channel 1, skeletal muscle (Th	2.2
	423045	AW967472	Hs.183302	PCTAIRE protein kinase 2	2.2
	409427	AW389668		gb:RC2-ST0168-071299-013-f06 ST0168 Homo	2.2
	434745	AW974445	Hs.185155	ESTs, Weakly similar to T12482 hypotheti	2.2
	400696				2.2
30	407259	L02256		gb:Human Fab fragment binding syncytial	2.2
	411893	R82845	Hs.273789	ESTs	2.2
	428192	AA424051	Hs.304742	ESTs	2.2
	435634	T82384		gb:yc14f05.r1 Stratagene lung (937210) H	2.2
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
35	458303	AI264628	Hs.125428	ESTs	2.2
	405692				2.2
	403572				2.2
	415380	F07953	Hs.16085	putative G-protein coupled receptor	2.2
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.2
40	417859	T26453		gb:AB214F6R Infant brain, LLNL array of	2.2
	456472	AK001714	Hs.95744	hypothetical protein similar to ankyrin	2.2
	444106	AI123922	Hs.138215	Homo sapiens cDNA FLJ11400 fis, clone HE	2.2
	428231	U17989	Hs.183105	nuclear autoantigen	2.2
	454086	AW885909	Hs.6975	PRO1073 protein	2.2
45	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.2
	416348	H65887	Hs.272163	ESTs	2.2
	403780				2.2
	414262	AW975616	Hs.291469	ESTs	2.2
	419423	D26488	Hs.90315	KIAA0007 protein	2.2
50	442078	AW268583	Hs.262629	ESTs	2.2
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.2
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.2
	416588	H66558		gb:yu16e04.r1 Soares fetal liver spleen	2.2
	425368	AB014595	Hs.155976	cullin 4B	2.2
55	425686	M73531	Hs.1937	retinal degeneration, slow (retinitis pi	2.2
	441638	AW293202	Hs.133451	ESTs	2.2
	446845	AI343645	Hs.156108	ESTs	2.2
	422563	BE299342	Hs.19348	hypothetical protein FLJ13119	2.2
	436574	AW293527	Hs.126465	ESTs	2.2
60	424584	H10692	Hs.13310	ESTs	2.2
	456347	U00803	Hs.89426	fyn-related kinase	2.2
	446901	AI347274		gb:tc05d02x1 NCL_CGAP_Co16 Homo sapiens	2.2
	459364	W69284		gb:zd46c03.r1 Soares_fetal_heart_NbHH19W	2.2
	430686	NM_001942	Hs.2633	desmoglein 1	2.2
65	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	2.2
	425707	AF115402	Hs.11713	E74-like factor 5 (els domain transcript	2.2
	403525				2.2
	453343	AA905353	Hs.121622	ESTs	2.2
	421574	AJ000152	Hs.105924	defensin, beta 2	2.2
70	449327	AI638743	Hs.224672	ESTs	2.2
	454769	AW819848		gb:QV0-ST0294-070300-151-b04 ST0294 Homo	2.2
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I78885 serine/th	2.2
	401614				2.2
	404767				2.2
75	403534				2.2
	410594	AW770778	Hs.281238	ESTs	2.2
	436193	AA706059	Hs.255286	ESTs	2.2
	439626	N22415	Hs.189080	ESTs	2.2
	456481	AA258033	Hs.108110	DKFZP547E2110 protein	2.2
80	441453	AW176106	Hs.285459	ESTs	2.2
	424946	M64572	Hs.153932	protein tyrosine phosphatase, non-recept	2.2
	437332	AA814943		gb:cc07d06.s1 NCL_CGAP_GC81 Homo sapiens	2.2
	454419	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	2.2
	416225	AA577730	Hs.188884	ESTs, Weakly similar to PC4259 ferritin	2.2
	450579	AW136774	Hs.48614	ESTs	2.2
	400664				2.2
	447613	AL041057	Hs.33363	DKFZP434N093 protein	2.2

	402689	AK001334	Hs.15470	putative ring zinc finger protein NY-REN	2.2
	430884	AF053748	Hs.248114	glial cell derived neurotrophic factor	2.2
	432797	AA565264	Hs.136443	ESTs	2.2
	405608				2.2
5	426365	AA376667	Hs.10283	RNA binding motif protein 8B	2.2
	405634				2.2
	423646	H02364		gb:yj35d06.r1 Soares placenta Nb2HP Homo	2.2
	434690	AI867679	Hs.148410	ESTs	2.2
	436572	AA723274	Hs.279596	ESTs	2.2
10	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	448828	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	2.2
	457802	T78013	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.2
	444585	AW170015	Hs.6594	ESTs	2.2
	433781	AA609379	Hs.192083	ESTs	2.2
15	450587	AI828854	Hs.258538	striatin, calmodulin-binding protein	2.2
	434077	AF116659	Hs.321151	Homo sapiens PRO1412 mRNA, complete cds	2.2
	448756	AI739241	Hs.171480	ESTs	2.2
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.2
20	454471	AW902125		gb:QVO-NN1022-120500-220-h12 NN1022 Homo	2.2
	419107	AW085152	Hs.292987	ESTs	2.2
	455114	AW857121		gb:RC1-CT0302-040400-017-a12 CT0302 Homo	2.2
	416548	H62953		gb:yr4706.r1 Soares fetal liver spleen	2.2
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	2.2
25	456056	AA463550	Hs.337532	ESTs, Weakly similar to A47582 B-cell gr	2.2
	409998	M78345	Hs.98265	KIAA1877 protein	2.2
	422352	AA766296	Hs.99200	ESTs	2.2
	409191	AW818390	Hs.175613	homolog of Xenopus Caspin	2.2
	433919	AA746311		gb:oa56d12.r1 NCI_CGAP_GC81 Homo sapiens	2.2
	455771	BE084820	Hs.186711	hypothetical protein FLJ120070	2.2
30	431632	AK000992	Hs.333144	Homo sapiens cDNA FLJ10130 fis, clone HE	2.2
	454716	AW850684		gb:IL3-CT0219-160200-063-D12 CT0219 Homo	2.2
	413752	BE161807		gb:MR3-HT0446-300300-203-h01 HT0446 Homo	2.2
	458037	AF074962	Hs.226031	ESTs, Highly similar to KIAA0535 protein	2.2
	434239	AF119910	Hs.283047	hypothetical protein PRO2964	2.2
35	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	2.2
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.2
	400697				2.2
	455685	BE066976		gb:PM0-BT0340-211299-003-c12 BT0340 Homo	2.2
40	447039	AV661798	Hs.282915	ESTs	2.2
	404593				2.2
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.2
	421976	AL138443	Hs.23450	mitochondrial ribosomal protein S25	2.2
	401673				2.2
	425001	U55184	Hs.154145	hypothetical protein FLJ11585	2.2
45	447816	NM_007233	Hs.274329	TP53 target gene 1	2.2
	416143	AI955650	Hs.79033	glutamyl-peptidyl cyclotransferase (glu	2.2
	419118	AA234223	Hs.139204	ESTs	2.2
	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	2.2
	449808	AA694220	Hs.15403	ESTs, Moderately similar to ALU7_HUMAN A	2.2
50	454749	AW818649		gb:RC1-ST0278-040400-018-e02 ST0278 Homo	2.2
	456933	AA363946	Hs.20969	ESTs	2.2
	402942				2.2
	437064	AI023264		gb:zv64h08.s1 Soares_testis_NHT Homo sap	2.2
	458623	AI305223	Hs.148056	ESTs	2.2
55	415257	F03016	Hs.27513	ESTs	2.2
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp586A1046 (f	2.2
	442783	AI017586	Hs.131181	ESTs	2.2
	444313	AI140494	Hs.197955	KIAA0704 protein	2.2
	453444	AL036531		gb:DKFZp564I1162_r1 564 (synonym: hibr2)	2.2
60	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.2
	430013	AA463833	Hs.151275	ESTs, Weakly similar to TRHY_HUMAN TRICH	2.2
	437138	AI935622	Hs.271245	ESTs	2.2
	406298				2.2
	409723	AW885757	Hs.257862	ESTs	2.2
65	414481	AW451956	Hs.8383	bromodomain adjacent to zinc finger doma	2.2
	433266	AI863224	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	2.2
	435090	BE217923	Hs.149595	ESTs	2.2
	457187	AA443927	Hs.144360	EST	2.2
	445061	AI253094	Hs.145227	ESTs	2.2
70	442617	AW340093	Hs.130538	ESTs	2.2
	438298	H23542	Hs.181788	ESTs	2.2
	454916	BE067246		gb:PM1-BT0348-151299-001-d04 BT0348 Homo	2.2
	428017	AA424983	Hs.98312	ESTs	2.2
	451149	AL047586	Hs.10283	RNA binding motif protein 8B	2.2
75	418076	R61388	Hs.6724	ESTs	2.2
	403306	NM_006825	Hs.74368	transmembrane protein (53kD), endoplasmic	2.2
	441811	AI073548	Hs.164597	ESTs	2.2
	434763	AA648618		gb:ns07a11.r1 NCI_CGAP_Ew1 Homo sapiens	2.2
	447453	AW808645	Hs.18800	hypothetical protein FLJ20281	2.2
80	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.2
	415424	Z44766		gb:HSC28G081 normalized infant brain cDN	2.2
	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	2.2
	421216	AV649282	Hs.102664	vesicle-associated membrane protein 4	2.2

	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	2.2
	448700	BE614182	Hs.123075	ESTs	2.2
	457741	BE044740		gb:hm55g10.x1 NCI_CGAP_RDF1 Homo sapiens	2.2
	437927	AI039789	Hs.25982	hypothetical protein FLJ21031	2.2
5	401694				2.2
	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	424419	AK001563	Hs.146589	hypothetical protein FLJ10701	2.2
	436640	AA724411	Hs.156065	ESTs	2.2
	438290	AA843719	Hs.122341	ESTs	2.2
10	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
	455735	BE161124		gb:PM0-HT0425-141299-001-A06 HT0425 Homo	2.2
	458455	AV648310	Hs.213488	ESTs	2.2
	430680	AW138724	Hs.168974	ESTs, Highly similar to ALU7_HUMAN ALU S	2.2
	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypotheti	2.2
15	424063	NM_002019	Hs.138671	fms-related tyrosine kinase 1 (vascular	2.2
	441874	AA970389	Hs.128055	ESTs	2.2
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.2
	433629	R13140	Hs.13359	ESTs	2.2
	415266	AA184199	Hs.270152	ESTs	2.2
20	440633	AJ140686	Hs.263320	ESTs	2.2
	442789	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.2
	417563	AA203701		gb:zx52a10.r1 Soares_fetal_liver_spleen_	2.2
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.2
	401240				2.2
25	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
	411151	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	2.2
	436992	AA741074	Hs.120750	ESTs	2.2
	439634	W79377	Hs.167	microtubule-associated protein 2	2.2
30	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	2.1
	400040				2.1
	458762	AW802754		gb:IL2-UM0076-030400-061-H01 UM0076 Homo	2.1
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	2.1
	419953	BE267154	Hs.125752	ESTs	2.1
35	410648	AW792909		gb:CM0-UM0001-010300-258-c05 UM0001 Homo	2.1
	423717	AA330036	Hs.152003	ESTs	2.1
	436683	AW991278	Hs.57787	ESTs	2.1
	445225	AJ216555	Hs.202398	ESTs	2.1
	410991	AW812790		gb:RC3-ST0186-141299-014-g08 ST0186 Homo	2.1
40	412639	AW961284	Hs.296235	ESTs	2.1
	447777	AJ424223		gb:te95a05.x1 NCI_CGAP_Pr28 Homo sapiens	2.1
	451270	AW341392	Hs.235795	ESTs	2.1
	404526	AJ912555	Hs.157195	peptide YY, 2 (seminaplasmin)	2.1
	452492	BE063096		gb:CM4-BT0266-091199-039-a02 BT0266 Homo	2.1
45	417154	AI674701	Hs.21388	ESTs	2.1
	428152	AA422030		gb:zv26h05.r1 Soares_NhHMPu_S1 Homo sapi	2.1
	442312	AJ820617	Hs.129216	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	456513	AA279143	Hs.88561	ESTs	2.1
	430712	AW044647	Hs.196284	ESTs	2.1
50	441445	AJ221959	Hs.187937	ESTs	2.1
	420288	AW071225	Hs.245558	ESTs	2.1
	412329	AW937445		gb:QV3-DT0043-090200-080-c09 DT0043 Homo	2.1
	447033	AJ357412	Hs.157601	ESTs	2.1
	436853	BE328074	Hs.148661	ESTs	2.1
55	455189	AW864176		gb:PM0-SN0014-260400-002-b08 SN0014 Homo	2.1
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	2.1
	458356	AJ024855	Hs.131575	ESTs	2.1
	457040	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.1
	424480	AA341442	Hs.205299	ESTs	2.1
60	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
	406018				2.1
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	2.1
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	2.1
	415871	R55995	Hs.283309	ESTs, Moderately similar to ALU1_HUMAN A	2.1
65	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	2.1
	417725	R25257	Hs.21503	ESTs	2.1
	424856	AA347746	Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	2.1
	439474	AJ824060	Hs.211501	ESTs	2.1
	446895	AA166655	Hs.282803	ESTs	2.1
70	448582	AI538880	Hs.94812	ESTs	2.1
	452783	AA028167	Hs.61486	ESTs	2.1
	442430	R89164	Hs.48320	double ring-finger protein, Doriin	2.1
	428908	AW303529	Hs.144955	ESTs	2.1
	427335	AA448542	Hs.251677	G antigen 7B	2.1
75	428336	AA503115	Hs.183752	microsomal protein, beta-	2.1
	419290	AJ128114	Hs.112885	spinal cord-derived growth factor-B	2.1
	416951	AA190926	Hs.190785	ESTs, Moderately similar to S65657 alpha	2.1
	439950	AW937417	Hs.293561	ESTs	2.1
	458227	Z40670	Hs.181340	ESTs	2.1
80	447179	AW015633	Hs.157299	ESTs	2.1
	454950	AW847460		gb:RC3-CT0208-270999-021-e04 CT0208 Homo	2.1
	404453				2.1
	420844	AA595522		gb:nh22c09.s1 NCI_CGAP_Pr1 Homo sapiens	2.1

	426456	AA580748	Hs.130658	ESTs	2.1
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
	430879	BE149423	Hs.10554	hypothetical protein FLJ12761	2.1
5	444584	AI168422		gb:ok30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.1
	446296	AA985662	Hs.63131	Homo sapiens cDNA FLJ13155 fis, clone NT	2.1
	453853	AL040600	Hs.188083	ESTs	2.1
	414083	AL121282	Hs.257786	ESTs	2.1
	401645				2.1
10	436577	W84774	Hs.17643	ESTs	2.1
	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	2.1
	409168	N94037	Hs.312938	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	410276	AI554545	Hs.68301	ESTs	2.1
	443372	AI792557	Hs.133107	ESTs	2.1
	422093	AF151852	Hs.111449	CGI-94 protein	2.1
15	402333				2.1
	409374	R87083	Hs.19081	ESTs	2.1
	412011	NM_000406	Hs.73064	gonadotropin-releasing hormone receptor	2.1
	412798	AW998657	Hs.119120	E3 ubiquitin ligase SMURF1	2.1
20	416085	H18072	Hs.92576	ESTs	2.1
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.1
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.1
	452374	AL037405	Hs.339639	ESTs	2.1
	450061	AI797034	Hs.201115	ESTs	2.1
	450180	AW449644	Hs.257182	ESTs	2.1
25	405120				2.1
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.1
	458890	AW865523		gb:PM4-SN0020-010400-009-b05 SN0020 Homo	2.1
	435600	AL047034	Hs.119747	ESTs	2.1
30	440964	AI733106	Hs.130218	ESTs	2.1
	417455	AW007066	Hs.18949	ESTs, Weakly similar to CA2B_HUMAN COLLA	2.1
	436461	AW511956	Hs.293261	ESTs	2.1
	436777	AA731199	Hs.293130	ESTs	2.1
	427521	AW973352	Hs.290585	ESTs	2.1
35	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	2.1
	413231	D87461	Hs.75244	BCL2-like 2	2.1
	423969	AI830571	Hs.331633	hypothetical protein DKFZp566N034	2.1
	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	2.1
	443777	AV846510	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	2.1
40	416148	H22453	Hs.169187	ESTs	2.1
	402528				2.1
	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	2.1
	436820	AI684535	Hs.200811	ESTs	2.1
	446209	AI375025	Hs.153368	ESTs	2.1
45	453362	H14988	Hs.107375	ESTs	2.1
	417430	AA984546		gb:am88e08.s1 Stralagene schizo brain S1	2.1
	401069				2.1
	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	2.1
	410966	AW812088		gb:RC4-ST0173-191099-032-a07 ST0173 Homo	2.1
50	447124	AW976438	Hs.17428	RBP1-like protein	2.1
	449939	T86420	Hs.272139	ESTs	2.1
	411693	AW857271		gb:CM0-CT0307-210100-158-g09 CT0307 Homo	2.1
	438005	BE151746		gb:PM1-HT0305-061289-003-a06 HT0305 Homo	2.1
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	2.1
55	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	2.1
	404694				2.1
	406668	T62745	Hs.184411	albumin	2.1
	441092	T99289	Hs.126556	EST	2.1
60	454843	BE006345		gb:RC2-BN0127-240300-011-d05 BN0127 Homo	2.1
	426646	AA382787	Hs.122713	ESTs	2.1
	431605	AW972407		gb:EST384498 MAGE resequences, MAGL Homo	2.1
	414452	AA454038	Hs.29032	ESTs	2.1
	401991				2.1
	457176	AA436837		gb:zv57g07.s1 Soares_testis_NHT Homo sap	2.1
65	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	428208	AA442327	Hs.104854	ESTs	2.1
	445049	AV652718		gb:AV652718 GLC Homo sapiens cDNA clone	2.1
	419116	AF292402	Hs.283093	neuromedin U receptor 2	2.1
	427894	AL135709	Hs.28921	zinc finger protein	2.1
70	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	2.1
	424323	AA338791	Hs.177788	ESTs	2.1
	404582				2.1
	418831	AA225921	Hs.115105	ESTs	2.1
	424872	AA347923		gb:EST54302 Fetal heart II Homo sapiens	2.1
75	452539	AW105321	Hs.49367	ESTs	2.1
	454658	AW812330	Hs.11123	DKFZP564G092 protein	2.1
	440310	AA878939	Hs.125406	ESTs	2.1
	433297	AV658581	Hs.282633	ESTs	2.1
	410900	AW810169		gb:MR4-ST0124-040500-007-h07 ST0124 Homo	2.1
80	419386	AA236867	Hs.143868	ESTs, Weakly similar to I38022 hypothi	2.1
	402451				2.1
	447842	AW160804	Hs.247302	twisted gastrulation	2.1
	453880	AI803166	Hs.28462	ESTs, Weakly similar to I38022 hypothi	2.1
	425189	H16622		gb:ym26c07.r1 Soares infant brain 1N1B H	2.1

	457225	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.1
	400612				2.1
	402318				2.1
5	410534	AW905138		gb:QV0-NN1071-280400-207-g07 NN1071 Homo	2.1
	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
	412029	AW886238		gb:RCS-OT0078-280300-022-F01 OT0078 Homo	2.1
	414494	AA768491	Hs.6783	hypothetical protein FLJ22724	2.1
	427027	AJ924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
10	444498	AJ151413	Hs.26330	ESTs	2.1
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	2.1
	425324	M89470	Hs.155644	paired box gene 2	2.1
	430719	AA488988	Hs.293796	ESTs	2.1
	432577	BE208545	Hs.317590	hypothetical protein FLJ14640	2.1
15	407593	AW044083	Hs.237008	ESTs	2.1
	401098				2.1
	440299	AJ871778	Hs.250112	ESTs	2.1
	414146	BE549372	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	2.1
	428527	BE002993	Hs.187660	putative Rab5 GDP/GTP exchange factor ho	2.1
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	2.1
20	431912	AJ660552	Hs.154903	ESTs, Weakly similar to A56154 ABl subst	2.1
	439831	AW136488	Hs.25545	ESTs	2.1
	451829	AW964081	Hs.247377	ESTs	2.1
	404595				2.1
25	421498	AA292084	Hs.191575	ESTs, Moderately similar to ALU2_HUMAN A	2.1
	456083	U46922	Hs.77252	fragile histidine triad gene	2.1
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	2.1
	406413				2.1
	439483	T69980	Hs.58323	Homo sapiens cDNA FLJ11613 fis, clone HE	2.1
30	446242	N66336	Hs.7360	ESTs	2.1
	449625	NM_014253	Hs.23796	odx (odd Oz/ten-m, Drosophila) homolog 1	2.1
	457938	AJ373638	Hs.133900	ESTs	2.1
	413101	BE085215		gb:RC1-BT0314-310300-015-f01 BT0314 Homo	2.1
	408350	AW183350	Hs.250127	ESTs	2.1
35	419812	NM_000562	Hs.93210	complement component 8, alpha polypeptid	2.1
	430881	NM_000809	Hs.248112	gamma-aminobutyric acid (GABA) A recepto	2.1
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	2.1
	409955	U60655	Hs.57692	chromosome 6 open reading frame 10	2.1
	435579	AJ332373	Hs.156924	ESTs	2.1
40	436088	AA704687	Hs.191294	ESTs	2.1
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.1
	416100	H18700	Hs.268799	ESTs	2.1
	403218	AL134878	Hs.119500	ribosomal protein, large P2	2.1
	409747	H60964	Hs.331250	ESTs	2.1
45	428764	W21550		gb:zb5212r1 Soares_fetal_Jung_NbHL19W	2.1
	425075	AA506324	Hs.1852	acid phosphatase, prostate	2.1
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.1
	428299	AL038004	Hs.29419	ESTs	2.1
	406817	AJ936028		gb:wo47a09.x1 NCI_CGAP_Gas4 Homo sapiens	2.1
50	411940	AW876686		gb:CM4-PT0031-180200-507-e05 PT0031 Homo	2.1
	412446	AJ768015	Hs.92127	ESTs	2.1
	414012	AW452334	Hs.128148	ESTs	2.1
	421956	AA904519	Hs.130710	ESTs	2.1
	430566	AA481282	Hs.190149	ESTs	2.1
55	456606	AA292862	Hs.275369	ESTs	2.1
	451604	T65365	Hs.172851	arginase, type II	2.0
	440926	AW196772	Hs.131323	ESTs	2.0
	420687	AA279392	Hs.88605	Homo sapiens cDNA FLJ13427 fis, clone PL	2.0
	459082	BE551721	Hs.282149	ESTs	2.0
60	413241	BE073771	Hs.302414	Homo sapiens clone FLB8945 PRO2411 mRNA,	2.0
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	2.0
	447552	AJ394125	Hs.160413	ESTs	2.0
	420905	AA521307	Hs.186651	ESTs	2.0
	428052	AA420477	Hs.26993	ESTs	2.0
65	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.0
	432527	AW975028	Hs.102754	ESTs	2.0
	430202	T85775		gb:yd60g02r1 Soares fetal liver spleen	2.0
	446610	AV659433	Hs.282984	ESTs, Weakly similar to I38022 hypothe	2.0
	427961	AW293165	Hs.143134	ESTs	2.0
70	455290	U75810		gb:HSU75810 Human Homo sapiens cDNA clon	2.0
	445564	AB028957	Hs.12898	KIAA1034 protein	2.0
	412811	H06382	Hs.21400	ESTs	2.0
	413783	AA314337	Hs.301547	ribosomal protein S7	2.0
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.0
75	429418	AJ381028	Hs.118769	ESTs	2.0
	431511	NM_012386	Hs.258581	Homo sapiens p95 paxillin-kinase linker	2.0
	445829	AJ452457	Hs.145526	ESTs	2.0
	452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
	453123	AJ953718	Hs.221849	ESTs	2.0
80	455401	AW936369		gb:QV4-OT0021-301299-071-d07 OT0021 Homo	2.0
	406666	VD0495	Hs.184411	albumin	2.0
	445688	AJ248205	Hs.153244	ESTs	2.0
	446131	NM_000929	Hs.290	phospholipase A2, group V	2.0
	440388	AJ693520	Hs.223000	ESTs	2.0

	457128	AI932995	Hs.183475	Homo sapiens clone 25051 mRNA sequence	2.0
	404416				2.0
	444187	AW138466	Hs.151274	ESTs	2.0
	431552	AI815863	Hs.259873	axonal transport of synaptic vesicles	2.0
5	455814	BE141689		gb:CM1-HT0092-220999-016-b09 HT0092 Homo	2.0
	454759	AW819455		gb:RC5-ST0293-021299-031-A04 ST0293 Homo	2.0
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cd	2.0
	404420				2.0
10	408112	AW451982	Hs.248613	ESTs	2.0
	432702	AW973953	Hs.293744	ESTs	2.0
	448587	AI539652	Hs.28338	KIAA1546 protein	2.0
	446854	BE268103	Hs.208914	hypothetical protein MGC10999	2.0
	410569	AA766825	Hs.205675	ESTs	2.0
	432596	AJ224741	Hs.278461	matrilin 3	2.0
15	402341				2.0
	452919	AW962167		gb:EST374240 MAGE resequences, MAGG Homo	2.0
	433632	AA649921	Hs.112553	ESTs	2.0
	435079	AA664192		gb:rac05b03.s1 Stratagene lung (937210) H	2.0
20	451927	AL355687	Hs.27261	Homo sapiens mRNA full length insert cDN	2.0
	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	2.0
	450895	N66727	Hs.10957	ESTs	2.0
	408459	H09701	Hs.278366	ESTs, Weakly similar to I38022 hypothi	2.0
	400842				2.0
25	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.0
	400859				2.0
	405829				2.0
	411863	BE075244	Hs.12420	ESTs	2.0
	415258	AW752247	Hs.293853	ESTs	2.0
30	416093	R60685	Hs.268698	ESTs, Moderately similar to ALUC_HUMAN I	2.0
	420314	H81671	Hs.320921	ESTs, Weakly similar to T22688 hypothi	2.0
	428002	AA418703		gb:zv98c03.s1 Soares_NhhMPu_S1 Homo sapi	2.0
	437733	AI792574	Hs.122876	ESTs	2.0
	453118	AW195849	Hs.252757	ESTs	2.0
35	457039	H29990	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.0
	454578	AW809178		gb:MR4-ST0118-261099-012-c07 ST0118 Homo	2.0
	411565	AW851728		gb:MR2-CT0222-011199-007-d06 CT0222 Homo	2.0
	419986	AJ345455	Hs.78915	GA-binding protein transcription factor,	2.0
	415173	AW501735	Hs.253015	ESTs	2.0
40	449011	AI655376	Hs.192693	ESTs	2.0
	410365	AJ287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	2.0
	416057	AI927382	Hs.29857	ESTs	2.0
	455688	BE067238		gb:PM1-BT0348-151299-001-a12 BT0348 Homo	2.0
	408531	AW207553	Hs.253639	ESTs	2.0
45	434663	AA641972	Hs.130058	ESTs	2.0
	428085	AA421081	Hs.12388	ESTs	2.0
	425006	R38685	Hs.332622	ESTs	2.0
	446139	H77395	Hs.39749	ESTs	2.0
	400049				2.0
50	428333	AW972668	Hs.293044	ESTs	2.0
	429458	BE161832	Hs.292689	ESTs	2.0
	425087	R62424	Hs.126059	ESTs	2.0
	457122	AJ026157	Hs.33728	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
	400310	X63966	Hs.135631	H.sapiens synthetic gene for platelet-de	2.0
55	451805	AI968300	Hs.208220	ESTs	2.0
	401986				2.0
	415318	T06544		gb:EST04433 Fetal brain, Stratagene (cat	2.0
	417756	Z43056		gb:HSC128021 normalized infant brain cDN	2.0
60	418301	AW976201	Hs.53913	hypothetical protein FLJ10252	2.0
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	2.0
	429110	L29301	Hs.2353	opioid receptor, mu 1	2.0
	433755	AW085934	Hs.120868	ESTs	2.0
	434118	AF116715	Hs.256256	Homo sapiens PRO2829 mRNA, complete cds	2.0
	435413	AI267476	Hs.46669	ESTs	2.0
65	443748	AW206447		gb:UH-BH1-afg-g-02-D-UI.s1 NCI_CGAP_Su	2.0
	445205	D63776	Hs.12413	KIAA0191 protein	2.0
	458175	AW296024	Hs.150434	ESTs	2.0
	446419	AW576760	Hs.160726	Homo sapiens cDNA FLJ11680 fis, clone HE	2.0
	441627	AA947552	Hs.58086	ESTs	2.0
70	457653	AJ820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	2.0
	455614	AI693369	Hs.202274	ESTs	2.0
	449899	AI610700	Hs.103280	ESTs	2.0
	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	2.0
75	437354	AA749215	Hs.291886	ESTs	2.0
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.0
	419691	W03298	Hs.193521	ESTs	2.0
	439724	AF086565	Hs.60351	EST	2.0
	413362	BE088812		gb:CM2-BT0693-230300-129-d08 BT0693 Homo	2.0
80	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	2.0
	434361	AF129755	Hs.117772	ESTs	2.0
	442479	AF063484		gb:AF089484 Homo sapiens astrocytoma fib	2.0
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	2.0
	459323	AW062490		gb:MR0-CT0065-100899-001-d01 CT0065 Homo	2.0
	449438	AA927317	Hs.554	Sjogren syndrome antigen A2 (60kD, ribon	2.0

400285				2.0
407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
411459	BE142707		gb:MR0-HT0157-191199-002-g12 HT0157 Homo	2.0
417383	W02642	Hs.136102	KIAA0853 protein	2.0
447153	AA805202	Hs.315562	ESTs	2.0
447313	U92981	Hs.18081	Homo sapiens clone DT1P186 mRNA, CAG rep	2.0
455696	BE067870		gb:RCO-BT0362-021299-031-b06 BT0362 Homo	2.0
456510	AK001652	Hs.99423	ATP-dependent RNA helicase	2.0
449815	AI671000	Hs.199739	ESTs	2.0
425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	2.0
400238				2.0
451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.0
445073	AW291389	Hs.13056	hypothetical protein FLJ13920	2.0
455221	AW867751		gb:MR0-SN0038-290300-001-a03 SN0038 Homo	2.0
413174	AA723564	Hs.191343	ESTs	2.0
435810	BE349853	Hs.2785	keratin 17	2.0
418687	R61650	Hs.22581	ESTs	2.0
438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	2.0
431750	AA514986	Hs.283705	ESTs	2.0
453242	T98327	Hs.18343	ESTs	2.0
437074	AI286235	Hs.128905	hypothetical protein FLJ13204	2.0
459411	N52920		gb:yyv34h09.s1 Soares fetal liver spleen	2.0
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	2.0
409929	R38772	Hs.172619	myelin transcription factor 1-like	2.0
406378				2.0
459208	BE261314	Hs.149039	ESTs, Weakly similar to I38022 hypotheti	2.0
445260	AI218133	Hs.147617	ESTs	2.0
416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	2.0
445020	AI205655	Hs.147221	ESTs	2.0
402048				2.0
412695	AW984439		gb:PM3-HN0011-220300-002-c05 HN0011 Homo	2.0
416408	R94725	Hs.35354	ESTs	2.0
423347	AI660412	Hs.234557	ESTs	2.0
427836	AA416642	Hs.116176	ESTs	2.0
433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
436902	AW247145	Hs.192729	ESTs	2.0
440122	AI733011	Hs.127678	ESTs	2.0
442901	AI023654	Hs.114191	ESTs	2.0
444097	AW517412	Hs.150757	ESTs	2.0
447278	AI934935	Hs.158569	ESTs	2.0
451361	AA053854		gb:z52f02.r1 Soares retina N2b4HR Homo	2.0
451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.0
454423	AW603985		gb:RC4-CN0048-140100-011-a04 CN0048 Homo	2.0
458801	N98648	Hs.276860	ESTs, Weakly similar to C Chain C, Human	2.0

TABLE 30B

50	Key:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
55	Play	CAT number	Accession
	407593	1003161_1	AW044083 AW044094 AW370634
	407594	1003220_1	AW057584 AW057585 AW044153 R34370
	407639	1006924_1	AW205369 AW058599 AW207608
	407676	1008294_1	AW064111 AW054450 AW064429
60	407721	10108_1	Y12735 NM_003582 AW238970 R38268 R41411 R41419 T16717 AA002193 H62028 AJ359545 AW105201 AW087158 AA699728 AI095264
	407726	101126_1	AA002065 H62029 AJ289101 AA884804 AA904950 AA609672 AJ139874 H77896
	407762	101439_1	AA435679 AA470655 H22526 AA044031 AA876426 W63767 AI221140 AI418990 H42329 H88910 AL041066 H88909 W94610 AW352277 W94648
	407764	1014849_1	W94167 AW952568 AI419553 AA335501 AA393641 AA044353 H41626 H22525 R58582 AW297645 C75230 AW368034 AW468904 AI272755
	407788	10163_1	AW235638 AA346882 AW866803 AA381281 AW963163 AA044373 AA136755
65			BE008347 BE008320 BE083307 BE083311 AW075968
			BE514982 BE614814 AW393078 AW238480 AA055637 N27644 AA641158 M87068 AA161019 AA161003 AA587315 AA716746 AA593632
			AJ354870 AW183492 Y07755 NM_005978 AW872948 AI608987 H64656 AF086003 AA643149 AI819402 H64555 AA858398 AA594885 AA436747
			BE122811 AA587026 AW857106 AI950679 AA596012 AA654004 AW238238 AI971395 AA459074 AA458884 AI608591 BE181995 BE181970
			AW195797 C00271 BE182043
70	407803	1017498_1	AW081681 N36967 N36959
	407809	1017982_1	AW082279 AW082688
	407811	10180_1	AW190902 AJ802788 AI041650 AI037867 AF110137 NM_013372 H99469 N35377 AW151676 AI678451 AW078795 AW087935 AI884505
			AW044602 AB032372 AF045800 AI621183 AI750578 AA376403 AI910477 AA373348 AA373673 AI752124 AL359060 W48619 AA373298 AA373975
75			AW604409 AW604404 AW368603 AA545734 AW361415 AA373557 AW956164 AW853798 AI750595 AL359059 AA344024 N31127 AW580737
			N27040 AA071138 AI753050 AA599801 W48852 AA669811 AA112124 AI940705 W52686 AA084001 C01826 AI940729 AA373544 AW957491
			AW383224 AW383184 AW383192 AW383125 AW383194 AW842507 AI940795 H80042 AW631119 W47324 W42884 AI750594 AI754387 AI753734
			AA372833 AW069006 AI750577 AW473621 AJ88605 AA600082 AI041803 W51909 W25447 AI521673 AI087351 AA670070 W47325 AA071381
			W42791 AI090390 AJ085102 AJ302125 AA788723 AW069430 AW069485 AI754608 AA373014 BE140150 BE140166 BE140102 BE140143
			BE140157 BE140117 BE140098 AW005943 BE140108 BE140176 BE140171 BE140144 BE140175 BE140160 BE140152 BE140099 BE140177
			BE140167 BE140145 BE140109 BE140163 BE140172 BE140161 BE140179 BE140147 BE140107 BE140146 BE140155 BE140173 BE140148
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5	407834 407851 407884 407938	1020170_1 10212_1 1023626_1 102759_1	NW084991 R54179 N64486 NM_014496 AF184965 H82896 H82897 BE075316 AW090150 AW589417 H47391 D61911 BE173252 AA905097 AI734242 BE044545 N86431 AA344041 C03245 AW963097 AI567324 AA045934 AW079233 R58274 AI744425 AI167427 R58176 R58588 AI969945 AI921684 AW013864 AI204559 AA909648 N84115 AA897468 AI686637 BE221753 AI355307 AI139542 N80934 W21483 U15590 NM_006308 N56314 AA126678 AA426507 Y17782 W24740 W05062 W21042 AA649552 AA093507 AA092088 AA476830 N88299 AA429090 AA095643 AI224915 AA443775 AI204315 AI333690 AA586584 AI275037 AI193915 AA659647 T82641 AA136048 T82643 T82647 F36041 N74099 AI572217 T82650 T82642 T82640 R47360 R47361 R47357 N74672 R47356 R47355 N93086 R47354 R47353 R47342 R47362 R47358 N93441 N56384 N93566 T82622 T82618 AI094748 AW241797 AI759976 T10509 AI814441 AI421977 AI423762 N73686 T11392 AA046406 L11690 NM_001723 M69225 H99655 AI750335 BE000199 M63618 N31521 AA112876 AW265395 AA088909 N21507 X58677 U04850 AW864903 AI830854 AW361101 AW379356 AA301170 T29232 AW965998 H26216 H44230 H44784 AA808916 AA514765 H44575 AA705179 AA586735 AW589403 H25843 AA654993 AI783826 BE087370 AW451982 AW157117 AW161544 W02488 AW167479 AW361027 AW833243 AA912183 AA541622 AI673341 AI266109 AI335896 AI421010 AA053327 AI982962 AI372854 AI674348 AA531087 AI801016 AI372855 AI817816 N52151 D62928 AI401633 AI378549 AI378800 AI337972 D62536 AW972977 AA135826 BE222491 D62195 BE326453 AA225293 AA236461 R85586 AA625141 AA058641 AA135825 AA234644 H50784 R71663 AA053381 W95901 AA053387 AA121501 Y00787 M26130 D14283 BE439795 BE439924 AA362187 BE439515 M17017 C05929 AA381897 AA346136 AA381472 C06304 AA381670 AA381679 AA381965 T11274 AA381318 AA381601 AA381700 AA381952 AW950718 AA381992 D82198 AA381914 AV653399 AA362140 AA381592 AA381967 AA381454 M26383 AA362188 AA382057 AA381781 AA362246 AA381669 AA381395 AA381845 AA381848 AA381603 W40425 AW663238 AA381702 AA381355 AA381356 AA381653 AA362127 AA374516 AA381426 AA381767 AA362270 AA381459 AA362358 AA362160 AA304441 T27482 D83848 AA381877 AA381623 D83851 AA362133 AA381999 AA372837 AA362192 AA362196 AA381806 D82132 AA362107 AA363589 AA296403 T11316 D82218 D83813 Z11686 T10915 AW367405 AW604306 AA363550 AA363514 BE004230 AA381218 W40279 T68485 D82618 W52958 W39356 T27467 D83813 Z11686 T10915 AW367405 AW604306 AA363550 AA363514 BE004230 AA381218 W40279 AA363545 AW377023 AA363453 AA363559 AA381833 AW850620 AA381813 AA381710 AA381584 AA381577 AA381715 AW376990 T11334 AA305271 AA363554 W52491 AW631242 AA363599 D82254 AA363540 AA363596 AW951160 BE122704 AA380985 AW850702 AW630501 AA381229 AA381228 AA381576 AA381795 AA381816 AI274317 AA360958 AA381517 AA381618 AA381891 AI310352 T11037 BE122702 AA834388 W38334 C01358 AW059870 AA371394 AW075978 AI922031 AA381189 AW468452 AI375262 AI870149 C06055 AA381309 AA381625 AA381252 AI620395 AW467642 AJ227913 AW780131 AI742278 AI564251 C75569 AW272612 AI634748 AW339521 AI079248 C75557 AI569162 C75493 AW581509 AW769268 C75524 AI469809 AI579895 C75486 AI697109 AI475413 AI355474 AI282685 AI087873 AI469815 C06100 AA568576 AW014817 C05914 AW272671 C75615 AW337841 AI380580 AW467270 AA847352 W46290 AW780211 AW440851 W45324 C06017 C75643 AI346866 W45400 C05898 C05704 AA381931 AA381177 AA382015 AI476632 AA381274 C05758 C75413 W45362 AW951601 C05910 C75382 W60423 AA095727 C75410 AW188453 AW341742 W60450 AW613454 AI469266 AI473944 BE042737 AW273112 AW467973 C05893 AW272835 W45409 C05668 AI431254 T29157 AI953422 AW510601 W45271 C75538 BE138893 AW662358 AA102526 AI457250 AW615017 AW662707 AW051250 AW470168 AI952442 AA362337 AW015490 AA362269 BE122713 C06363 C06353 AW779405 T68419 AA381217 AA362139 T11140 T11198 AA363591 AA362138 AA362357 AA362344 D56519 AA362132 AA361981 AA362159 AA362110 D83856 D82102 D83842 AW959358 AI373550 AA362225 BE141183 AW178167 AW178162 AW178166 AW178172 AW845893 AW178159 AW178222 AW178213 AW178215 AW178090 AW178091 AW178161 AW178207 AW178210 AW178214 AW178212 BE140918 BE140917 AW178135 AW178205 AW178209 AW178223 AW178220 AW178206 AW178203 AW178165 AW178168 AW178160 AW178136 AW845878 AW178131 AW178138 AW178105 AW845894 AW178129 AW845810 AW845828 AW178216 AW178112 AW178211 AW178224 BE140915 AW178221 AW178130 AW178134 AW178096 AW178108 AW178133 AW178164 AW178218 AW178171 AW178157 AW178158 AW178103 BE141189 AW178170 AW845816 BE141586 AW178156 AW178104 AW178163 AW178093 AW178208 AW178137 AW178140 AW178219 BE141592 AW845901 BE141580 AW178155 BE141598 BE140957
45	408281	1050256_1	H91230 AW182672 AW514652 AW612492 AW182695 AW183350 C03487 C05115 AF070571 H70949 AW149569 AI804276 AA936447 AA987912 N35082 N35065 N43822 N43804 H69776 T80170 H09701 R35799 R19028 AW196589 AI207553 BE221925 BE551043 R61736 AW242757 R53961 T33418 Z45363 AW250525 BE265117 AA195764 AA167076 AW937980 AA166917 AA056984 AI206035 AW023639 AA195520 AA329676 AA678589 AI784331 H55489 AW876581 AW876552 AW268587 N91553 AW268820 AW566003 W19061 BE397160 AW274839 BE296227 AF008551 Z43879 AA313688 AW409753 AA298501 AW957623 BE299015 BE093498 AA431134 N64029 AI038260 AW732512 AI917458 AA628301 AA291514 BE092461 H63889 AI126792 BE092286 H72166 H57843 AI884785 R96793 AW516673 W78726 H78488 BE011847 AI638439 AA834453 AW014897 AI004050 AA804577 AI207188 AW365500 AI689761 AA432153 AA767736 AI738674 R19158 BE503915 AA629662 BE465533 AA602467 AI859635 N58083 AI828708 AI859629 AI148444 R97724 AI652950 BE243218 AI318096 AA704673 AI318060 BE465518 AA745859 AI026750 AW409660 AI265728 AA748628 H58486 AA486497 AI750284 H79032 H54313 H78390 H63492 AW272138 AA488685 R07581 AA736853 AW594462 AI500164 AA832366 Z39943 AA598643 W80533 AA243133 AF011468 NM_003600 AA373999 H54104 AW136695 BE547389 H70678 AB033025 AL359061 AL045836 AI751521 AI752804 AI752650 AA853580 AI752290 AA853460 AI752769 AA852309 AA853785 AA853219 AW068503 AI752069 AI049389 AW068368 BE439518 W52813 BE141833 AI940574 AI750606 AL109718 AA242845 AA315795 AA307741 AW954603 AI752070 AA30794 AI752849 AA307755 AW951677 AA298896 BE439692 AA852453 AW068826 AW853984 AA418236 AA639417 AW290917 AI750592 AI752768 AL045837 AI926513 AW262903 BE439819 AI459360 AW339074 AW295181 AW029483 AI750945 AI750659 AI752525 AI147688 BE440122 AI751522 AI473816 AI752291 AI694639 AI925816 AA599476 AA242752 AW021892 AI755098 AW469299 AW769363 AA853579 AI784082 AA852454 AI925501 AA976657 AW150473 AW166734 AI129586 AA455078 BE536256 AA834910 AI264121 AA715165 AI675186 AA878884 AI937502 H41127 AI613527 AA136856 AI858126 AA062762 AI351420 AW195729 AI433903 W78038 BE143223 AA136950 AA193470 AA082447 AW796079 AW996023 BE065712 AA063003 AI880645 AI880644 AA063458 AA063018 AI444822 AF251237 AA412359 T19106 AW975988 AA948244 AI954712 AA620697 AA758618 AI631681 AA648117 BE620755 BE620196 AW386187 AA747475 AI205793 AA730288 AW467539 AW468376 AW467312 AW337844 AW337833 AW467317 AW467401 AW468247 AW440988 AW440830 AW467337
50	408332 408334 408350 408408 408459 408531 408617 408691 408729 408749 408751 408812 408908	1052056_1 1052079_1 1052676_1 10566_1 1059830_1 1064578_1 1070070_1 1074933_1 107722_1 1078708_1 1078907_1 1083877_1 10893_2	
55			
60			
65			
70	409041	10962_2	
75	409044	109648_1	
80	409070 409073 409103 409105	109839_1 109851_1 109_1 1100052_1	

	409156	110362_1	N76186 R69723 AW444682 BE220376 W49490 AA961099 BE218202 N53704 W73451 A1823360 AW675687 N64773 AA064629 AA064753 AA527475 AW473807 AA199658 A1090188 A1374757 A1769715 A1026060 A1801785 W49491 R72390 R63399 A1742199 A190947 R69629 A1287331 A1769707 A1219372 D20803 A187711 A1472100 W73390 N94037 N94055 AA064789 AW835560 T84873 AW818390 AW818237 AW858911 AW858977 BE072544 W26498 AA070211 AA070030 AA070114 AA070198 AA070217 AA070106 AA070265 AA070334 AA070101 AA070302 AA070278 AA070231 R87083 R01811 T81648 AW383308 AW389668 AW389657 AW609198 AW389649 D49372 Z75668 Z92709 NM_002986 U46572 U46573 AA125790 AW294260 AA127067 A1080514 U34780 A1867933 AA910483 A1446061 A1913625 A1913629 A1537716 A1357416 W69211 AW805343 C21564 AF278761 AA461577 AA460289 A1561173 AA600224 AA074612 AW382145 AL045940 X90780 C03339 C03114 W07136 C02994 C03103 C04896 C05070 W17389 C04180 C05502 W19390 C04558 C04543 AA311399 C05351 C04551 C04456 X54163 NM_000363 C02730 C05613 C05482 R57607 BE140258 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AW751957 AW846083 AW846087 AW846090 AW905138 AW753008 R13818 Z43519 AA373210 H91768 BE172318 AA371497 AA085843 A1307247 A1824005 AW261982 A1625754 N27830 A1679467 A1078259 AW594323 A1335252 AA122264 AA994930 AA111902 N21680 A1498311 AA633551 AA455980 A1625756 AA938642 AA768825 AA811180 AA085906 A1762946 AW977820 AW770523 BE503941 BE219626 AW770778 BE551458 BE550838 BE549582 BE328860 BE550143 AW792909 AW876101 AW792964 AW876100 AW876099 AW792910 AA497117 AA497039 AA996105 A1042190 A1910528 AA088543 A1733733 AA732081 A1269879 AJ001873 R58869 AJ001874 AW301235 AA496916 Z41363 AW857191 AW857192 AW804060 AW805687 H88503 H88502 AW807182 AW807328 AW807063 AW807183 AW807192 AW807033 AW807061 AW807286 AW807097 AW807270 AW807372 AW807280 AW807283 D78367 NM_000223 AF137286 AB007119 C00499 AW809201 AW809176 AW809258 AW809268 AW809236 AW809213 AW809243 AW809187 AW809235 AW809142 AW809186 AW809152 AW809146 AW809144 AW809141 AW809145 AW809170 AW809248 AW809149 AW861207 AW809508 AW810169 AW809654 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	409434	112_1	
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	409632	11445_1	
25	409642	1145579_1	
	409718	11505_1	
	409723	1150962_1	
	409747	1152417_1	
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	409929	1160241_1	
	409955	11619_1	
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	410181	118148_1	
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	410307	11935_1	
	410318	119440_1	
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	410483	1204995_1	
	410500	1206323_1	
	410534	1207247_1	
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	410585	1210225_1	
	410594	1210463_1	
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	410685	121605_1	
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	410797	1221640_1	
	410811	1222814_1	
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	410878	1225667_1	
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	410966	1228071_1	
	410991	1228659_1	
80	410999	1228809_1	
	411018	1229132_1	
	411024	1229310_1	
	411036	122971_1	

			AW854691 AW854689 AW814776 AW854617 AW854635 AW854621 AW854693 AW854694
			BE067650 AW817053
			AW819212 AW819170 BE158474 AW819172 AW819213 AW819200 AW819256 AW819254 AW819178 AW819214 AW819215 AW819233
			AW819171
5	411045	1230222_1	AW865497 AW819775 AW819868 AW866602 AW866561
	411093	1231970_1	AW819944 AW820182 AW820168 AW819959 AW819953
	411131	1233576_1	AW821257 AW821267 AW821283
	411151	1234022_1	AW887330 AI560214 AI629040 N21397 AW770023 AA092291 AA777320 AI612725 AI669633 AI249763 AA703485 AI913790 AI376778 AA846775
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	455964	1389912_1	AI803972 AI493307 AI245155 AA918722 R50713 N35686 AI278165 AW025706 AI885436 R86314 AI582390 AA256123 AI468521 R53094 T89183
	455992	1398552_1	AA621493 AW372583 R05964 AW819303 AI417763 AW293203 BE247001 AA864207 AW819302 AW393209 AW393195 AI870522 R05963
	456027	142104_1	AA380267 AL117573 R51476 AA131283 AA305730 AW960438 T7291 AW504410 W77631 AA243239 AA426041 AA927639 AW792877 AA055133
80			AW291315 AI589104 AI949122 AW025986 AW275328 N51358 AA131190 AA723731 N88864 AA091367 AI738620 AA345291 AA774160 R51372
	456056	14855_1	AI373904 R37681 W72195 AA476597 AI025596 AI242078 AA384072 BE349121 AI023442 AA885019 AI424214 AI964081 AI219465 AW103904
	456083		AA017216 AW591839 AI890043 BE247650 AW793376 AA224322 AI784198 AW190649 BE247646 AA055073 D19892 AA428076 AA165625

			R34233 AA469355 AI302148 AI690055 AA946756 AI697829 BE218045 AA027985 AI734957 AA436215 AW362506 AA469277 AA436214 AW362508 R79964 AW362504 AW362505 AA027984 AI417795 BE066043 AW967592 AA165661 AA251567 C05877 R19957 R53161 R52318 Z44555 BE066030 AW769414 R35560 H08481 AA017309 H91010 N39092 N48447 AW299698 BE270312 AI333779 R68946 AF154846 AA00924 AF075093 AA626790 AI202783 H53869 H53499 AI001163 AA714166 L32164 AA768900 AW182419 AW977135 AI915355 AA994468 AI377886 AI654131 AI674302 AW074683 AA224872 AI791642 AA228308 AI821503 AA230172 AA224838 U00803 NM_002031 AW195632 C05922 W28481 AW967500 AW966876 AW976565 AI417020 AI057022 AA251316 AA744820 AI806037 AW966871 AA251713 AF080576 T49825 AA281037 T49826 AK001714 AW960785 AK001831 BE075311 AW273355 AA928445 AI698734 AW977909 AW268863 AI392846 AA811609 AI565035 AW007245 AI754385 AI092244 AA906509 AW438768 AW751668 AA459681 AA861761 AW118314 D63077 AI537049 AA782718 AW050550 AA430988 AA130556 AA383461 AA337522 AA130593 AA258033 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5	456189	1620717_1	
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10	456303	176884_1	
	456347	18004_1	
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	456443	188540_1	
	456472	19126_1	
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	456510	19507_1	
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	456555	199748_1	
	456561	200378_1	
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	456606	203847_1	
	456737	22551_1	
30	456869	24619_1	
35	456933	256540_2	
	457003	27203_1	
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55	457024	274501_1	
	457030	27473_1	
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70	457039	275248_1	
	457040	27530_2	
75			
80	457041	275843_1	
	457122	287827_1	

457128	28930_1	AI932995 BE064464 AW371902 AW371841 AI885885 BE064457 AA524113 AA721037 AA504343 AA778099 AI800598 AI693112 AI864633 AI690228 AI400990 AW969089 AW371927 AW371912 AW383562 BE151089 AW383568 BE218503 AW383570 AW371899 BE151097 AW371900 AW293095 AW292008 AA434179 AA714780 R45868 W01182 AW957767 AW119223 AI207864 W01578 AA354403 AA805177 AI613299 AW269636 AA481528 AW079101 AF131777 R60489 T81289 AA481594 BE181020 AA465433 AW808125 T84992 AA749191
5	457176 296527_1 457187 298994_1 457225 30546_1	AA436837 AA442594 AA443927 AA444106 AW820035 T20260 T20259 AL049415 AA737756 W46965 W00799 AW340968 AW027417 AW263261 AI420674 AA814921 AA736509 N69991 W368643 W47065 AI090172 AI924139 BE468071 AA375842 AA375767 AW628849 AI422731 AA494558 AA969233 AI142954 AI161089 AI167233 W94484 AI681576 AA249694 AI695943 AA832347 AA476621 AA937792 AI702870 AA455748 AW195100 AI638530 BE502479 AI383418 AA039630 C20777
10	457314 318637_1 457460 340038_1 457506 34672_1 457620 371514_1 457630 373784_1 457652 37972_1 457653 37979_2 457741 395767_1 457756 3_1	AA479597 Z45151 H28821 AI143312 AI394343 AW205239 AA523980 AI831223 AI347180 BE263197 AA765781 AI654500 AF131757 T79901 AA602711 BE078290 AI680903 AI703329 AA609004 AI305245 AI457796 AW295787 AF116656 AI114583 AW838134 AW838525 AW885447 H83251 AW838349 AW838378 AW838175 H83252 AI820719 AI273515 AW592687 AI263784 AI351926 R46866 BE044740 AW827360 AW827623 BE161439 BE044718 BE046207 BE046551 AA653908 BE166581 AA126136 H62964 BE245159 AF280094 AA431918 BE386201 AA707576 AI074267 AA969194 AA693596 H62844 AW134991 AA126014 AI077443 AA689881 AI037956 AA961277 AW204185 AI540791 AI273273 AW627957 AA926890 AI014851 AW081056 AA443705 AW137571 BE139390 AI583851 AI583822 AI583814 AW268341 AI590502 AW302642 AI053871 AI254692 AI591255 AI590260 AI583359 AI583341 AI583752 AI224227 AW302089 AW466960 AA810124 AW302684 AI272921 AI141003 AW589738 AA074714 AA621482 AI796501 AW024557 AA621074 T62627 AA639206 AI913538 AA075135 R54613 AA352975 AW206892 AI688280 AW449243 AA907317 AW134573 AI590492 AI610050 AI834309 AI375556 AI284991 AW968038 BE065030 AA670100 AA781546 AI022472 AA846803 AI497780 N68386 AI382890 T78013 AA699327 W87785 W88613 AW976692 AA806542 AA745856 AI373638 AI073389 AI087143 AA764776 AA913318 AW978161 AW978165 AI016938 AI539270 AW294958 AW511089 AA814849 AF074982 R27906 R31333 R31591 R27812 AW979009 AA828038 AA828148 AA393603 Z19481 AA252342 AI807614 AI913804 AA040176 AA971879 H53388 AF085972 AI291424 H53349 AW015078 AA768307 AA127921 AA723700 AA040841 AA933954 AA213655 AA127972 AA913063 BE327712 AI017585 AA988186 AA628183 AI205930 AA833558 AA974107 AI004390 H48931 AA724004 AW296024 AA897109 AI015000 Z40670 BE504110 BE219908 AW468668 AI002334 U48351 AA969182 BE327312 AW138276 BE467567 AI680815 AI422668 AI264628 AF017648 AI872732 AI024855 AI024877 AI084514 N46645 AW183984 AV648310 AV661871 AI928475 AV647819 T55845 AI185703 AI805813 AW292764 AW136139 AI216724 AI305223 AI458577 AI275569 AI362790 AI275996 N48887 AI299789 BE551384 BE281115 T53860 AV659439 AV659421 BE539929 AI554946 AW362008 AW362553 AI683342 AI376781 AW802754 BE619228 AI693417 AI418256 AW627792 F32979 AW295151 AI425004 AW470228 AI693738 H50554 R99198 H50553 R99197 AW001835 AW612725 AW136670 AI798965 BE467368 AA280216 AI216764 BE622057 AL121193 AW853470 AW853450 AW369075 AW369108 AW578479 AW369106 AW361242 AW361190 N78183 N98648 AI458157 BE041652 BE218014 BE622355 AA369340 AA369515 AW962780 AW962704 AI522129 T56009 R53849 AW236702 AI566105 Z40396 AI630223 AI630470 AW865523 AW865128 AW865467 AW865127 AW865466 R15891 R61471 R61469 N69765 AI014624 AA007214 AW592075 H09780 AA709038 AI335898 H11055 AI559229 F09750 T72573 AA935558 AA988654 AA826438 AI002431 AI299721 AW968226 AI139249 AI701692 AA017303 AW469622 AA259148 AA811690 AA807996 AA744260 AA824494 AA731710 T25332 AA258101 AA970687 AW439497 AI826059 AA018402 AA837392 BE551721 H51878 AI823338 C01488 AW813562 AW301478 AW301560 AI869207 AW138410 AI912712 N40186 BE281314 AI243408 AA027322 AI808913 AW028342 W81290 AI571379 AI382808 AA037071 W79688 R48751 N31808 AI870233 R48752 AW024895 AI333754 AW294659 AI204928 AA351653 H51220 R86843 AA93182 U79298 R15294 F05089 Z42963 R17818 T77498 AA332319 W56049 AA331586 AW881873 AW881865 AW881876 R52345 AI652070 AA400044 AA401512 T08151 W05486 N68378 T33846 AI190920 R43021 AI949980 Z39084 T63413 W37269 F01343 R86669 AI621055 AW117593 AI193211 AW297932 AI500709 AA400056

75 Table 30C

80

Przy: Unique number corresponding to an Eos probe set.
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Przy	Ref	Strand	NL_position
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	400462	9929659	Minus	197610-197785
	400608	9887666	Minus	96756-97558
	400612	9928646	Minus	151513-151662
5	400631	8247025	Minus	56203-56313,56424-56482,57073-57185,57513-57593,57747-57941
	400641	8117693	Plus	4786-4992
	400664	8118496	Plus	13558-13721,13942-14090,14554-14679
	400696	8118812	Minus	77737-77899
	400697	8118812	Minus	79073-79198
10	400706	7249204	Minus	78299-78686
	400816	8569993	Plus	161221-162078
	400842	1927148	Plus	90462-90673
	400859	9757499	Minus	91888-92018,98131-98294,99474-99570
	400861	9757506	Plus	163855-164016
15	400889	9958234	Minus	169782-170036
	401069	3927852	Minus	45682-45831
	401098	9965518	Minus	85632-86174
	401132	8705350	Minus	85679-85795
	401189	9690246	Minus	90815-90929
20	401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
	401240	3355450	Plus	77433-77636
	401324	9863791	Plus	234057-234174
	401355	9796180	Minus	119572-119672
	401368	8670914	Minus	65508-65662
25	401459	9212270	Minus	182001-183323
	401462	6682291	Plus	112763-112909
	401497	7381770	Plus	92607-92813
	401526	7770561	Plus	91570-93177
30	401596	3293210	Plus	63639-63890
	401614	7839924	Plus	17350-17735
	401626	8575943	Minus	238100-238432
	401645	7657839	Minus	34986-35133
	401673	7689903	Minus	122587-122705,122765-123047
35	401694	3540172	Minus	64056-64168
	401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
	401878	8099802	Minus	162268-162474,163089-163195
	401887	7229981	Plus	93973-94120
	401899	7230209	Minus	155620-155815
40	401986	4406829	Minus	31137-31293
	401989	4309964	Minus	118611-118821
	401991	4156128	Plus	2398-2513
	402048	8072512	Plus	43936-44078
	402076	8117410	Plus	128316-128627
45	402090	7249154	Minus	104806-104939,106898-107052
	402112	8139750	Plus	10507-10713
	402131	7704961	Minus	33114-33209,33496-33678
	402145	8018280	Plus	113086-114800
	402318	7582559	Minus	12843-13403
50	402333	8844110	Minus	165693-165856
	402341	7656696	Plus	22583-23699
	402369	9558577	Minus	50417-50522
	402451	9796677	Minus	48137-48343
	402528	7630857	Minus	169609-169742
55	402603	9909396	Minus	141663-141852
	402615	9926801	Plus	131390-132157
	402689	8348025	Minus	5885-6209
	402942	9368398	Plus	102152-102386
	403011	6693597	Minus	3468-3623
60	403053	8748888	Plus	146588-146659,147539-147811
	403089	8954241	Plus	171964-172239
	403188	9838289	Minus	157618-157755
	403218	7630969	Plus	58039-58149
	403271	7230852	Plus	134283-134485
65	403281	8072630	Minus	7521-7728
	403306	8099945	Plus	127100-127251
	403310	8139936	Minus	183883-184026
	403317	8318526	Minus	50623-50834
	403329	8516120	Plus	96450-96598
70	403341	8569175	Plus	30699-30910
	403344	8569726	Plus	70823-70990
	403356	8569930	Plus	92639-93036
	403513	7656757	Minus	155310-155436,158402-158535
	403515	7656757	Minus	173358-179553
75	403525	7960440	Plus	152431-153243
	403534	8076917	Minus	46652-47332
	403568	8101145	Minus	85509-85658
	403572	8101156	Minus	1253-1675
	403574	8101156	Plus	5542-6176
80	403623	8569879	Minus	3519-5426
	403625	8569879	Plus	6551-7111
	403637	8671936	Minus	142647-142771,145531-145762
	403678	7331517	Minus	119573-120430
	403691	7387384	Minus	88280-88463

	403776	7770611	Minus	1414-1513,1624-1756
	403780	8076989	Plus	93160-93409
	403786	8083636	Minus	73028-73217
5	403891	7331467	Minus	191508-193220
	403937	7711761	Minus	12609-12773
	404042	9558573	Plus	5140-5208,8633-8763
	404043	9558573	Plus	29042-29135,46597-46699
	404068	3168621	Minus	18123-18766
10	404108	8247074	Minus	63603-64942
	404166	7596822	Plus	86147-86509
	404193	3881948	Minus	94185-94322
	404196	3805917	Minus	67928-68109
	404249	8655533	Plus	64270-64833
	404367	9965011	Minus	114391-114628
15	404404	7272262	Plus	82112-82244
	404414	7382165	Plus	143127-143398
	404416	7382420	Minus	143042-143216,144704-144853,145800-146048
	404420	7407952	Minus	129817-130586
	404443	7579073	Minus	87198-87441
20	404453	7657714	Plus	27768-29179
	404476	8080699	Plus	101841-102043
	404518	8151988	Plus	84494-84603
	404526	8152087	Plus	121918-122123,125198-125348
	404531	8247909	Plus	20152-20362
25	404561	9795980	Minus	69039-70100
	404569	7249169	Minus	104257-104348,104822-104970
	404582	9739220	Plus	53230-53424
	404587	8698840	Minus	69781-70096
	404588	6456726	Minus	40059-40210
30	404593	9944086	Minus	74922-75788
	404595	9958262	Minus	16764-16900
	404638	9796751	Minus	99433-99528,100035-100161
	404652	9796969	Minus	108172-108296
	404694	9799957	Minus	128092-128227
35	404708	9800828	Plus	77522-77658
	404731	7230299	Minus	168609-168781,182951-183081
	404767	7882827	Minus	23244-23759
	404793	7232206	Minus	61087-61590
	404822	3810614	Plus	7541-8132
40	404834	6911603	Minus	37948-38226
	404957	7407927	Plus	147512-148011
	404967	7523744	Minus	89944-90729
	404988	4662677	Minus	72406-72600,72779-72856
45	405001	6015406	Minus	104646-104819
	405008	6088019	Minus	64091-64267
	405090	8072525	Minus	38552-39202
	405120	8099940	Plus	140176-140340
	405229	7249019	Plus	51081-51701
50	405230	7249032	Minus	97493-97682
	405302	2078453	Minus	121688-121840
	405347	2979602	Minus	977-1116
	405443	7408143	Plus	90716-90887,101420-101577
	405455	7656675	Plus	134112-134671
	405456	7656676	Plus	150052-150208
55	405494	8050952	Minus	70284-70518
	405521	9454643	Plus	65096-65247,77508-77637,81242-81364,84246-84395
	405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
	405605	5836195	Minus	117070-117270
	405608	5815499	Minus	66822-66925
60	405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
	405654	4895155	Minus	53624-53759
	405692	4314424	Plus	61379-62562
	405738	9943998	Plus	44370-45410
	405747	8469069	Minus	153933-154060
65	405780	7248203	Minus	48204-48371
	405783	5738434	Minus	27238-27885
	405784	7417368	Minus	77798-78000
	405829	7109593	Minus	15628-16127
	405920	6758795	Plus	120621-120971
70	405935	6758795	Minus	163112-163652
	405970	8247789	Minus	45795-46295
	406005	8247801	Minus	39912-40220
	406018	6758904	Minus	37795-38168
	406076	9123123	Plus	89972-90319
75	406092	9123919	Plus	251370-251797,252168-252882
	406190	7289992	Minus	22395-22901
	406288	7549620	Plus	111718-112008
	406298	5686278	Minus	30084-30770
	406333	9213235	Plus	64689-64798
80	406364	9256114	Minus	50715-50833
	406378	9256142	Minus	126408-126800
	406413	9256407	Plus	43858-44003,46993-47136
	406468	9795553	Plus	4373-4616,8870-9046,11366-11509,11625-11880

406603 8272659 Minus 39506-38894

5 TABLE 31A: ABOUT 1884 GENES UP-REGULATED IN IPF COMPARED TO NSIP

10 Table 31A lists about 1884 genes whose expression levels are up regulated in idiopathic pulmonary fibrosis (IPF) samples as compared with non-specific interstitial pneumonia (NSIP) samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" idiopathic pulmonary fibrosis sample expression level to "average" non-specific interstitial pneumonia sample expression was greater than or equal to about 2.0. The "average" idiopathic pulmonary fibrosis level was set to the 90th percentile amongst idiopathic pulmonary fibrosis samples. The "average" non-specific interstitial pneumonia level was set to the 90th percentile amongst non-specific interstitial pneumonia samples.

15 Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of IPF (idiopathic pulmonary fibrosis) to NSIP (non-specific interstitial pneumonia)

20	Pkey	ExAccn	Unigene ID	Unigene Title	R1
	450478	AW451709	Hs.271200	ESTs	20.2
	405554				16.1
	432365	AK001105	Hs.274419	hypothetical protein FLJ10244	11.9
	403637				11.2
25	431548	AJ834273	Hs.9711	novel protein	10.8
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	10.4
	439606	W79123	Hs.58561	G protein-coupled receptor 87	10.3
	403574				10.1
	416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.3
30	441233	AA972965	Hs.135568	ESTs	9.1
	415817	U89967	Hs.78867	protein tyrosine phosphatase, receptor-t	8.8
	409532	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	8.4
	432437	W07088	Hs.293685	ESTs	8.3
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	8.2
35	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	8.1
	403329				8.0
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	8.0
	441519	AA972740	Hs.127092	ESTs	7.9
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	7.8
40	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	7.7
	416379	N38857	Hs.203933	ESTs	7.7
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	7.5
	407305	AA715284		gb:mv35f03.r1 NCL_CGAP_Br5 Homo sapiens	7.2
	434683	AW298724	Hs.202639	ESTs	7.2
45	441802	AA968636	Hs.127877	ESTs	6.9
	431242	AA987742	Hs.251278	KIAA1201 protein	6.9
	442377	AA993807	Hs.167367	ESTs	6.9
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	6.8
	428908	AW303529	Hs.144955	ESTs	6.8
50	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	6.7
	457673	AA551569	Hs.272034	hypothetical protein PRO2622	6.7
	458771	AW295151	Hs.163612	ESTs	6.6
	426800	AA385085		gb:EST98959 Thyroid Homo sapiens cDNA 5'	6.6
	440504	AJ948966	Hs.130017	ESTs, Weakly similar to JN0908 H--transp	6.6
55	415025	AW207091	Hs.72307	ESTs	6.5
	438557	AW364104	Hs.143509	hypothetical protein FLJ21924	6.5
	416128	AA173632	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	6.4
	457242	AA457011		gb:aa90c11.r1 Stratagene fetal retina 93	6.3
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	6.3
60	404793				6.2
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	6.2
	415672	N53097	Hs.193579	ESTs	6.2
	455488	AA102322		gb:z19f03.r1 Stratagene colon (937204)	6.2
	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	6.1
65	412282	BE160188		gb:QV1-HT0413-010200-059-g05 HT0413 Homo	6.1
	431622	AW979271	Hs.293184	ESTs	6.1
	405523				6.0
	424693	BE169810	Hs.47557	ESTs	6.0
70	436397	AA715013	Hs.169835	ESTs	6.0
	456476	AA256753		gb:z522b12.r1 NCL_CGAP_GCB1 Homo sapiens	5.9
	434784	AA649051	Hs.164007	ESTs	5.9
	422977	AA631498		gb:mp83h04.s1 NCL_CGAP_Thy1 Homo sapiens	5.9
	442849	R10099	Hs.269805	ESTs	5.9
	451519	AJ800600	Hs.209573	ESTs	5.8
75	412474	AJ791451		gb:n150c09.y5 NCL_CGAP_Ov2 Homo sapiens	5.8
	457081	AA916785	Hs.180510	splicing factor proline/glutamine rich (5.8
	444827	R09764	Hs.20416	ESTs	5.8
	404822				5.7
	402430				5.7
80	457900	AW976692	Hs.291665	ESTs	5.7
	400292	AA250737	Hs.72472	ESTs	5.7
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	5.7
	440172	AA868584	Hs.126154	ESTs	5.7

5	431374	BE258532	Hs.251871	CTP synthase	5.7
	409816	AW500954		gb:U1-HF-BP0p-ai-h-12-0-ULr1 NIH_MGC_5	5.6
	447613	AL041057	Hs.33363	DKFZP434N093 protein	5.6
	417919	AI928203	Hs.86379	ESTs	5.6
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.6
10	439063	AF085922	Hs.113968	ESTs	5.6
	406053				5.5
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	5.5
	451830	H18433	Hs.21542	KIAA1035 protein	5.5
	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	5.5
15	413849	BE173561	Hs.15384	AP1 gamma subunit binding protein 1	5.5
	459458	AW270957	Hs.254577	ESTs, Weakly similar to B34087 hypothetical	5.5
	416154	Z46122		gb:HSCOV8031 normalized infant brain cDN	5.5
	404561				5.4
	428895	AA437124	Hs.187247	ESTs	5.4
20	419247	S65791	Hs.89764	fragile X mental retardation 1	5.4
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	5.4
	440925	AW511090	Hs.130419	ESTs	5.4
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	5.4
	448477	BE612572		gb:601452090F1 NIH_MGC_66 Homo sapiens c	5.4
25	454039	AW079064	Hs.245540	ESTs	5.3
	459664				5.3
	401497				5.3
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	5.3
	444931	AV652066	Hs.75113	general transcription factor IIIA	5.3
30	456680	AL137758	Hs.116072	Homo sapiens mRNA; cDNA DKFZp434H245 (fr	5.3
	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo	5.2
	411402	BE297855	Hs.69855	NRAS-related gene	5.2
	404957				5.2
	436445	AA922213	Hs.121735	ESTs	5.2
35	442617	AW340093	Hs.130538	ESTs	5.2
	416045	H15990	Hs.31403	ESTs	5.2
	425178	H16097	Hs.161027	ESTs	5.2
	441918	AI733373	Hs.128119	ESTs	5.2
	455464	AW983901		gb:RC1-HN0003-220300-011-f10 HN0003 Homo	5.2
40	420929	AI694143	Hs.298251	programmed cell death 4	5.2
	448844	AI581519	Hs.177164	ESTs	5.2
	430686	NM_001942	Hs.2633	desmoglein 1	5.2
	405229				5.1
	417641	AA205015	Hs.54617	hypothetical protein FLJ20060	5.1
45	434167	AA626334	Hs.116153	ESTs	5.1
	450438	AI696071	Hs.253800	ESTs	5.1
	456394	W28506		gb:48f1 Human retina cDNA randomly prime	5.0
	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.0
	417420	T85150	Hs.268814	ESTs	5.0
50	409545	BE298182	Hs.19002	hypothetical protein MGC4675	5.0
	426750	AA383950		gb:EST97403 Thymus II Homo sapiens cDNA	5.0
	440615	AI733055	Hs.130806	ESTs	5.0
	408959	AW890878	Hs.211610	CUG triplet repeat, RNA-binding protein	4.9
	454482	BE147919		gb:RC3-HT0230-160200-016-a08 HT0230 Homo	4.9
55	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	4.9
	452046	AB018345	Hs.27657	KIAA0802 protein	4.9
	407415	AF073328		gb:Homo sapiens tetracycline transporter-	4.9
	450090	AW448940	Hs.202259	ESTs	4.9
	406333				4.9
60	434188	AI765848	Hs.281680	peroxisomal trans 2-enoyl CoA reductase;	4.8
	403344				4.8
	448466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	4.8
	405455				4.8
	411387	AW842339	Hs.130815	hypothetical protein FLJ21870	4.8
65	426097	BE327369	Hs.112238	ESTs	4.8
	427768	T78402	Hs.174880	ESTs	4.8
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	4.8
	415257	F03016	Hs.27513	ESTs	4.8
	441107	AA917075	Hs.190520	ESTs	4.8
70	419519	AI198719	Hs.176376	ESTs	4.8
	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
	426217	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	4.8
	424188	AW954552	Hs.142634	zinc finger protein	4.8
	456987	AI557290	Hs.173536	ESTs	4.8
75	405303				4.8
	414955	C15506		gb:C15506 Clontech human aorta polyA+ mR	4.8
	451620	AW449888	Hs.257224	ESTs	4.7
	421948	L42583	Hs.334309	keratin 6A	4.7
	424780	U39576	Hs.153058	butyrophilin, subfamily 1, member A1	4.7
80	443271	BE568568	Hs.195704	ESTs	4.7
	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	402230				4.7
	422246	AA461032	Hs.5306	hypothetical protein DKFZp586F1122 simil	4.7
	431508	NM_012481	Hs.182979	ribosomal protein L12	4.7
	415236	R41400		gb:y94b12.s1 Soares infant brain 1N1B H	4.7
	413101	BE065215		gb:RC1-BT0314-310300-015-R01 BT0314 Homo	4.6
	444774	AW052174	Hs.196030	ESTs	4.6

5	444414	AW293214	Hs.8752	transmembrane protein 4	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	436853	BE328074	Hs.148661	ESTs	4.6
	445334	AJ610081	Hs.9475	glucose transporter protein 10	4.6
	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	4.6
10	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
	404638				4.6
	447617	AI400762	Hs.176675	ESTs	4.6
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	4.6
	442360	AJ374621	Hs.29055	ESTs	4.5
15	411738	AW859353		gb:MR1-CT0353-150300-102-a12 CT0353 Homo	4.5
	444157	AI125785	Hs.153351	ESTs	4.5
	401365				4.5
	459592	AL037421	Hs.208746	ESTs, Moderately similar to pol. ORF 1 [4.5
	436269	AA707472	Hs.190760	ESTs	4.5
20	459448	AA416773	Hs.275012	EST	4.5
	452090	AA022684	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	4.5
	414899	AW975433	Hs.36288	ESTs	4.5
	443764	F23283		gb:HSPD22980 HM3 Homo sapiens cDNA clone	4.5
	444898	AI201548	Hs.308338	ESTs	4.5
25	417428	N87579		gb:LL2030F Human fetal heart, Lambda ZAP	4.5
	428528	AI004034	Hs.98638	ESTs	4.5
	405605				4.5
	457982	AW856093	Hs.183617	ESTs	4.4
	427731	AA411750	Hs.20943	ESTs	4.4
30	420691	AA829433	Hs.275343	ESTs	4.4
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	4.4
	453080	AI423056	Hs.23921	hypothetical protein DKFZp547A023	4.4
	412147	AW895984		gb:QV4-NN0039-040500-197-e08 NN0039 Homo	4.4
	435747	AI079519	Hs.134398	ESTs	4.4
35	453824	AL138012	Hs.183840	ESTs, Moderately similar to ALU7_HUMAN A	4.4
	458865	T05095	Hs.19597	KIAA1694 protein	4.4
	459037	AW439497	Hs.290656	EST	4.4
	403310				4.4
	425578	U65652	Hs.158313	chromosome 17 open reading frame 1A	4.4
40	427500	AW970017	Hs.293948	ESTs, Weakly similar to S65657 alpha-1C-	4.4
	432020	AJ251509	Hs.272345	phospholipase A1A	4.4
	453043	AW136440	Hs.224277	ESTs	4.4
	456293	AW131715	Hs.311561	ESTs, Weakly similar to CYA7_HUMAN ADENY	4.4
	447879	BE503405	Hs.170437	ESTs, Weakly similar to PRP4_HUMAN SALIV	4.4
45	426646	AA382787	Hs.122713	ESTs	4.4
	454864	AW835775		gb:QV4-LT0016-240200-110-d04 LT0016 Homo	4.4
	404898				4.4
	435434	AA680387	Hs.187850	ESTs	4.3
	443314	AW771701	Hs.54646	ESTs	4.3
50	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	4.3
	441700	AA233556	Hs.126908	hypothetical protein FLJ12994	4.3
	455000	AW850283	Hs.324429	Homo sapiens cDNA FLJ14015 fis, clone HE	4.3
	404767				4.3
	445189	AJ936450	Hs.147482	ESTs	4.3
55	452393	H87398	Hs.99858	ribosomal protein L7a	4.3
	428740	AA433838		gb:zw53e12.r1 Soares_tetal_fetus_Nb2HF8_	4.3
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H	4.3
	410615	AW772721		gb:h195c01.x1 NCL_CGAP_Thy8 Homo sapiens	4.3
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.3
60	406073				4.3
	405692				4.3
	436033	H75391	Hs.255748	ESTs	4.3
	410733	D84284	Hs.66052	CD38 antigen (p45)	4.3
	455587	BE007829		gb:QV0-BN0147-280400-213-d03 BN0147 Homo	4.3
65	459084	H01699	Hs.27289	CGI-125 protein	4.3
	401189				4.3
	435451	AF195420	Hs.303006	ESTs, Weakly similar to gamma-heretulin	4.3
	456407	AW968614		gb:EST380690 MAGE resequences, MAGJ Homo	4.3
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	4.3
70	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3
	436659	AI217900	Hs.144464	ESTs	4.3
	435463	AA682507		gb:zj18f08.s1 Soares_fetal_liver_spleen_	4.3
	455675	BE065984		gb:RC3-BT0319-120200-014-a06 BT0319 Homo	4.3
	439481	AF086294	Hs.125844	ESTs	4.3
75	405287				4.3
	405784				4.3
	436461	AW511956	Hs.293261	ESTs	4.2
	437636	AA764781	Hs.291844	ESTs	4.2
	409629	AW449589	Hs.279724	ESTs	4.2
80	412999	BE046255		gb:hn38g10.x2 NCL_CGAP_RDF2 Homo sapiens	4.2
	403281				4.2
	427531	AA405097	Hs.97957	ESTs	4.2
	451882	AI821324	Hs.100445	ESTs	4.2
	418856	AA362658		gb:EST72900 Ovary II Homo sapiens cDNA 5	4.2
	405494				4.2
	456027	BE327387	Hs.13913	KIAA1577 protein	4.2
	414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens c	4.2

5	421106	AA877124	Hs.172844	ESTs	4.2
	409076	N57559	Hs.82273	hypothetical protein	4.2
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	4.2
	411688	AW953440		gb:EST365510 MAGE resequences, MAGB Homo	4.1
	416614	T83391	Hs.111849	ESTs	4.1
	454434	AA083558	Hs.261288	ESTs	4.1
	404526	AI912555	Hs.157195	peptide YY, 2 (serinalplasmin)	4.1
	446393	AW014174	Hs.301956	zinc finger protein	4.1
	405302				4.1
10	432669	AL043482	Hs.267115	ESTs	4.1
	416972	BE019670		gb:bb28cd01.x1 NIH_MGC_5 Homo sapiens cDN	4.1
	423841	AW753957		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	4.1
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.1
	430484	D82880	Hs.241548	RAS p21 protein activator 2	4.1
15	403895				4.1
	420457	AA482280	Hs.191656	ESTs	4.1
	438993	AA828995		gb:cd77b08.s1 NCI_CGAP_Ov2 Homo sapiens	4.1
	458421	AI279978	Hs.22547	ESTs	4.1
20	458722	AA741545	Hs.282832	ESTs, Weakly similar to T24961 hypotheti	4.1
	411382	BE067246		gb:PM1-BT0348-151299-001-d04 BT0348 Homo	4.1
	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fis, clone L	4.1
	430749	AJ242956	Hs.25960	v-myc avian myelocytomatosis viral relat	4.1
	403625				4.1
25	401887				4.1
	403667				4.1
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.0
	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi	4.0
	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
30	432792	AA448114	Hs.278950	protocadherin beta 1	4.0
	405443				4.0
	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	4.0
	431822	AA516049		gb:mg65d01.s1 NCI_CGAP_Lip2 Homo sapiens	4.0
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinasefructose-2,6-bi	4.0
35	448324	AI571356	Hs.34174	ESTs, Moderately similar to ALU8_HUMAN A	4.0
	456536	AW135986	Hs.257859	ESTs	4.0
	415811	AA450191	Hs.172963	hypothetical protein FLJ14624	4.0
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	4.0
	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	4.0
40	449327	AI638743	Hs.224672	ESTs	4.0
	426062	N57014	Hs.75874	pregnancy-associated plasma protein A	4.0
	433485	AA93076	Hs.201967	aldo-keto reductase family 1, member C2	4.0
	434849	AW292765	Hs.8053	ESTs	4.0
	400268				4.0
45	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	4.0
	445414	AV653692	Hs.146105	ESTs	4.0
	406470				3.9
	429809	AL162010	Hs.223603	Homo sapiens mRNA; cDNA DKFZp761D09121 (3.9
	453098	Z25935	Hs.86379	ESTs	3.9
50	402867				3.9
	431071	AA491379		gb:aa65f05.r1 NCI_CGAP_GCB1 Homo sapiens	3.9
	436298	AW293496	Hs.180138	ESTs	3.9
	440356	AI933184	Hs.127922	ESTs, Moderately similar to S65657 alpha	3.9
	419091	T85332	Hs.178294	ESTs	3.9
55	422591	L07648	Hs.118630	MAX-interacting protein 1	3.9
	426076	AW962714		gb:EST374787 MAGE resequences, MAGG Homo	3.9
	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.9
	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell	3.9
	430072	X13294	Hs.300592	v-myb avian myeloblastosis viral oncogen	3.9
60	413499	BE144884		gb:CMO-HT0182-041099-065-e11 HT0182 Homo	3.9
	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	3.9
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.9
	424029	AB014594	Hs.137579	KIAA0694 gene product	3.9
	455993	BE179085		gb:RCO-HT0613-140300-021-d06 HT0613 Homo	3.9
65	420111	AA255652		gb:aa21h11.r1 NCI_CGAP_GCB1 Homo sapiens	3.9
	403956	W28077	Hs.79389	nel (chicken)-like 2	3.9
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retroviru	3.9
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	3.9
	430140	AW296771	Hs.221999	ESTs	3.8
70	457042	AI382130	Hs.97703	ESTs	3.8
	450236	AW162998	Hs.24684	KIAA1376 protein	3.8
	417705	T90797	Hs.268623	ESTs	3.8
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	3.8
	413071	BE064032		gb:QV3-BT0296-010300-111-b08 BT0296 Homo	3.8
75	437354	AA749215	Hs.291886	ESTs	3.8
	403381				3.8
	425798	AA384002		gb:EST74529 Pineal gland II Homo sapiens	3.8
	459429	AA278779	Hs.335696	EST	3.8
	426365	AA376667	Hs.10283	RNA binding motif protein 88	3.8
80	430757	AI458623		gb:fd04g09.x1 NCI_CGAP_Lu24 Homo sapiens	3.8
	430205	AB025904	Hs.235168	carbonic anhydrase XIV	3.8
	433887	AW204232	Hs.279522	ESTs	3.8
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	3.8
	404043				3.8

5	431333	AA708488	Hs.120127	Homo sapiens cDNA: FLJ22769 fis, clone K	3.8
	451073	AI758905	Hs.206063	ESTs	3.8
	417663	R07483	Hs.180461	ESTs	3.8
	432363	AA534489		gb:mf76g11.s1 NCI_CGAP_Co3 Homo sapiens	3.8
	436975	AA740723	Hs.212644	ESTs	3.8
10	405959				3.8
	400631	AF173937	Hs.109494	secreted protein of unknown function	3.7
	425937	NM_013240	Hs.163846	putative N6-DNA-methyltransferase	3.7
	446158	AI277603	Hs.145990	ESTs, Weakly similar to I38022 hypotheti	3.7
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	3.7
15	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	3.7
	436020	AA778177	Hs.121724	ESTs	3.7
	424989	AA985520	Hs.23575	ESTs	3.7
	426447	AV655843	Hs.169919	electron-transfer-flavoprotein, alpha po	3.7
	441416	AI990139	Hs.148609	ESTs	3.7
20	456443	AW967500	Hs.133543	ESTs	3.7
	402112	R58624	Hs.2186	eukaryotic translation elongation factor	3.7
	404453				3.7
	451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.7
	421037	AI684808	Hs.197653	ESTs	3.7
25	427088	AA398085	Hs.142390	ESTs	3.7
	453375	AI990114	Hs.240091	ESTs	3.7
	453530	AW021633		gb:df26c02.y1 Morton Fetal Cochlea Homo	3.7
	406964	M21305		gb:Human alpha satellite and satellite 3	3.7
	432291	AK001108	Hs.274274	hypothetical protein FLJ10246	3.7
30	449623	C00719	Hs.120440	EST	3.7
	419691	W03298	Hs.193521	ESTs	3.7
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.7
	403271				3.7
	453123	AI953718	Hs.221849	ESTs	3.7
35	400462				3.7
	449804	AI535663	Hs.39379	ESTs	3.7
	443305	AI050693	Hs.133318	ESTs	3.7
	411186	AW821257		gb:PM3-ST0307-231299-001-b11 ST0307 Homo	3.6
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	3.6
40	432189	AA527941		gb:xnh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	3.6
	403296				3.6
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	3.6
	436026	AI349764	Hs.217081	ESTs	3.6
	429864	AA460039	Hs.286	ribosomal protein L4	3.6
45	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	3.6
	442910	AI365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	3.6
	446304	AW104432	Hs.149761	ESTs	3.6
	441216	BE299830	Hs.192908	ESTs	3.6
	421494	AI763322	Hs.152104	ESTs	3.6
50	404476				3.6
	416327	R99822	Hs.36172	ESTs	3.6
	414146	BE549372	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.6
	417401	AA426026	Hs.187615	ESTs	3.6
	401200				3.6
55	411560	AW851186	Hs.179909	hypothetical protein FLJ22995	3.6
	426306	AA447310	Hs.164059	Homo sapiens cDNA FLJ13338 fis, clone OV	3.6
	437918	AI761449	Hs.121629	ESTs	3.6
	447917	AL048037	Hs.164588	ESTs, Moderately similar to neuronal thr	3.6
	421328	BE466506	Hs.3981	ESTs	3.6
60	447290	AI476732	Hs.263912	ESTs	3.6
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.6
	425403	AL023753	Hs.156406	Human DNA sequence from clone 1198H6 on	3.6
	403515				3.6
	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232 (fr	3.6
65	435554	AF208502	Hs.185708	early B-cell factor	3.6
	420481	U50525	Hs.98201	Human BRCA2 region, mRNA sequence CG029	3.6
	410500	R09442		gb:yr26c09.r1 Soares fetal liver spleen	3.6
	439326	W07140	Hs.54721	ESTs	3.6
	426296	R14454	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.6
70	411311	AW836491		gb:PM3-LT0032-281299-002-f02 LT0032 Homo	3.6
	418019	R68911	Hs.176275	ESTs	3.6
	417490	AA203335		gb:zxc56g02.r1 Soares_fetal_liver_spleen_	3.6
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
	416575	W02414	Hs.38383	ESTs	3.5
75	414400	X06948	Hs.897	Fc fragment of IgE, high affinity I, rec	3.5
	418405	AI688282	Hs.11889	ESTs, Highly similar to KIAA1370 protein	3.5
	450350	T97817	Hs.174880	ESTs	3.5
	451704	AI755209	Hs.205616	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	421013	M62397	Hs.1345	mutated in colorectal cancers	3.5
80	407404	AF040257		gb:Homo sapiens TNF receptor homolog mRN	3.5
	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
	430533	AA480895	Hs.201552	ESTs, Weakly similar to T17288 hypotheti	3.5
	457141	AA521410	Hs.41371	ESTs	3.5
	411772	BE170301		gb:QV4-HT0538-040500-193-f05 HT0536 Homo	3.5
	440737	AI375167	Hs.132221	hypothetical protein FLJ12401	3.5
	452728	AI915676	Hs.239708	ESTs	3.5
	423266	AA323875	Hs.193674	ESTs	3.5

5	413543	AA130228	Hs.324611	ESTs, Moderately similar to ALU8_HUMAN A	3.5
	454447	BE163557		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	3.5
	458057	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.5
	437608	AA761605	Hs.292308	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	415549	F11942		gb:HSC33F061 normalized Infant brain cDN	3.5
10	420910	AL049437	Hs.100292	Homo sapiens mRNA; cDNA DKFZp586E1120 (f	3.5
	435793	AB037734	Hs.4993	KIAA1313 protein	3.5
	453211	W84829		gb:zh53f04.r1 Soares_fetal_liver_spleen_	3.5
	418717	AI334430	Hs.86984	ESTs	3.5
	400641				3.5
15	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	3.5
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	3.5
	440364	AA910460	Hs.128626	ESTs	3.5
	458340	AJ457102	Hs.6986	Human glucose transporter pseudogene	3.5
	412281	AJ810054	Hs.14119	ESTs	3.5
20	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	3.5
	416616	H68270		gb:yr81h09.r1 Soares fetal liver spleen	3.5
	444338	AJ937026	Hs.146642	ESTs	3.4
	436946	AW137748	Hs.125956	ESTs	3.4
	431632	AK000992	Hs.333144	Homo sapiens cDNA FLJ10130 fis, clone HE	3.4
25	403306	NM_008825	Hs.74368	transmembrane protein (53kD), endoplasmic	3.4
	422093	AF151852	Hs.111449	CGI-94 protein	3.4
	428816	AA004986	Hs.193852	ATP-binding cassette, sub-family C (CFTR	3.4
	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	3.4
	405970				3.4
30	409434	AF278761	Hs.131581	Homo sapiens testis transcript Y 7 (TTY7	3.4
	416100	H18700	Hs.268799	ESTs	3.4
	431418	X68242	Hs.252722	Hin-1	3.4
	431954	AK001874	Hs.272242	hypothetical protein FLJ11112	3.4
	440388	AJ693520	Hs.223000	ESTs	3.4
35	421072	AJ215069	Hs.89113	ESTs	3.4
	424578	AK001973	Hs.150890	hypothetical protein	3.4
	436331	AJ239495	Hs.120189	ESTs	3.4
	444053	AI122614		gb:qa96b05.x1 Soares_fetal_heart_NbHH19W	3.4
	444453	AW379394	Hs.145126	ESTs	3.4
40	404196				3.4
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	3.4
	409555	AW410788	Hs.256185	ESTs	3.4
	417669	T99898		gb:ye68g01.r1 Soares fetal liver spleen	3.4
	416057	AJ927382	Hs.29857	ESTs	3.4
45	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	3.4
	447738	AJ871000	Hs.161330	ESTs	3.4
	430664	AW969834	Hs.303303	ESTs	3.4
	411377	AW841462		gb:RC6-CN0014-080300-012-B09 CN0014 Homo	3.4
	415769	H94186	Hs.5912	F-box only protein 7	3.4
50	429382	AJ791249	Hs.278054	ESTs, Weakly similar to I38022 hypotheti	3.4
	431474	AL133990	Hs.190642	ESTs	3.4
	456908	AJ953671	Hs.220994	hypothetical protein FLJ14129	3.4
	442826	AJ018777	Hs.131241	ESTs	3.4
	400608				3.4
55	436111	AJ803082	Hs.157212	ESTs	3.4
	452807	AA028933	Hs.162434	ESTs	3.4
	436577	W84774	Hs.17643	ESTs	3.4
	412209	AW901456		gb:RC0-NN1012-270300-031-c07 NN1012 Homo	3.4
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	3.4
60	423871	AA331906		gb:EST35805 Embryo, 8 week 1 Homo sapien	3.4
	447516	W05365	Hs.102971	hypothetical protein FLJ14751	3.4
	409623	AW449185		gb:UJ-H-BI3-akg-e-05-0-UJ.s1 NCI_CGAP_Su	3.4
	416182	NM_004354	Hs.79069	cyclin G2	3.4
	420854	AW296927		gb:UJ-H-BW0-ajc-c-07-0-UJ.s1 NCI_CGAP_Su	3.4
65	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.4
	432404	AA535246	Hs.50852	ESTs	3.4
	458695	AV660159	Hs.282284	ESTs, Weakly similar to I38022 hypotheti	3.4
	440727	AJ073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	3.3
	428766	AA477989	Hs.98800	ESTs	3.3
70	439667	AJ056618	Hs.134314	ESTs	3.3
	456231	H73183	Hs.129885	ESTs, Weakly similar to 2004399A chromos	3.3
	454318	AW367764	Hs.7857	erythrocyte membrane protein band 4.1-1	3.3
	411966	AA099113	Hs.118609	ESTs	3.3
	443644	AJ080491	Hs.93270	ESTs, Moderately similar to S65657 alpha	3.3
75	437037	T63804		gb:yc21e09.r1 Stratagene lung (937210) H	3.3
	407664	AW063476	Hs.279080	ESTs	3.3
	405780				3.3
	426567	AA381579	Hs.182962	ESTs	3.3
	400432	AX015809	Hs.287757	Sequence 8 from Patent WO9950285	3.3
80	403356				3.3
	404518	AJ815601	Hs.79197	CD83 antigen (activated B lymphocytes, I	3.3
	413581	BE150618		gb:RC3-HT0272-110100-013-c06 HT0272 Homo	3.3
	429875	AJ091815		gb:qa58b06.s1 Soares_NhHMPu_S1 Homo sapi	3.3
	433785	BE044593	Hs.112704	ESTs	3.3
	437876	AA770151	Hs.126424	ESTs	3.3
	444870	AJ200621	Hs.148504	ESTs	3.3
	453324	W26592	Hs.232089	ESTs	3.3

5	437963	BE396279		gb:601309785F1 NIH_MGC_44 Homo sapiens c	3.3
	425361	AA355933	Hs.132221	hypothetical protein FLJ12401	3.3
	406813	AI580090	Hs.48295	RNA helicase family	3.3
	426692	AK001751	Hs.171835	hypothetical protein FLJ10889	3.3
	407456	AJ237589		gb:Homo sapiens mRNA for T-box transcrip	3.3
	433183	AF231338	Hs.222024	transcription factor BMAL2	3.3
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE	3.3
	438456	AA913381	Hs.190513	ESTs	3.3
10	453242	T98327	Hs.18343	ESTs	3.3
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	3.3
	412040	D86519	Hs.73086	neuropeptide Y receptor Y6 (pseudogene)	3.3
	435070	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	3.3
	444443	AI149286	Hs.55099	rab5 GTPase activating protein (GAP and	3.3
15	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	3.3
	454145	AA046872	Hs.62798	ESTs	3.3
	405264				3.3
	411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro	3.3
	416816	T71168	Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	3.3
20	435325	AI038388	Hs.119309	ESTs	3.3
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	3.3
	428356	AL046991	Hs.10338	ESTs	3.3
	429216	AI369472	Hs.65407	ESTs	3.3
	429106	AA446612		gb:zw85g07.s1 Soares_total_fetus_Nb2HF8_	3.3
25	405720				3.3
	400889				3.3
	416294	D86980	Hs.79170	KIAA0227 protein	3.3
	422094	AF129535	Hs.272027	F-box only protein 5	3.3
	425374	AI904013		gb:MR-BT041-220199-104 BT041 Homo sapien	3.3
30	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	3.3
	427374	AI150033	Hs.143686	ESTs	3.3
	443367	AW071349	Hs.215937	ESTs	3.3
	446645	AI336596	Hs.156294	ESTs	3.3
	457604	AI004397	Hs.334552	Homo sapiens cDNA FLJ14930 fis, clone PL	3.3
35	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.3
	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	3.3
	458885	AA411303	Hs.30022	ESTs, Weakly similar to NAH6_HUMAN SODIU	3.2
	429508	U9250	Hs.210862	T-box, brain, 1	3.2
	437454	AL390159	Hs.269812	Homo sapiens mRNA; cDNA DKFZp761M0415 (f	3.2
40	430503	AA533574	Hs.152274	ESTs	3.2
	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	3.2
	421698	T89677	Hs.324323	ESTs	3.2
	412321	AW936913		gb:RC1-DT0029-030200-012-08 DT0029 Homo	3.2
	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.2
45	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	441705	AI087052	Hs.55993	ESTs	3.2
	403619				3.2
	435608	AW183971	Hs.250896	ESTs	3.2
	426701	AI968103	Hs.209461	Homo sapiens cDNA FLJ12836 fis, clone NT	3.2
50	401132				3.2
	407764	BE008347		gb:CM0-BN0154-080400-325-h04 BN0154 Homo	3.2
	409425	U40462	Hs.54452	zinc finger protein, subfamily 1A, 1 (lk	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	443603	BE502601	Hs.134289	ESTs, Weakly similar to KIAA1063 protein	3.2
55	419936	AI792788		gb:xl91d05.y5 NCL_CGAP_Kid5 Homo sapiens	3.2
	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	3.2
	406592				3.2
	446530	AV658909	Hs.282642	ESTs	3.2
	454466	AA984138	Hs.155101	ATP synthase, H+ transporting, mitochond	3.2
60	401449				3.2
	431196	AW974436	Hs.154929	ESTs	3.2
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	3.2
	459459	AA460445		gb:zx66h11.r1 Soares_total_fetus_Nb2HF8_	3.2
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	3.2
65	427335	AA448542	Hs.251677	G antigen 7B	3.2
	455236	AW875972		gb:CM3-PT0014-071299-051-b05 PT0014 Homo	3.2
	425156	AA351364		gb:EST59099 Infant brain Homo sapiens cD	3.2
	404588				3.2
	413087	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
70	444910	AI201849		gb:xs76g04.x1 NCL_CGAP_Pt28 Homo sapiens	3.2
	426660	NM_002719	Hs.171734	protein phosphatase 2, regulatory subuni	3.2
	438315	R56795	Hs.82419	ESTs	3.2
	425523	AB007948	Hs.158244	KIAA0479 protein	3.2
	419340	AA236590	Hs.87530	ESTs	3.2
75	425636	AK001243	Hs.158370	hypothetical protein FLJ10381	3.2
	430553	AW392821		gb:CM4-ST0275-021299-053-h09 ST0275 Homo	3.2
	457030	AI301740	Hs.173381	dihydropyrimidine-like 2	3.2
	447375	AI376660	Hs.257822	ESTs	3.2
	408334	AW514652	Hs.321637	ESTs	3.2
80	410085	AA428482	Hs.58589	glycogenin 2	3.2
	410536	N39533		gb:yr27d04.s1 Soares fetal liver spleen	3.2
	448495	AW136516	Hs.208515	ESTs	3.2
	405634				3.2
	431098	AW501465	Hs.249230	ribonuclease L (2',5'-oligoadenylate	3.2

	421581	U89331	Hs.105932	short stature homeobox	3.1
	440633	AJ140686	Hs.263320	ESTs	3.1
	453264	AA034137	Hs.271955	ESTs	3.1
5	411656	AW855576		gb:CAA-CT0278-221099-027-d01 CT0278 Homo	3.1
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypothe	3.1
	426591	AA431127	Hs.98685	ESTs	3.1
	446966	C01448	Hs.300511	ESTs	3.1
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
10	455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	3.1
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.1
	423657	AL045128	Hs.1691	glucan (1,4-alpha-), branching enzyme 1	3.1
	400816				3.1
	410307	AF022913	Hs.62187	phosphatidylinositol glycan, class K	3.1
15	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.1
	400315	U46120	Hs.193392	Human expressed unknown mRNA	3.1
	411965	BE467339	Hs.280115	ESTs	3.1
	416316	H58721	Hs.271628	ESTs	3.1
	400613				3.1
20	414819	BE177320	Hs.156148	hypothetical protein FLJ13231	3.1
	434833	AF156548	Hs.192969	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.1
	418693	AI750878	Hs.87409	thrombospondin 1	3.1
	416258	N45661	Hs.90011	adenylosuccinate synthase	3.1
25	405093				3.1
	415273	Z39840	Hs.22229	ESTs	3.1
	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
	422654	AA314316	Hs.163725	ESTs	3.1
	414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens c	3.1
30	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	3.1
	402790				3.1
	438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	3.1
	447524	D80449	Hs.45177	ESTs	3.1
	448835	BE277929	Hs.11081	UBX domain-containing 2	3.1
35	415979	H16427	Hs.271501	ESTs, Weakly similar to I54374 gene NF2	3.1
	434479	AI138213	Hs.162035	olfactory receptor, family 52, subfamily	3.1
	426724	AA383623	Hs.293616	ESTs	3.1
	418105	AW937488	Hs.178000	ESTs, Weakly similar to FV1 MOUSE FRIEND	3.1
	405608				3.1
	406506				3.1
40	421216	AV649282	Hs.102664	vesicle-associated membrane protein 4	3.1
	452755	AW138937	Hs.213436	ESTs, Weakly similar to A34087 hypothe	3.1
	404288				3.1
	429878	AA460188	Hs.127263	ESTs	3.1
45	439834	AI754576	Hs.124523	ESTs	3.1
	454564	AW807573		gb:MR1-ST0088-021299-004-g01 ST0088 Homo	3.1
	450491	BE045604	Hs.202301	ESTs	3.1
	409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	3.1
	400579				3.1
50	402953				3.1
	404285				3.1
	426890	AA393167	Hs.41294	ESTs	3.1
	457770	BE065030	Hs.124179	ESTs	3.1
	435477	BE218708	Hs.117270	hypothetical protein FLJ14345	3.1
55	436391	AJ227892	Hs.146274	ESTs	3.1
	456083	U46922	Hs.77252	fragile histidine triad gene	3.1
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.1
	430101	AF110002	Hs.233363	guanylate cyclase activator 1C	3.1
	449238	AA428229	Hs.331561	muscle-specific RING-finger protein 3	3.1
60	452605	AW968557	Hs.90012	hypothetical protein FLJ23441	3.1
	456323	AW752389	Hs.87296	Homo sapiens cDNA FLJ20269 fis, clone HE	3.1
	429828	AB019494	Hs.225767	IDN3 protein	3.1
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	3.1
	452762	AW501435	Hs.278582	v-akt murine thymoma viral oncogene homo	3.1
65	401344				3.1
	455511	BE144762		gb:CMD-HT0180-041099-065-b04 HT0180 Homo	3.1
	455280	AW886156		gb:RCS-OT0078-150300-021-E08 OT0078 Homo	3.1
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.1
	423600	AI633559	Hs.310359	ESTs	3.1
70	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	3.0
	407257	AB006834		gb:Homo sapiens mRNA for HRV Fab N6-VH,	3.0
	457041	AA399018	Hs.250835	ESTs	3.0
	421482	AL135462	Hs.104715	inversin	3.0
	459062	AA059246	Hs.110293	ESTs	3.0
75	436475	R58805	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.0
	411622	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	3.0
	417489	AW953341	Hs.22573	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
	409699	BE154650		gb:PM3-HT0344-071299-003-c08 HT0344 Homo	3.0
80	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-1	3.0
	443741	AW451759	Hs.145420	ESTs	3.0
	405090				3.0
	432267	AK000872	Hs.274227	Homo sapiens cDNA FLJ10010 fis, clone HE	3.0
	445409	AI949081	Hs.147862	ESTs	3.0

	449347	AV649748	Hs.295901	KIAA0493 protein	3.0
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	3.0
	406364				3.0
5	418409	AA219332	Hs.120869	ESTs, Weakly similar to R107_HUMAN H-REV	3.0
	427050	AA397789	Hs.161803	ESTs	3.0
	431778	AL080276	Hs.268562	regulator of G-protein signalling 17	3.0
	448405	AW207634	Hs.170849	ESTs	3.0
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	3.0
10	438165	AA779344	Hs.138136	ESTs, Weakly similar to 1510254A L1 repe	3.0
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	3.0
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	3.0
	426424	BE081745	Hs.272188	Homo sapiens cDNA FLJ12090 fis, clone HE	3.0
	419505	AA243660	Hs.143061	ESTs	3.0
	403743				3.0
15	415452	F09134	Hs.12839	ESTs	3.0
	426579	NM_005756	Hs.184942	G protein-coupled receptor 64	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
	455851	BE146879		gb:QV4-HT0222-261099-014-c11 HT0222 Homo	3.0
	400227				3.0
20	436219	AK001695	Hs.146589	hypothetical protein FLJ10701	3.0
	439037	AF075084		gb:Homo sapiens full length insert cDNA	3.0
	439693	AI741816	Hs.125897	ESTs	3.0
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	3.0
	403513				3.0
25	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	3.0
	440122	AI733011	Hs.127678	ESTs	3.0
	448446	AI521251	Hs.171030	ESTs	3.0
	422563	BE299342	Hs.19348	hypothetical protein FLJ13119	3.0
	448130	AW271635	Hs.170717	ESTs	3.0
30	420288	AW071225	Hs.245556	ESTs	3.0
	428201	AA424158	Hs.206461	ESTs	3.0
	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	3.0
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.0
	404513				3.0
35	412074	S74683	Hs.73139	ADP-ribosyltransferase 1	3.0
	407762	AW236638	Hs.29475	ESTs	3.0
	403396				3.0
	436938	AW139680	Hs.161393	ESTs	3.0
40	458090	AI282149	Hs.55213	ESTs, Highly similar to FXD3_HUMAN FORKH	2.9
	400706				2.9
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	2.9
	444600	R41398	Hs.6996	ESTs	2.9
	403786				2.9
45	430187	AI799909	Hs.158989	ESTs	2.9
	451700	AI470262	Hs.29553	ESTs	2.9
	456649	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	2.9
	457503	AW970244	Hs.162188	ESTs	2.9
	446251	AW867156	Hs.282589	ESTs, Weakly similar to I38022 hypotheti	2.9
	406327				2.9
50	434671	R34758		gb:yg01g02.r1 Soares infant brain 1N1B H	2.9
	430175	AA468724		gb:ne09a06.s1 NCI_CGAP_Co3 Homo sapiens	2.9
	454186	BE141030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	2.9
	449459	BE546846	Hs.195048	ESTs	2.9
55	435934	R19382	Hs.117869	ESTs	2.9
	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	414514	BE327365	Hs.280187	ESTs	2.9
	423717	AA330036	Hs.152003	ESTs	2.9
60	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
	430982	R17432	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	2.9
	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fis, clone HE	2.9
	456186	W26642		gb:34b8 Human retina cDNA randomly prime	2.9
	412222	AA528283	Hs.292737	ESTs	2.9
65	459201	AW391177		gb:MR3-ST0203-221299-023-d05 ST0203 Homo	2.9
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.9
	435579	AI323273	Hs.156924	ESTs	2.9
	417027	AA192306	Hs.23926	triadin	2.9
	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.9
	445909	BE262656	Hs.32603	hypothetical protein MGC3279 similar to	2.9
70	418343	AA216372	Hs.159501	ESTs	2.9
	459440	BE048054		gb:tz46c03.y1 NCI_CGAP_Bm52 Homo sapien	2.9
	403341				2.9
	445635	AI769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	453830	AA534296	Hs.20953	ESTs	2.9
75	455866	BE149024		gb:CMO-HT0249-291099-084-c04 HT0249 Homo	2.9
	407676	AW064111	Hs.279823	ESTs	2.9
	437913	AI140825	Hs.121623	ESTs	2.9
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
	457049	AW631495	Hs.27135	B-cell receptor-associated protein BAP29	2.9
80	400491	H25530	Hs.50668	solute carrier family 22 (organic cation	2.9
	456189	H91010	Hs.44940	ESTs	2.9
	441874	AA970389	Hs.128055	ESTs	2.9
	416483	H58311	Hs.165077	ESTs	2.9

	420879	N31165	Hs.238837	ESTs, Weakly similar to S43603 RNA bindi	2.9
	446447	AJ300402	Hs.202250	ESTs	2.9
	439953	AA918129	Hs.124638	ESTs	2.9
	400643				2.9
5	436594	AI419982	Hs.156189	ESTs	2.9
	438402	D16902	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	2.9
	451353	N21043	Hs.42932	ESTs	2.9
	419791	AI579909	Hs.105104	ESTs	2.9
	415628	F13080		gb:HSC3ID041 normalized infant brain cDN	2.9
10	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (f	2.9
	454747	AW818535		gb:RC1-ST0278-140300-016-05 ST0278 Homo	2.9
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.9
	457178	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	2.9
	401526				2.9
15	408751	N91553	Hs.258343	ESTs	2.9
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	2.9
	417320	AA195667	Hs.86022	ESTs	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
	444125	AI124882	Hs.118121	ESTs	2.9
20	453901	BE065902		gb:RC2-BT0318-150200-011-b09 BT0318 Homo	2.9
	421847	NM_014717	Hs.108884	KIAA0390 gene product	2.8
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.8
	422225	BE245652	Hs.118281	zinc finger protein 266	2.8
	403011				2.8
25	405170				2.8
	435878	R08330	Hs.20152	ESTs	2.8
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	2.8
	400394	AF040257	Hs.283818	Homo sapiens TNF receptor homolog mRNA,	2.8
	411244	AW833768		gb:QV4-TT0008-130100-077-e06 TT0008 Homo	2.8
30	418117	AW969708	Hs.293332	ESTs	2.8
	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
	417801	AA417383	Hs.82582	Integrin, beta-like 1 (with EGF-like rep	2.8
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypothei	2.8
	402131				2.8
35	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	2.8
	438160	AA779332	Hs.122671	ESTs	2.8
	407594	AW057584	Hs.160681	ESTs	2.8
	417877	AI025829	Hs.86320	ESTs	2.8
	439235	N45513	Hs.46608	ESTs	2.8
40	451257	AA016255	Hs.31856	ESTs, Weakly similar to KIAA1453 protein	2.8
	437113	AA744693		gb:ny26c10.s1 NCI_CGAP_GCB1 Homo sapiens	2.8
	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	2.8
	409978	D31897	Hs.57714	double C2-like domains, alpha	2.8
	410672	AW794600		gb:RC6-UM0014-170300-022-C05 UM0014 Homo	2.8
45	412236	AW902583		gb:QV3-NN1024-260400-171-f10 NN1024 Homo	2.8
	417827	T79366	Hs.108258	actin binding protein; macrophilin (microf	2.8
	420206	M91463	Hs.95958	solute carrier family 2 (facilitated glu	2.8
	449676	AW380579	Hs.209657	ESTs	2.8
	454778	AW820199		gb:QV2-ST0296-190100-029-a07 ST0296 Homo	2.8
50	451203	AW070604	Hs.46517	ESTs	2.8
	450180	AW449644	Hs.257182	ESTs	2.8
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.8
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
	450003	AA777809	Hs.191995	ESTs	2.8
55	401602				2.8
	413986	Z43567		gb:HSC1FC021 normalized infant brain cDN	2.8
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	2.8
	415652	T79213	Hs.272073	ESTs	2.8
	404076				2.8
60	409416	AW388359	Hs.10667	ESTs	2.8
	420814	AA721158	Hs.190440	ESTs	2.8
	426960	AA393713		gb:zf71h04.r1 Soares_testis_NHT Homo sap	2.8
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.8
	448597	BE613250	Hs.98265	KIAA1877 protein	2.8
65	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	2.8
	433077	AA314262	Hs.301917	YDD19 protein	2.8
	436720	AW975902		gb:EST388011 MAGE resequences, MAGN Homo	2.8
	447410	AI470235	Hs.172698	EST	2.8
	414652	AI620599	Hs.72058	ESTs	2.8
70	430454	AW469011	Hs.105635	ESTs	2.8
	412417	AA102268	Hs.158622	ESTs	2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	430660	R11884	Hs.100826	ESTs	2.8
	401098				2.8
75	454036	AA374766	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	2.8
	403549				2.8
	414394	AI904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.8
	412323	AW937143		gb:PM1-DT0041-281299-001-01 DT0041 Homo	2.8
	433513	AI566356	Hs.171437	ESTs	2.8
80	446677	AI800311	Hs.156291	ESTs	2.8
	457756	AA126136	Hs.38125	interferon-induced protein 75, 52kD	2.8
	450895	N66727	Hs.10957	ESTs	2.8
	434352	AF129505	Hs.86492	small muscle protein, X-linked	2.8

	449358	AA001229	Hs.131436	ESTs	2.8
	422816	AA323586	Hs.93235	ESTs	2.8
	420756	AA411800	Hs.189900	ESTs	2.8
5	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
	448870	BE181783	Hs.175358	ESTs, Weakly similar to A47582 B-cell gr	2.8
	451206	H86228	Hs.271780	ESTs, Weakly similar to 138022 hypothe	2.8
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
	458023	AW978161	Hs.268555	5'-3' exonuclease 2	2.8
10	422260	AA315993	Hs.105484	regenerating gene type IV	2.8
	429638	AI916662	Hs.211577	kinectin 1 (kinesin receptor)	2.8
	408936	AL138043	Hs.293549	ESTs	2.8
	411762	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	2.8
	416192	NM_005036	Hs.998	peroxisome proliferative activated recep	2.8
15	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.7
	406992	S82472		gb:beta -pot=DNA polymerase beta (exon a	2.7
	421003	T72080	Hs.95667	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
	445611	AW418497	Hs.145583	ESTs	2.7
20	445747	AI820863	Hs.145328	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	445017	AI205493	Hs.176860	ESTs	2.7
	411726	AW858612		gb:CM3-CT0341-190400-152-h12 CT0341 Homo	2.7
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	2.7
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.7
25	427134	AA398409	Hs.173561	EST	2.7
	435689	AA694284		gb:zi35c02.s1 Soares_fetal_liver_spleen_	2.7
	429282	N27596	Hs.21342	ESTs	2.7
	435731	AA695581	Hs.186811	ESTs	2.7
30	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.7
	421274	BE160327	Hs.104572	ESTs	2.7
	403776				2.7
	409526	BE298751	Hs.55014	hypothetical protein FLJ10206	2.7
	410201	AA126129		gb:zm78c07.r1 Stratagene neuroepithelium	2.7
35	427839	AA608823	Hs.98244	ESTs	2.7
	447884	H29505		gb:ym60d10.r1 Soares infant brain 1NIB H	2.7
	449396	BE169100	Hs.195029	ESTs	2.7
	422988	AW673847	Hs.97321	ESTs	2.7
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.7
40	434890	AF161345	Hs.283930	Homo sapiens HSPC082 mRNA, partial cds	2.7
	412400	AW948066		gb:RC0-MT0012-280300-031-h10 MT0012 Homo	2.7
	413998	AW103807	Hs.243933	ESTs	2.7
	403677				2.7
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	2.7
45	430698	AA492071		gb:ne97b04.s1 NCI_CGAP_Kid1 Homo sapiens	2.7
	432591	AA643238	Hs.146144	ESTs	2.7
	446800	AI341635	Hs.156486	ESTs	2.7
	454938	AW846134		gb:QV0-CT0179-091199-049-d02 CT0179 Homo	2.7
	456859	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.7
50	445233	AV653034	Hs.297559	ESTs	2.7
	448756	AI739241	Hs.171480	ESTs	2.7
	418379	AA218940	Hs.137516	fidgetin-like 1	2.7
	435068	H16262	Hs.31415	ESTs	2.7
	406092				2.7
55	422036	AA302647	Hs.271891	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.7
	441541	AA938663	Hs.199828	ESTs	2.7
	451395	AI082419	Hs.114761	ESTs	2.7
	456880	BE153208		gb:PM0-HT0335-050400-007-F10 HT0335 Homo	2.7
	459275	AI808913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.7
60	423949	AI014546	Hs.130912	ESTs	2.7
	435420	AI928513	Hs.59203	ESTs	2.7
	439418	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	2.7
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	2.7
	447453	AW608645	Hs.18800	hypothetical protein FLJ20281	2.7
65	454767	BE069199		gb:QV3-BT0379-010300-105-g03 BT0379 Homo	2.7
	413252	BE074910		gb:RCS-BT0580-170300-021-F12 BT0580 Homo	2.7
	402429				2.7
	403760				2.7
	433128	AB021923	Hs.23367	EST-YD1 protein	2.7
70	435448	H17132	Hs.27085	ESTs	2.7
	445706	AA305520	Hs.108812	hypothetical protein FLJ22004	2.7
	422171	U50529	Hs.112434	Novel human gene mapping to chromosome 13	2.7
	459023	AW968226	Hs.60798	ESTs	2.7
	443246	T75157	Hs.337603	ESTs, Weakly similar to T08680 hypothe	2.7
75	404569				2.7
	410181	AA682210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
	422897	AA679784	Hs.4290	ESTs	2.7
	427038	NM_014633	Hs.173288	KIAA0155 gene product	2.7
	449880	AI673006	Hs.231948	ESTs	2.7
80	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
	415268	R53935	Hs.287827	ESTs, Highly similar to MDR3_HUMAN MULTI	2.7
	446554	AA151730	Hs.301769	nudix (nucleoside diphosphate linked mol	2.7
	452512	AW363486	Hs.337635	ESTs	2.7
	440728	AW066077	Hs.153272	Homo sapiens cDNA: FLJ22715 fis, clone H	2.7

	419481	AI879195	Hs.90606	15 kDa selenoprotein	2.7
	454352	AW389668		gb:RC2-ST0168-071299-013-06 ST0168 Homo	2.7
	422831	R02504	Hs.332943	ESTs	2.7
5	413646	BE155042		gb:PMO-HT0349-101299-002-E04 HT0349 Homo	2.7
	426872	AA410446	Hs.112011	ESTs, Weakly similar to unknown [H.sapi	2.7
	459160	AI904723		gb:CM-BT066-120299-092 BT066 Homo sapien	2.7
	421338	AA287443		gb:zs52c10.r1 NCI_CGAP_GCB1 Homo sapiens	2.7
	446002	AI346468	Hs.145789	ESTs	2.7
10	454716	AW850684		gb:IL3-CT0219-160200-063-D12 CT0219 Homo	2.7
	406664	L34041	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	2.7
	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	2.7
	408691	AW250525		gb:2821626.5prime NIH_MGC_7 Homo sapiens	2.7
	454754	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	2.7
15	439451	AF086270	Hs.278554	heterochromatin-like protein 1	2.7
	445225	AI216555	Hs.202398	ESTs	2.7
	427175	H06924	Hs.23782	hypothetical protein FLJ12847	2.7
	411816	AW884609		gb:PM3-SN0017-240300-001-h03 SN0017 Homo	2.7
	438135	AI253025	Hs.190426	ESTs	2.7
	405981				2.7
20	406005				2.7
	430762	AI343652	Hs.105667	ESTs	2.7
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	2.7
	412105	H07971	Hs.94319	VPS10 domain receptor protein	2.7
25	434684	AA737282	Hs.190911	ESTs	2.7
	445660	AI702668	Hs.201955	ESTs	2.7
	400844				2.6
	415725	BE219771	Hs.237146	hypothetical protein FLJ12752	2.6
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.6
30	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 Integrin	2.6
	430052	AF102850	Hs.227933	Alg5, S. cerevisiae, homolog of	2.6
	440310	AA878939	Hs.125406	ESTs	2.6
	425659	AK000590	Hs.158836	hypothetical protein FLJ20583	2.6
	417252	AA195014	Hs.85971	ESTs	2.6
35	427167	AI239607	Hs.99196	hypothetical protein MGC11324	2.6
	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.6
	414546	BE379492		gb:601236215F1 NIH_MGC_44 Homo sapiens c	2.6
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.6
40	442240	AI791883	Hs.292719	ESTs	2.6
	452821	AW471181	Hs.160874	ESTs	2.6
	410238	N94320	Hs.144225	ESTs	2.6
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	2.6
	440801	AA906366	Hs.190535	ESTs	2.6
45	440274	R24595	Hs.7122	scrapie responsive protein 1	2.6
	411597	AW852925		gb:PMO-CT0248-131099-001-f10 CT0248 Homo	2.6
	417956	AA210704	Hs.190465	ESTs	2.6
	420621	AA278808		gb:zs79c09.r1 NCI_CGAP_GCB1 Homo sapiens	2.6
	425176	AW015844	Hs.155005	TEA domain family member 1 (SV40 transcr	2.6
50	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	2.6
	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
	426098	NM_014906	Hs.166351	KIAA1072 protein	2.6
	435113	AA665469	Hs.117136	ESTs	2.6
	438188	AA779975	Hs.128859	ESTs	2.6
55	445550	AI242754	Hs.137306	ESTs	2.6
	458804	AL157625		gb:DKFZp761L2016_r1 761 (synonym: hamy2)	2.6
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.6
	436407	T88803	Hs.271507	ESTs, Weakly similar to TIM_HUMAN PROBAB	2.6
	425195	AA352026	Hs.94319	VPS10 domain receptor protein	2.6
60	418282	AA215535	Hs.98133	ESTs	2.6
	442757	AI739528	Hs.28345	ESTs	2.6
	413470	N20934		gb:yx54c11.s1 Soares melanocyte 2NbHM Ho	2.6
	428527	AI902398	Hs.34492	Cyt19 protein	2.6
	441209	AA922939	Hs.135742	ESTs	2.6
	458679	AW975460	Hs.143563	ESTs	2.6
65	442279	AW867006	Hs.159970	ESTs	2.6
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.6
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	2.6
	404845				2.6
70	411693	AW857271		gb:CMO-CT0307-210100-158-g09 CT0307 Homo	2.6
	438298	H23542	Hs.181788	ESTs	2.6
	444517	AI939339	Hs.146883	ESTs	2.6
	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6
	457630	AI680803	Hs.112627	ESTs	2.6
75	424015	N95696	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	2.6
	417563	AA203701		gb:zx52a10.r1 Soares_fetal_liver_spleen_	2.6
	413174	AA723564	Hs.191343	ESTs	2.6
	438875	AA827640	Hs.189059	ESTs	2.6
	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	2.6
80	423257	AW161039	Hs.125878	synapsin III	2.6
	431086	AI829692	Hs.211561	ESTs	2.6
	409337	H71289	Hs.220535	ESTs	2.6
	442818	AK001741	Hs.8739	hypothetical protein FLJ10879	2.6
	410004	AI298027	Hs.5057	carboxypeptidase D	2.6

	455935	BE158687	gb:CMD-HT0395-280100-169-b09 HT0395 Homo	2.6
	403273			2.6
	445955	AA332209	Hs.158196 transcriptional adaptor 3 (ADA3, yeast h	2.6
	425626	AI537536	Hs.173519 ESTs	2.6
5	451531	AA018311	Hs.114762 ESTs	2.6
	428085	AA421081	Hs.12388 ESTs	2.6
	429761	AI276780	Hs.135173 ESTs	2.6
	437958	BE139550	Hs.121668 ESTs, Moderately similar to PC4259 ferri	2.6
	442656	W74633	Hs.303720 ESTs	2.6
10	413088	BE064962	gb:RC1-BT0313-130400-016-c02 BT0313 Homo	2.6
	419107	AW085152	Hs.292987 ESTs	2.6
	435766	R11673	Hs.186498 ESTs	2.6
	452879	AW905328	Hs.180842 ribosomal protein L13	2.6
	440400	AA594364	Hs.125594 ESTs, Weakly similar to T25472 hypotheti	2.6
15	440460	H92571	Hs.234478 Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
	424146	AA705092	Hs.202368 ESTs	2.6
	439950	AW937417	Hs.293561 ESTs	2.6
	410366	AI267589	Hs.302689 hypothetical protein	2.6
	417485	AA203304	Hs.32826 CGI-130 protein	2.6
20	412566	AW962574	gb:EST374847 MAGE resequences, MAGG Homo	2.6
	416498	U33632	Hs.79351 potassium channel, subfamily K, member 1	2.6
	440397	AA884448	Hs.157239 ESTs	2.6
	451236	AI767406	Hs.207026 ESTs, Weakly similar to B56205 transcrip	2.6
	411819	AW947884	gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.6
25	430357	AW976789	Hs.165607 ESTs	2.6
	432869	AW974094	gb:EST386197 MAGE resequences, MAGM Homo	2.6
	427506	AK000134	Hs.179100 hypothetical protein FLJ20127	2.6
	401614			2.6
	404531	Z25884	Hs.121483 chloride channel 1, skeletal muscle (Th	2.6
30	426698	AA394104	Hs.97489 ESTs	2.6
	440479	AA886461	Hs.208161 ESTs	2.6
	443160	AI467915	Hs.36053 ESTs	2.5
	419323	AI092379	Hs.135275 ESTs	2.5
	442813	AI018435	Hs.270970 ESTs	2.5
35	436198	AK001084	Hs.333498 Homo sapiens cDNA FLJ10222 fis, clone HE	2.5
	433561	BE540937	Hs.20104 hypothetical protein FLJ00052	2.5
	434059	AA649162	Hs.236456 ESTs	2.5
	454836	AW833711	gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
	458589	AV654623	Hs.288141 hypothetical protein MGC3156	2.5
40	459716			2.5
	436340	R42246	Hs.21606 ESTs	2.5
	428020	L19058	Hs.181581 glutamate receptor, ionotropic, kainate	2.5
	416951	AA190926	Hs.190785 ESTs, Moderately similar to S65657 alpha	2.5
	401078			2.5
45	410644	AW902125	gb:QV0-NN1022-120500-220-h12 NN1022 Homo	2.5
	411660	AW855718	gb:RC1-CT0279-070100-021-a06 CT0279 Homo	2.5
	425201	AA352111	gb:EST60061 Activated T-cells XX Homo sa	2.5
	455252	AW876627	gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
	439096	AA630185	Hs.269680 ESTs	2.5
50	442627	AI027990	Hs.132303 ESTs	2.5
	457799	AF220188	Hs.236510 uncharacterized hypothalamus protein HTM	2.5
	428799	AI478619	Hs.104677 ESTs	2.5
	450402	BE218027	Hs.89969 ESTs	2.5
	411156	AW819939	Hs.273629 ESTs	2.5
55	431673	AW971302	Hs.293233 ESTs	2.5
	415706	BE182587	Hs.57485 ESTs	2.5
	412882	BE006919	Hs.134106 ESTs	2.5
	441300	R35063	Hs.181536 ESTs	2.5
	413257	BE075035	gb:PM3-BT0584-260300-002-g05 BT0584 Homo	2.5
60	434662	AA641957	gb:ms18d08.r1 NCI_CGAP_GCB1 Homo sapiens	2.5
	455255	AW877139	gb:QV2-PT0010-160400-133-g01 PT0010 Homo	2.5
	417137	U46265	Hs.81281 mitochondrial ribosomal protein S21	2.5
	417909	R35614	gb:yg66e08.r1 Soares infant brain 1N1B H	2.5
	458043	AW979009	Hs.326108 ESTs	2.5
65	417006	AW673606	Hs.80758 aspartyl-LRNA synthetase	2.5
	442006	AW975183	Hs.292663 ESTs, Weakly similar to S72482 hypotheti	2.5
	455766	BE079307	gb:RC1-BT0623-120200-011-g09 BT0623 Homo	2.5
	454032	W31790	Hs.194293 ESTs, Weakly similar to I54374 gene NF2	2.5
	444963	AI916973	Hs.213603 ESTs	2.5
70	443626	AW792804	Hs.134002 ESTs	2.5
	454532	AA344685	Hs.58831 regulator of Fas-induced apoptosis	2.5
	428832	AA578229	Hs.324239 ESTs, Moderately similar to ZN91_HUMAN Z	2.5
	442003	AW297497	Hs.201891 ESTs	2.5
	452768	AW069459	Hs.61539 ESTs	2.5
75	411355	AW838479	Hs.22692 ESTs	2.5
	458890	AW865523	gb:PM4-SN0020-010400-009-b05 SN0020 Homo	2.5
	400074			2.5
	405241			2.5
	413096	BE065209	gb:RC1-BT0314-310300-015-b12 BT0314 Homo	2.5
80	414349	BE512968	gb:50117229GF1 NIH_MGC_15 Homo sapiens c	2.5
	422884	AW860875	Hs.13256 ESTs	2.5
	429515	AL031228	Hs.204370 DNA segment on chromosome 6 (unique, pse	2.5
	431925	AK000890	gb:Homo sapiens cDNA FLJ10028 fis, clone	2.5

	442653	BE269247		gb:601185486F1 NIH_MGC_8 Homo sapiens cD	2.5
	401882				2.5
	458257	U48351	Hs.201219	ESTs, Weakly similar to S18946 ultra hig	2.5
	405336				2.5
5	439492	AF086310	Hs.103159	ESTs	2.5
	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	2.5
	436359	ZB3806		gb:Hsapiens mRNA for axonemal dynein he	2.5
	429322	D86984	Hs.199243	KIAA0231 protein	2.5
	431699	NM_0011173	Hs.267831	Rho GTPase activating protein 5	2.5
10	437107	AA745598	Hs.291840	ESTs, Weakly similar to I78885 serine/th	2.5
	441953	H11695	Hs.322901	disrupter of silencing 10	2.5
	442777	AW341541	Hs.271153	ESTs	2.5
	453361	AA035197	Hs.107375	ESTs	2.5
	455275	AW977806		gb:EST389810 MAGE resequences, MAGO Homo	2.5
15	457824	R84938		gb:yt6504.r1 Soares retina N2b4HR Homo	2.5
	428550	AW297880	Hs.98661	ESTs	2.5
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	2.5
	456359	AJ567991	Hs.93574	homeo box D3	2.5
	414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sapiens c	2.5
20	452528	AA742457	Hs.291479	ESTs	2.5
	408444	AW661839	Hs.253204	ESTs	2.5
	440327	R12581	Hs.191146	ESTs	2.5
	410406	AJ969703	Hs.1466	glycerol kinase	2.5
25	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ121897 fis, clone H	2.5
	418948	AI217097		gb:qd43h07.x1 Soares fetal_heart_NbHH19W	2.5
	435427	AA682573	Hs.188982	ESTs, Weakly similar to organic anion tr	2.5
	427791	AA412446	Hs.98138	ESTs	2.5
	403509	AF231919	Hs.18759	KIAA0539 gene product	2.5
	436590	AI393115	Hs.127655	ESTs	2.5
30	455556	AW995423		gb:QV0-BN0042-010400-183-g08 BN0042 Homo	2.5
	405869				2.5
	408274	R17315		gb:yg12g11.r1 Soares infant brain 1N1B H	2.5
	448015	AI458065	Hs.23196	ESTs	2.5
	454190	AW177821		gb:IL3-HT0059-180699-007-C05 HT0059 Homo	2.5
35	436154	AA764950	Hs.119898	ESTs	2.5
	406377				2.5
	437030	AA742577	Hs.303781	EST	2.5
	420815	AA280684	Hs.270584	ESTs	2.5
	418421	R58620	Hs.85050	phospholamban	2.5
40	423638	AI003521	Hs.130310	Homo sapiens mRNA for cyclin B3 isoform	2.5
	415425	F08365		gb:HSCZSA121 normalized infant brain cDN	2.5
	404577				2.5
	403568				2.5
	425967	NM_007159	Hs.4007	Sarcolemmal-associated protein	2.5
45	449899	AI610700	Hs.103280	ESTs	2.5
	451078	AI927694	Hs.204470	ESTs	2.5
	453343	AA905353	Hs.121622	ESTs	2.5
	428728	NM_016625	Hs.191381	hypothetical protein	2.5
	409642	AW450809	Hs.257347	ESTs	2.5
50	426235	AI631964	Hs.34447	ESTs	2.5
	452043	H86231		gb:yt03f02.r1 Soares retina N2b5HR Homo	2.5
	401992				2.5
	419910	AA662913	Hs.190173	ESTs, Weakly similar to A46010 X-linked	2.5
55	411038	AA857218	Hs.297007	membrane-bound transcription factor prot	2.5
	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	2.5
	449311	AI657014		gb:t49a12.x1 NCL_CGAP_GC6 Homo sapiens	2.5
	454566	AW807605		gb:MR4-ST0098-120100-001-b06 ST0098 Homo	2.5
	454597	AW809648		gb:MR4-ST0124-261099-015-d01 ST0124 Homo	2.5
60	413875	BE176776		gb:RC3-HT0588-110300-011-g09 HT0588 Homo	2.4
	421583	AA293333		gb:zt53c09.r1 Soares ovary tumor NbHOT H	2.4
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	2.4
	454437	AI248173	Hs.191460	hypothetical protein MGC12936	2.4
	419187	AA234852	Hs.44693	ESTs	2.4
65	444493	R59410	Hs.282094	ESTs, Moderately similar to I38022 hypot	2.4
	405547				2.4
	454086	AW885909	Hs.6975	PRO1073 protein	2.4
	417508	BE163512	Hs.180877	H3 histone, family 3B (H3.3B)	2.4
	416277	W78765	Hs.180145	HSPC030 protein	2.4
70	420976	AJ924940	Hs.108082	ESTs, Weakly similar to T31636 hypotheti	2.4
	406468				2.4
	408617	R61736	Hs.124128	ESTs	2.4
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	2.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	2.4
75	454137	AW500340	Hs.313876	ESTs, Weakly similar to I38022 hypotheti	2.4
	455328	AW896438		gb:PM1-NN0047-040400-001-d09 NN0047 Homo	2.4
	409500	U08098	Hs.54576	sulfotransferase, estrogen-preferring	2.4
	434138	AA625804		gb:zu86h01.s1 Soares testis_NHT Homo sap	2.4
	419511	AA429750	Hs.75113	general transcription factor IIIA	2.4
80	437980	R50393	Hs.278436	KJAA1474 protein	2.4
	439999	AA115811	Hs.6838	ras homolog gene family, member E	2.4
	403501				2.4
	446845	AI343645	Hs.156108	ESTs	2.4
	401775				2.4

	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	2.4
	411836	AW901879	Hs.314453	ESTs	2.4
	412879	BE092219		gb:IL2-BT0734-240400-071-B04 BT0734 Homo	2.4
	421083	AA283628	Hs.298016	ESTs, Weakly similar to I38022 hypothe	2.4
5	423513	AF035960	Hs.129719	transglutaminase 5	2.4
	428882	AA436915	Hs.131748	ESTs, Moderately similar to ALU7_HUMAN A	2.4
	428945	AW192803	Hs.98974	ESTs, Weakly similar to S65824 reverse t	2.4
	434627	AI221894	Hs.39311	ESTs	2.4
	435256	AF193766	Hs.13872	cytokine-like protein C17	2.4
10	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.4
	458239	BE439877	Hs.283389	ESTs	2.4
	414093	BE544867	Hs.283077	centrosomal P4.1-associated protein; unc	2.4
	441262	AI809130	Hs.176906	ESTs	2.4
	402076				2.4
15	427962	AA946582	Hs.8700	deleted in liver cancer 1	2.4
	400587				2.4
	403053	R58624	Hs.2186	eukaryotic translation elongation factor	2.4
	411203	AW872430	Hs.273743	ESTs	2.4
	447849	AI538147	Hs.164277	ESTs	2.4
20	454201	AB023191	Hs.44131	KIAA0974 protein	2.4
	424131	AA335714	Hs.199665	ESTs	2.4
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	2.4
	440385	AA884283	Hs.192136	ESTs	2.4
	417976	BE565892	Hs.83077	Interleukin 18 (interferon-gamma-inducin	2.4
25	447179	AW015833	Hs.157299	ESTs	2.4
	412977	AA125910	Hs.191461	ESTs	2.4
	436958	AA740322	Hs.293539	Homo sapiens mRNA for KIAA1758 protein,	2.4
	401381				2.4
	403891				2.4
30	408419	AW250092	Hs.305953	zinc finger protein 83 (HPF1)	2.4
	417002	T79613	Hs.14613	ESTs	2.4
	439446	AI927629	Hs.57873	ESTs	2.4
	458570	AW971698	Hs.12627	TJ6 protein	2.4
	458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
35	459344	AW499533	Hs.257976	ESTs	2.4
	413488	BE144017		gb:MR0-HT0165-191199-004-d09 HT0165 Homo	2.4
	412114	AW893891	Hs.240833	ESTs, Weakly similar to I38022 hypothe	2.4
	423296	AW957193	Hs.3327	Homo sapiens cDNA: FLJ22219 fls, clone H	2.4
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	2.4
40	428268	AA424957	Hs.294132	ESTs	2.4
	450947	AI745400	Hs.204662	ESTs	2.4
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	2.4
	438142	T90309	Hs.269651	ESTs	2.4
	409239	AA740875	Hs.44307	ESTs, Moderately similar to I38022 hypot	2.4
45	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.4
	429063	AW363845	Hs.122142	ESTs, Weakly similar to A46010 X-linked	2.4
	433868	AA612860	Hs.337300	ESTs	2.4
	401645				2.4
	432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	2.4
50	453393	AW956392	Hs.110376	ESTs	2.4
	436054	AI076262	Hs.119813	ESTs	2.4
	425433	AA357471		gb:EST66274 LNCAP cells I Homo sapiens c	2.4
	417712	AA205569	Hs.194193	ESTs, Moderately similar to ALU1_HUMAN A	2.4
	420639	AI683116	Hs.25328	ESTs, Moderately similar to ALU7_HUMAN A	2.4
55	453369	BE551550	Hs.232630	ESTs	2.4
	405017				2.4
	405385				2.4
	435633	AI248152	Hs.270047	ESTs	2.4
	457128	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.4
60	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	2.4
	434544	C05875	Hs.91575	ESTs	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
	455219	AW879403		gb:PMO-OT0019-150300-002-d01 OT0019 Homo	2.4
	458734	AI554946	Hs.158794	ESTs	2.4
65	442179	AA983842	Hs.333555	chromosome 2 open reading frame 2	2.4
	444313	AI140494	Hs.197955	KIAA0704 protein	2.4
	440448	AA885428	Hs.125646	ESTs	2.4
	441498	AI379248	Hs.58742	ESTs	2.4
	438205	AA780365	Hs.122161	ESTs	2.4
70	402615				2.4
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.4
	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	2.4
	413697	AA131315	Hs.47144	DKFZP586N0819 protein	2.4
	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.4
75	449007	AI620433	Hs.193201	EST, Weakly similar to NIP2_HUMAN BCL2/A	2.4
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	2.4
	418857	D10216	Hs.89394	POU domain, class 1, transcription facto	2.4
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	2.4
	458914	BE327696	Hs.280922	ESTs	2.4
80	435061	AI651474	Hs.163944	ESTs	2.4
	416458	AA180511		gb:zp53f03.r1 Stratagene NT2 neuronal pr	2.4
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.4
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase 1, l	2.4

	403003				2.4
	405347				2.4
	406091				2.4
5	428402	AW237531	Hs.326876	Homo sapiens SOX6 mRNA, complete cds	2.4
	438762	AW844412	Hs.65450	reticulation 4	2.4
	455780	BE088828		gb:CM2-BT0693-230300-129-g09 BT0693 Homo	2.4
	457024	AA397546	Hs.119151	ESTs	2.4
	404249				2.4
10	443921	AI091310	Hs.134848	ESTs	2.4
	407055	X89211		gb:H.sapiens DNA for endogenous retrovir	2.4
	417154	AI674701	Hs.21388	ESTs	2.4
	419720	AA249131	Hs.337778	hypothetical protein FLJ11068	2.4
	405230				2.4
	405935				2.4
15	436998	AA745625	Hs.291414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	445748	U80766	Hs.13252	Human EST clone 22453 mariner transposon	2.4
	419233	AA458873	Hs.178306	ESTs	2.3
	414277	BE269910		gb:601186291F1 NIH_MGC_8 Homo sapiens cD	2.3
20	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.3
	453736	AL118674	Hs.34871	zinc finger homeobox 18	2.3
	410888	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo	2.3
	434239	AF119910	Hs.283047	hypothetical protein PRO2954	2.3
	434098	AA625499		gb:af69g08.r1 Soares_NhHMPu_S1 Homo sapi	2.3
25	414195	BE263293	Hs.89605	cholinergic receptor, nicotinic, alpha p	2.3
	445688	AI248205	Hs.153244	ESTs	2.3
	451656	BE327088	Hs.212752	ESTs	2.3
	423956	W28203	Hs.136169	Homo sapiens clone 25215 mRNA sequence,	2.3
	413445	BE141022		gb:MR0-HT0067-201099-002-d10 HT0067 Homo	2.3
30	436149	AF754308	Hs.159452	ESTs	2.3
	405629				2.3
	432702	AW973953	Hs.293744	ESTs	2.3
	433377	AI752713	Hs.43845	ESTs	2.3
	444711	AI188739	Hs.148488	ESTs	2.3
35	445621	AI733818	Hs.145549	ESTs	2.3
	456432	AW966931	Hs.179662	nucleosome assembly protein 1-like 1	2.3
	449236	AJ403126	Hs.26373	Homo sapiens cDNA: FLJ23449 fis, clone H	2.3
	459024	AA020799	Hs.262869	plasminogen-like	2.3
	441037	AA913360	Hs.126468	ESTs	2.3
40	431577	T34523	Hs.302040	Homo sapiens DNA sequence from PAC 43401	2.3
	438782	AA828380	Hs.126733	ESTs	2.3
	412329	AW937445		gb:QV3-DT0043-090200-080-c09 DT0043 Homo	2.3
	410999	AW813004		gb:RC3-ST0186-230300-019-h02 ST0186 Homo	2.3
	429044	AI261490	Hs.145527	ESTs	2.3
45	431655	AW971119		gb:EST383206 MAGE resequences, MAGL Homo	2.3
	439642	W81441	Hs.153967	ESTs	2.3
	441721	AI288259	Hs.127652	ESTs	2.3
	443482	AW188093	Hs.250385	ESTs	2.3
	403416	AI744626	Hs.151385	KIAA0564 protein	2.3
50	416443	N69469	Hs.194225	ESTs	2.3
	419714	AA758751	Hs.98216	ESTs	2.3
	415511	AI732617	Hs.182362	ESTs	2.3
	412344	AW938384	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.3
	449264	AI637649	Hs.196105	ESTs	2.3
55	451664	AA889081	Hs.153952	5' nucleotidase (CD73)	2.3
	441269	AW015206	Hs.178784	ESTs	2.3
	402333				2.3
	453649	Y07494	Hs.34114	ATPase, Na+/K+ transporting, alpha 2 (+)	2.3
60	430680	AW138724	Hs.168974	ESTs, Highly similar to ALU7_HUMAN ALU S	2.3
	404367				2.3
	403696				2.3
	441622	AW450957	Hs.224864	ESTs	2.3
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo	2.3
	411093	BE067650		gb:MR4-BT0358-090300-003-e01 BT0358 Homo	2.3
65	428548	AA430058	Hs.98649	EST	2.3
	404059				2.3
	446861	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.3
	413640	BE158118		gb:MR2-HT0378-240200-205-d09 HT0378 Homo	2.3
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	2.3
70	435338	AA678071	Hs.194300	ESTs, Weakly similar to 138022 hypotheti	2.3
	442710	AI015831	Hs.23210	ESTs	2.3
	444206	AW301017	Hs.146492	ESTs	2.3
	451250	AA491275	Hs.236940	hypothetical protein FLJ12542	2.3
	454784	AW820626		gb:RC0-ST0299-190100-012-e10 ST0299 Homo	2.3
75	458455	AV648310	Hs.213488	ESTs	2.3
	458521	AI651039	Hs.148559	ESTs	2.3
	407938	AA905097	Hs.85050	phospholamban	2.3
	439546	AF088056		gb:Homo sapiens full length Insert cDNA	2.3
	441274	AW593781	Hs.131357	ESTs	2.3
80	454314	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo	2.3
	409660	AW452065	Hs.258905	ESTs	2.3
	428532	AF157326	Hs.184786	TBP-interacting protein	2.3
	411384	AW842115		gb:RC0-CN0026-090200-031-e11 CN0026 Homo	2.3
	453687	T55674	Hs.283108	hemoglobin, gamma G	2.3

	410140	AL134435	Hs.22269	neurexin 3	2.3
	422443	NM_014707	Hs.116753	histone deacetylase 7B	2.3
	409071	AW316932	Hs.181982	ESTs	2.3
	421253	AI188102	Hs.31028	ESTs	2.3
5	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypotheti	2.3
	448458	AW614367	Hs.171054	ESTs	2.3
	457225	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.3
	443718	AI083580	Hs.221373	ESTs	2.3
	445568	H00918	Hs.268744	KIAA1796 protein	2.3
10	400582				2.3
	411262	AW834480		gb:MR2-TT0014-151199-011-b07 TT0014 Homo	2.3
	401145				2.3
	407440	AF227135		gb:Homo sapiens candidate taste receptor	2.3
	455121	BE156459		gb:QV0-HT0368-040100-082-f06 HT0368 Homo	2.3
15	459077	N20370	Hs.235883	ESTs	2.3
	448117	H49129	Hs.172982	ESTs	2.3
	453331	AI240665	Hs.8895	ESTs	2.3
	443751	AI285839	Hs.153324	EST	2.3
	402038				2.3
20	402176				2.3
	456605	AI827786	Hs.259044	ESTs	2.3
	432479	AL042844	Hs.275675	katanin p80 (WD40-containing) subunit B	2.3
	402527				2.3
	449272	AW137656	Hs.197645	ESTs	2.3
25	411024	BE062590		gb:QV1-BT0260-281099-023-f05 BT0260 Homo	2.3
	455608	BE011437		gb:CM4-BN0220-080500-170-f03 BN0220 Homo	2.3
	458818	AI523857	Hs.232257	ESTs	2.3
	419875	AA853410	Hs.93557	proenkephalin	2.3
	405521				2.3
30	436517	BE080932	Hs.135225	ESTs	2.3
	456801	AW961886	Hs.138263	Homo sapiens clone 24528 mRNA sequence	2.3
	430444	AW296421	Hs.121035	ESTs	2.3
	456208	AW299698	Hs.334625	Homo sapiens cDNA FLJ14890 fis, clone PL	2.3
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.3
35	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
	419337	AW291112	Hs.209978	ESTs	2.3
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypotheti	2.3
	454456	AW850984		gb:IL3-CT0220-150200-068-H08 CT0220 Homo	2.3
40	454633	AW811380		gb:IL3-ST0143-290999-019-D05 ST0143 Homo	2.3
	457028	AW449838	Hs.97562	ESTs	2.3
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.3
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.3
	430850	BE144152		gb:MR0-HT0165-060200-006-e02 HT0165 Homo	2.3
45	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	2.3
	421227	R78581	Hs.266308	mosaic serine protease	2.3
	426902	AI125334	Hs.97408	ESTs	2.3
	430789	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	2.3
	447475	AI380797	Hs.158992	ESTs	2.3
50	452148	AF007143	Hs.28205	Homo sapiens clone 23738 mRNA sequence	2.3
	430712	AW044647	Hs.196284	ESTs	2.3
	458103	AW780192	Hs.267596	ESTs	2.3
	420959	AA282119	Hs.88975	ESTs	2.3
	444098	AV647969	Hs.109594	KIAA1451 protein	2.3
55	445841	AI245987	Hs.149442	ESTs	2.3
	449276	AW241510	Hs.252713	ESTs	2.3
	452294	AI871925	Hs.117895	ESTs, Moderately similar to A47582 B-cell	2.3
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	2.3
	459497	AA825742	Hs.87517	ESTs	2.3
60	412852	BE004117	Hs.37415	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	437539	AA974673	Hs.121419	ESTs	2.3
	421813	BE048255		gb:tz49b05.y1 NCL_CGAP_Bm52 Homo sapien	2.3
	411994	R67298	Hs.109087	Homo sapiens cDNA: FLJ22845 fis, clone K	2.3
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOT	2.3
	452463	R36452	Hs.300817	ESTs	2.3
65	404936				2.3
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.3
	440836	AW370882	Hs.222080	ESTs	2.3
	405120				2.3
	400238				2.3
70	407609	AW082279	Hs.244106	ESTs	2.3
	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.3
	420478	AA521259	Hs.193796	ESTs	2.3
	441417	AI733297	Hs.144474	ESTs	2.3
	445117	AI208754	Hs.147369	ESTs	2.3
75	431162	AW971180		gb:EST383268 MAGE resequences, MAGL Homo	2.2
	437036	AI571514	Hs.133022	ESTs	2.2
	455849	BE146866		gb:QV4-HT0222-211099-014-f06 HT0222 Homo	2.2
	447624	AI640326	Hs.62713	ESTs	2.2
80	439780	AL109588		gb:Homo sapiens mRNA full length insert	2.2
	405706				2.2
	447732	AI758398	Hs.161318	ESTs	2.2
	440625	BE539853	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	2.2
	404257				2.2

	437722	AW292947	Hs.122872	ESTs, Weakly similar to JU0033 hypothel	2.2
	449133	AI531655	Hs.197919	ESTs	2.2
	456555	AW592167	Hs.293299	ESTs	2.2
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiesterase	2.2
5	428192	AA424051	Hs.304742	ESTs	2.2
	435634	T82384		gb:yc1405.r1 Stratagene lung (937210) H	2.2
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
	446096	AI276454		gb:q17a12.x1 Soares_NhHMPu_S1 Homo sapi	2.2
10	448106	AI800470	Hs.171941	ESTs	2.2
	450232	BE300815	Hs.201326	ESTs	2.2
	436134	AK000618	Hs.123784	ESTs	2.2
	448466	AI522109	Hs.171066	ESTs	2.2
	420678	AW593288	Hs.3530	TLS-associated serine-arginine protein 2	2.2
	430692	X80240		gb:H.sapiens endogenous retrovirus HERV-	2.2
15	446453	AV658469	Hs.188646	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	423611	AB011163	Hs.129908	KIAA0591 protein	2.2
	444050	AW138295	Hs.135024	ESTs	2.2
	431532	AI537817	Hs.270311	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
20	422669	H12402	Hs.119122	ribosomal protein L13a	2.2
	403388				2.2
	403780				2.2
	419423	D26488	Hs.90315	KIAA0007 protein	2.2
	424719	H90452		gb:yo1c03.r1 Soares fetal liver spleen	2.2
25	431453	AW753917		gb:RC0-CT0299-291199-031-F02 CT0299 Homo	2.2
	442078	AW268583	Hs.262629	ESTs	2.2
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.2
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	2.2
	427119	AW880562	Hs.114574	ESTs	2.2
	400486				2.2
30	448482	AW294078	Hs.171092	ESTs	2.2
	402621				2.2
	408363	NM_003389	Hs.44396	coronin, actin-binding protein, 2A	2.2
	424584	H10692	Hs.13310	ESTs	2.2
35	445061	AI253094	Hs.145227	ESTs	2.2
	431065	AA491286	Hs.128792	ESTs	2.2
	411908	L27943	Hs.72924	cytidine deaminase	2.2
	441826	AW503603	Hs.129915	phosphotriesterase related	2.2
	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	2.2
40	422677	AL046388	Hs.208206	hypothetical protein FLJ21162	2.2
	455534	AW991925		gb:PM3-BN0011-130100-002-b07 BN0011 Homo	2.2
	400163				2.2
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.2
	409206	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo	2.2
45	410556	R32158		gb:yh67a07.s1 Soares placenta Nb2HP Homo	2.2
	432584	AA928829	Hs.47099	hypothetical protein FLJ21212	2.2
	439482	W70045	Hs.58089	ESTs	2.2
	447877	AI435184	Hs.164252	ESTs	2.2
	418297	R91254		gb:yp94e12.s1 Soares fetal liver spleen	2.2
50	403534				2.2
	410594	AW770778	Hs.281238	ESTs	2.2
	414000	BE242814	Hs.323494	ESTs, Weakly similar to T27544 zinc resi	2.2
	432762	NM_014099	Hs.278924	PRO1768 protein	2.2
	437606	AA761594	Hs.122440	ESTs	2.2
55	438550	AW976002	Hs.258402	ESTs	2.2
	439628	N22415	Hs.189080	ESTs	2.2
	444540	AI693927	Hs.265165	ESTs	2.2
	450024	AA005129		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.2
60	456481	AA256033	Hs.108110	DKFZP547E2110 protein	2.2
	435138	BE314734		gb:601152976F1 NIH_MGC_19 Homo sapiens c	2.2
	412887	BE007420		gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.2
	454204	AW816498		gb:QV0-ST0236-171299-075-b02 ST0236 Homo	2.2
	408253	AW807476	Hs.21051	Homo sapiens mRNA for FLJ00012 protein,	2.2
	432887	AI926047	Hs.162859	ESTs	2.2
65	448063	AI459108	Hs.159818	ESTs	2.2
	416171	H23896	Hs.125790	leucine-rich repeat-containing 2	2.2
	433098	AW190593	Hs.151143	ESTs	2.2
	409781	AW812266	Hs.15220	zinc finger protein 106	2.2
	423441	R68849	Hs.278359	absent in melanoma 1 like	2.2
70	423846	H02364		gb:yl35d06.r1 Soares placenta Nb2HP Homo	2.2
	436572	AA723274	Hs.279596	ESTs	2.2
	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	448828	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	2.2
	444585	AW170015	Hs.6594	ESTs	2.2
75	437334	AL353947	Hs.283780	hypothetical protein DKFZp761N1814	2.2
	431917	D16181	Hs.2868	peripheral myelin protein 2	2.2
	400843				2.2
	455688	BE067238		gb:PM1-BT0348-151299-001-a12 BT0348 Homo	2.2
80	449560	AA001767	Hs.17924	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	408940	M58583	Hs.662	cerebellin 1 precursor	2.2
	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.2
	413617	BE155373	Hs.279518	amyloid beta (A4) precursor-like protein	2.2
	459495	BE544158		gb:601076707F1 NIH_MGC_12 Homo sapiens c	2.2
	433225	AW816515	Hs.173540	ATPase, Class V, type 10D	2.2

	444547	AV650207	Hs.282437	ESTs, Weakly similar to I38022 hypothe	2.2
	417156	N49476	Hs.166563	replication factor C (activator 1) 1 (14	2.2
	416761	H85422	Hs.108556	ESTs	2.2
5	408867	AA437199	Hs.656	cell division cycle 25C	2.2
	406748	AW339106	Hs.217493	annexin A2	2.2
	427443	AA402713	Hs.97872	ESTs	2.2
	452843	AJ796769	Hs.208320	ESTs	2.2
	427473	AW274439	Hs.252709	ESTs	2.2
10	433919	AA746311		gb:aa56d12.r1 NCL_CGAP_GC81 Homo sapiens	2.2
	431058	AW968865		gb:EST380941 MAGE resequences, MAGJ Homo	2.2
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	2.2
	415250	F02614	Hs.27319	ESTs	2.2
	440253	AI651329	Hs.160289	ESTs	2.2
	434470	AA634818	Hs.298138	ESTs	2.2
15	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	2.2
	432463	AA548518	Hs.186733	ESTs	2.2
	400861				2.2
	407287	AI678812		gb:tu59d08.x1 NCL_CGAP_Gas4 Homo sapiens	2.2
20	414817	AW902892	Hs.23782	hypothetical protein FLJ12847	2.2
	416143	AI956650	Hs.79033	glutamyl-peptide cyclotransferase (glu	2.2
	449808	AA694220	Hs.15403	ESTs, Moderately similar to ALU7_HUMAN A	2.2
	412314	AA825247	Hs.250899	heat shock factor binding protein 1	2.2
	442952	AJ743261	Hs.131860	ESTs	2.2
25	425187	AW014489	Hs.22509	ESTs	2.2
	408221	AA912183	Hs.47447	ESTs	2.2
	411480	AW848022		gb:IL3-CT0214-231299-053-A09 CT0214 Homo	2.2
	459881				2.2
	414784	NM_000344	Hs.288986	survival of motor neuron 1, telomeric	2.2
30	442726	AW136065	Hs.19145	ESTs	2.2
	450433	AW444538	Hs.231863	ESTs	2.2
	437642	AL079309		gb:Homo sapiens mRNA full length insert	2.2
	406298				2.2
	409723	AW885757	Hs.257862	ESTs	2.2
35	433266	AI863224	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	2.2
	435090	BE217923	Hs.149595	ESTs	2.2
	457187	AA443927	Hs.144360	EST	2.2
	446534	AI307356	Hs.175225	ESTs	2.2
	403764				2.2
40	442735	R91949		gb:yq06h06.s1 Soares fetal liver spleen	2.2
	455221	AW867751		gb:MRO-SN0038-260300-001-a03 SN0038 Homo	2.2
	405965				2.2
	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	2.2
	441679	BE502267	Hs.65996	ESTs	2.2
45	432781	NM_014133	Hs.278940	PRO0618 protein	2.2
	448470	AW026226	Hs.309479	ESTs	2.2
	419637	W27493		gb:31h10 Human retina cDNA randomly prim	2.2
	443180	R15875	Hs.258576	claudin 12	2.2
	422213	AA306385	Hs.133160	ESTs	2.2
	423119	AA322201	Hs.131976	ESTs	2.2
50	450192	AA263143	Hs.24596	RAD51-interacting protein	2.2
	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	2.2
	400734				2.2
	430499	AW969408	Hs.231991	ESTs	2.2
55	451134	AA318315	Hs.25599	hypothetical protein FLJ22195	2.2
	401694				2.2
	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	424419	AK001563	Hs.146589	hypothetical protein FLJ10701	2.2
	431364	AW971382	Hs.294016	ESTs, Moderately similar to B34087 hypot	2.2
60	436640	AA724411	Hs.156065	ESTs	2.2
	436802	N34486	Hs.170504	ESTs	2.2
	443994	AI094805	Hs.135522	ESTs, Weakly similar to S38038 hypothe	2.2
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
	446412	AW135313	Hs.150098	ESTs	2.2
	448390	AL035414	Hs.21068	hypothetical protein	2.2
65	449939	T86420	Hs.272139	ESTs	2.2
	412700	BE222433	Hs.201262	ESTs, Weakly similar to I38022 hypothe	2.2
	453125	AW779544	Hs.115497	hypothetical protein FLJ22655	2.2
	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.2
70	452864	AA033714	Hs.287629	hypothetical protein FLJ14260	2.2
	452441	BE222078	Hs.113069	ESTs	2.2
	402395				2.2
	459659				2.2
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	2.2
75	438432	AW444990	Hs.258800	ESTs, Weakly similar to I38022 hypothe	2.2
	409446	AI561173	Hs.67688	ESTs	2.2
	408764	BE087164	Hs.302415	ESTs	2.2
	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	2.2
	436992	AA741074	Hs.120750	ESTs	2.2
80	439634	W79377	Hs.167	microtubule-associated protein 2	2.2
	444199	AI128931	Hs.260681	ESTs, Moderately similar to ALUF_HUMAN 1	2.2
	446009	AI989885	Hs.231926	ESTs	2.2
	435510	BE143837		gb:MRO-HT0164-151299-012-b08 HT0164 Homo	2.1

	403691				2.1
	458333	AI000792	Hs.108209	ESTs	2.1
	454560	AW807281		gb:MR4-ST0062-240300-003-g01 ST0062 Homo	2.1
5	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	2.1
	421498	AA292084	Hs.191575	ESTs, Moderately similar to ALU2_HUMAN A	2.1
	414428	BE296906	Hs.182625	VAMP (vesicle-associated membrane protel	2.1
	406941	X58140		(NONE)	2.1
	445712	AI458246	Hs.167451	ESTs	2.1
10	451270	AW341392	Hs.235795	ESTs	2.1
	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	2.1
	437073	AI885608	Hs.94122	ESTs	2.1
	434789	AW292515	Hs.194317	ESTs, Weakly similar to T08680 hypotheti	2.1
	430884	AF053748	Hs.248114	glial cell derived neurotrophic factor	2.1
15	445944	H06336	Hs.13480	Homo sapiens clone 24875 mRNA sequence	2.1
	405233				2.1
	446512	H30351	Hs.207982	ESTs	2.1
	403188				2.1
	404443				2.1
20	433645	AI821746	Hs.190258	ESTs, Moderately similar to ALU6_HUMAN A	2.1
	414456	H74314		gb:yu56e10.r1 Soares fetal liver spleen	2.1
	433479	AW511459	Hs.249972	ESTs	2.1
	455482	AW948353		gb:RC0-MT0015-130400-031-d07 MT0015 Homo	2.1
	446384	AB006624	Hs.14912	KIAA0286 protein	2.1
25	452004	AU827815	Hs.277359	ESTs	2.1
	406059				2.1
	425457	AW964212		gb:EST376285 MAGE resequences, MAGH Homo	2.1
	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	2.1
30	415871	R55995	Hs.283309	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	432774	AA564946	Hs.156280	ESTs	2.1
	436349	AA45255	Hs.115315	ESTs	2.1
	445532	BE138944	Hs.146200	ESTs	2.1
	456313	AA225741		gb:nc17b10.s1 NCI_CGAP_Pr1 Homo sapiens	2.1
35	412818	NM_003337	Hs.811	ubiquitin-conjugating enzyme E2B (RAD6 h	2.1
	450271	AI693900	Hs.200920	ESTs	2.1
	401521				2.1
	422880	AF228704	Hs.121524	glutathione reductase	2.1
	448871	BE616709	Hs.159265	kruppel-related zinc finger protein hckr	2.1
40	449233	BE048401	Hs.196511	ESTs	2.1
	408217	AI433201	Hs.279860	tumor protein, translationally-controlle	2.1
	457003	S78234	Hs.172405	cell division cycle 27	2.1
	417448	AA203135	Hs.130186	ESTs	2.1
	402103				2.1
45	450579	AW136774	Hs.48614	ESTs	2.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.1
	456596	AA291834	Hs.78950	branched chain keto acid dehydrogenase E	2.1
	415333	H24415	Hs.13273	KIAA0592 protein	2.1
	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocorticotr	2.1
50	434985	AA658229	Hs.291228	ESTs	2.1
	414729	BE466928	Hs.261901	ESTs	2.1
	400510				2.1
	420844	AA595522		gb:nh22c09.s1 NCI_CGAP_Pr1 Homo sapiens	2.1
55	427434	BE538374	Hs.301732	hypothetical protein MGC5306	2.1
	432188	AI362962	Hs.2928	solute carrier family 7 (cationic amino	2.1
	446296	AA985682	Hs.63131	Homo sapiens cDNA FLJ13155 fis, clone NT	2.1
	453853	AL040600	Hs.188083	ESTs	2.1
	459108	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	2.1
	430118	AI377255	Hs.183287	ESTs	2.1
60	456964	BE166924		gb:CM4-HT0501-240300-519-f01 HT0501 Homo	2.1
	437981	AA774445	Hs.192095	ESTs, Weakly similar to KIAA1397 protein	2.1
	439957	AI453184	Hs.66357	ESTs	2.1
	423734	H02217		gb:yj38d11.r1 Soares placenta Nb2HP Homo	2.1
	450721	AI732271	Hs.25567	ESTs	2.1
65	429392	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN	2.1
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	2.1
	432919	AL079800		gb:DKFZp434O2330_r1 434 (synonym: htes3)	2.1
	434791	AA649235	Hs.116457	ESTs, Weakly similar to NIP3_HUMAN BCL2/	2.1
	445273	AI218441	Hs.153846	ESTs	2.1
70	400514				2.1
	412798	AW998657	Hs.119120	E3 ubiquitin ligase SMURF1	2.1
	416085	H18072	Hs.92576	ESTs	2.1
	437846	AA773866	Hs.244569	esophagus cancer-related geno-2	2.1
	439391	AW975638	Hs.293490	ESTs, Weakly similar to I38022 hypotheti	2.1
75	428414	AL049980	Hs.184216	DKFZP564C152 protein	2.1
	429430	AI381837	Hs.155335	ESTs	2.1
	449689	AF228421	Hs.23889	DKFZP564A032 protein	2.1
	430909	AF034632	Hs.248126	G protein-coupled receptor 38	2.1
	453116	AI276680	Hs.146086	ESTs	2.1
80	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	2.1
	423019	AI640185	Hs.283626	ESTs	2.1
	414007	AI733895	Hs.103813	ESTs	2.1
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	2.1
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	2.1

	421279	AW664878	Hs.106645	ESTs	2.1
	443167	AI202009	Hs.132087	ESTs	2.1
	459124	AW301478	Hs.184592	protein kinase, lysine deficient 1	2.1
5	448078	AI460117	Hs.170464	ESTs, Highly similar to A53933 myosin I	2.1
	436858	BE545498		gb:601070344F1 NIH_MGC_12 Homo sapiens c	2.1
	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	2.1
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	2.1
	407401	AF029325		gb:Homo sapiens laminin beta-4 chain pre	2.1
10	426336	AA375802		gb:EST88135 HSC172 cells II Homo sapiens	2.1
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	2.1
	425541	AA359119		gb:EST68172 Fetal lung II Homo sapiens c	2.1
	406504				2.1
	410626	BE407727		gb:601299771F1 NIH_MGC_21 Homo sapiens c	2.1
15	415186	AA160945	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	2.1
	416175	H24230	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	436820	AI684535	Hs.200811	ESTs	2.1
	442095	AI733162	Hs.128470	ESTs	2.1
	451878	AI821027	Hs.8429	ESTs	2.1
20	449178	AI633748	Hs.197597	ESTs	2.1
	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	2.1
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	2.1
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	2.1
	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	2.1
	441543	AI733014	Hs.269715	ESTs	2.1
25	403065				2.1
	428811	AA436062	Hs.99487	ESTs	2.1
	451803	BE541174	Hs.252058	ESTs, Moderately similar to PC4259 ferri	2.1
	442906	AW296888	Hs.170939	ESTs	2.1
30	409171	R17126		gb:yg09c11.r1 Soares infant brain 1N1B H	2.1
	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	2.1
	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	2.1
	412039	AW887384		gb:RCO-OT0089-130300-021-d07 OT0089 Homo	2.1
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	2.1
35	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	2.1
	455022	AW850845		gb:IL3-CT0220-111199-028-D11 CT0220 Homo	2.1
	447972	AL137275	Hs.20137	hypothetical protein DKFZp434P0116	2.1
	422942	AF054839	Hs.122540	tetraspan 2	2.1
	400451				2.1
40	406668	T62745	Hs.184411	albumin	2.1
	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	2.1
	404834				2.1
	448732	BE614063	Hs.334689	KIAA1838 protein	2.1
	423453	AW450737	Hs.128791	CGI-09 protein	2.1
45	421447	AB005216	Hs.104481	Nck, Ash and phospholipase C binding pro	2.1
	408774	AW270899	Hs.254569	ESTs, Weakly similar to B34087 hypothei	2.1
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.1
	405732				2.1
	417848	AA206581	Hs.39457	ESTs, Weakly similar to JC5314 CDC28/cdc	2.1
50	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.1
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	2.1
	455778	BE088746		gb:CMZ-BT0693-210300-123-d09 BT0693 Homo	2.1
	426953	AI769281	Hs.97439	ESTs	2.1
	440454	AI733037	Hs.129990	ESTs	2.1
55	433917	AI809325	Hs.122814	Human DNA sequence from clone RP5-1028D1	2.1
	424872	AA347923		gb:EST54302 Fetal heart II Homo sapiens	2.1
	454658	AW812330	Hs.11123	DKFZP564G092 protein	2.1
	441963	AI733307	Hs.128002	ESTs	2.1
	439498	AA908731	Hs.58297	CLL8 protein	2.1
60	456224	AW292905	Hs.128770	ESTs	2.1
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	2.1
	444702	AI220122	Hs.326560	hypothetical protein MGC2780	2.1
	417787	R14948	Hs.23883	ESTs	2.1
	400612				2.1
	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
65	414494	AA768491	Hs.6783	hypothetical protein FLJ22724	2.1
	427027	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
	451067	BE172186		gb:MR0-HT0559-110300-005-h11 HT0559 Homo	2.1
	455032	AI830890	Hs.192422	ESTs	2.1
70	417945	R29072		gb:F1-101D 22 week old human fetal liver	2.1
	438268	AA782163	Hs.293502	ESTs	2.1
	424754	R09692		gb:y23b12.r1 Soares fetal liver spleen	2.1
	404599				2.1
	459655				2.1
75	402455				2.1
	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	2.1
	421987	AI133161	Hs.286131	CGI-101 protein	2.1
	400339	X57131	Hs.248209	H2A histone family, member F, pseudogene	2.1
	438206	AA780385	Hs.187885	ESTs	2.1
	458451	AW297181	Hs.195922	ESTs	2.1
80	447534	AW953935	Hs.30837	ESTs	2.1
	417687	AI828596	Hs.250691	ESTs	2.1
	412717	W00973	Hs.334728	ESTs	2.1
	405759				2.1

	406413				2.1
	442081	AA401863	Hs.22380	ESTs	2.1
	457938	AI373638	Hs.133900	ESTs	2.1
	420687	AA279392	Hs.88605	Homo sapiens cDNA FLJ13427 lis, clone PL	2.1
5	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
	415635	F13168		gb:HSC3JF101 normalized infant brain cDN	2.1
	411421	BE272110	Hs.21177	ESTs	2.1
	437825	AA769123	Hs.291947	ESTs	2.1
	437083	AW082597	Hs.244862	ESTs	2.1
10	409466	AA436207	Hs.226666	ESTs, Moderately similar to 154374 gene	2.1
	433523	H29882	Hs.162614	ESTs	2.1
	446868	AV660737	Hs.135100	ESTs	2.1
	445882	AJ948717	Hs.225155	ESTs, Weakly similar to A46302 PTB-assoc	2.1
15	438005	BE151746		gb:PM1-HT0305-061299-003-e06 HT0305 Homo	2.1
	406817	AJ936028		gb:wo47e09.x1 NCL_CGAP_Gas4 Homo sapiens	2.1
	410486	AW235094	Hs.69233	zinc finger protein	2.1
	411940	AW876686		gb:CM4-PT0031-180200-507-e05 PT0031 Homo	2.1
	412446	AJ768015	Hs.92127	ESTs	2.1
	457289	AW573204	Hs.137078	ESTs	2.1
20	400335	Y13187	Hs.248067	Homo sapiens dmd gene, intron 11	2.0
	435959	AW296243	Hs.118375	ESTs	2.0
	448188	AW001835	Hs.13323	hypothetical protein FLJ22059	2.0
	416339	AA639902	Hs.104215	ESTs, Moderately similar to SPON_HUMAN S	2.0
	420430	A703192		gb:wd92h04.x1 NCL_CGAP_Lu24 Homo sapiens	2.0
25	445717	AW664658	Hs.149332	ESTs	2.0
	451862	H09260	Hs.32333	ESTs	2.0
	459886				2.0
	441996	BE349537	Hs.38383	ESTs	2.0
30	412194	AW900282	Hs.115412	hypothetical protein FLJ13881	2.0
	444229	AV648613	Hs.282397	ESTs	2.0
	441635	AJ908538	Hs.133000	ESTs, Weakly similar to S26689 hypotheti	2.0
	421387	AF059566	Hs.103983	solute carrier family 5 (sodium iodide s	2.0
	414373	AW162907	Hs.75969	proline-rich protein with nuclear target	2.0
	428209	AA424197	Hs.98947	ESTs, Weakly similar to S33496 trypsin [2.0
35	443520	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO	2.0
	409248	AB033035	Hs.51965	KIAA1209 protein	2.0
	444518	A1160278	Hs.146884	ESTs	2.0
	422237	M13149	Hs.1498	histidine-rich glycoprotein	2.0
40	409316	U28251	Hs.53237	ESTs, Highly similar to Z169_HUMAN ZINC	2.0
	402725				2.0
	413783	AA314337	Hs.301547	ribosomal protein S7	2.0
	423887	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.0
	425008	AW675764	Hs.174248	ESTs	2.0
45	427271	AW195922	Hs.188758	connexin 59	2.0
	444102	AV647953	Hs.83077	Interleukin 18 (interferon-gamma-inducin	2.0
	445829	AJ452457	Hs.145526	ESTs	2.0
	452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
	457652	AF116656	Hs.273809	Homo sapiens PRO1167 mRNA, complete cds	2.0
50	429540	M85776		gb:EST02297 Fetal brain, Stragene (cat	2.0
	459456	AA486036	Hs.190124	ESTs	2.0
	409840	AW502122		gb:UL-HF-BR0p-ajr-c-08-0-ULr1 NIH_MGC_5	2.0
	441025	AA913880	Hs.176379	ESTs	2.0
	457802	T78013	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.0
	445627	AW818475	Hs.7363	ESTs	2.0
55	440299	AJ871778	Hs.250112	ESTs	2.0
	401236	H24185	Hs.92918	hypothetical protein	2.0
	429996	N90822	Hs.48969	ESTs	2.0
	455135	AW857889		gb:PM2-CT0328-281299-003-e04 CT0328 Homo	2.0
	411537	BE073250		gb:MR0-BT0551-060300-102-e05 BT0551 Homo	2.0
60	433449	AW772282		gb:hn71b05.x1 NCL_CGAP_K0d11 Homo sapien	2.0
	454197	BE140966		gb:MR0-HT0065-081199-002-b06 HT0065 Homo	2.0
	445297	BE544163	Hs.87128	hypothetical protein FLJ23309	2.0
	403977				2.0
	458948	AJ695359	Hs.280943	ESTs	2.0
65	418653	AK001100	Hs.41690	desmocollin 3	2.0
	411479	AW848047		gb:IL3-CT0214-281299-052-A12 CT0214 Homo	2.0
	426536	AJ949749	Hs.44441	ESTs	2.0
	442765	BE567353	Hs.99480	ESTs	2.0
	400859				2.0
70	405829				2.0
	411863	BE075244	Hs.12420	ESTs	2.0
	415258	AW752247	Hs.293853	ESTs	2.0
	416093	R60685	Hs.268698	ESTs, Moderately similar to ALUC_HUMAN I	2.0
	416184	R48481	Hs.269177	ESTs, Weakly similar to ALU6_HUMAN ALU S	2.0
75	437733	AJ792574	Hs.122876	ESTs	2.0
	453118	AW195849	Hs.252757	ESTs	2.0
	457039	H29990	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.0
	444292	AJ139794	Hs.146569	ESTs	2.0
	431360	NM_000427	Hs.251680	lorixin	2.0
80	407644	D16815	Hs.37288	nuclear receptor subfamily 1, group D, m	2.0
	412029	AW886238		gb:RCS-OT0078-280300-022-F01 OT0078 Homo	2.0
	438522	AA809431	Hs.258886	ESTs	2.0
	422634	NM_016010	Hs.118821	CGI-62 protein	2.0

	418790	H95693		gb:y95d11.s1 Soares_pineal_gland_N3HPG	2.0
	442950	A1500417	Hs.46764	ESTs	2.0
	457040	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.0
	436464	A1016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
5	402674				2.0
	408733	AW264812	Hs.254290	ESTs	2.0
	408767	AA057279	Hs.211928	ESTs	2.0
	432801	NM_016260	Hs.278953	zinc finger DNA binding protein Helios	2.0
10	418205	L21715	Hs.83760	tropoin I, skeletal, fast	2.0
	404604				2.0
	413627	BE182082	Hs.248973	ESTs	2.0
	402341				2.0
	438090	AA777534	Hs.191992	ESTs	2.0
	421303	T06464		gb:EST04353 Fetal brain, Stratagene (cat	2.0
15	411417	AW845481		gb:MR1-CT0056-201199-008-b04 CT0056 Homo	2.0
	401986				2.0
	415318	T06544		gb:EST04433 Fetal brain, Stratagene (cat	2.0
	417756	Z43056		gb:HSC12B021 normalized infant brain cDN	2.0
	418301	AW976201	Hs.53913	hypothetical protein FLJ10252	2.0
20	433755	AW085934	Hs.120868	ESTs	2.0
	435413	A1267476	Hs.46689	ESTs	2.0
	435648	H24347	Hs.27524	ESTs	2.0
	447555	A1391682	Hs.160963	Homo sapiens, clone MGC:12318, mRNA, com	2.0
	458175	AW296024	Hs.150434	ESTs	2.0
25	458433	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.0
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	2.0
	447678	BE385257	Hs.336457	Homo sapiens dopamine receptor Interacti	2.0
	448150	A1472167	Hs.302739	ESTs	2.0
	453445	AL036532	Hs.91453	ESTs	2.0
30	444420	A1148157	Hs.146766	ESTs	2.0
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	2.0
	413758	BE162391		gb:PM2-HT0451-090100-002-404 HT0451 Homo	2.0
	428231	U17989	Hs.183105	nuclear autoantigen	2.0
	455873	BE152239		gb:QV4-HT0316-091199-028-f12 HT0316 Homo	2.0
35	430970	A1018210	Hs.144083	ESTs	2.0
	412277	BE277592	Hs.73799	guanine nucleotide binding protein (G pr	2.0
	413025	AA805265	Hs.291646	ESTs	2.0
	424083	AF065018	Hs.139137	Homo sapiens clone 24442 mRNA sequence	2.0
	427654	AA410183	Hs.137475	ESTs	2.0
40	410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.0
	423942	AF209704	Hs.135723	glycolipid transfer protein	2.0
	430340	AA476777		gb:zw94g11.r1 Soares_tetal_fetus_Nb2HF8_	2.0
	425686	M73531	Hs.1937	retinal degeneration, slow (retinitis pi	2.0
	425075	AA506324	Hs.1852	acid phosphatase, prostate	2.0
45	400285				2.0
	405966				2.0
	407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
	411459	BE142707		gb:MR0-HT0157-191199-002-g12 HT0157 Homo	2.0
	415105	D60166		gb:HUM089G11B Clontech human fetal brain	2.0
50	434531	AA642007	Hs.116369	ESTs	2.0
	447153	AA805202	Hs.315562	ESTs	2.0
	447185	AW377092	Hs.99601	hypothetical protein FLJ12553	2.0
	455696	BE067870		gb:RC0-BT0362-021299-031-b06 BT0362 Homo	2.0
	456510	AK001652	Hs.99423	ATP-dependant RNA helicase	2.0
55	400617	AF151064	Hs.36069	hypothetical protein	2.0
	418647	AA226198		gb:nc26a07.s1 NCL_CGAP_Pr1 Homo sapiens	2.0
	401785				2.0
	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	2.0
	420777	AA280223	Hs.130865	ESTs	2.0
60	439509	AF086332	Hs.58314	ESTs	2.0
	430203	L36140	Hs.235069	RecQ protein-like (DNA helicase Q1-like)	2.0
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	2.0
	455540	BE080231		gb:RC4-BT0629-120200-012-f11 BT0629 Homo	2.0
	437620	AW976930	Hs.128760	ESTs	2.0
65	407528	X64990		gb:H.sapiens mRNA HTPCRX16 for olfactory	2.0
	402048				2.0
	403623				2.0
	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	2.0
70	417531	NM_003157	Hs.1087	serine/threonine kinase 2	2.0
	422600	BE143586	Hs.87	retinoblastoma-like 1 (p107)	2.0
	423347	A1660412	Hs.234557	ESTs	2.0
	424560	AA158727	Hs.150555	protein predicted by clone 23733	2.0
	433153	AA578512		gb:nh22e11.s1 NCL_CGAP_Pr1 Homo sapiens	2.0
	433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
75	435373	AW665538	Hs.117689	ESTs	2.0
	442988	A1026130	Hs.131683	ESTs	2.0
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.0
	454423	AW603985		gb:RC4-CN0048-140100-011-a04 CN0048 Homo	2.0
80					

Table 31B

5	Pkey: Unique Eos probeset identifier number		
	CAT number: Gene cluster number		
10	Accession: Genbank accession numbers		
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	409171	1104879_1	R17126 R38456 H02771
	409206	1108161_1	AW364844 AW364847 AW937534 AW937593 AW937659
20	409623	1144047_1	AW449185 AW449665 BE220971
	409699	1149033_1	BE154650 BE154785 AW468343 BE154816 BE154667
	409816	1155396_1	AW500954 AW501111 AW501394
	409840	1156071_1	AW502122 AW502125 AW501663 AW501720
	410201	118365_1	AA126129 AA126033 AA082561
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	410500	1206323_1	R09442 AW846115 AW846108 AW751967 AW846083 AW846087 AW846090
	410536	1207322_1	N39533 AW753094 AW753093
	410556	1208157_1	R32158 AW754055 AW754054 AW754053 AW754045 AW857320
	410615	1212203_1	AW772721 AW873372 H89212
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	410644	1213795_1	AW902125 AW792853 AW837703 AW837710
	410672	1214882_1	AW794600 AW794730
	410845	1223881_1	AW807182 AW807328 AW807063 AW807183 AW807192 AW807033 AW807061 AW807286 AW807097 AW807270 AW807372 AW807280
	410888	1225955_1	AW807283
35	410901	1226077_1	AW861207 AW809508
	410934	1227240_1	AW810001 AW810092 AW810170 AW809884 AW809664 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786
	410999	1228809_1	AW810006 AW809672 AW809694 AW810552 AW810345 AW810432 AW809960
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	411093	1231970_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
	411186	1235090_1	BE062590 AW813565 BE147101
	411244	1236407_2	BE067650 AW817053
	411262	1236998_1	AW821257 AW821267 AW821283
45	411311	1238530_1	AW833768 AW833631 AW833435 AW833533 AW833554 AW833543 AW833557
	411377	1242238_1	AW834480 AW834531 AW834637 AW834618 AW834653 AW834487
	411382	1242594_1	AW836491 AW836461 AW836673
	411384	1242702_1	AW841462 BE156657 BE156668 BE092475
	411417	1245075_1	BE067246 BE067241 BE067254 BE067249 AW841860
50	411459	1246724_1	AW842115 AW842111 AW842103
	411479	1247077_1	AW845481 AW845474 AW850849
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	411537	1248899_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069
	411597	1250843_1	AW848905 AW848214
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	411660	1253078_1	AW850246 AW850251 AW850302
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	411745	1256160_1	AW853440 T08189 AW857085
	411762	1256906_1	AW857271 AW857308 AW857296 AW857258
	411772	1257386_1	AW858612 AW861964 AW858600 AW861945 AW858445 AW861901 AW858546 AW861921 AW858395 AW861968 AW858394 AW858401
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	412209	1283610_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
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75	412321	1288608_1	AW887384 AW887372 AW887461 AW887315
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			BE064806 BE064796 BE064818 BE064975 BE064819 BE064810 BE064668 BE065059
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	413257	1355963_1	BE075035 BE074999 BE075006 BE075005 BE075032 BE075008 BE075037
	413445	1370833_1	BE141022 BE141513 BE141532 BE141488 BE141481 BE141526 BE141516 BE141471 BE141478 BE141476 BE141475 BE141021 BE141533
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20	413470	1371600_1	N20934 BE141875 BE141877
	413488	1373234_1	BE144017 BE185527 BE144023
	413499	1373910_1	BE144884 H97942
	413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
	413581	1378335_1	BE150618 BE150616 BE150626
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	413758	1386900_1	BE162391
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	413986	140720_1	Z43567 H24159 AA134240
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	414349	1437515_1	BE512668
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	415549	1538692_1	F11942 T78047 R13266
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	418297	1736343_1	R91254 T97156 R58711
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	418856	179649_1	AA362858 AW863761 AA228428
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	419637	186639_1	WZ7493 AA248063 AA249685 AA429579
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	435510	407286_1	BE143837 AW749652 AA683327
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	446901	697809_1	AI347274 AW844024
75	447884	740749_1	H28505 R18575 Z43580 T48738 AI435454 BE004683
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 459201 925883_1 AW391177 W45021

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TABLE 31C

20 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400451	8113550	Minus	82189-82320
400462	9929659	Minus	197610-197785
400486	8569885	Plus	181108-181605
400510	9796540	Minus	139633-139910,140469-140979
400514	9796594	Minus	78844-79025,80850-80991,89754-89941,93750-93891
400579	9887603	Plus	21323-21526
400582	9887609	Plus	88642-88726,89716-89866
400587	9887626	Plus	25435-25588,25668-25747
400608	9887666	Minus	96756-97558
400612	9929646	Minus	151513-151662
400613	9864507	Plus	92278-92472
400641	8117693	Plus	4786-4992
400643	8117693	Plus	12818-13016
400706	7249204	Minus	78299-78686
400734	8118979	Plus	122853-123971
400816	8569993	Plus	161221-162078
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
400844	9188605	Plus	24746-24872,25035-25204
400859	9757499	Minus	91888-92018,98131-98294,99474-99570
400861	9757506	Plus	163855-164016
400889	8958234	Minus	169782-170038
401078	3687273	Plus	105052-105171
401098	9965518	Minus	85632-86174
401132	8705350	Minus	85679-85795
401145	2547238	Plus	17599-17776
401189	9690246	Minus	90815-90929
401200	9743387	Minus	111586-111806,114781-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
401344	9926411	Minus	82478-82602,86952-87110
401361	9958062	Plus	153093-154106
401365	9796180	Minus	119572-119672
401449	8574316	Minus	144928-145030
401497	7381770	Plus	92607-92813
401521	7705251	Plus	9127-9234
401526	7770561	Plus	91570-93177
401602	7689963	Plus	101096-101253
401614	7839924	Plus	17350-17735
401645	7657839	Minus	34986-35133
401694	3540172	Minus	64056-64168
401775	9966311	Minus	110228-110340
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401882	8139716	Plus	86466-87077
401887	7229981	Plus	93973-94120
401986	4406829	Minus	31137-31293
401992	4153858	Plus	31452-31649
402038	7684482	Minus	100751-100885
402048	8072512	Plus	43936-44078
402076	8117410	Plus	128316-128627
402103	7249203	Plus	14453-15414
402131	7704961	Minus	33114-33209,33496-33678
402176	7543687	Minus	10-750
402230	9966312	Minus	29782-29932
402333	8844110	Minus	165693-165856
402341	7656696	Plus	22583-23699
402395	9929693	Minus	131016-131998
402429	9796372	Minus	57622-57793,59282-59402,59624-59827
402430	9796372	Minus	62382-62552
402455	9796753	Minus	139640-139779,140568-140660
402527	9800806	Plus	4722-4916,17858-18037,19964-20140,24423-24605,26699-26881

	402615	9926801	Plus	131390-132157
	402621	9930950	Plus	130806-131036
	402674	8077108	Minus	39290-39502
	402725	8979991	Plus	107231-107383
5	402790	4835258	Minus	147744-147861
	402857	5596716	Plus	52806-53106,53500-53818
	402953	9408724	Minus	122603-122743
	403003	5441423	Minus	79403-79560,79712-80021
	403011	6693597	Minus	3468-3623
10	403065	8954197	Minus	71615-71773,73930-74144
	403188	9838289	Minus	157618-157755
	403271	7230852	Plus	134283-134485
	403273	8018055	Plus	133809-134099
	403281	8072630	Minus	7521-7728
15	403296	8096530	Minus	35913-36520
	403310	8139936	Minus	183883-184026
	403329	8516120	Plus	96450-96598
	403341	8569175	Plus	30699-30910
	403344	8569726	Plus	70823-70990
20	403356	8569930	Plus	92839-93036
	403381	9438267	Minus	26009-26178
	403388	9438331	Plus	112733-113001,114599-114735
	403396	9438367	Minus	952-1160
	403501	7534005	Minus	108903-110438
25	403513	7656757	Minus	155310-155436,158402-158535
	403515	7656757	Minus	173358-179553
	403534	8076917	Minus	46652-47332
	403549	8081591	Minus	137150-137362
	403568	8101145	Minus	85509-85658
30	403574	8101156	Plus	5542-6176
	403619	8569810	Plus	62501-62653
	403623	8569879	Minus	3519-5426
	403625	8569879	Plus	6651-7111
	403637	8671936	Minus	142647-142771,145531-145762
35	403667	6850483	Minus	1344-1442,1545-1697
	403677	7331517	Minus	55008-55083,62860-63051
	403691	7387384	Minus	88280-88463
	403696	3135242	Minus	143467-143634
	403743	7652003	Minus	135463-136646
40	403760	7712202	Minus	45910-46260,47563-47824
	403764	7717105	Minus	118692-118853
	403776	7770611	Minus	1414-1513,1624-1756
	403780	8076989	Plus	93160-93409
	403786	8083636	Minus	73028-73217
45	403891	7331467	Minus	191508-193220
	403895	7381715	Minus	3502-4002,4070-4308
	403977	7657840	Minus	115573-115820
	404043	9558573	Plus	29042-29135,46597-46699
	404059	3548785	Plus	104326-106788
50	404076	9931752	Minus	3848-3967
	404196	3805917	Minus	67928-68109
	404249	8655533	Plus	64270-64633
	404257	9367215	Plus	15262-16227
	404285	2326514	Plus	32282-32416
55	404288	2769644	Plus	3512-3691
	404367	9965011	Minus	114391-114628
	404443	7579073	Minus	87198-87441
	404453	7657714	Plus	27768-29179
	404476	8080699	Plus	101841-102043
60	404513	8151941	Minus	112837-113339
	404561	9795980	Minus	69039-70100
	404569	7249169	Minus	104257-104348,104822-104970
	404577	4020145	Plus	17991-18420
	404588	6456726	Minus	40059-40210
65	404599	8705107	Plus	110443-110733
	404604	9212537	Minus	72019-72509
	404638	9796751	Minus	99433-99528,100035-100161
	404767	7882827	Minus	23244-23759
	404793	7232206	Minus	61087-61590
70	404822	3810614	Plus	7541-8132
	404834	6911603	Minus	37948-38226
	404845	7958980	Minus	47174-47326,52928-53146,53312-53602
	404898	7331420	Minus	177015-177328
	404936	6850774	Plus	191519-191664
75	404957	7407927	Plus	147512-148011
	405017	8532084	Plus	35551-35690
	405059	7656683	Plus	349-822
	405090	8072525	Minus	38552-39202
	405093	8072575	Plus	95878-96020
80	405120	8099940	Plus	140176-140340
	405170	9966524	Plus	37047-37198
	405229	7249019	Plus	51081-51701
	405230	7249032	Minus	97493-97682

	405233	7249045	Plus	9588-10065
	405241	7249178	Minus	69927-70526
	405264	7329374	Plus	28556-28684
	405287	3928029	Plus	89802-89999
5	405302	2078453	Minus	121688-121840
	405303	2078453	Minus	130607-130802
	405336	6094635	Plus	33267-33563
	405347	2979602	Minus	977-1116
	405385	6552772	Plus	48332-48454
10	405443	7408143	Plus	90716-90887,101420-101577
	405455	7656675	Plus	134112-134671
	405494	8050952	Minus	70284-70518
	405521	9454643	Plus	65096-65247,77508-77637,81242-81364,84246-84395
	405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
15	405547	1054740	Plus	124361-124520,124914-125050
	405605	5836185	Minus	117070-117270
	405608	5815499	Minus	66822-66925
	405629	4508116	Minus	101678-101866
	405634	5308288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
20	405654	4895155	Minus	53624-53759
	405692	4314424	Plus	61379-62562
	405706	4165003	Plus	44307-44431,49619-49802
	405720	9797144	Plus	13409-13861
	405732	7534017	Plus	146981-147316
25	405759	3288022	Minus	18283-18399
	405780	7248203	Minus	48204-48371
	405784	7417368	Minus	77798-78000
	405829	7109593	Minus	15628-16127
	405869	6758731	Minus	89867-90358
30	405935	6758795	Minus	163112-163652
	405959	6758815	Plus	1-642
	405965	8247786	Minus	179930-180373
	405966	8247788	Minus	51762-51978
	405970	8247789	Minus	45795-46295
35	405981	8247790	Plus	4771-5338
	406005	8247801	Minus	39912-40220
	406053	6758997	Plus	30921-31532
	406073	9119150	Plus	60495-60610
40	406091	9123919	Minus	197370-197935
	406092	9123919	Plus	251370-251797,252168-252882
	406298	5686278	Minus	30084-30770
	406327	9212407	Plus	168241-168492
	406333	9213235	Plus	64689-64798
45	406364	9256114	Minus	50715-50833
	406377	9256135	Plus	126826-126979,129755-129942
	406413	9256407	Plus	43858-44003,46993-47136
	406468	9795553	Plus	4373-4616,8870-9046,11366-11509,11625-11880
	406470	9795562	Minus	15532-15697
50	406504	7711360	Minus	107068-107277
	406506	7711374	Minus	6843-8077F
	406592	4567182	Plus	352560-352963

55

Table 32A lists about 969 genes upregulated in lung fibrosis relative to normal body tissues. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

60

Table 33A lists about 800 genes upregulated in lung fibrosis relative to normal lung. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

65

Table 34A lists about 703 genes upregulated in idiopathic pulmonary fibrosis (IPF) relative to hypersensitivity pneumonitis (HP) or non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

70

Table 35A lists about 323 genes upregulated in hypersensitivity pneumonitis (HP) relative to idiopathic pulmonary fibrosis (IPF) or non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

75

Table 36A lists about 52 genes upregulated in non-specific interstitial pneumonitis (NSIP) relative to hypersensitivity pneumonitis (HP) or idiopathic pulmonary fibrosis (IPF). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

80

Table 37A lists about 206 genes downregulated in lung fibrosis relative to normal lung. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

Table 38A lists about 207 genes upregulated in lung fibrosis relative to normal tissues. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

TABLE 32A: About 969 genes upregulated in lung fibrosis relative to normal body tissues

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of lung fibrosis AIs divided by 90th percentile of normal tissue AIs, where the minimum value for the numerator and denominator was set to 50.
 R2: 90th percentile of lung fibrosis AIs divided by 90th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator. The minimum value for the numerator and denominator was set to 50.

	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
	414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	22.45	28.63
	406964	M21305		FGENES predicted novel secreted protein	16.10	7.65
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	15.83	14.86
	442275	AW449467	Hs.54795	ESTs	15.74	21.96
	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	13.83	34.53
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	12.40	7.38
	431089	BE041395		ESTs, Weakly similar to unknown protein	12.38	6.05
	421110	AJ250717	Hs.1355	cathepsin E	11.86	6.49
	457200	U33749	Hs.197764	thyroid transcription factor 1	11.38	9.79
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	10.89	15.94
	443709	AI082692	Hs.134662	ESTs	10.84	8.27
	431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	10.06	8.92
	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	9.96	5.43
	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	9.90	7.87
	421798	N74880		N-acylsphingosine amidohydrolase (acid c	9.38	8.35
	400269			Eos Control	9.03	6.48
	444325	AW152618	Hs.16757	ESTs	8.31	6.76
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	8.14	5.51
	413048	M93221	Hs.75182	mannose receptor, C type 1	7.70	4.09
	432985	T92363	Hs.178703	ESTs	7.56	7.83
	443324	R44013	Hs.164225	ESTs	7.06	4.47
	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	6.90	2.89
	408562	AI435323	Hs.31141	roundabout (axon guidance receptor, Dros	6.88	4.00
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.56	4.25
	421952	AA300900	Hs.98849	dynein light chain 2B (DNL2B)	6.46	4.47
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	6.30	13.57
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	6.28	3.38
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	5.99	13.26
	446428	AW082270	Hs.12495	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.88	4.10
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kd, chr	5.88	3.35
	442652	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	5.87	5.69
	414812	X72755	Hs.77367	monokine induced by gamma Interferon	5.84	3.34
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.72	5.90
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	5.59	6.89
	436954	AA740151	Hs.130425	ESTs	5.58	4.72
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	5.48	5.33
	421340	F07783	Hs.1369	decay accelerating factor for complement	5.48	2.69
	420656	AA279098	Hs.187636	ESTs	5.45	3.99
	432441	AW292425	Hs.163484	intron of hepatocyte nuclear factor-3 al	5.38	3.65
	408380	AF123050	Hs.44532	diubiquitin	5.37	3.11
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	5.30	3.98
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.29	4.00
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	5.28	2.48
	442632	AW206560	Hs.253569	ESTs	5.20	3.78
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	5.11	3.81
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	5.11	2.88
	424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.07	3.46
	428043	T92248	Hs.2240	uteroglobin	5.06	9.46
	431745	AW972448	Hs.163425	ESTs	5.04	4.16
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.04	3.68
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	5.02	4.26
	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	4.97	3.35
	428927	AA441837	Hs.90250	ESTs	4.92	3.15
	432222	AI204995		gb:am03c03.x1 Stratagene schizo brain S1	4.79	3.05
	442994	AI026718	Hs.16954	ESTs	4.76	2.65
	416030	H15261	Hs.21948	ESTs	4.76	4.26
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	4.73	3.24
	453142	AA033648	Hs.7473	ESTs	4.66	2.92
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	4.64	4.88
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	4.60	2.60
	432810	AA863400		ESTs	4.54	2.42
	418259	AA215404		ESTs	4.54	2.54
	453310	X70597	Hs.553	solute carrier family 6 (neurotransmitte	4.48	4.86
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	4.46	3.62
	423575	C18863	Hs.163443	intron of periosin(OSF-2os)	4.44	3.41
	428667	AI375550	Hs.346868	nucleolar protein p40; homolog of yeast	4.42	3.41

	429228	AI553633		ESTs	4.32	2.98
	432435	BE218886	Hs.282070	ESTs	4.30	2.26
	446932	AA961459	Hs.125644	ESTs	4.30	2.81
5	408369	R38438	Hs.182575	SLC15A2 Solute carrier family 15 (H+/pep	4.30	2.39
	409435	AI810721	Hs.95424	ESTs	4.30	2.60
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	4.29	2.48
	452561	AI692181	Hs.49169	KIAA1634 protein	4.23	2.26
	427698	AW972594	Hs.335499	ESTs	4.22	3.49
10	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	4.22	13.34
	446608	N75217	Hs.257846	ESTs	4.20	3.62
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.18	3.14
	459702	AI204995	gb:an03c03.x1 Stratagene schizo brain S1	ESTs	4.16	2.64
	445885	AI734009	Hs.127699	KIAA1603 protein	4.16	3.99
	430280	AA361258	Hs.237868	interleukin 7 receptor	4.13	2.79
15	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.12	2.19
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	4.12	3.02
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	4.08	3.13
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	4.08	3.48
20	432731	R31178	Hs.287820	fibronectin 1	4.06	2.66
	439398	AA284267	Hs.221504	ESTs	4.06	2.86
	409153	W03754	Hs.50813	hypothetical protein FLJ20022	4.05	3.51
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	4.04	2.44
	436120	AI248193	Hs.119860	ESTs	4.04	3.11
25	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.03	2.69
	421462	AF016495	Hs.104624	aquaporin 9	4.00	2.51
	443257	AI334040	Hs.11614	HSPC065 protein	4.00	2.61
	421659	NM_014459	Hs.106511	protocadherin 17	4.00	3.00
	424273	W40460	Hs.144442	phospholipase A2, group X	3.98	2.30
30	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.97	3.36
	450656	AA010539	Hs.18912	ESTs	3.96	4.37
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	3.94	2.44
	424527	AW138558	Hs.334873	ESTs, Weakly similar to I54374 gene NF2	3.93	3.08
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	3.92	3.53
	452416	AA026115	Hs.114777	ESTs	3.92	2.90
35	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	3.90	5.06
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.90	2.00
	453204	R10799	Hs.191990	ESTs	3.90	2.22
	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	3.81	3.82
40	422173	BE365828	Hs.250619	phorbol-like protein MDS019(CEM15)	3.80	2.23
	425538	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	3.78	2.86
	406672	M26041	Hs.198253	major histocompatibility complex, class	3.78	3.70
	457411	AW085961	Hs.130093	iroquois-class homeobox protein IRX2	3.76	2.56
	432605	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.76	2.76
45	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.74	2.83
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.72	2.55
	428820	AA436187	Hs.172631	integrin, alpha M (complement component	3.71	2.25
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	3.70	2.26
	419556	U29615	Hs.91093	chitinase 1 (chitinobiosidase)	3.69	7.71
50	417412	X16896	Hs.82112	interleukin 1 receptor, type I	3.68	2.17
	426174	AA547959	Hs.115838	ESTs	3.65	2.93
	408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513	3.64	2.62
	435990	AI015862	Hs.131793	ESTs	3.62	2.27
	427621	BE621182	Hs.179882	hypothetical protein FLJ12443	3.62	3.48
55	425555	AA359281	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	3.61	3.18
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	3.60	3.05
	426116	AA868729	Hs.144694	ESTs	3.60	2.80
	419235	AW470411	Hs.288433	neurotrophin	3.58	2.88
	424054	AA334511	Hs.26638	membrane-spanning 4-domains, subfamily A	3.56	2.58
60	422667	H25642		ESTs	3.55	2.44
	406673	M34996	Hs.198253	major histocompatibility complex, class	3.54	3.98
	414142	AW368397	Hs.334485	hemiscentin(fibulin 6)	3.54	3.30
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.54	3.11
	430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	3.53	2.38
65	417318	AW953937	Hs.240845	ESTs	3.52	2.02
	456034	AW450979		gb:U1-H-B13-ata-a-12-0-UI.s1 NCI_CGAP_Su	3.50	3.21
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	3.48	2.35
	430709	R34356		gb:yh85d01.s1 Soares placenta Nb2HP Homo	3.48	2.13
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3.47	2.93
70	424711	NM_005795	Hs.152175	calcitonin receptor-like	3.47	2.69
	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	3.46	2.31
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	3.46	2.37
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	3.45	2.07
	447183	AI554733	Hs.173182	ESTs	3.42	2.01
	435299	AI745458	Hs.343026	ESTs, Weakly similar to T20593 hypotheti	3.40	3.49
75	425922	AL157466	Hs.162751	Homo sapiens mRNA; cDNA DKFZp761E2423 (f	3.40	2.42
	413714	AI560944	Hs.71428	ESTs	3.38	2.52
	407361	AA744622	Hs.292645	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.36	2.13
	436043	AW953838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	3.36	2.41
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	3.36	2.06
80	407756	AA116021	Hs.38250	ubiquitin specific protease 18	3.35	2.42
	410606	AW418779	Hs.114889	ESTs	3.35	2.39
	450726	AW204600		retinoic acid receptor, alpha	3.34	6.35
	430573	AA744550	Hs.136345	ESTs	3.33	1.94

5	421585	U95626	Hs.302043	chemokine (C-C motif) receptor-like 2(3.32	2.75
	433658	L03678	Hs.156110	immunoglobulin kappa constant	3.31	2.22
	454076	AW204712	Hs.61957	ESTs	3.31	1.95
	452039	AI922988	Hs.172510	ESTs	3.30	2.95
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.30	2.37
10	430414	AW365665	Hs.120388	ESTs	3.30	2.48
	417958	AA767382	Hs.193417	ESTs	3.30	2.04
	423001	AA320014	Hs.208603	ESTs	3.29	2.62
	443774	AL117428	Hs.9740	DKFZP434A236 protein	3.28	2.35
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	3.28	2.05
15	424238	AA337401	Hs.137635	ESTs	3.28	2.45
	429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	3.27	2.63
	448869	AI792798	Hs.12495	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.26	2.67
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020.1 E2IG5	3.26	2.04
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.22	2.36
20	440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	3.22	3.87
	422109	S73265	Hs.1473	gastrin-releasing peptide	3.20	2.79
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfamily	3.20	2.30
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	3.18	2.42
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	3.18	2.12
25	438568	R98865	Hs.11135	major histocompatibility complex, class	3.18	3.86
	451497	H83294	Hs.284122	Wnt1 inhibitory factor-1	3.18	2.99
	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	3.17	2.02
	446094	AK001760	Hs.13801	KJAA1685 protein	3.17	2.42
	442048	AA974603		gb:rop34f05.s1 Soares_NFL_T_GBC_S1 Homo s	3.17	2.27
30	406685	M18728		gb:Human nonspecific crossreacting antig	3.17	2.80
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.16	1.95
	424943	AJ077260	Hs.153924	death-associated protein kinase 1	3.16	2.18
	436805	AA731533	Hs.270751	ESTs	3.16	1.95
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.15	3.63
35	409799	D11928	Hs.76845	phosphoserine phosphatase-like	3.14	1.74
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.13	3.35
	420729	AW964897	Hs.290825	ESTs	3.12	2.09
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.12	2.06
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	3.12	2.58
40	451820	AW058357	Hs.199248	ESTs	3.10	2.26
	440028	AW473675		ESTs, Weakly similar to T17227 hypotheti	3.10	3.01
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	3.10	2.32
	437866	AA156781		metallothionein 1E (functional)	3.10	1.80
	428513	BE220806	Hs.184697	plexin C1	3.10	2.11
45	438607	AW080237	Hs.252884	ESTs	3.10	2.20
	445034	AW293376	Hs.143659	ESTs	3.08	2.81
	458332	AI000341		ESTs	3.08	1.87
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	3.08	1.87
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.08	1.94
50	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	3.07	2.12
	452960	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	3.07	2.16
	425509	AF079363	Hs.158213	sperm associated antigen 6	3.06	2.75
	431087	H12723	Hs.290791	ESTs	3.06	2.41
	452235	AL039743	Hs.28514	testes development-related NYD-SP21	3.06	2.64
55	449328	AI962493		ESTs	3.06	2.78
	422900	AA641201	Hs.222051	ESTs	3.05	1.87
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.05	1.99
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	3.05	2.49
	437527	AJ241019	Hs.145644	ESTs	3.04	2.17
60	432340	AA534222		gb:nj21d02.s1 NCL_CGAP_AA1 Homo sapiens	3.04	1.78
	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	3.02	2.43
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	3.02	1.77
	411252	AB018549	Hs.69328	MD-2 protein	3.02	1.95
	439981	AJ348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	3.02	2.24
65	420683	AA830168	Hs.271305	ESTs	3.01	2.14
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.00	2.13
	410434	AF051152	Hs.63668	tol-like receptor 2	3.00	2.60
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	3.00	1.81
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.00	1.89
70	435800	AI248285	Hs.118348	ESTs	3.00	2.08
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	3.00	2.18
	449057	AB037784	Hs.22941	KIAA1363 protein	2.99	2.46
	413195	AA127382	Hs.22404	protease, serine, 12 (neurolysin, moto	2.99	2.76
	436198	AK001125		Homo sapiens cDNA FLJ10263 fis, clone HE	2.99	2.16
75	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.98	2.21
	444020	R92952	Hs.35052	ESTs	2.98	2.08
	427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.98	2.40
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	2.96	2.03
	457675	AF119917	Hs.306574	Homo sapiens PRO3098 mRNA, complete cds	2.96	1.74
80	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	2.96	2.40
	429950	AW081608	Hs.105053	ESTs	2.95	2.46
	420394	AB023161	Hs.97403	KIAA0944 protein	2.95	4.13
	406698	X03068	Hs.73931	major histocompatibility complex, class	2.94	1.72
	419038	AW134924	Hs.190325	ESTs	2.94	2.93
	449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	2.94	1.94
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	2.94	1.94
	400880			NM_000611*Homo sapiens CD59 antigen p18	2.94	1.74

5	430382	AA477908	Hs.282267	ESTs, Moderately similar to I38022 hypot	2.94	2.12
	419034	NM_002110	Hs.89555	hemopoietic cell kinase	2.93	2.25
	439335	AA742697	Hs.62492	NM_052863:Homo sapiens secretoglobulin, fa	2.93	3.72
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.92	1.91
	419981	AA897581	Hs.128773	ESTs	2.92	2.18
	400419	AF084545		Target	2.92	1.83
	435176	AA744875	Hs.189413	ESTs	2.91	2.15
	413283	R78669	Hs.23756	hypothetical protein similar to swine ac	2.90	2.25
10	444339	T96555	Hs.31562	ESTs	2.90	3.16
	429272	W25140	Hs.110667	ESTs	2.90	2.43
	435047	AA454985	Hs.54973	cadherin-like protein VR20	2.90	2.29
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	2.90	2.40
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	2.88	2.47
15	421554	AW137676	Hs.97775	ESTs	2.88	3.37
	422770	AL117544	Hs.120021	DKFZP4341092 protein	2.88	2.00
	434658	AJ624436	Hs.310286	ESTs	2.88	2.06
	440248	AA876138		ESTs	2.86	2.24
	442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	2.86	4.32
20	430515	AA746503	Hs.283313	ESTs	2.86	2.96
	446063	AJ720140	Hs.151079	ESTs	2.86	2.47
	438177	BE327015		ESTs	2.86	1.70
	429083	Y09397	Hs.227817	BCL2-related protein A1	2.85	2.06
	417105	X60992	Hs.81226	CD6 antigen	2.85	3.00
25	433230	AW136134	Hs.220277	ESTs	2.84	1.97
	438676	AA813745	Hs.123446	ESTs	2.84	2.62
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	2.82	4.33
	420252	AW270404	Hs.193161	ESTs	2.82	3.22
	415788	AW628686	Hs.78851	KIAA0217 protein	2.82	1.78
30	428065	AI634046	Hs.157313	ESTs	2.81	2.47
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.81	2.67
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.78	3.39
	435517	AA928626	Hs.130177	ESTs	2.78	2.36
	439883	AL359652	Hs.171096	Homo sapiens EST from clone DKFZp434A041	2.78	1.82
35	434158	T86534	Hs.14372	ESTs	2.78	1.96
	428923	BE047698	Hs.188785	ESTs	2.78	2.07
	413786	AW613780	Hs.13500	ESTs	2.78	1.97
	406387			Target Exon	2.77	4.22
40	421168	AF182277	Hs.330780	cytochrome P450, subfamily IIB (phenobar	2.76	3.24
	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	2.76	2.11
	427484	N32859	Hs.37288	nuclear receptor subfamily 1, group D, m	2.76	1.94
	417728	AW138437	Hs.24790	KIAA1573 protein	2.76	1.78
	435154	AA668764		ESTs	2.76	2.10
45	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.76	2.21
	423387	AJ012074		vasoactive intestinal peptide receptor 1	2.76	2.36
	432060	AW971364	Hs.324775	ESTs	2.75	2.02
	434164	AW207019	Hs.148135	serine/threonine kinase 33	2.74	2.48
	423706	U95218	Hs.131924	G protein-coupled receptor 65	2.74	1.93
	442703	AL044949	Hs.116298	ESTs	2.74	1.89
50	450247	AF123303	Hs.24713	hypothetical protein	2.74	1.73
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	2.74	2.85
	426535	AJ077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	2.74	1.88
	409196	NM_001874	Hs.334873	carboxypeptidase M	2.73	1.86
	422389	AF240635	Hs.115897	protocadherin 12	2.72	2.26
55	444324	AI301330	Hs.143838	ESTs	2.72	1.74
	417831	H16423	Hs.82685	CD47 antigen (Rh-related antigen, integr	2.72	2.40
	428769	AW207175	Hs.106771	ESTs	2.72	2.19
	404277			NM_019111*:Homo sapiens major histocompa	2.72	3.12
60	409653	AW451693	Hs.220826	ESTs	2.72	2.62
	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	2.72	2.25
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	2.72	2.09
	444381	BE387335	Hs.283713	hypothetical protein BC014245	2.71	2.26
	443547	AW271273		hypothetical protein FLJ12666	2.71	1.74
65	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.70	2.39
	402874			Target Exon	2.70	1.85
	438068	AI927209	Hs.306210	Homo sapiens cDNA: FLJ23133 fis, clone L	2.70	2.23
	415075	L27479	Hs.77889	Friedreich ataxia region gene X123	2.69	2.11
	444314	AI140497		gb:row76b09.s1 Soares_fetal_liver_spleen_	2.69	2.28
70	428656	AB037798	Hs.188790	KIAA1377 protein	2.68	1.91
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.68	3.95
	443951	F13272		ferritin, light polypeptide	2.68	2.66
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.68	1.74
	432639	AW973785		gb:EST385886 MAGE resequences, MAGM Homo	2.68	1.78
	445423	AW139555	Hs.150120	ESTs	2.68	2.29
75	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	2.67	2.07
	431779	AW971178	Hs.268571	apolipoprotein C-I	2.67	3.00
	458124	AW005548	Hs.124590	ESTs	2.67	3.78
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-I	2.66	1.64
	445745	AB007924	Hs.13245	KIAA0455 gene product	2.66	1.64
80	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	2.65	1.82
	432231	AA339977	Hs.274127	CLST 11240 protein	2.64	4.23
	442200	AW590572	Hs.235768	ESTs	2.64	2.46
	426828	NM_000020	Hs.172870	activin A receptor type II-like 1	2.64	2.00
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.63	3.23

	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	2.63	2.48
	411213	AA676939	Hs.69285	neuropilin 1	2.62	1.73
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	2.62	2.69
	446570	AV659177	Hs.127160	ESTs	2.61	2.44
5	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	2.60	3.39
	434792	AA649253	Hs.132458	ESTs	2.60	1.74
	426782	R14614	Hs.33846	ESTs	2.60	2.36
	425371	D49441	Hs.155981	mesothelin	2.60	6.97
	447720	AL038765	Hs.161304	ESTs	2.59	3.06
10	444623	AI183829	Hs.202111	ESTs	2.59	2.77
	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	2.58	2.01
	444542	AI161293	Hs.280380	aminopeptidase	2.58	2.31
	439549	AW837885	Hs.137314	ESTs	2.58	2.37
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	2.58	2.56
15	417015	M83772	Hs.80876	flavin containing monooxygenase 3	2.56	2.47
	433308	AA582718	Hs.291650	ESTs	2.56	2.01
	443885	H91806	Hs.15284	ESTs	2.55	1.71
	408170	AW204516	Hs.31835	ESTs	2.55	1.59
20	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatid	2.54	1.63
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	2.54	2.98
	428791	AA435661	Hs.264750	ESTs	2.53	2.29
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	2.53	3.91
	447357	AI375922	Hs.159367	ESTs	2.52	2.83
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	2.52	1.90
25	424105	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1	2.52	3.45
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	2.52	1.98
	438698	AW297855		ESTs, Weakly similar to I38022 hypotheti	2.52	1.98
	420991	AW504814	Hs.287379	Homo sapiens mRNA for FLJ00111 protein,	2.52	2.41
	424049	AB014524	Hs.138380	KIAA0624 protein	2.51	2.19
30	438543	AA810141	Hs.192182	ESTs	2.51	2.06
	414061	NM_000699	Hs.335493	amylase, alpha 2A; pancreatic	2.51	2.14
	424806	AA382523	Hs.105689	MSTP031 protein	2.51	2.11
	438580	AA811262	Hs.299202	ESTs	2.50	1.83
	434445	AI349306	Hs.11782	ESTs	2.50	3.13
35	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	2.50	1.76
	413638	H71252		gbys12h12.s1 Soares fetal liver spleen	2.50	2.00
	421281	AI299139	Hs.17517	ESTs	2.50	2.40
	441384	AA447849	Hs.288660	retinoic acid induced 3	2.50	2.75
	436772	AW975688		metallothionein 1E (functional)	2.49	1.80
40	433102	AI343966	Hs.158528	ESTs	2.49	2.25
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	2.48	2.09
	445612	N94126	Hs.12969	hypothetical protein	2.48	2.28
	445261	T79759	Hs.250651	ESTs, Weakly similar to I38022 hypotheti	2.48	1.87
45	433854	AA610649	Hs.333239	ESTs	2.48	2.09
	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	2.48	2.75
	411069	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	2.48	2.01
	440594	AW445167	Hs.126036	ESTs	2.48	1.57
	450295	AI766732	Hs.210628	ESTs	2.48	1.99
50	431316	AA502663	Hs.145037	ESTs	2.48	1.80
	438564	AA381553	Hs.198253	major histocompatibility complex, class	2.48	2.80
	439593	BE073597	Hs.124863	ESTs	2.48	1.89
	422355	AW403724	Hs.300697	coagulation factor VII (serum prothrombi	2.47	3.74
	453134	AA032211	Hs.118493	ESTs	2.46	2.72
55	417169	R13550	Hs.21388	ESTs	2.46	1.88
	434411	AA632649	Hs.201372	ESTs	2.46	1.95
	440381	AA917808	Hs.190495	ESTs	2.46	2.09
	448782	AL050295		KIAA0758 protein	2.46	2.69
	404240			NM_018950:Homo sapiens major histocompat	2.45	2.83
60	450843	AI741483	Hs.205383	ESTs	2.44	2.25
	434137	AA907734	Hs.124895	ESTs	2.44	1.94
	438315	R56795	Hs.82419	ESTs	2.44	1.61
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.44	1.90
	439402	W02753	Hs.103002	ESTs	2.44	2.32
65	445903	AI347487	Hs.132781	class I cytokine receptor	2.44	1.70
	437323	AA371145	Hs.194397	leptin receptor	2.44	1.58
	433923	AI823453	Hs.146625	ESTs	2.43	1.68
	442201	AW516704	Hs.208726	ESTs	2.43	3.22
	437982	N93466	Hs.121764	ESTs, Weakly similar to testicular lekti	2.43	2.21
70	452698	NM_001295	Hs.301921	chemokine (C-C motif) receptor 1	2.43	2.13
	407904	W44735	Hs.9286	Homo sapiens cDNA: FLJ21278 lis, clone C	2.43	2.68
	406973	M34996	Hs.198253	major histocompatibility complex, class	2.42	2.05
	428055	AA420564	Hs.101760	ESTs	2.42	2.79
	428970	BE276891	Hs.194691	retinoic acid induced 3 (RAIG1); metabo	2.42	1.88
	433138	AB029496	Hs.59729	semaphorin sem2	2.42	2.02
75	415757	AA830854	Hs.187810	ESTs	2.42	2.08
	438507	AA809052		ESTs	2.42	1.97
	450811	AI739486	Hs.245497	ESTs	2.42	2.76
	424027	AW337575	Hs.201591	ESTs	2.41	3.15
80	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.41	2.08
	435978	AF272899	Hs.135118	Homo sapiens PR-domain zinc finger prote	2.40	1.76
	426291	U58913	Hs.169191	small inducible cytokine subfamily A (Cy	2.40	1.97
	416370	N90470	Hs.203697	CD38 antigen (p45)	2.40	1.63
	415688	AA166963		gb:zo86d01.s1 Stratagene ovarian cancer	2.40	

5	445633	AI453386	Hs.17287	ESTs, Weakly similar to S26689 hypotheti	2.39	1.99
	431300	AA502346		gb:ne26b03.s1 NCL CGAP_Co3 Homo sapiens	2.39	1.79
	407690	R47799	Hs.266957	hypothetical protein FLJ14281	2.39	1.84
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.39	2.21
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	2.38	2.09
10	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.38	1.78
	437479	R61866	Hs.101277	ESTs	2.38	3.00
	445784	AI253155	Hs.146065	ESTs	2.38	1.61
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	2.38	2.25
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	2.37	1.55
15	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	2.37	2.41
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	2.37	1.61
	418262	Z38968		ESTs	2.37	2.05
	420943	AI718702	Hs.279930	major histocompatibility complex, class	2.37	2.00
	442762	AF035119	Hs.8700	deleted in liver cancer 1	2.37	2.05
20	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	2.37	1.67
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.36	1.88
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	2.36	2.61
	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	2.36	2.84
	427250	R35941	Hs.25418	ESTs	2.36	2.15
25	452194	AI694413		olfactory receptor, family 2, subfamily	2.36	3.41
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	2.36	3.05
	407242	M18728		gb:Human nonspecific crossreacting antig	2.35	2.34
	418875	W19971	Hs.233459	ESTs	2.35	1.95
	425023	AW956889	Hs.154210	EDG-1 (endothelial differentiation, sph	2.35	1.85
30	432608	AI492660	Hs.170935	ESTs	2.35	2.06
	408048	NM_007203	Hs.42322	A kinase (PKA) anchor protein 2	2.35	1.91
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	2.35	2.34
	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	2.35	2.13
	410577	X91911	Hs.64639	glioma pathogenesis-related protein	2.34	1.73
35	422099	AA156022	Hs.111518	hypothetical protein	2.34	1.80
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIIb, r	2.34	2.24
	427541	AI798983	Hs.82921	solute carrier family 35 (CMP-sialic aci	2.33	2.62
	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	2.32	2.52
	431848	AI378867	Hs.271605	ESTs, Highly similar to AF175283 1 zinc	2.32	2.50
40	446354	AW449650		ESTs	2.32	2.21
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	2.32	4.34
	423961	D13666	Hs.136348	perostin(OSF-2os)	2.31	2.19
	410798	BE178622	Hs.16291	gb:PM3-HT0605-270200-001-a02 HT0605 Homo	2.31	2.34
	457250	AA811987	Hs.125779	ESTs	2.31	1.66
45	445291	BE397753	Hs.14623	Interferon, gamma-inducible protein 30	2.31	2.96
	426839	M74782	Hs.172689	Interleukin 3 receptor, alpha (low affin	2.30	2.12
	422746	NM_004484	Hs.119651	glypican 3	2.30	2.16
	439920	H05430	Hs.288433	neurotrophin	2.30	4.06
	414942	C14898	Hs.192986	ESTs	2.30	2.02
50	419092	J05581	Hs.89603	mucin 1, transmembrane	2.29	3.08
	424878	H57111	Hs.221132	ESTs	2.29	1.84
	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.29	2.76
	411605	AW006831		ESTs	2.29	1.58
	416965	N26223	Hs.160436	ESTs	2.29	4.71
55	428713	AA432067		ESTs, Moderately similar to CYA4 RAT ADE	2.29	1.73
	435106	AA100847	Hs.5978	ESTs, Highly similar to AF174600 1 F-box	2.28	1.90
	420380	AA640891	Hs.102406	ESTs	2.28	2.82
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.28	1.52
	410361	BE391804	Hs.62661	guanylate binding protein 1, Interferon-	2.28	2.09
60	447160	AA330310	Hs.24181	ESTs	2.28	1.71
	421114	AW975051	Hs.293156	ESTs, Weakly similar to T78885 serine/th	2.27	1.98
	453686	AL110328	Hs.304679	ESTs, Moderately similar to Z195_HUMAN Z	2.27	1.91
	452114	N22687	Hs.8236	ESTs	2.27	1.88
	417355	D13168	Hs.82002	endothelin receptor type B	2.26	1.63
65	434927	H46612	Hs.293815	Homo sapiens HSPC265 mRNA, partial cds	2.26	1.84
	442262	BE170651	Hs.8700	deleted in liver cancer 1	2.26	1.86
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	2.26	1.72
	425354	U62027	Hs.155935	complement component 3a receptor 1	2.26	1.70
	409190	AU076536	Hs.50984	sarcoma amplified sequence	2.26	1.56
70	414221	AW450979		gb:U1-H-B13-ala-a-12-0-UI.s1 NCL CGAP_Su	2.26	2.12
	435272	AA906415	Hs.110041	ESTs	2.25	2.15
	414991	C17898		gb:C17898 Human placenta cDNA (TFujiwara	2.24	3.58
	424623	AW963062	Hs.270737	ESTs	2.24	1.87
	424665	AW368576	Hs.139851	caveolin 2	2.24	2.15
75	422426	W79117	Hs.58559	ESTs	2.22	3.33
	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	2.22	2.39
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	2.22	3.28
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.22	1.59
	446142	AI754693	Hs.145968	ESTs	2.22	1.88
80	410503	AW975746	Hs.188682	KIAA1702 protein	2.22	1.56
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	2.22	2.49
	437629	AW574774	Hs.121692	ESTs	2.22	1.70
	429688	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	2.21	1.64
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.20	2.73
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/V	2.20	2.58
	429496	AA453800	Hs.192793	ESTs	2.20	2.97
	425516	BE000707	Hs.29567	ESTs	2.20	1.58

	422404	AL133571	Hs.336189	Homo sapiens mRNA; cDNA DKFZp434F1135 (f	2.19	1.92
	423526	AB011086	Hs.129739	KIAA0514 gene product	2.19	2.85
	436485	X59135	Hs.156110	Immunoglobulin kappa constant	2.19	2.01
	426251	M24283	Hs.168383	Intercellular adhesion molecule 1 (CD54)	2.19	2.53
5	443441	AW291196	Hs.92195	ESTs	2.18	1.73
	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	2.18	2.53
	408705	AA312135	Hs.48967	HSPC034 protein	2.18	1.54
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	2.18	1.93
	430915	AA488953		gb:aa55e05.r1 NCL_CGAP_GCB1 Homo sapiens	2.18	1.57
10	418791	AA935633	Hs.194628	ESTs	2.17	2.05
	432620	AA777749	Hs.5978	LIM domain only 7	2.17	1.75
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	2.17	2.01
	406646	M33600	Hs.308026	major histocompatibility complex, class	2.17	3.12
	424450	AL137526		dynein intermediate chain 2	2.17	4.14
15	426410	BE298446	Hs.305890	BCL2-like 1	2.16	2.19
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	2.16	1.70
	421077	AK000061	Hs.101590	hypothetical protein	2.16	1.60
	424563	AA446932	Hs.151428	net finger protein 2	2.16	1.83
	405102			C15001220*:g[4469558]gb[AA021311.1] (AF	2.16	1.78
20	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-fin	2.15	1.87
	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	2.15	1.65
	418067	AI127958	Hs.83393	cystatin E/M	2.15	2.40
	436372	AW972301	Hs.310286	ESTs	2.15	2.35
	418728	AW970937	Hs.293843	ESTs	2.14	2.58
25	450400	AI694722	Hs.279744	ESTs	2.14	2.06
	409031	AA376836		ESTs	2.14	2.14
	435143	R12375	Hs.194800	ESTs	2.14	1.69
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	2.14	2.03
	453927	AA082465	Hs.125031	choline/ethanolaminephosphotransferase	2.14	1.57
30	418304	AA215702		gb:zr97g10.r1 NCL_CGAP_GCB1 Homo sapiens	2.14	1.68
	418299	AA279530	Hs.83968	Integrin, beta 2 (antigen CD18 (p95), ly	2.14	2.04
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	2.13	1.72
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	2.13	1.68
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	2.13	2.47
35	452353	C18825	Hs.29191	epithelial membrane protein 2	2.12	2.31
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	2.12	2.76
	424005	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	2.12	2.11
	437581	N59284	Hs.288010	ESTs	2.12	2.85
	410976	R36207	Hs.25092	hypothetical protein MGC10744	2.12	2.04
40	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.12	2.00
	423069	W15613	Hs.1613	adenosine A2a receptor	2.12	1.72
	432860	AW974077	Hs.283349	ESTs	2.12	1.75
	449509	AA001615	Hs.84561	ESTs	2.12	1.84
	456062	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	2.11	4.42
45	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.11	1.65
	459680	H96982	Hs.42321	ESTs	2.11	2.20
	449677	AA002071		gb:zh85d01.s1 Soares_fetal_liver_spleen_	2.10	2.12
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	2.10	2.48
	443021	AA368546	Hs.8904	Ig superfamily protein	2.10	2.42
50	437838	AI307229		ESTs	2.10	1.67
	429421	AL031658		Human DNA sequence from clone RP1-310013	2.10	1.91
	407202	N58172	Hs.109370	ESTs	2.10	1.68
	443669	AI140462	Hs.134587	ESTs	2.10	1.64
	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	2.10	1.71
55	408410	AA447438	Hs.44697	ATPase, Class V, type 10C	2.10	2.05
	436293	AI601188	Hs.120910	ESTs	2.10	2.01
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	2.10	1.66
	427876	AI494291		ESTs	2.10	2.48
	456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	2.09	3.11
60	434987	AW975114		ESTs	2.09	1.69
	433735	AA608955	Hs.109653	ESTs	2.09	1.78
	433226	AW503733	Hs.9414	KIAA1488 protein	2.09	1.62
	425787	AA363867	Hs.155029	ESTs	2.09	1.85
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	2.08	3.41
65	442369	AI565071		ESTs	2.08	1.60
	430478	NM_014349	Hs.241535	apolipoprotein L, 3	2.08	2.39
	434421	AI915927	Hs.34771	ESTs	2.08	1.66
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	2.08	1.72
	431728	NM_007351	Hs.268107	multimerin	2.08	1.51
70	444929	AI685841	Hs.161354	ESTs	2.08	3.14
	408873	AL046017		calmodulin 2 (phosphorylase kinase, delt	2.08	2.09
	437634	AW293046	Hs.255158	ESTs	2.08	1.66
	400277			Eos Control	2.08	1.46
	443601	AI078554	Hs.42658	ESTs	2.08	1.87
75	432212	AW137742		ESTs	2.08	2.84
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	2.07	1.48
	406122			Target Exon	2.06	2.75
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	2.06	1.66
	408788	AL134947	Hs.213956	Homo sapiens BAC clone RP11-10205 from Y	2.06	1.70
80	421057	T58283		Homo sapiens cDNA: FLJ22063 fis, clone H	2.06	1.78
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	2.06	2.30
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	2.06	2.31
	449444	AW818436		solute carrier family 16 (monocarboxylic	2.06	1.41

	421464	AA291553	Hs.190086	ESTs	2.06	2.61
	424831	H61453		ESTs	2.06	2.12
	434542	AA769310		hypothetical protein FLJ13164	2.06	1.44
5	418323	NM_002118	Hs.1162	major histocompatibility complex, class	2.05	2.61
	418836	AI655499	Hs.161712	ESTs	2.05	1.73
	431315	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	2.05	1.99
	400750			Target Exon	2.05	1.75
	406851	AA609784		major histocompatibility complex, class	2.05	3.94
10	414936	C14774		gb:C14774 Clontech human aorta polyA mRNA	2.05	2.41
	453459	BE047032	Hs.257789	ESTs	2.04	1.86
	443450	N66045	Hs.133529	ESTs	2.04	2.46
	430015	AW768399		ESTs	2.04	1.63
	429399	AA452244	Hs.16727	ESTs	2.04	1.51
15	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	2.04	1.73
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	2.04	1.46
	421757	Z20897	Hs.296259	paraoxonase 3	2.04	2.13
	441942	AF182645	Hs.8024	IK cytokine, down-regulator of HLA II	2.04	1.82
	431843	AA516420		ESTs, Weakly similar to I38022 hypothe	2.04	1.57
20	432006	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	2.04	3.23
	414154	AW205314	Hs.323060	ESTs	2.03	2.96
	449987	AW079749	Hs.184719	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.03	1.59
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	2.03	2.01
	406645	M57466	Hs.814	major histocompatibility complex, class	2.03	2.49
25	414516	AJ307802		ESTs, Weakly similar to T43458 hypothe	2.02	1.56
	417032	AA192469	Hs.271838	ESTs	2.02	1.48
	414875	H42679	Hs.77522	major histocompatibility complex, class	2.02	2.79
	414522	AW518944	Hs.76325	immunoglobulin J chain	2.02	1.84
	410511	AA743475	Hs.285655	ESTs	2.02	1.87
30	423533	NM_014339	Hs.129751	interleukin 17 receptor	2.02	2.26
	437259	AJ377755	Hs.120695	ESTs	2.02	2.34
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypothe	2.02	1.86
	426722	U53823	Hs.171952	occludin	2.02	1.57
	421229	AJ056590	Hs.7086	hypothetical protein MGC12435	2.02	1.79
35	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.02	1.97
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	2.02	2.09
	449317	AW293413	Hs.132906	19A24 protein	2.02	1.84
	439556	AI623752	Hs.163603	ESTs	2.02	1.62
40	443031	AW134696	Hs.49418	ESTs	2.01	1.58
	444838	AV651680	Hs.208558	ESTs	2.01	1.69
	453108	AJ311457	Hs.99472	ESTs	2.01	1.64
	432967	AA572949	Hs.207566	ESTs	2.01	1.83
	441390	AI692560	Hs.131175	ESTs	2.01	1.63
	448076	AJ133123	Hs.20196	adenylate cyclase 9	2.01	1.80
45	420258	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.01	2.32
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	2.01	1.90
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.01	1.90
	415443	T07353	Hs.7948	ESTs	2.00	1.54
	424925	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	2.00	2.74
50	404394			ENSP00000241075:TRRAP PROTEIN.	2.00	2.99
	459557	N58315		gb:yv68g06.s1 Soares fetal liver spleen	2.00	1.89
	437204	AL110216		ESTs, Weakly similar to I55214 salivary	2.00	1.46
	429295	AA682377	Hs.99216	ESTs, Moderately similar to ALU8_HUMAN A	2.00	1.37
	440667	BE076969	Hs.7337	hypothetical protein FLJ10936	2.00	1.51
55	431193	AW749505	Hs.296770	KIAA1719 protein	1.99	2.01
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	1.99	2.11
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	1.98	1.79
	417072	BE243915	Hs.81118	leukotriene A4 hydrolase	1.98	2.47
	429073	AA446167	Hs.47385	ESTs	1.98	1.92
60	448133	AA723157	Hs.73769	folate receptor 1 (adult)	1.98	2.94
	420838	AW118210	Hs.42321	ESTs	1.98	1.67
	436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	1.97	2.10
	430702	U56979	Hs.278568	H factor 1 (complement)	1.97	1.84
	456804	AI421645	Hs.139851	caveolin 2	1.97	1.58
65	439195	H89360		gb:yyw28d08.s1 Morton Fetal Cochlea Homo	1.97	1.93
	459299	BE094291	Hs.155651	hepatocyte nuclear factor 3, beta	1.97	2.28
	413836	W92003	Hs.70614	ESTs	1.97	1.80
	400417	X72475		Target	1.97	1.75
	427814	W28383	Hs.180900	Williams-Beuren syndrome chromosome regi	1.96	1.46
70	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	1.96	2.18
	446135	AW130288	Hs.170318	hypothetical protein FLJ10147	1.96	2.06
	455615	BE045344	Hs.274923	ESTs, Moderately similar to unnamed prot	1.96	2.21
	414572	AJ077174	Hs.288181	cathepsin H	1.96	2.65
	433891	AA613792		gb:zno97h03.s1 NCI_CGAP_Pr2 Homo sapiens	1.95	1.71
75	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	1.95	2.88
	451609	AL046019	Hs.209276	ESTs	1.94	3.26
	447131	NM_004585	Hs.17466	retinoid acid receptor responder (lazar	1.94	2.94
	430887	N66801	Hs.260287	KIAA1841 protein	1.94	1.62
	414700	H63202	Hs.38163	ESTs	1.94	1.72
	417874	BE516160	Hs.82829	protein tyrosine phosphatase, non-recept	1.94	1.56
80	443907	AJ076484	Hs.9963	TYRO protein tyrosine kinase binding pro	1.93	2.22
	425252	AW391162		calreticulin	1.92	2.14
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	1.92	2.19
	425810	AI923627	Hs.31903	ESTs	1.92	1.76

	433618	AA602539	Hs.345494	ESTs	1.92	1.84
	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	1.92	2.27
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	1.92	1.76
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	1.92	1.72
5	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA	1.91	1.83
	426780	BE242284	Hs.172199	adenylate cyclase 7	1.91	1.67
	452386	R12499	Hs.20468	ESTs	1.91	2.64
	438670	AI275803	Hs.123428	ESTs	1.91	3.12
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	1.91	1.82
10	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	1.90	2.06
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	1.90	1.85
	444745	AF117754	Hs.11861	thyroid hormone receptor-associated prot	1.90	1.65
	428166	AA423849	Hs.79530	MS-14 protein	1.90	1.70
	426721	AA383588	Hs.131816	ESTs, Weakly similar to T29012 hypotheti	1.89	3.22
15	449271	AW338067	Hs.7869	Homo sapiens cDNA FLJ11946 fis, clone HE	1.88	2.07
	436576	AI458213	Hs.77542	ESTs	1.88	2.25
	437751	AA767373		ESTs, Moderately similar to ALU1_HUMAN A	1.88	2.41
	449618	AI076459	Hs.15978	KIAA1272 protein	1.88	1.63
	430634	AI860651	Hs.26685	calcyphosine	1.88	3.01
20	440663	AW452976	Hs.247112	hypothetical protein FLJ10902	1.88	1.65
	440099	AL080058	Hs.6909	DKFZP564G202 protein	1.88	1.78
	414662	AL036058	Hs.76807	major histocompatibility complex, class	1.88	2.37
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	1.87	2.07
	414464	AI870175	Hs.13957	ESTs	1.87	2.68
25	427792	M63928	Hs.180841	tumor necrosis factor receptor superfam	1.87	2.25
	415801	R24219	Hs.278443	Fc fragment of IgG, low affinity IIb, re	1.87	2.05
	430027	AB023197	Hs.227743	KIAA0980 protein	1.87	1.70
	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.87	2.18
	412443	AW951103	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	1.86	2.27
30	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	1.86	2.31
	420361	N92054	Hs.194718	zinc finger protein 265	1.86	1.63
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	1.86	2.13
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	1.85	1.77
	442434	AA995787	Hs.129583	ESTs	1.85	2.15
35	422735	AA169685	Hs.119529	Niemann-Pick disease, type C2 gene	1.85	2.77
	444083	AI123195		gb:0017a10.x1 Soares_NSF_F8_9W_OT_PA_P_S	1.84	1.73
	449679	AI823951	Hs.129700	toll-like-like 1	1.84	1.57
	418183	NM_001772	Hs.83731	CD33 antigen (gp67)	1.84	2.02
40	414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.84	1.72
	414803	X03100	Hs.914	Human mRNA for SB class II histocompatibi	1.84	2.47
	408669	AA493591	Hs.78146	platelet/endothelial cell adhesion molec	1.84	2.29
	455508	AW976165		gb:EST388274 MAGE resequences, MAGN Homo	1.84	1.69
	410290	AA02307	Hs.322844	hypothetical protein DKFZp564A176	1.83	2.12
	426457	AW894667	Hs.22660	chimerin (chimaerin) 1	1.83	1.59
45	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	1.83	1.57
	417086	AA194446		ESTs, Weakly similar to S55024 nebulin,	1.83	1.45
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	1.83	2.18
	429952	AF080158	Hs.226573	inhibitor of kappa light polypeptide gan	1.83	1.75
	438596	AA829427	Hs.243081	ESTs	1.83	2.83
50	436486	AA742221	Hs.120633	ESTs	1.82	2.14
	433365	AF026944	Hs.293797	ESTs	1.82	2.50
	449943	AF104266	Hs.24212	latrophilin	1.82	2.08
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	1.82	2.37
	421563	NM_006433	Hs.105806	granulysin	1.82	2.48
55	449161	N53431	Hs.47647	ESTs, Weakly similar to T00057 hypotheti	1.81	2.81
	453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	1.81	2.66
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	1.81	2.50
	432946	U60899	Hs.279854	mannosidase, alpha, class 2B, member 1	1.81	2.05
	432297	AW663632	Hs.285625	Homo sapiens mRNA; cDNA DKFZp434A119 (fr	1.80	3.13
60	428677	AI657119	Hs.120036	troponin I, cardiac	1.80	2.94
	409485	S80990	Hs.252136	ficollin (collagen/tibronogen domain-cont	1.80	2.28
	423081	AF262992	Hs.123159	sperm associated antigen 4	1.80	1.55
	425458	H89317	Hs.182889	ESTs	1.80	2.21
	425390	AI092634	Hs.156114	protein tyrosine phosphatase, non-recept	1.80	1.41
65	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	1.80	2.20
	430570	AI417881	Hs.292464	ESTs	1.80	1.62
	439425	AF086244	Hs.114659	ESTs	1.80	2.37
	408688	AI634522	Hs.152925	KIAA1268 protein	1.80	2.13
	440675	AW005054	Hs.279788	ESTs, Weakly similar to KCC1_HUMAN CALCI	1.80	1.80
70	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	1.79	1.57
	406621	X57809	Hs.8997	immunoglobulin lambda locus	1.79	2.18
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.79	1.68
	403421			NM_016369*Homo sapiens claudin 18 (CLDN	1.79	2.47
	430423	AI190548	Hs.143479	ESTs, Weakly similar to hypothetical pro	1.79	2.92
75	416384	AU076903	Hs.79283	selectin P ligand	1.79	1.87
	440638	AI376551		gb:ta64e10.x1 Soares_NFL_T_GBC_S1 Homo s	1.78	1.69
	422003	AA361760	Hs.296326	ESTs	1.78	2.05
	412288	NM_003005	Hs.73800	selectin P (granule membrane protein 140	1.77	1.82
	432987	AI864771	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	1.77	2.03
80	441602	AI655043	Hs.133456	ESTs	1.77	2.01
	458194	AW383618		ESTs, Moderately similar to ALU2_HUMAN A	1.76	2.35
	432565	AA553477	Hs.152428	ESTs	1.76	2.63
	421071	AI311238	Hs.104476	ESTs, Weakly similar to OGHU1E collagen	1.75	2.59

	408989	AW361666	Hs.49500	KIAA0746 protein	1.75	1.66
	414807	AJ738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	1.75	1.54
	403903			C5001632-gi10645308jgb AAG21430.1)AC00	1.75	3.20
5	421461	AW291023		ESTs, Weakly similar to A46010 X-linked	1.74	2.67
	430850	BE144152		gb:MRD-HT0165-060200-006-e02 HT0165 Homo	1.74	2.52
	424377	AF081675	Hs.146322	killer cell lectin-like receptor subfamily	1.74	2.15
	443884	N20617	Hs.194397	lactin receptor	1.74	1.51
	423057	AW961597	Hs.130816	ESTs, Moderately similar to I38022 hypot	1.74	1.63
10	448262	AW880830	Hs.186273	ESTs	1.73	2.57
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subunit	1.73	1.87
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	1.73	2.21
	412896	AW804157	Hs.308026	major histocompatibility complex, class	1.72	2.37
	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	1.72	2.16
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	1.72	1.52
15	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	1.71	1.55
	438606	NM_014859	Hs.6336	KIAA0672 gene product	1.71	1.57
	434795	BE620794	Hs.4147	translocating chain-associating membrane	1.71	2.21
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	1.71	1.46
	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	1.71	2.49
20	421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	1.71	1.57
	423857	N48902	Hs.133481	Homo sapiens mRNA; cDNA DKFZp564O0862 (f	1.71	1.56
	408393	AW015318	Hs.23165	ESTs	1.70	1.43
	432409	AA806538	Hs.130732	KIAA1575 protein	1.70	1.54
	440817	AJ341423	Hs.288433	neurotrophin	1.70	2.17
25	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	1.69	2.54
	453691	H12235	Hs.226505	ESTs	1.69	2.07
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	1.68	1.54
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.68	2.29
	434951	AF161442	Hs.191591	Homo sapiens HSPC324 mRNA, partial cds	1.68	2.24
30	444301	AK000136	Hs.10760	asporin (LRR class 1)	1.68	1.44
	407775	NM_004914	Hs.38772	RAB36, member RAS oncogene family	1.68	2.03
	437119	AJ379921	Hs.177043	ESTs	1.68	4.21
	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	1.68	2.28
	453498	BE181412	Hs.23245	hypothetical protein FLJ11767	1.68	2.76
35	428289	M26301	Hs.2253	complement component 2	1.67	2.40
	404854			Target Exon	1.67	1.76
	450954	AJ904740	Hs.25691	receptor (calcitonin) activity modifying	1.67	2.32
	410048	W76467	Hs.343874	proline oxidase homolog	1.67	3.03
	407857	AJ928445	Hs.92254	synaptotagmin-like 2	1.66	1.51
40	447827	U73727	Hs.19718	protein tyrosine phosphatase, receptor t	1.66	2.01
	417193	AJ922189	Hs.288390	hypothetical protein FLJ22795	1.66	2.05
	421237	U25029	Hs.102761	Human glucocorticoid receptor alpha mRNA	1.66	2.20
	433350	BE563152	Hs.10362	Homo sapiens cDNA: FLJ20944 fls, clone A	1.66	2.11
	417451	AW007280	Hs.115537	putative dipeptidase	1.65	2.11
45	443791	N64458	Hs.143345	ESTs	1.65	2.11
	440475	AJ807671	Hs.24040	potassium channel, subfamily K, member 3	1.65	2.04
	431743	AW972642	Hs.293055	ESTs	1.64	2.64
	400328	X87344		transporter 2, ATP-binding cassette, sub	1.64	2.43
50	451876	T63141		gb:yg99a12.s1 Stralagene lung (937210) H	1.64	2.02
	417321	N68722	Hs.191368	ESTs	1.64	2.53
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	1.64	2.01
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	1.63	2.17
	432176	AW090386	Hs.112278	arrestin, beta 1	1.63	2.04
55	450708	AA376654		eukaryotic translation initiation factor	1.62	2.05
	429570	BE242256	Hs.2441	KIAA0022 gene product	1.62	1.39
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	1.62	1.57
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	1.62	1.44
	452424	AJ964028	Hs.48353	ESTs	1.62	2.53
60	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	1.62	1.38
	416316	H58721	Hs.271628	ESTs	1.62	1.39
	431808	AF188114	Hs.270737	tumor necrosis factor (ligand) superfamily	1.62	2.67
	452203	X57522		transporter 1, ATP-binding cassette, sub	1.62	2.45
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a)	1.62	1.51
65	438089	W05391		nuclear receptor subfamily 1, group 1, m	1.61	1.45
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	1.61	1.52
	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	1.61	2.40
	444009	AJ380782	Hs.135104	ESTs	1.60	2.15
	436057	AJ004832	Hs.5038	neuropathy target esterase	1.60	2.60
70	437352	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	1.60	2.57
	433614	W07475	Hs.277101	cytochrome c oxidase subunit IV isoform	1.60	3.30
	410494	M36564	Hs.64016	protein S (alpha)	1.59	1.42
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	1.59	2.02
	446616	R65984	Hs.334873	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.59	2.52
	419918	X80700	Hs.93728	pre-B-cell leukemia transcription factor	1.59	2.04
75	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	1.59	1.98
	434308	N15157	Hs.47282	ESTs	1.58	2.29
	447341	AF106941	Hs.18142	arrestin, beta 2	1.58	2.09
	454315	AW373564	Hs.251928	BANP homolog, SMAR1 homolog	1.58	2.10
	423281	AJ271684	Hs.126355	C-type (calcium dependent, carbohydrate-	1.57	1.75
80	433671	AW138797	Hs.132906	19A24 protein	1.57	2.05
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	1.57	2.71
	436906	H95990	Hs.181244	major histocompatibility complex, class	1.57	2.24
	417771	AA804698	Hs.82547	retinoic acid receptor responder (lazarus	1.57	1.43

5	406825	AI982529	Hs.84298	CD74 antigen (invariant polypeptide of m	1.57	2.37
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.56	1.61
	423329	AF054910	Hs.127111	tektin 2 (testicular)	1.56	2.51
	424909	ST8187	Hs.153752	cell division cycle 25B	1.55	2.00
	431921	N46466	Hs.58879	ESTs	1.54	3.04
10	437400	AB011542	Hs.55599	EGF-like-domain, multiple 5	1.54	1.44
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfamily	1.54	3.04
	415078	AA311223	Hs.283091	found in inflammatory zone 3	1.53	2.61
	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	1.53	2.18
	401854			Target Exon	1.53	2.08
15	406850	AI624300	Hs.172928	collagen, type I, alpha 1	1.52	1.52
	433815	AI696602	Hs.112757	ESTs	1.52	2.57
	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	1.52	1.36
	453870	AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fis, clone L	1.51	1.43
	414763	U97276	Hs.77266	quiescin Q6	1.50	2.07
20	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuo	1.50	1.46
	412870	N22788	Hs.82407	CXC chemokine ligand 16	1.50	2.83
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	1.50	2.04
	432894	AW167668	Hs.279772	brain specific protein	1.50	2.25
	457941	AI004525	Hs.14587	ESTs, Weakly similar to AF151859 1 CGI-1	1.49	2.22
25	442743	AI801351	Hs.302110	ESTs, Weakly similar to MUC2_HUMAN MUCIN	1.49	2.09
	419542	AA366037	Hs.90911	solute carrier family 16 (monocarboxylic	1.49	2.40
	433124	U51712	Hs.13775	hypothetical protein SMAP31	1.49	1.39
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	1.49	1.39
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.48	1.76
30	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.48	1.41
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	1.48	1.44
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	1.47	1.31
	427872	AA835058		Human DNA sequence from clone RP1-261G23	1.47	2.50
	449853	AF006823	Hs.24040	potassium channel, subfamily K, member 3	1.47	2.21
35	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (1.47	1.50
	415149	X12451	Hs.78056	cathepsin L	1.46	1.84
	447217	BE465754	Hs.17778	neurotrophin 2	1.46	1.40
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	1.46	2.16
	445672	AI907438	Hs.282862	ESTs	1.46	2.01
40	432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.46	2.10
	458208	AI380016		ESTs, Weakly similar to T4S4_HUMAN TRANS	1.46	1.60
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	1.45	1.40
	419577	L36531	Hs.91296	integrin, alpha 8	1.45	1.40
	439620	AA838727	Hs.124405	ESTs, Weakly similar to A46010 X-linked	1.45	1.57
45	423804	AW403448	Hs.16725	Interferon-stimulated transcription fact	1.45	2.10
	424658	NM_002406	Hs.151513	mannosyl (alpha-1,3)-glycoprotein beta-	1.44	2.00
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005	1.44	1.45
	431573	AW971070	Hs.291160	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.44	1.40
	409524	AW402151	Hs.54673	tumor necrosis factor (ligand) superfamily	1.43	2.01
50	405767	AW090702	Hs.240615	tubulin alpha 1	1.42	1.86
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.42	1.95
	406422			Target Exon	1.41	2.02
	421341	AJ243212		deleted in malignant brain tumors 1	1.41	1.47
	421195	BE464560	Hs.133017	ESTs	1.41	2.42
55	425998	AL076629	Hs.165950	fibroblast growth factor receptor 4	1.41	2.05
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	1.41	1.34
	451220	AF124251	Hs.26054	novel SH2-containing protein 3	1.40	2.10
	409238	AL049990	Hs.51515	Homo sapiens mRNA: cDNA DKFZp564G112 (fr	1.40	3.64
	411880	AW872477		gb:hm30f03.x1 NCL_CGAP_Thy4 Homo sapiens	1.40	3.24
60	432133	AB033088	Hs.272567	KIAA1282 protein	1.40	2.78
	428833	AI928355		ESTs	1.40	2.02
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	1.39	1.55
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	1.39	2.09
	427732	NM_002980	Hs.2199	secretin receptor	1.38	2.44
65	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	1.38	1.85
	407568	AA740964	Hs.62699	ESTs	1.38	3.13
	422573	AW297985	Hs.295726	integrin, alpha V (vitronectin receptor	1.38	1.38
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	1.37	1.12
	457918	AL359590	Hs.162604	hypothetical protein DKFZp762M186	1.36	2.01
70	423696	Z92546	Hs.131819	Sushi domain (SCR repeat) containing	1.36	2.54
	416700	AW498958	Hs.343475	cathepsin D (lysosomal aspartyl protease	1.36	2.04
	407244	M10014		fibrinogen, gamma polypeptide	1.36	1.29
	451109	F11875	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	1.35	1.34
	406654	M90686	Hs.73885	HLA-G histocompatibility antigen, class	1.35	2.47
75	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	1.34	1.66
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	1.34	1.92
	436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular mat	1.34	1.86
	427507	AF240467	Hs.179152	toll-like receptor 7	1.34	2.11
	446967	AI699629	Hs.156781	ESTs	1.34	3.75
80	436553	AW407157	Hs.8997	immunoglobulin lambda locus	1.34	2.18
	456637	AW161450	Hs.109201	CGI-86 protein	1.33	1.78
	422129	AL076635	Hs.1478	serine (or cysteine) proteinase inhibito	1.33	1.95
	417785	X59812	Hs.82568	cytochrome P450, subfamily XXVIIA (stero	1.32	2.05
	414849	AW372721	Hs.291623	ESTs, Weakly similar to unnamed protein	1.32	2.08
	436986	AA740983	Hs.210792	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.32	2.06
	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	1.32	2.08
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	1.31	1.29

5	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)	1.30	1.25
	413474	T86312	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.30	1.92
	406659	AA663985	Hs.277477	major histocompatibility complex, class	1.30	2.22
	451049	AA013353		gb:ze28h10.s1 Soares retina N2b4HR Homo	1.30	2.12
	436494	AA720997	Hs.128295	ESTs	1.29	2.30
	438374	AA321866	Hs.6193	hypothetical protein FLJ14590	1.28	2.34
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	1.28	2.39
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.28	1.69
10	428458	AA428820	Hs.251399	neurogranin (protein kinase C substrate,	1.27	2.00
	443180	R15875	Hs.258576	claudin 12	1.26	1.25
	421764	AI681535	Hs.148135	serine/threonine kinase 33	1.26	2.01
	414217	AI308298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	1.26	1.21
	433283	BE041135	Hs.175622	ESTs	1.24	3.05
15	428759	AI590401	Hs.21213	ESTs	1.23	1.20
	436446	AW016809	Hs.119021	ESTs	1.23	1.20
	421467	AA291590	Hs.97252	ESTs	1.22	1.54
	431353	AA828032		ESTs	1.22	3.00
	427403	AA402107	Hs.257146	ESTs, Moderately similar to I38022 hypot	1.22	1.91
20	453037	AA045175	Hs.17914	ESTs	1.22	2.40
	437608	AA761605	Hs.292308	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.22	2.26
	439941	AI392640	Hs.18272	amino acid transporter system A1	1.22	1.22
	451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	1.21	1.49
	400496			ENSP00000224716*:GTP-binding protein SAR	1.20	1.25
25	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	1.20	1.44
	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	1.19	2.06
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	1.18	2.02
	445033	AV652402	Hs.72901	cyclin-dependent kinase inhibitor 2B (p1	1.17	1.14
	439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	1.14	1.16
30	440555	D31292	Hs.6853	hypothetical protein FLJ22167	1.14	2.19
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	1.13	1.12
	432203	AA305746	Hs.49	macrophage scavenger receptor 1	1.12	2.43
	432798	AA565309	Hs.194015	ESTs	1.10	2.23
	411274	NM_002776	Hs.69423	kalikrein 10	1.10	1.09
35	438856	N40027	Hs.7473	ESTs	1.09	1.52
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	1.09	1.07
	448253	H25899	Hs.201591	ESTs	1.08	2.10
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	1.08	2.08
	409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN IIII	1.06	1.58
40	449321	AA001150	Hs.132937	ESTs	1.06	2.06
	418693	AI750878	Hs.87409	thrombospondin 1	1.06	1.02
	402333			Target Exon	1.03	1.03
	421814	L12350	Hs.108623	thrombospondin 2	1.02	1.02
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	1.00	2.36
45	458158	AW296778	Hs.144734	Human DNA sequence from clone RP3-416F21	1.00	2.73
	406517			nel (chicken)-like 2	1.00	2.07
	442526	AW277221		ESTs	1.00	2.21
	446164	AW273539		hypothetical protein FLJ23577	1.00	2.52
	449122	AI631310	Hs.196955	ESTs	1.00	2.23
50	438038	AI732629		ESTs, Weakly similar to TA2R HUMAN, BETA	1.00	2.04
	429420	AK001679	Hs.202289	hypothetical protein DKFZp434P1735	1.00	2.02
	453672	U73531	Hs.34526	G protein-coupled receptor	1.00	2.57
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	1.00	2.64
	438909	AF085839		gb:Homo sapiens full length insert cDNA	1.00	2.23
55	423609	AA328348	Hs.218289	ESTs	1.00	2.19
	419261	X07876	Hs.89791	wingless-type MMTV integration site fam1	1.00	2.28
	436284	AA708016	Hs.190389	ESTs	1.00	2.22
	440932	AI801509	Hs.182080	ESTs	1.00	1.66
	403420			Target Exon	1.00	1.86
60	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	1.00	2.02
	425916	NM_006788	Hs.162200	urotensin 2	1.00	2.11
	419721	NM_001650		aquaporin 4	1.00	2.26
	421761	AL120297	Hs.108043	Friend leukemia virus integration 1	1.00	1.86
	425781	AF001622	Hs.159523	class-I MHC-restricted T cell associated	1.00	1.96
65	415094	D59513	Hs.330778	ESTs	1.00	2.32
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	1.00	2.26
	420727	H75701	Hs.99886	complement component 4-binding protein,	1.00	1.84
	430049	AW277085	Hs.99819	ESTs	1.00	1.87
	446868	AV660737		ESTs	1.00	1.79
70	418786	AI796317	Hs.203594	Homo sapiens uncharacterized gastric pro	1.00	1.44
	436391	AJ227892	Hs.146274	ESTs	1.00	1.30
	413059	BE151498		gb:RC0-HT0295-291199-031-E11 HT0295 Homo	1.00	1.42
	427739	AW195755	Hs.98105	NYD-SP14 protein	1.00	2.41
	452788	AW294571	Hs.136040	ESTs	1.00	2.23

TABLE 32B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
431089	125941_2	BC940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826

421798	3042_4	BC017829 AW276646 AI984209 AA663933 AA634104 AA551528 AA634041 AA298038 BG483990 T89297 BF853958 H64685 T90329 T60644 T57747 BF852694 T92529 BG482852 BF883064 BF883066 N74880 AA829796 N90716 X65018 BC022318 NM_003019 BE465060 AI732255 BF446634 AI820677 AI002217 AI924488 BI821373 BI770406 BI823937 BI820265 BI489632 BG482911 AA617783 AI807697 AW205576 T94427 AA871101 T94513 BI819407 BI822450 BI820618 BI824619 BG542824 BG537862
400269	2726_1	
432222	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
432810	101919_1	BG292389 C06094 AI668930 AW104534 AA310513 AA830127 AW134897 AA046953 AW965490 AI810530 BF092924 AA334151 AA334725 D31302 R20723 AA263003 BI824635 AI276287 AI684428 AI524234 AI335035 AW014704 AI911443 AA972102 AI367512 AI126670 AW016017 AI286003 AI147163 AA626033 AI539156 AA565542 AI094253 AW512612 BE889628 AA744752 BE646306 AW471324 AA999975 AA863400 H17550 AI991439 R46187 BE929954 AA333976 D63102 BF744491
418259	133853_1	BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969 BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563 AA459408 AA459633 AA418444 W23607 BG940150 AI493445 AW054729 AI221929 AI868744 AA215405 AA766713 AA621546 BF928317 BE464132 AI990909 AW271459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 R69057 BF766886 BE769254 W05240
429228	215430_1	BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW969605 AI553633
459702	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
422667	224778_1	AI758223 AW469334 BF940841 AW080348 AI270363 AI055892 BE464168 BF431797 BE350144 BF448739 AI693409 BF432999 D62848 AA398070 AI383375 AW611490
456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
430709	1234627_1	AW969880 AA484613 AA501874 R34356
450726	666520_1	AI732297 AW204600 T95017
442048	750422_1	AW340495 AI984319 AA974603
406685	0_0	M18728
440028	598730_1	AW473675 AI190744 W69997 AW104913 AI221098 W69996 AA885487 AA861491
437866	34267_1	U52054 AL581000 AA156850 AW293839 BI335865 AA024963 BF149420 BE073977 AW602574 BE164012 BE163992 BE163974 AW402161 BM194134 AW966609 W84374 BF916380 AA385173 W84366 AA383743 BF903598 AA043776 W84421 AA778446 AW444904 BF446960 AA837481 AV755539 AW468444 AW468002 AA811830 AA581806 AI866686 AI572124 AA687333 D20160 AA812489 AU185248 AU186004 AA156781 AI536733 BM144850 AI471883 AA040926 BF507639 AA043777 AW874142 BE832523 BE163972 BI022546 BI021204 AI000341 AI766341 AW873274
458332	1139885_1	AA602964 AA609200
407192	2200202_1	AI884781 AI652306 AI651694 AI638744 AI962493
449328	3030726_1	AA534222 AA632632 T81234
432340	1619980_1	AF119847 AA437261 AA436987 AI132965
434194	62680_1	AK001125 AU120581 AU146612 AW301393
436198	28727_1	AA876138 AI239602 AI698953
440248	2616908_1	AW975183 AA973583 AI365103 AI699495 AI301787
442006	1239046_1	AK024965 AU158033 AA978370 R79120 BE327015 AA779740 R79121
438177	9337_12	AW972063 AA668764 AA804491 AW665688 AA765069
435154	126605_1	L13288 AA928785 AI608912 AW872978 AA565655 AI022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805 R46356
423387	2612_2	AA418798 BM129553 BM129126 BM129292 BM128865 AI808418 AI689932 AI806573 BF431808 AW872985 AW166269 H73241 T16182 AI264547 R73391 R72085 R72840 T83751 X75299 BF764348 R94105 AW449839 R73300 NM_004624 AI797007 BE045543 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902 BI763932 BI910138 AV645808 AA701657 AW271273 AI796734 AI472316 AI017531 AI061178 BF109096 AA548964 N83805 AA131648 AA156589 BE708349 AW952494 D30877 AV684717 Z24837 F00167 BF576150 T63841 R78995 N87474
444314	1027984_1	AW749625 AW749626 AW749644 AI140497
443951	MH1768_18	AI334106 R63583 AI028079 AI140098 AI911625 AI890637 F34815 T65959 N40935 W52768 AA854747 AA661945 AA878472 AA778270 W32249
432639	1237887_1	AA026061 W52662 W15352 W79670 W95384 T94283 AA002155 R82052 BE825493 BE825520
438698	598828_1	AW973785 H60163 AA557608
413638	1525406_1	AW975851 AI911033 AI540093 AA932284 AW297855 AA829228 AA814442 AW105017
436772	1239464_1	H71252 BE154642 BE154668
448782	34980_1	AA156151 Z25109 C05177 AW976688 AA731063 N67084
		AB018301 AL050295 BF513128 AW385080 AL551708 AI325542 AI829703 AI819388 AW629019 AW073189 AW273857 AW118768 AI453845 AI452494 AA866341 AI057144 AA904647 AI423547 AW263913 AI094774 AI434419 AI039546 AI002491 AI240412 Z25099 AA995178 AW050649 AW026140 AI796309 AI584012 BE166666 AI767991 AI309041 AA724059 AI695284 AI245095 T63971 Z40627 BE166681 BG570071 BF921915 BI562702 BG506502 AV658066 R48378 AA121543 AI096938 AA618131 H40993 R48277 AI352281 BG540263 BG538901 N95226 AI356752 AI221152 Z28777 R16574 AW966449 AA044116 AW797518 BI010405 AA044288 AI093508 BE140169 T64039 BG433106 AW130367 AW130361 N73937 AA127680 AW044037 AI096437 AA384077 BF941499 T93764 BG003285
438507	2729_4	BG698329 AI417878 AI080171 AI190332 AI092344 AI357100 AA744522 AA412653 AA977007 BF438628 AA743264 AA365279 AW073197 BI493198 AA169355 BI493197 AI283051 BF436642 AA809052 AI833263
415688	1235745_1	AW971218 AA483942 AA166963
431300	1529181_1	BE159863 AA502346 AI186097 R86267 H71358
418262	5824_2	AK055180 AA490810 AI420925 AI473832 AA127397 AA127409 AW820078 AI214567 AA876961 AA283985 AI904240 D20426 BC015835 N28408 Z42826 AI927925 AW590850 AW195543 AI675823 W84675 AA767204 AW207335 AI051690 AI434786 AI051699 AW139875 BF195790 AI250256 AI767042 AI521899 AA829382 AA526451 AI971192 R08173 N20059 AA215409 Z38968 H13200 H01182 R82482 AW972928 BF242637 H01273 H13567 R82532
452194	90339_1	AI694413 AW994700 AI912946 N73548 AI082035 AW271652 W24189 W24182 AI719718 AA024658 AW810120 AW015394 T79755 AA988043 AI709339
446354	831448_1	AI701583 AI291038 AW449650
406687	0_0	M31126
411605	10026_3	BG256892 H10532 N46614 R52610 AW977696 BM460488 W56819 BI042183 BG977498 BE767451 BF870009 BG477472 R61137 R14274 R20259 R09686 BI838226 BF034269 AA429173 BE741829 AW867495 AI123683 AW006831 BE831162 AW452753 AV742717 W86152 BF115102 AI633815 BF921562 AA094230 BE092587 W86151 AA526153 AI672156 BF914496 R12579 BF852352 AA699780 T57386 BF903022 R09933 AA678298
428713	21322_7	AA432057 AW572442
414221	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
414991	1785135_1	D78831 C17898 D78863
447197	2176805_1	R39075 R36167 AI366546
430915	197844_1	BG425760 BF997600 N48516 W73454 BF816344 BF997601 AA488953
424450	1674_1	NM_023036 AJ295276 AF250288 AL137526 AW517074 AI870459 AI215420
409031	9531_1	BF036043 AW190446 BG194731 AW662036 AI445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 AI270167 AI857345 AA937302 AW818444 BE929780 BG498678 BF155010 BI598271 BI599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608 AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 AI018009 N42850 AW573242 AI417258

			AA463483 AI676131 AI167170 AA836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW474332 BI043239 AW474342 BG708553 AW362423 BF090028 BE827256 R16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AW966405 AW994425 D81879 BE093545 AW901107 AA383529 BI021552 R56420 N39976 AA573281 H82595 AA234955 BE093539 AW367006 BF358697 BF366318 AA663856 BE702099 BF035969 AI267384 AI267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836 AV724531 D53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 AL118798 BM126728 AA193411 AW444709 AW952455 AI887612 BF431948 BI495876 AI264159 BM128481 AI624657 AI689301 AI969467 AA861685 AA251595 AA625761 AA872090 AI826790 AA328366 BE827416 R75951 D56918 R68122 BE827384 AL118797 AI184164 AA164411 BI495332 BE858113 AI863860 H00660 T69849 AW780389 C14667 BE934995 BI018652 R92801 AA154410 H00752 AW373305 AW373299 AW373302 BE883520 BI057842 AA215702 AA215703 AA368006 BE006876 BE066555 AA002232 T99209 AA002071 AI308202 AI307229 AA769348 AW341668 AI201382 AW104364 AA648367 AA897604 AW977914 AA811957 AI352198 AL040620 BG427950 AA826016 AI903441 BG939868 AW979154 AA640872 BG547134 AA457091 AW368860 W88852 R94779 AA088823 AI494291 AI582807 AA417018 AA608841 AW975114 AI096634 AI767001 AA658364 AW517542 AA993566 AI521958 AI565071 AI864217 AL046017 AW504804 AA532433 AI634701 AI126421 AW151275 AA620782 AA933047 AI828223 AI624555 AI624489 AV749032 BI495751 AI672288 AA342944 AV748076 AV747586 AA058597 H56073 W87367 R71630 H84499 AI866297 D25918 AV746788 H78995 H63752 H82985 R46600 BE786692 R71128 AA608909 R29728 BG534018 Y00281 NM_002950 BC010839 BC007995 BG675232 BM468552 AL555484 BG831516 BF035300 BG677277 BF852972 BE314901 BF850656 AI371816 AA292474 AA375747 AA308414 BM454544 BI333370 BM049921 BI461428 BI465007 BI223401 BE856245 AW821164 BF914775 BF914761 AU125835 BI222678 BI091137 BF340536 BM462798 BI224452 BG707915 AI569160 AA443815 AW572867 AW363410 BF739268 BG010283 BI013120 BF818845 BF763468 AA305165 AI630370 AA039826 R24906 H02046 T96891 BF981330 AW936510 AA478169 H04587 BG166574 BI869342 BE562482 BE539633 AA165089 AL579118 AL553699 BE044054 AW117440 AI520674 BF435417 AW245648 AI952404 T29534 AU153459 AU152168 AW591591 AU146918 AI393187 AA478013 AU148143 AI224471 AI640728 AI871537 AW264752 N93787 AI189357 AV756134 AI471659 AU147466 AA779206 AU149419 AU149104 AU159135 AA312221 AW445119 AW021912 AI799771 F04407 AI285530 AI914643 AW068751 AA513325 AA164627 AA639285 AA569644 T96892 AI923594 BF439180 BI770936 BF032438 AU154884 AA682793 AW072992 AU158815 AI884444 AL048031 AU158922 AU152546 AI695187 AL048033 AI245650 AU148507 AW467451 BE356868 BF913001 BF062707 AL573082 AW067993 AA523354 BE886727 AI890705 AU159092 AI982693 AI817553 AA236729 BI687858 BG163767 AI524675 AI678155 AA127100 AI762661 AU159718 AI469720 AA483627 AW131696 R26868 AI199885 AW875614 AW938694 AW578974 BI763988 BG819168 BE874767 BG978292 BE162948 AL555483 AW189719 T56783 AI018819 AI476552 BI492837 AI824440 BG986262 AA932887 AI380726 R79530 AA622108 AI262575 T56782 R27437 BE784153 AW129549 AI675567 AI866759 BG987935 AW972351 AW182936 AI478370 AA528309 BG997292 AW137742 AI632006 AA775020 AA961625 W86628 BF112014 AI275423 AI680786 BE222349 AA830545 BF224127 H99396 N81017 N81016 AI525205 T58283 U59185 NM_004696 AV734324 AI245349 AA369517 H88760 D79128 AA970406 H01059 H88761 H03446 BG620383 AU135008 AU136895 AU158158 AU155762 R73608 R65751 R23756 N74630 AW078687 BE439761 BE786351 R68994 BE785867 AW297502 AW297553 BG431545 AW814843 BF382644 BG429539 BE929862 BF811258 H61453 AA838765 AI693104 AA721107 AF392454 AK023074 AI884890 AI814455 AW966220 BF736545 AA026021 AA286843 AA251918 BG197710 AA026294 AA337356 BC010422 AK023226 NM_022776 BM459496 AA769310 AI826460 AU153650 AU160375 AW166211 AW292992 BF433538 AI823888 AI684798 AI655985 AW770982 AI400454 AI276257 AA639510 AI689818 AW772604 AA807639 AU130298 AU132028 BF900889 BF804822 AY007102 AU143256 BG621460 AA829630 AI864665 AI084922 AA025234 AI360060 AA766554 AA026295 AA825817 AA251762 BE180751 BM464530 AV715833 AA779447 AI452519 AW418525 AA435643 D25894 AA435651 AA286844 N64369 AI702262 BG288063 BE170545 BM466232 BE299160 AA169573 AL567428 BF217285 BE967276 AA609784 R97304 C14774 C17911 D79033 BC011717 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 BI759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399 AI365196 AW337884 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF888930 BM475542 AW246215 BE501897 BE903610 BE581530 BE560537 BE903782 BE732947 BIZ72704 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AI423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG765947 BF363829 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW026983 AT789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AI134894 BF104082 H80591 AW970134 AA516420 AA543007 BG057526 BI001430 AI498371 D60181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818 C15161 D60184 D60656 AK057782 AI146454 BG703115 AI765980 AI948811 AA889263 AA947457 BG547193 H11947 Z38147 F10426 BF447329 H11946 T74958 F06195 BG548563 AI004988 AA148735 AI307802 AI439791 BE041453 AI984904 AA148734 F12823 BG623239 N58315 AI524952 AL110216 AI816283 AI688476 AA928351 AW157672 AI288740 BE468242 AI452476 AI291665 AW192364 BE503635 AW526772 AA857393 AW162770 AI680660 AI879565 AI347717 BF808000 AI266646 AA834381 AI291667 AI264567 Z38449 T03352 AI929432 BF673697 AI124770 AI350389 AA910378 R54042 AV746670 AW089037 AV729218 H28971 R38549 AI692560 BE671562 BE669918 BE672206 BF445152 BF445151 AI914323 AI684406 AA932348 BE670597 AA932080 AF086037 H89360 H89546 AW182329 AA613792 T05304 AW858385 AK056513 AL553942 AL553941 BG924307 BE879339 AA576941 BG054674 BF431361 BE467806 BF445874 BE138798 AA425029 BF084265 BE814324 BM466426 BE819467 AW594593 AA341536 AI823511 BI792998 AW296213 AW800506 AW378236 BE819553 AW341342 BE146513 BE146525 BE146515 AW295699 BE146518 BE146516 BF349828 AL50587 AW803944 BE931092 BF376188 BG657670 BF832746 BG696737 AW391179 AI582980 AW582217 AW814484 BE672215 AW391162 AW814336 AW814302 AW814444 AL520586 AI333134 AI378333 AW243412 BE350482 AI628661 AI925481 AI246159 AW593633 AI273558 AI494388 AA806280 AW005606 BE048135 AW341024 AA969419 AA912778 AA621100 AA478920 AI867584 AI290391 BE348490 BF340755 AI225038 AI867592 BG113588 AI566808 AW195841 BF087184 AA353524 AW957546 BF340833 BF037221 BE146523 BI030997 AA921874 AW188822 BI027862 AI347618 BI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445 AW978796 AA767373 AW173343 AA836163 N27563 AA905328 R97032
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5	444083	10908_12	BI836699 AI123195
	455508	1239880_1	AW976165 C04000
	417086	1154_2	AK056605 AK056969 AW380724 AA195950 F21243 Z17422 AA176595 AA176955 AA194350 BC005933 BC017866 AA196396 Z24810 AA181361
			AA193115 AA086465 F25194 F30130 AA180013 AJ346143 F20589 F20620 F29371 F32439 F25163 F32146 F26110 F28506 F25307 F27533
			F20375 F32370 AA653078 BF574897 Z24852 F00172 T30560 AW449825 AI620346 BG986374 BE706521 C02691 AL596834 F31902 F26078
			AA670099 BF475555 F30818 F37524 AJ346558 F28050 F17933 F31637 C03413 AI092152 AA180743 AA085730 F21998 F20854 F18944 F31180
			F37937 F37738 AA193162 Z17344 AA192546
	409208	10117_2	AK074047 AI144342 AW014280 BM145128 N28267 AW206231 AA989041 H93197 AW594063 BG236296 AW236606 AW081031 AA765843
			BM144372 AA989341 AI824838 AI963970 AI637671 AW196330 BG427526 BM148789 BF893644 BF881946
10	440638	371165_1	BG009500 AJ376551 AA897445 T87714
	458194	506272_1	AI692525 AW005307 AW383618 AI689861 AI342712 AA906899
	421461	128918_1	AA291529 AI629027 AI890447 AA677465 BF001179 AI301102 AW452003 AA704419 AA706883 T68871 AW291023
	430850	296806_1	BE144152 AA487799 BF916865 AA937952
	400328		
15	451876	2328579_1	T63141 AI821021 BF370092 BF370127 BF370060 T62998
	450708	12745_1	AK055196 AW952031 AI694545 AJ742403 AW874431 AW204731 AI887383 BE220997 AA011287 AA115112 AI306385 AW571707 BF433009
			AW197042 AI367086 H23002 H11743 R37085 Z39208 AI002267 H10206 T23948 W74801 R51633 R37677 R59986 H10833 BG012000 R13817
			H22794 Z43122 H10257 BG984543 H10875 BG984542 AA318232 BF849799 W76367 AA376654 R18795 AA114979 AA303838 AW139819
			AI674165 AI686172 W94102 R67170 H11820 BG15023
20	452203	2630_1	BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL558882 AL541576 AL550654 BI823519
			BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470
			BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644
			AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW107777 AA586956 AL571889
			AL556850 AL576404 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377
			AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222
25			BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198
			AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054
			AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927
			H23433 R42244 N79997 AW366665 AW366601 AA878742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586
			BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440
30	438089	22448_4	AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW697824 AI811204 AA344646 BE009112 BG899664
			H91240 R60548 AI1701
			BI826340 BI868674 R12615 AW887767 BF439409 AI424995 BG059893 AA417003 AI220270 AA418740 AI190974 Z39070 AA742556 AA835058
	427872	4983_5	AA694436 R20520 AA418795 BG460307 BI560147
35	458208	45807_4	AI990640 AI380018 BM273298 BM273060
	421341	1407_1	NM_007329 AF159456 AJ243212 AI297935 AA295769 NM_017579 AJ243224 AI492875 AI796676 AJ749838 AA918144 AI814590 AI923531
			BF513992 AI720725 AI150879 AI279072 AW612904 AI492104 AI284510 AI141231 AA613554 AW662148 AW769047 AA565985 AW612888
			AU100513 BG955585 BG955588 AA295763 BE829414 BF760645 BG954398 AA295332 AA295795 BE932867 AW769569 T89953 BE934311
			BE088101 T06990 AW872477
40	411880	1139083_1	AI928355 AI709178 AA436447 AI431274 BF946000
	428833	317753_1	BE091833 BE091874 BE091871
	455797	1511159_1	
	407244		
	451049	83923_1	W92422 AA013353
	431353	1241126_1	AW977507 AA503803 AA767137 AA828032 AA828033
45	451385	85022_1	AA019761 AA017656 AA017374
	442526	450370_1	AF150283 AW182000 AW277221 AV735848
	446164	41648_2	AK026817 AI559708 AW273539 AW892986
	438038	2523501_1	AI732629 AI732631 AA776249
	438909	4045_1	AF085839 R69254 R69137 AW188788
50	431169	1235760_1	AW971240 AA493723 AA93843
	419721	40816_1	AK026728 AL138136 BF059437 AI657037 AL600872 C15206 C14676 AA001003 AL157562 BG706081 H24162 BF841047 H15952 Z45355
			AL157565 AV721762 AW953127 AA324171 BF476417 R52508 N54211 R46734 BG485659 BF810747 BE786227 AI538364 R19964 T15657
			AW197333 R16235 R40826 BG152309 AV729035 R45066 AA016969 BE504976 BF593783 N51085 R61284 BE702264 AI216994 Z41068 N72577
			R37645 AW237014 AW197630 AI359402 AA707906 AL119885 H23480 T16037 AI950756 T62597 T91684 R40195 D60186 H23014 T89715 H05749
55			H24054 AA001565 H15041 C15205 D59987 R13787 R61283 H23478 H07874 R14070 R52555 R21139 H05856 AA348655 AL120460 T62525
			AV725241 AA046875 AI361912 H13341 BG150488 AL119338 Z42792 F05895 H07966 F06492 R59866 D31594 H09436 R35726 BI917845
			BG704196 BF735198 AL036526 BG569879 AW195713 R59867 AA016968 H09087 BE841173 AW893631
			AK074473 BC017997 BI831060 BF971101 AI886394 AI082824 AV708785 W86073 W07772 AV660737 AI816793 R52250 BG183529 AA633473
	446868	15525_1	AI191256 R44763 R19947 BF571346 W86257
60	413059	1488711_1	BE063078 BE151503 BE151498

TABLE 32C:

65	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	NL_position:	Indicates nucleotide positions of predicted exons.		
70	Pkey	Ref	Strand	NL_position
	400880	9931121	Plus	29235-29336,36363-36580
	402474	7547175	Minus	53526-53628,55755-55820,57530-57757
	406387	9256180	Plus	116229-116371,117512-117651
	404277	1834458	Minus	91665-91946
75	402674	8077108	Minus	39290-39502
	404240	5002624	Minus	116132-116407,116653-116922
	405102	8076881	Minus	120922-121296
	406122	9144087	Minus	30940-31386
	400750	8119067	Plus	198991-199168,199316-199548
80	404394	3135305	Minus	37121-37205,37491-37762,41053-41140,4132
	403421	9666041	Minus	126609-126773,139986-140205
	403903	7710671	Minus	101165-102597
	404854	7143420	Plus	14260-14537

5	401854	7770538	Plus	151483-151637,151902-152008,152146-15231
	406422	9256411	Plus	163003-163311
	400496	9743564	Plus	41515-41695
	402333	8844110	Minus	165693-165856
	406517	7711431	Plus	7151-7402
	403420	9664969	Plus	159835-159938

10 TABLE 33A: About 800 genes upregulated in lung fibrosis relative to normal lung

15 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of lung fibrosis AIs divided by 90th percentile of normal lung AIs, where the minimum value for the numerator and denominator was set to 50

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
20	406964	M21305		FGENES predicted novel secreted protein	16.10
	431089	BE041396		ESTs, Weakly similar to unknown protein	12.38
	421110	AJ250717	Hs.1355	cathepsin E	11.86
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	11.62
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	9.90
25	444381	BE387335	Hs.283713	hypothetical protein BC014245	8.58
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	8.26
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)	8.24
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.72
	408380	AF123050	Hs.44532	diubiquitin	7.24
30	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	7.15
	456034	AW450979		gb:U1-H-813-ala-a-12-0-UI.s1 NCL_CGAP_Su	7.12
	453355	AW295374	Hs.31412	myopodin	6.96
	408562	AI436323	Hs.31141	roundabout (axon guidance receptor, Dros	6.88
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.83
35	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	6.72
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	6.72
	438089	W05391		nuclear receptor subfamily 1, group I, m	6.62
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.56
	421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	6.46
40	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	6.32
	439195	H89360		gb:yy28d08.s1 Morton Fetal Cochlea Homo	6.29
	444301	AK000136	Hs.10760	asporin (LRR class 1)	6.28
	414061	NM_000699	Hs.335493	amylase, alpha 2A; pancreatic	6.13
	423057	AW961597	Hs.130816	ESTs, Moderately similar to I38022 hypot	6.11
45	430702	U56979	Hs.278568	H factor 1 (complement)	6.10
	424878	H57111	Hs.221132	ESTs	6.00
	417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	6.00
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	5.94
	408491	AJ088063	Hs.7882	ESTs	5.94
50	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	5.92
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	5.92
	407857	AI928445	Hs.92254	synaptotagmin-like 2	5.90
	433230	AW136134	Hs.220277	ESTs	5.86
	412719	AW016810	Hs.816	ESTs	5.86
55	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	5.82
	426759	AI590401	Hs.21213	ESTs	5.72
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (Interstitial	5.72
	421814	L12350	Hs.108623	thrombospondin 2	5.71
	430887	N66801	Hs.260287	KIAA1841 protein	5.70
60	453870	AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fis, clone L	5.62
	436954	AA740151	Hs.130425	ESTs	5.58
	411573	AB029000	Hs.70823	KIAA1077 protein	5.55
	432441	AW292425	Hs.163484	intron of hepatocyte nuclear factor-3 al	5.38
	410606	AW418779	Hs.114889	ESTs	5.38
65	410800	BE280421	Hs.94499	ESTs	5.32
	413195	AA127382	Hs.22404	protease, serine, 12 (neurotrypsin, moto	5.28
	406687	M31126		matrix metalloproteinase 11 (stromelysin	5.26
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	5.22
	412622	AW664708	Hs.171959	ESTs	5.22
70	439941	AI392640	Hs.18272	amino acid transporter system A1	5.18
	440675	AW005054	Hs.279788	ESTs, Weakly similar to KCC1_HUMAN CALCI	5.15
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	5.13
	425177	AF127577	Hs.155017	nuclear receptor interacting protein 1	5.12
	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	5.11
75	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.04
	452239	AW379378		protein tyrosine phosphatase, receptor t	4.97
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	4.96
	443884	N20617	Hs.194397	leptin receptor	4.94
	444040	AF204231	Hs.182982	golgin-67	4.94
80	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuo	4.93
	440687	AL080222	Hs.7358	hypothetical protein FLJ13110	4.92
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	4.92
	432435	BE218886	Hs.282070	ESTs	4.92

	422573	AW297985	Hs.295726	integrin, alpha V (vitronectin receptor	4.90
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	4.90
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	4.90
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	4.82
5	430027	AB023197	Hs.227743	KIAA0980 protein	4.78
	408393	AW015318	Hs.23165	ESTs	4.76
	449509	AA001615	Hs.84561	ESTs	4.72
	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	4.72
10	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	4.68
	433226	AW503733	Hs.9414	KIAA1488 protein	4.68
	444745	AF117754	Hs.11861	thyroid hormone receptor-associated prot	4.66
	442994	AJ026718	Hs.16954	ESTs	4.66
	430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	4.66
15	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	4.65
	418005	AI186220	Hs.83164	collagen, type XV, alpha 1	4.64
	433586	T85301		gbvdy78d06.s1 Soares fetal liver spleen	4.64
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	4.64
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	4.64
20	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.62
	451109	F11875	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	4.62
	450086	AW016343	Hs.233301	ESTs	4.61
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	4.60
	426552	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypothei	4.59
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.58
25	418259	AA215404		ESTs	4.54
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	4.54
	432810	AA863400		ESTs	4.53
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.52
30	436100	AA704806	Hs.143842	ESTs, Weakly similar to 2004399A chromos	4.52
	412652	AI801777		ESTs	4.52
	436899	AF085833	Hs.135624	ESTs	4.52
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	4.52
	436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	4.52
	443324	R44013	Hs.164225	ESTs	4.51
35	407690	R47799	Hs.266957	hypothetical protein FLJ14281	4.51
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.51
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypothei	4.50
	431843	AA516420		ESTs, Weakly similar to I38022 hypothei	4.50
40	436865	AW880358	Hs.339808	hypothetical protein FLJ10120	4.46
	452561	AI692181	Hs.49169	KIAA1634 protein	4.46
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	4.45
	442048	AA974603		gbvdy34f05.s1 Soares_NFL_T_GBC_S1 Homo s	4.44
	436120	AI248193	Hs.119860	ESTs	4.44
45	423575	C18863	Hs.163443	Intron of perlestin (OSF-2os)	4.44
	429697	AW298451	Hs.24605	ESTs	4.43
	439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	4.43
	429688	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	4.42
	414462	BE622743	Hs.301064	araplin 1	4.42
50	428698	AA852773	Hs.334838	KIAA1866 protein	4.41
	420838	AW118210	Hs.42321	ESTs	4.40
	458584	AF217518	Hs.8360	PTD012 protein	4.40
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypothei	4.40
	400076			Eos Control	4.38
55	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to	4.38
	445773	H73456	Hs.13299	Homo sapiens mRNA: cDNA DKFZp761M0111 (f	4.36
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.36
	433339	AF019226	Hs.8036	glioblastoma overexpressed	4.36
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	4.34
60	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	4.34
	421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	4.33
	409342	AU077058	Hs.54089	BRCA1 associated RING domain 1	4.33
	429228	AI553633		ESTs	4.32
	426458	D83032	Hs.169984	nuclear protein	4.30
65	408369	R38438	Hs.182575	SLC15A2 Solute carrier family 15 (H+/pep	4.30
	432476	T94344	Hs.326263	ESTs	4.29
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	4.28
	436446	AW016809	Hs.119021	ESTs	4.27
	439556	AI623752	Hs.163603	ESTs	4.26
70	428179	AI127772	Hs.279696	serum/glucocorticoid regulated kinase-II	4.26
	428411	AW291454	Hs.10338	ESTs	4.26
	434936	AI285970	Hs.183817	ESTs	4.23
	413048	M93221	Hs.75182	mannose receptor, C type 1	4.23
	432606	NM_002104	Hs.3068	granzyme K (serine protease, granzyme 3;	4.22
75	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	4.22
	409977	AW805510	Hs.97056	hypothetical protein FLJ21634	4.22
	441297	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	4.21
	421229	AI065690	Hs.7086	hypothetical protein MGC12435	4.20
	455844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	4.20
80	423578	AW960454	Hs.222830	ESTs	4.20
	445608	N75217	Hs.257846	ESTs	4.20
	424238	AA337401	Hs.137635	ESTs	4.19
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	4.18
	420674	NM_000055	Hs.1327	butyrylcholinesterase	4.18

	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.18
	439593	BE073597	Hs.124863	ESTs	4.17
	442369	AI565071		ESTs	4.16
5	445885	AI734009	Hs.127699	KIAA1603 protein	4.16
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	4.16
	452960	AK001335	Hs.31137	protein tyrosine phosphatase, receptor I	4.16
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (tr	4.15
	407347	AA829847		gb:cd40d07.s1 NCI_CGAP_GC81 Homo sapiens	4.14
10	409153	W03754	Hs.50813	hypothetical protein FLJ20022	4.13
	430168	AW968343	Hs.145582	DKFZP434I1735 protein	4.12
	451184	T87943		transcription factor 7-like 2 (T-cell sp	4.12
	426174	AA547959	Hs.115838	ESTs	4.12
	431562	AI884334	Hs.11637	ESTs	4.12
15	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.12
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (tr	4.12
	449437	AI702038	Hs.100057	Homo sapiens cDNA: FLJ22902 fis, clone K	4.12
	425053	AF046024	Hs.154320	ubiquitin-activating enzyme E1C (homolog	4.10
	444020	R92962	Hs.35052	ESTs	4.10
20	439424	AI478667	Hs.118183	hypothetical protein FLJ22833	4.10
	416987	D86957	Hs.80712	KIAA0202 protein	4.10
	457121	AI743770	Hs.180513	ESTs, Weakly similar to KIAA0822 protein	4.09
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	4.09
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.08
25	431193	AW749505	Hs.296770	KIAA1719 protein	4.08
	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	4.08
	433308	AA582718	Hs.291650	ESTs	4.08
	445756	AA290690	Hs.300776	ESTs	4.08
	431745	AW972448	Hs.163425	ESTs	4.08
30	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	4.07
	440099	AL080058	Hs.6909	DKFZP564G202 protein	4.06
	439398	AA284267	Hs.221504	ESTs	4.06
	432731	R31178	Hs.287820	fibronectin 1	4.06
	415075	L27479	Hs.77889	Friedreich ataxia region gene X123	4.05
35	433626	AF078859	Hs.86347	hypothetical protein	4.05
	428055	AA420564	Hs.101760	ESTs	4.04
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	4.04
	413243	AA769266	Hs.193657	ESTs	4.02
	431214	AA294921	Hs.348024	v-rat simian leukemia viral oncogene hom	4.02
40	453753	BE252983	Hs.35086	ubiquitin specific protease 1	4.02
	414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	4.02
	434404	AW445034	Hs.256578	ESTs	4.02
	407604	AW191562		collagen, type VIII, alpha 2	4.02
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	4.02
45	436772	AW975688		metallothionein 1E (functional)	4.00
	443257	AI334040	Hs.11614	HSPC065 protein	4.00
	450187	AA736788	Hs.78521	KIAA1717 protein	3.98
	433913	AI694106	Hs.72325	ESTs, Weakly similar to I38022 hypotheti	3.98
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEFS_HUMAN TRANS	3.98
50	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	3.98
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	3.98
	426818	AA554827	Hs.292996	DKFZp434A0131 protein	3.98
	440118	AB040893	Hs.6968	KIAA1460 protein	3.98
	413836	W92003	Hs.70614	ESTs	3.97
55	442647	AL038436	Hs.31388	ESTs	3.96
	449188	AW072939	Hs.347187	myotubularin related protein 1	3.96
	450656	AA010539	Hs.18912	ESTs	3.96
	410817	AI262789	Hs.93659	protein disulfide isomerase related prot	3.94
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	3.94
60	408483	AA464836	Hs.291079	ESTs, Weakly similar to T27173 hypotheti	3.94
	407879	AA045464	Hs.6557	zinc finger protein 161	3.93
	438146	Z36842	Hs.57548	ESTs	3.93
	433658	L03678	Hs.156110	immunoglobulin kappa constant	3.93
	429355	AW973253	Hs.292689	ESTs	3.92
65	437210	AA311443	Hs.293563	Homo sapiens mRNA; cDNA DKFZp588E2317 (f	3.92
	432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	3.92
	452416	AA026115	Hs.114777	ESTs	3.92
	413873	AI310151	Hs.173524	ESTs	3.91
	400196			Eos Control	3.91
70	437175	AW968078	Hs.87773	protein kinase, cAMP-dependent, catalyti	3.90
	453204	R10799	Hs.191990	ESTs	3.90
	454076	AW204712	Hs.61957	ESTs	3.90
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	3.90
	437158	AW090198		KIAA1150 protein	3.90
75	443970	AI280341	Hs.166571	ESTs	3.90
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	3.90
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.90
	444057	AA316896	Hs.257267	FYVE and coiled-coil domain containing 1	3.89
	411495	AP000693	Hs.70359	KIAA0136 protein	3.88
80	438452	AI220911	Hs.288959	hypothetical protein FLJ20920	3.88
	410297	AA148710		lumican	3.88
	427698	AW972594	Hs.335499	ESTs	3.88
	436769	AA748675		ESTs	3.86
	417819	AI253112	Hs.133540	ESTs	3.86

	445800	AA126419	Hs.32944	inositol polyphosphate-4-phosphatase, ly	3.86
	425838	NM_014071	Hs.159613	nuclear receptor coactivator RAP250; per	3.86
	422173	BE385828	Hs.250619	phorbol-like protein MDS019 (CEM15)	3.86
	428147	AW629565	Hs.234983	ESTs, Weakly similar to 2109260A B cell	3.85
5	445693	AW800444	Hs.76507	LPS-induced TNF-alpha factor	3.85
	432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma	3.85
	412636	NM_004415		desmoplakin (DPI, DPII)	3.84
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	3.84
	418876	AA740616		gb:ny97f11.s1 NCI_CGAP_GC81 Homo sapiens	3.84
10	436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypotheti	3.84
	430317	AB020645	Hs.239189	glutaminase	3.84
	442806	AW294522	Hs.149991	ESTs	3.84
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	3.82
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	3.82
15	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ110500 fis, clone NT	3.82
	430573	AA744550	Hs.136345	ESTs	3.82
	453394	AW960474	Hs.40289	ESTs	3.81
	431266	AW149321	Hs.105411	ESTs	3.80
	434987	AW975114		ESTs	3.80
20	452685	AI634651	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	3.79
	435176	AA744875	Hs.189413	ESTs	3.78
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	3.77
	430709	R34356		gb:yh85d01.s1 Soares placenta Nb2HP Homo	3.77
	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.76
25	441989	AA306207	Hs.286241	protein kinase, cAMP-dependent, regulato	3.76
	417228	AL134324	Hs.7312	ESTs	3.76
	418546	AA224827		gb:nc32g04.s1 NCI_CGAP_Pr2 Homo sapiens	3.76
	450779	AW204145	Hs.156044	ESTs	3.75
	412408	D51103	Hs.73851	ATP synthase, H transporting, mitochondr	3.75
30	443879	Z28462	Hs.9927	Homo sapiens mRNA; cDNA DKFZp564D156 (fr	3.75
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.75
	429494	AA769365	Hs.126058	ESTs	3.75
	447118	AB014599	Hs.330988	Homo sapiens, Similar to Bicaudal D (Dro	3.75
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	3.74
35	419591	AF090900	Hs.91393	Homo sapiens cDNA: FLJ21887 fis, clone H	3.74
	448121	AL045714	Hs.128653	hypothetical protein DKFZp564F013	3.74
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.74
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	3.73
	414883	AA926960		CDC28 protein kinase 1	3.72
40	416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.72
	452250	BE618654	Hs.28607	hypothetical protein A-211C6.1	3.72
	444099	D87432	Hs.10315	solute carrier family 7 (cationic amino	3.72
	438607	AW080237	Hs.252884	ESTs	3.72
	408221	AA912183	Hs.47447	ESTs	3.72
45	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.70
	419900	AI469960	Hs.170698	ESTs	3.70
	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	3.70
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	3.70
50	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	3.70
	413283	R78669	Hs.23756	hypothetical protein similar to swine ec	3.70
	447846	AA324057	Hs.77955	Homo sapiens cDNA: FLJ23527 fis, clone L	3.70
	436198	AK001125		Homo sapiens cDNA FLJ10263 fis, clone HE	3.70
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	3.69
	408495	W68796	Hs.237731	ESTs	3.69
55	424452	N41367	Hs.173002	ESTs, Weakly similar to I38022 hypotheti	3.68
	448479	H96115	Hs.21293	UDP-N-acetylglucosamine pyrophosphorylas	3.68
	431974	AW972689	Hs.200934	ESTs	3.68
	416354	NM_000633	Hs.79241	B-cell CLL/lymphoma 2 (BCL2)	3.68
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	3.68
60	413645	AA130992		gb:zo15e02.s1 Stratagene colon (937204)	3.67
	416221	BE513171	Hs.79086	mitochondrial ribosomal protein L3	3.67
	419111	AA234172	Hs.137418	ESTs	3.67
	423979	AF229181	Hs.136644	CS box-containing WD protein	3.66
65	418875	W19971	Hs.233459	ESTs	3.66
	451690	AW451469	Hs.209990	ESTs	3.66
	423032	AI684746	Hs.119274	RAS p21 protein activator (GTPase activa	3.66
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.66
	428347	AI264161	Hs.183773	golgi autoantigen, golgin subfamily a, 4	3.66
70	426779	AA384577	Hs.93714	ESTs, Weakly similar to T00365 hypotheti	3.66
	435335	AI693150	Hs.137928	ESTs	3.66
	410577	X91911	Hs.64639	glioma pathogenesis-related protein	3.66
	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	3.65
	429105	D87077	Hs.196275	KIAA0240 protein	3.64
	407813	AL120247	Hs.40109	KIAA0872 protein	3.64
75	425863	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	3.64
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	3.64
	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	3.64
	452408	AA306477	Hs.29379	hypothetical protein FLJ10687	3.64
	441466	AW673081	Hs.54828	ESTs	3.63
80	414013	AA766605	Hs.47099	hypothetical protein FLJ21212	3.62
	420056	AW043684	Hs.99804	ESTs	3.62
	424886	H88584	Hs.96900	hypothetical protein; KIAA1830 protein	3.62
	431774	BE348813	Hs.268561	hypothetical protein FLJ10726	3.62

5	435990	AJ015862	Hs.131793	ESTs	3.62
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	3.62
	414715	AA587891	Hs.904	amylase-1,6-glucosidase, 4-alpha-glucanot	3.62
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	3.62
	417008	AA191708	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone AD	3.62
	413823	AI341417	Hs.29406	ESTs	3.61
	435354	AA678267	Hs.117115	ESTs	3.60
	427832	AF038362	Hs.180930	TBP-associated factor 172	3.60
10	427846	AW499770	Hs.180948	KIAA0729 protein	3.60
	426116	AA868729	Hs.144694	ESTs	3.60
	457635	AV660976	Hs.3569	hypothetical protein	3.60
	443998	AI620661	Hs.296276	ESTs	3.60
	417867	AW952547	Hs.194603	ESTs, Moderately similar to I38022 hypot	3.58
	418182	AW016405	Hs.16648	ESTs	3.58
15	434941	AW073202	Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT	3.58
	424831	H61453		ESTs	3.58
	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	3.58
	421823	N40850	Hs.28625	ESTs	3.58
20	414781	D50917	Hs.77293	KIAA0127 gene product	3.57
	427393	AB029018	Hs.177635	KIAA1095 protein	3.57
	415664	NM_004939	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.56
	425465	L18964	Hs.1904	protein kinase C, iota	3.56
	417124	BE122762	Hs.25338	ESTs	3.56
25	416602	NM_006159	Hs.79389	Protein kinase C-binding protein NELL2	3.56
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	3.55
	421097	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	3.55
	410390	AA876905	Hs.125286	ESTs	3.54
	442073	AW973443	Hs.8086	RNA (guanine-7-) methyltransferase	3.54
30	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	3.54
	441499	AW298235	Hs.101689	ESTs	3.54
	453256	AI565587	Hs.32556	KIAA0379 protein	3.54
	414142	AW368397	Hs.334485	hemiscentin (fibulin 6)	3.54
	438023	AF204883	Hs.6048	FEM-1 (C.elegans) homolog b	3.54
35	412245	AI952669	Hs.22883	ESTs, Weakly similar to I38022 hypoteti	3.54
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	3.53
	446682	AW205632	Hs.211198	ESTs	3.52
	431392	AI371223	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HE	3.52
	433430	AI863735		ESTs	3.52
40	420394	AB023161	Hs.97403	KIAA0944 protein	3.52
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.52
	443547	AW271273		hypothetical protein FLJ12666	3.52
	420676	AI434780	Hs.4248	vav 2 oncogene	3.51
	410690	AA322579	Hs.130266	ESTs	3.50
45	459645	AA074346		ESTs	3.50
	401403			Target Exon	3.50
	451166	T98171	Hs.185675	ESTs	3.50
	418836	AI655499	Hs.161712	ESTs	3.50
	421462	AF016495	Hs.104624	aquaporin 9	3.50
50	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	3.50
	432401	NM_013330	Hs.274479	NME7	3.49
	408392	U28831	Hs.44566	KIAA1641 protein	3.49
	425836	AW955696	Hs.90960	ESTs	3.48
	452327	AK000196	Hs.29052	hypothetical protein FLJ20189	3.48
55	418721	NM_002731	Hs.87773	protein kinase, cAMP-dependent, catalyti	3.48
	433627	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone K	3.48
	422960	AW890487		cadherin 13, H-cadherin (heart)	3.48
	430570	AI417881	Hs.292464	ESTs	3.48
	406387			Target Exon	3.47
60	416585	XS4162	Hs.79386	leiomodlin 1, smooth muscle (LMOD1) (Thy	3.46
	432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	3.46
	412240	H72176		hypothetical protein FLJ13159	3.46
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	3.46
	443634	H73972	Hs.134460	ESTs	3.46
65	422963	M79141	Hs.13234	ESTs	3.46
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	3.46
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	3.46
	425100	AF051850	Hs.154587	supervillin	3.45
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.45
70	444250	R40815	Hs.12396	ESTs, Weakly similar to 2004399A chromos	3.44
	426386	R17298	Hs.295923	seven in absentia (Drosophila) homolog 1	3.44
	447764	NM_003776	Hs.19500	nuclear localization signal deleted in v	3.44
	411251	R19774	Hs.22835	HHGP protein	3.44
	432648	AA557952		gb:m17c05.s1 NCI_CGAP_HSC1 Homo sapiens	3.44
75	428708	NM_014897	Hs.190386	KIAA0924 protein	3.44
	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	3.43
	451743	AW074266	Hs.23071	ESTs	3.42
	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	3.42
	448705	H05072	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	3.42
80	414489	AI620677	Hs.73105	ESTs	3.42
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	3.41
	435841	R28522	Hs.186937	ESTs	3.41
	424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	3.40
	451198	AW964541		hypothetical protein FLJ21127	3.40

	429952	AF080158	Hs.226573	inhibitor of kappa light polypeptide gen	3.40
	436023	T81819	Hs.302251	ESTs	3.40
	449656	AA002008	Hs.188633	ESTs	3.40
5	437739	AW579216	Hs.264610	ESTs, Moderately similar to Ibd1 [H.sapi	3.40
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	3.40
	448474	AI792014	Hs.13809	hypothetical protein FLJ10648	3.40
	456505	AA504595		ESTs	3.40
	439867	AA847510	Hs.161292	ESTs	3.40
10	442113	BE622187		ESTs, Weakly similar to I38022 hypoteti	3.40
	425922	AL157466	Hs.162751	Homo sapiens mRNA; cDNA DKFZp761E2423 (f	3.40
	435299	AI745458	Hs.343026	ESTs, Weakly similar to T20593 hypoteti	3.40
	421263	AB020638	Hs.103000	KIAA0831 protein	3.40
	410300	AW903988	Hs.62119	hypothetical protein FLJ14800	3.39
15	440028	AW473675		ESTs, Weakly similar to T17227 hypoteti	3.39
	445070	N79110	Hs.21276	collagen, type IV, alpha 3 (Goodpasture	3.38
	432572	AI660840	Hs.191202	ESTs, Weakly similar to ALUE_HUMAN IIII	3.38
	442426	AI373062	Hs.332938	hypothetical protein MGC5370	3.38
	428412	AA428240	Hs.126083	ESTs	3.38
20	448772	AW390822	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	3.38
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.38
	413714	AI660944	Hs.71428	ESTs	3.38
	415663	AW296841	Hs.313332	ESTs	3.38
	407904	W44735	Hs.9286	Homo sapiens cDNA: FLJ21278 fis, clone C	3.37
25	421114	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	3.37
	440214	AA247118	Hs.7049	hypothetical protein FLJ11305	3.37
	440980	AL042005	Hs.1117	tripeptidyl peptidase II	3.36
	411975	AI916058	Hs.144583	ESTs	3.36
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	3.36
30	414783	AW069569		inactive progesterone receptor, 23 kD	3.36
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	3.36
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.36
	411213	AA676939	Hs.69285	neuropilin 1	3.36
	420613	AI873871	Hs.7041	ESTs, Weakly similar to A47582 B-cell gr	3.35
35	417534	NM_004998	Hs.82251	myosin IE	3.35
	431698	AI492369		ESTs	3.35
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3.35
	441623	AA315805		desmoglein 2	3.34
	420729	AW964897	Hs.290825	ESTs	3.34
40	440010	AA534930	Hs.127236	hypothetical protein FLJ12879	3.34
	448369	AW268982	Hs.111335	ESTs	3.34
	452820	N46161	Hs.35274	ESTs	3.34
	453271	AA903424	Hs.6786	ESTs	3.34
	428839	AI787756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.34
45	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	3.34
	443291	AA325633	Hs.136102	KIAA0853 protein	3.33
	418720	AI381687	Hs.39526	ESTs	3.33
	452107	AB020681	Hs.27973	KIAA0874 protein	3.33
	439943	AW083789	Hs.124620	ESTs	3.33
50	433282	BE539101		hypothetical protein	3.33
	410344	AW978436	Hs.62515	KIAA0494 gene product	3.33
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	3.32
	421379	Y15221	Hs.103962	small inducible cytokine subfamily B (Cy	3.32
	434210	AA665612		ESTs	3.32
55	431923	AI741770	Hs.292690	ESTs, Weakly similar to I38022 hypoteti	3.32
	453199	AI336266	Hs.32353	mitogen-activated protein kinase kinase	3.32
	419534	AA443691	Hs.90858	Homo sapiens clone 25023 mRNA sequence	3.32
	448939	BE267795	Hs.22595	hypothetical protein FLJ10637	3.32
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	3.32
60	422092	AB007883	Hs.111373	KIAA0423 protein	3.32
	412262	W26406		seven in absentia (Drosophila) homolog 1	3.32
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.32
	446094	AK001760	Hs.13801	KIAA1685 protein	3.32
	446493	AK001389	Hs.15144	hypothetical protein DKFZp564O043	3.32
65	420339	AW968259	Hs.186647	ESTs	3.31
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	3.31
	432331	W37862	Hs.274368	MSTP032 protein	3.31
	433697	AA600357	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.31
	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypoteti	3.31
70	430950	AA489525		ESTs	3.30
	409758	AW474960	Hs.182258	ESTs, Weakly similar to I78885 serine/th	3.30
	417958	AA767382	Hs.193417	ESTs	3.30
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	3.30
	419543	AA244170		gbnc05h02.s1 NCL_CGAP_Pr1 Homo sapiens	3.30
75	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.30
	452039	AI922988	Hs.172510	ESTs	3.30
	443798	R07848	Hs.188522	ESTs	3.29
	448378	AW664026	Hs.59892	ESTs	3.29
80	455657	BE065209		gbRC1-BT0314-310300-015-b12 BT0314 Homo	3.28
	420126	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	3.28
	444291	AI598022	Hs.193989	TAR DNA binding protein	3.28
	424084	AI940575	Hs.20914	hypothetical protein FLJ23056	3.28
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	3.28
	443774	AL117428	Hs.9740	DKFZP434A236 protein	3.28

425657	T89839	Hs.119471	ESTs	3.28
406672	M26041	Hs.198253	major histocompatibility complex, class	3.28
419905	AW248229	Hs.93659	protein disulfide isomerase related prot	3.27
425332	AA633306	Hs.127279	ESTs	3.27
418529	AW005695	Hs.250897	TRK-fused gene	3.27
417944	AL077196	Hs.82985	collagen, type V, alpha 2	3.27
433618	AA602539	Hs.345494	ESTs	3.27
408630	AA748009	Hs.173328	ESTs	3.26
415914	AA306033	Hs.78915	GA-binding protein transcription factor,	3.26
415102	M31899	Hs.77929	excision repair cross-complementing rode	3.26
432626	AA471098	Hs.278544	acetyl-Coenzyme A acetyltransferase 2 (a	3.26
429493	AL134708	Hs.145998	ESTs	3.26
445860	AA332145	Hs.13392	tethering factor SEC34	3.26
450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	3.26
426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020.1 E2IG5	3.26
420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	3.26
448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	3.26
436758	AW977167	Hs.155272	ESTs	3.26
438011	BE466173	Hs.145696	splicing factor (CC1.3)	3.26
426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	3.25
426860	U04953	Hs.172801	isoleucine-tRNA synthetase	3.25
437830	AB020658	Hs.5867	KIAA0851 protein; suppressor of actin 1	3.25
453368	W20296	Hs.288178	Homo sapiens cDNA FLJ11968 fis, clone HE	3.25
409939	AA463437	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	3.25
413715	AW851121	Hs.75497	Homo sapiens cDNA: FLJ22139 fis, clone H	3.24
407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	3.24
418283	S79895	Hs.83942	calhepsin K (pseudosostosis)	3.24
414405	AI362533		KIAA0306 protein	3.24
445893	AI610702	Hs.202613	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.24
434423	NM_006769	Hs.3844	LIM domain only 4	3.24
408951	AW407227	Hs.227591	hypothetical protein FLJ11088	3.24
408949	AF189011	Hs.49163	putative ribonuclease III	3.24
410337	M83822	Hs.62354	cell division cycle 4-like	3.24
409010	AI648675		Homo sapiens, Similar to RIKEN cDNA 1700	3.24
400419	AF084545		Target	3.24
454078	AA601518	Hs.22209	secreted modular calcium-binding protein	3.24
422461	NM_003417	Hs.117077	zinc finger protein 264	3.24
441604	AI683049	Hs.201282	ESTs	3.24
411960	R77776	Hs.18103	ESTs	3.23
414895	AW894856	Hs.116278	Homo sapiens cDNA FLJ13571 fis, clone PL	3.23
430522	N75750	Hs.242271	KIAA0471 gene product	3.23
426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	3.23
405268			ENSP00000223174-KIAA0783 PROTEIN.	3.23
429165	AW009886	Hs.118258	prostate cancer associated protein 1	3.22
427196	AW967522	Hs.191593	ESTs	3.22
439776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	3.22
417727	AL133623	Hs.82501	similar to mouse Xmi1 / Dhmi2 protein	3.22
410853	H04588	Hs.30469	ESTs	3.22
411962	AA099050		gb:z85d12.1 Soares_pregnanLuterus_NbH	3.22
451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.22
440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	3.22
427480	BE148769	Hs.334477	hypothetical protein FLJ11328	3.22
444623	AI183829	Hs.202111	ESTs	3.21
424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	3.21
435874	AA868688	Hs.93102	ESTs	3.20
443801	AW206942	Hs.253594	intron of trichorhinophalangeal syndro	3.20
434982	AW975084		gb:EST387190 MAGE resequences, MAGN Homo	3.20
430929	AA489168	Hs.156933	ESTs	3.20
426316	NM_002430	Hs.268515	meningioma (disrupted in balanced trans	3.20
430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	3.20
422109	S73265	Hs.1473	gastrin-releasing peptide	3.20
451119	AA805417	Hs.64753	ESTs	3.20
414893	AA215295	Hs.77578	ubiquitin specific protease 9, X chromos	3.20
432676	AI187366		gb:q129c01.x1 Soares_leslis_NHT Homo sap	3.19
428820	AA436187	Hs.172631	integrin, alpha M (complement component	3.19
422040	AA172106	Hs.110950	Rag C protein	3.18
437838	AI307229		ESTs	3.18
408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	3.18
420789	AI670057	Hs.199882	ESTs	3.18
419135	R61448	Hs.106728	ESTs, Weakly similar to KIAA1353 protein	3.18
446019	AI362520		histone deacetylase 3	3.18
430848	AW021726	Hs.345490	gb:d127a02.y1 Morton Fetal Cochlea Homo	3.18
425375	AA631977	Hs.155995	KIAA0643 protein	3.18
424075	AI807320	Hs.227630	RE1-silencing transcription factor	3.18
413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	3.18
453111	AB014598	Hs.31720	hephaestin	3.18
454042	H22570		hypothetical protein FLJ20093	3.18
407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.18
447183	AI554733	Hs.173182	ESTs	3.18
437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	3.18
431831	AW023204	Hs.302743	ESTs	3.18
420664	AI681270	Hs.99824	BCE-1 protein	3.18
451582	AI963026	Hs.289958	ESTs, Weakly similar to putative p150 [H	3.17

	432954	AI076345		ESTs	3.17
	444990	AI912410	Hs.27475	Homo sapiens cDNA FLJ12749 fis, clone NT	3.17
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	3.17
5	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.17
	441889	AI090455	Hs.268371	hypothetical protein FLJ20274	3.17
	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	3.16
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.16
	420623	BE245485	Hs.99437	Homo sapiens mRNA; cDNA DKFZp586G1924 (f	3.16
10	451475	T19093	Hs.26450	KIAA0725 protein	3.16
	452066	AA772149	Hs.16979	ESTs, Weakly similar to A43932 mucin 2 p	3.16
	429556	AW139399	Hs.98988	ESTs	3.16
	448514	AB020626	Hs.301866	KIAA0819 protein	3.16
	443732	AI188803	Hs.153944	ESTs	3.16
	436805	AA731533	Hs.270751	ESTs	3.16
15	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	3.16
	417511	AL049176	Hs.82223	chordin-like	3.16
	423595	R82826	Hs.220702	ESTs	3.16
	445837	AI261700	Hs.145544	ESTs	3.16
20	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUS protein d	3.16
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.16
	414183	AW957446	Hs.301711	ESTs	3.16
	433194	AB040883	Hs.83243	KIAA1450 protein	3.16
	453915	AA588721	Hs.286218	ribosomal protein L44	3.15
25	407725	BE388094	Hs.21857	ESTs	3.15
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.14
	440937	AF202724	Hs.7531	KIAA0810 protein	3.14
	449057	AB037784	Hs.22941	KIAA1363 protein	3.14
	446126	AW085909		pleckstrin homology domain interacting p	3.14
30	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.14
	419145	N99638		gbz339g11.r1 Soares fetal liver spleen	3.14
	418757	AI864193	Hs.169728	hypothetical protein FLJ13150	3.14
	430000	AW205931	Hs.99598	hypothetical protein MGC5338	3.14
	437296	AA350994	Hs.20281	KIAA1700	3.14
35	441381	H22195	Hs.31874	ESTs	3.14
	457250	AA811987	Hs.125779	ESTs	3.14
	422900	AA641201	Hs.222051	ESTs	3.14
	442787	W93048	Hs.250723	hypothetical protein MGC2747	3.14
	430589	AJ002744	Hs.245315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.14
40	419355	AA428520	Hs.90061	progesterone binding protein	3.14
	409509	AL036923	Hs.322710	ESTs	3.14
	417308	H60720	Hs.81892	KIAA0101 gene product	3.14
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	3.14
	429160	AW663083	Hs.144469	ESTs	3.14
45	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	3.14
	451107	AA235108	Hs.17639	Homo sapiens ubiquitin protein ligase (U	3.14
	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	3.14
	451518	AW340925	Hs.174918	ESTs	3.14
	435702	AI033647	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	3.13
50	439208	AK000299	Hs.180952	dynactin 4 (p62)	3.13
	451838	AW005866	Hs.193969	ESTs	3.13
	426369	AF134157	Hs.169487	Kreiser (mouse) maf-related leucine zip	3.13
	446945	AI193115	Hs.16611	tumor protein D52-like 1	3.13
	453920	AI133148	Hs.36602	I factor (complement)	3.13
55	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.13
	417105	X60992	Hs.81226	CD6 antigen	3.12
	433854	AA610649	Hs.333239	ESTs	3.12
	408089	H59799	Hs.42644	thioredoxin-like	3.12
	453686	AL110326	Hs.304679	ESTs, Moderately similar to Z195_HUMAN Z	3.12
60	426167	AF039023	Hs.167496	RAN binding protein 6	3.12
	452195	AA994712	Hs.116878	ESTs	3.12
	416580	T61572	Hs.79385	Human clone Z3574 mRNA sequence	3.12
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.12
	424001	W67883	Hs.137476	paternally expressed 10	3.12
65	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.12
	433401	AF039698	Hs.284217	serologically defined colon cancer antig	3.12
	409245	AA361037		RNA isopentenylpyrophosphate transferas	3.12
	414290	AI568801	Hs.71721	ESTs	3.12
	400294	N95798	Hs.276695	Homo sapiens protein mRNA, complete cds	3.12
70	429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	3.11
	448873	NM_003677	Hs.22393	density-regulated protein	3.11
	428471	X57348	Hs.184510	stratfin	3.11
	436288	AI361722	Hs.192410	ESTs	3.10
	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	3.10
75	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	3.10
	453468	W00712	Hs.32990	DKFZP556F084 protein	3.10
	412340	AA101809	Hs.182685	ESTs	3.10
	438716	AA814903	Hs.155113	ESTs	3.10
	419440	AB020689	Hs.90419	KIAA0882 protein	3.10
80	433017	Y15067	Hs.279914	zinc finger protein 232	3.10
	428513	BE220806	Hs.184697	plexin C1	3.10
	437866	AA156781		metallothionein 1E (functional)	3.10
	451027	AW519204	Hs.40808	Homo sapiens, Similar to RIKEN cDNA 2810	3.10
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	3.10

	435445	AA737345	Hs.294041	ESTs	3.10
	420997	AK001214	Hs.100914	hypothetical protein FLJ10352	3.09
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	3.09
5	406122			Target Exon	3.09
	435272	AA906415	Hs.110041	ESTs	3.09
	410726	AJ623859	Hs.15936	ESTs	3.09
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.08
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.08
10	417538	AW050865	Hs.275711	hypothetical protein MGC2452	3.08
	434938	AW500718	Hs.8115	Homo sapiens, clone MGC:16169, mRNA, com	3.08
	434733	AI334367	Hs.159337	ESTs	3.08
	434421	AI915927	Hs.34771	ESTs	3.08
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.08
15	424939	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	3.08
	458332	AI000341		ESTs	3.08
	445034	AW293376	Hs.143659	ESTs	3.08
	446570	AV659177	Hs.127160	ESTs	3.08
	429920	AW473208	Hs.115572	ESTs, Weakly similar to I38022 hypotheti	3.08
20	459513	AI032946		gb:ox06g09.s1 Soares_fetal_liver_spleen_	3.06
	419038	AW134924	Hs.190325	ESTs	3.06
	451079	AJ827988	Hs.240728	ESTs, Moderately similar to PC4259 ferri	3.06
	417386	AL037228	Hs.82043	D123 gene product	3.06
	453108	AI311457	Hs.99472	ESTs	3.06
25	449328	AI962493		ESTs	3.06
	426556	AB037798	Hs.188790	KIAA1377 protein	3.06
	425509	AF079363	Hs.158213	sperm associated antigen 6	3.06
	447957	NM_014821	Hs.20126	KIAA0317 gene product	3.06
	417226	AW505054	Hs.4283	ESTs	3.05
30	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	3.05
	426279	AJ648520	Hs.169084	tubby like protein 3	3.05
	433814	AA509738	Hs.16525	ESTs	3.05
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	3.05
	431341	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	3.04
35	441789	D52059	Hs.7972	KIAA0871 protein	3.04
	456437	AJ924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.04
	438771	NM_016289	Hs.6406	MO25 protein	3.04
	448497	BE613269	Hs.21893	hypothetical protein DKFZp761N0624	3.04
	416240	NM_001981	Hs.79095	epidermal growth factor receptor pathway	3.04
40	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	3.04
	424776	AJ867931	Hs.164595	ESTs	3.03
	408409	AW838181	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.03
	429693	BE254962	Hs.211612	SEC24 (S. cerevisiae) related gene famil	3.03
	425960	AW410646	Hs.164649	hypothetical protein DKFZp434H247	3.03
45	431625	AW750627	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	3.03
	451144	AW956103	Hs.61712	pyruvate dehydrogenase kinase, isoenzyme	3.02
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	3.02
	408683	R58665	Hs.46847	TRAF and TNF receptor-associated protein	3.02
	427735	AA916785	Hs.180610	splicing factor proline/glutamine rich (3.02
50	440603	AL121733	Hs.7299	Novel human gene mapping to chromosome 1	3.02
	415443	T07353	Hs.7948	ESTs	3.02
	439981	AI348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	3.02
	406685	M18728		gb:Human nonspecific crossreacting antig	3.02
55	446013	AI360167	Hs.152774	ESTs	3.02
	433902	AW292820	Hs.144906	ESTs	3.02
	412610	X90908	Hs.74126	fatty acid binding protein 6, ilaai (gas	3.02
	432505	AW274526	Hs.277721	KIAA0049	3.01
	440040	BE219431	Hs.302031	zinc finger protein, subfamily 1A, 4 (Eo	3.01
	433255	AI274270	Hs.96840	KIAA1527 protein	3.01
60	419726	U50330	Hs.1274	bone morphogenetic protein 1	3.01
	417258	N58885		gb:yy60a09.s1 Soares_multiple_sclerosis_	3.00
	435800	AI248285	Hs.118348	ESTs	3.00
	444838	AV651680	Hs.208558	ESTs	3.00
	456760	AW961251	Hs.127828	guanine nucleotide binding protein (G pr	3.00
65	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	3.00
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.00
	436396	AI683487	Hs.152213	wingless-type MMTV Integration site fami	3.00
	410434	AF051152	Hs.63668	toll-like receptor 2	3.00
	412095	AJ624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.00
70	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	2.98
	450247	AF123303	Hs.24713	hypothetical protein	2.98
	417865	AW086059	Hs.6529	ESTs, Weakly similar to I78885 serine/th	2.98
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.98
	438543	AA810141	Hs.192182	ESTs	2.98
75	415503	U36601	Hs.78473	N-deacetylase/N-sulfotransferase (hepara	2.98
	429138	AB020657	Hs.197298	NS1-binding protein	2.98
	447881	BE620886		GCN1 (general control of amino-acid synt	2.96
	425481	AW978162		ESTs	2.96
	453315	BE544203	Hs.24831	ESTs	2.96
80	440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	2.95
	433208	AW002834	Hs.24095	ESTs	2.95
	442495	AI184717		ESTs	2.94
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	2.94
	408170	AW204516	Hs.31835	ESTs	2.94

5	430382	AA477908	Hs.282267	ESTs, Moderately similar to I38022 hypot	2.94
	449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	2.94
	407361	AA744622	Hs.292645	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.94
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.93
	436005	BE551650	Hs.158126	Homo sapiens cDNA FLJ13350 ts, clone OV	2.93
	449458	AI805078	Hs.208261	ESTs	2.93
	449317	AW293413	Hs.132906	19A24 protein	2.92
	411118	N27944	Hs.221476	ESTs, Weakly similar to AF108460 1 ubinu	2.92
10	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 ts, clone L	2.91
	416311	D80529		gb:HUM081H05B Human fetal brain (TFujiwa	2.91
	433068	NM_006456	Hs.289215	sialyltransferase	2.90
	429272	W25140	Hs.110667	ESTs	2.90
	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	2.90
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.88
15	426782	R14614	Hs.33846	ESTs	2.88
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 ts, clone HE	2.88
	413882	AA132973	Hs.184492	ESTs	2.88
	421554	AW137676	Hs.97775	ESTs	2.88
20	446488	AB037782	Hs.15119	KIAA1361 protein	2.84
	421391	AW304350	Hs.191958	Immunoglobulin superfamily receptor tran	2.84
	424527	AW138558	Hs.334873	ESTs, Weakly similar to t54374 gene NF2	2.82
	419284	AW820869	Hs.215558	ESTs, Moderately similar to ZN91_HUMAN Z	2.82
	415788	AW828686	Hs.78851	KIAA0217 protein	2.82
	448481	W15284	Hs.74832	ESTs	2.82
25	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.80
	443441	AW291196	Hs.92195	ESTs	2.80
	422725	AA315703	Hs.199993	ESTs, Weakly similar to ALUB_HUMAN IIII	2.80
	431926	AW972724		gb:EST384816 MAGE resequences, MAGL Homo	2.80
30	420406	AA741024	Hs.88378	ESTs	2.79
	437678	AA829860	Hs.122834	ESTs	2.78
	440115	R41808	Hs.144924	ESTs, Weakly similar to B Chain B, Solut	2.78
	439883	AL359652	Hs.171096	Homo sapiens EST from clone DKFZp434A041	2.78
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.77
35	451273	NM_014811	Hs.26163	KIAA0649 gene product	2.76
	435154	AA668764		ESTs	2.76
	432451	AW972771	Hs.292471	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.75
	442703	AL044949	Hs.116298	ESTs	2.74
	419341	N71463	Hs.118888	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.74
40	435861	AF254956	Hs.16608	candidate tumor suppressor protein	2.72
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TTT3 co	2.70
	438441	AW664960	Hs.205319	ESTs	2.70
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	2.67
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	2.66
45	416239	AL038450	Hs.48948	ESTs	2.62
	434792	AA649253	Hs.132458	ESTs	2.60
	424852	AI222779	Hs.144848	ESTs	2.58
	425538	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	2.57
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	2.56
50	450571	AF158240	Hs.60397	ESTs	2.56
	442435	AI986208	Hs.244760	ESTs, Highly similar to B34087 hypotheti	2.56
	424148	BE242274	Hs.1741	integrin, beta 7	2.56
	445784	AI253155	Hs.146065	ESTs	2.53
	408072	BE005566	Hs.16773	Homo sapiens clone TCCCA00427 mRNA sequ	2.52
55	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, s	2.52
	450295	AI766732	Hs.210628	ESTs	2.48
	440381	AA917808	Hs.190495	ESTs	2.46
	433923	AI823453	Hs.146625	ESTs	2.44
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.44
60	429670	L01087	Hs.211593	protein kinase C, theta	2.44
	437908	AI082424		ESTs	2.43
	438676	AA813745	Hs.123446	ESTs	2.37
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.28
	444969	AI203334	Hs.160628	ESTs	2.28
65	446423	AW139655	Hs.150120	ESTs	2.27
	435517	AA928626	Hs.130177	ESTs	2.27
	425354	U62027	Hs.155935	complement component 3a receptor 1	2.26
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	2.00
	429073	AA446167	Hs.47385	ESTs	1.98
70	433834	AA620742	Hs.130786	ESTs	1.72
	417365	D50583	Hs.82028	transforming growth factor, beta recepto	1.52
	414521	D28124	Hs.76307	neuroblastoma, suppression of tumorigen	1.30
	402550			Target Exon	1.09

TABLE 33B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

80	Pkey	CAT Number	Accession
	431089	125941_2	BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826
	456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	407192	2200202_1	AA602964 AA609200

438089	22448_4	BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344546 BE009112 BG899664 H91240 R60548 N41701 AF086037 H89360 H89546 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354 M31126 AW749625 AW749626 AW749644 AI140497 BG034853 AW173315 AW303375 BG190225 BG939153 BF057308 AA600736 AI751258 AI090486 BE939504 AW631492 AI768270 AI862133 AA417652 BE378218 AA599207 AW794702 AA024968 AA446024 AI148235 AI191710 BI493797 AI272646 BI493796 AA634323 AI754332 AA258414 C05155 AI218226 AI039656 AI350380 AI084698 AI754989 AI673545 AI432010 AI751035 AA375571 AA446297 BG216743 BC011194 AW517087 AA601054 T85512 BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969 BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563 AA459408 AA459633 AA418444 W23607 BG940150 AM93445 AW054729 AI221929 AI868744 AA215405 AA766713 AA621546 BF928317 BE464132 AI990909 AW271459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 R69057 BF766886 BE769254 W05240 BG292389 C06094 AI668930 AW104534 AA310513 AA830127 AW134897 AA046953 AW965490 AI810530 BF092924 AA334151 AA334725 D31302 R20723 AA263003 BI824635 AI276287 AI684428 AI524234 AI335035 AW014704 AI911443 AA972102 AI367512 AI126670 AW016017 AI286003 AI147163 AA626033 AI539156 AA555542 AI094253 AW512612 BE889628 AA744752 BE646306 AW471324 AA999975 AA863400 H17550 AI991439 R46187 BE928954 AA333976 D63102 BF744491 AI801777 BE677762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AA670058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF449023 AI289476 AW074381 BF972912 AI991780 AA889119 AI537472 Z39730 AI868953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981 AW970134 AA516420 AA543007 BG057526 BI001430 AI498371 D60181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818 C15161 D60184 D60656 AW340495 AI984319 AA974603 BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE465812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW969605 AI553633 AA993566 AI521958 AI565071 AI864217 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354 T23514 AI655785 Z99386 AV716301 BE222333 AI949687 BF732426 AI494086 AV721430 AW577332 N68315 BE672030 AI084440 AI250908 N50901 AA757364 BF515264 AI186231 BE466036 AW631313 AA993514 N54411 BG057515 AW013895 N77963 AA708723 AI273295 N59093 AA522665 AI871574 AA505521 AA812256 AA553941 AW467057 W68650 AI168772 AA988308 AA910057 AI868258 AA918322 AI335847 AA821494 AA904390 AI760007 AI146694 AV758440 BM142582 N66507 AI874563 AW628584 AI263902 BF223368 AI090490 AI452918 N71423 AA062767 T94332 AA016003 BG681608 AA082426 AA029451 N71873 BF437845 T54154 AV741757 AI174783 R12271 R83569 AK074129 AI138071 AI806793 AI453544 AI084616 BF062435 BE672932 AI828296 BF062464 AI803443 AI264326 AI280956 AI743547 AW295227 AI139967 AI972561 AI863570 AW062752 AW062756 AW062757 AW176904 AW062755 AW062750 AW062749 AW176886 AI751694 BG251391 AA043621 W30872 BI524827 N4581 AI084614 AA776976 AI377572 AI751695 AI016576 AW439994 AW194255 AW627763 AA668249 AI079870 AW022524 AI968540 AI248360 AA702490 AA043262 AA631511 AW176883 AW751767 AW176887 AW062748 AW062745 AW176862 AW176815 AW176814 AW176846 AW176841 AW176871 AW176874 AW176819 AI927437 AW191962 R36548 AA853713 AW196059 AA618567 AW176881 AW062754 AW062751 AW062746 AW176888 AW751772 AW176859 AW751765 AW751762 AW176833 AW176873 AW751745 AA694513 AA780815 AW176857 AW176834 AW176839 AW751771 AW176878 AW176843 AW176842 AW751755 AW176847 AW176812 AW176830 AW176849 AW176844 AW176877 AW751757 AW176850 AW176851 AW751758 AW751746 AW176858 AW176853 AW751766 AW176845 AW176872 AW176840 AW176876 AW176852 AW751754 AW176836 AW176856 AW751773 AW751760 AW751751 AI138070 AA639738 AL602588 AA853712 AA317570 R38469 AW291569 AI156151 Z25109 C05177 AW975688 AA731063 N67084 AL050068 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021968 BF063327 BF593552 AA630766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602 AA962057 AW516069 AI582546 BF221924 BF222543 AI801808 AW468599 AW000736 AI866625 AW235356 BM021837 AA911958 AI680606 W86516 T03370 AW611634 H41653 AI468349 H19588 AW090198 AW043993 R39847 BC013939 BI494690 BI491211 AI928393 AA843540 BG938644 AU185628 BI495842 AW173255 BM052709 AI743999 AI690144 AI922209 AI740907 AW340368 AA928759 AW118737 BF511370 AA707807 BF435295 AI339463 AI373842 AI433809 BE222392 AA602308 AA28261 BI460355 AW662760 AI888087 AI342098 AA722418 W78151 N64382 BE221848 AW025901 AA452120 AI150479 AI016168 AA779515 AA661791 BM474307 BI911169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BM461961 BG681168 BI602483 BE889592 AW954311 BM052988 BI962893 AI989299 Z42328 BF029504 T35688 BG402602 AU185770 AI023271 AA147719 AI434079 AI569000 AW276488 AA92453 AA342821 AI4648303 AI349364 AI051008 AA926941 AA350894 AW071451 N22249 AI784138 AA083847 N22258 AW440825 AA661570 AA376687 AA659125 AI356299 R70463 AI383586 AA827189 BI494872 AW021094 BI494871 AA905500 AA460923 BI492041 AW028955 AI624611 BG271780 AI497723 H88862 D59588 N89979 AA658425 N81154 D62341 AI274437 N66697 H96993 AI370663 AA728850 H05232 R59374 H12223 AI935759 AI362553 D60006 N29572 AI916833 N75273 AA148710 BI597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA452342 AW965441 W19723 R32986 BE883841 R61003 AI910374 AI865282 R56325 AI468927 R34681 H96211 Z39807 BF954386 AW975804 AA748675 AA731006 M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951765 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985842 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE831048 BF999889 BF368816 BE184924 BE159646 BE714832 BE184948 BG986845 AA131128 AA098991 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705968 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE719915 AW789309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715186 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094833 BF094833 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946935 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939852 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181
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 H61453 AA838765 AI693104 AA721107
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 T09030 AI886230 U70056 AU119916 BF446537 BE503207 BE502849 AI698102 AA258553 AV718529 AV719917 BF724133 BI438668 AI804000
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 AW975199 AA935418 T74315 F12666 AA022923 T89028 AA258606 W26406 BE838620 AV700706 AA101321 R41382 H14479 AA253044 R54810
 R42784 R44804 R41278
 AI525877 AA489525 AW088177

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414405	112689_1	AL047596 AA393792 AI670731 AI037957 AW874364 AI038137 N62286 AI241379 BE501095 AW090696 AI927369 AI669226 AI369437 AI371075
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		BG283489 BE090666 BE090664 BE090662 H26545
409010	10331_1	AL575207 AL551714 BMD14781 BG542863 BG771232 AA429722 AI377511 AI770155 AA716665 BG003427 AA810811 AA442760 AA128610
		AA059411 AI796263 AI494075 AI572127 AA420992 BF436083 AI648675 AA878813 BI488614 BG700888 AA128609 AV702879 AA731146
		AI580336 AI373224 AA919169 AI758175 AA976350 BG701414 BF057794 AW135598 AA062583 BI549631 AI185077 AA933879 AW024454
10		AA193289 AA045194 BG928396 BE856883 BF435859 AA196423 AW237471 R99289 D61992 BE856637 BF368270 AA194235 N51319 AA383499
		N63065 BG548812 BF027898 BG779448
411962	2307710_1	AA099050 AA099526 T47733
434982	121871_1	AW975084 T90204 AA658177
432676	3503_22	AI187366 AA618478 AA558869
437838	2512601_1	AI308202 AI307229 AA769348
15	658727_1	AI362520 D25917 AI670784 AI742347 AW269789 AI270700 AW610541 AW793036 AW793035 AW610540 AW362220 AW362166 AW362214
		AW362225 AW362228 AL119827
454042	30254_1	AJ420458 AI018523 AA708686 BF949633 AL119553 BF945960 AI081305 AA041432 AI921013 AI684910 AI654847 AW874199 AI206120
		AW241428 R43035 T66767 AW103715 W28478 BF953052 H45926 BF807568 AW903943 BE170143 BI040435 BF931989 BI600000 AV722350
		W27787 H45331 BI549761 R53955 BI549855 BG991583 BI491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199
20		AI431587 BE858679 AW292267 AI421678 AA041195 BE466753 AI243913 AI358894 AW137298 AI366468 N64350 AA779107 AW025969 R49056
		AA347011 R55722 AW771106 F04969 Z38381 F01659 H17396 BI493714 AI880103 AW771447 AI202561 AA788851 AI494436 BF856114 H22570
	432954	AI076345 AI887648 AA572691
446126	2159612_1	BF946219 BF946218 BF851494 AL536879 AA457150 AI590194 AI582629 AA464515 AA916242 AA337109 AA336509 N46906 AA336322
	610_2	AA336407 AA337222 AA319240 BI026817 BI027058 AL536880 AI693827 AA651730 AI701013 BMD68789 AW339506 AA293021 BF891108
25		AI458885 AW361203 AW974652 AI761251 AI655763 AA628063 BE047125 AW085916 AI129587 N52070 AW172361 AA052951 AW085909
		AI000008 AA962570 AI371342 AI364207 AA464514 AI962506 AI824603 AW376300 AA058439 AW361192 AV656660 N50282 BF820514 BF891008
		H40784 BF891112 BE708029 AW043567 AA056762
419145	248375_1	BM456602 AV706711 BF379357 H90994 AA234435 AA558020 BF351723 AA328271 R94815 N99638 BG223375 AW973760 N59599
409245	3199_2	AF030234 BC017465 BG008526 AW505550 BM460141 N47324 AA361037 AA321632 N45606 AV752798 AV657116 AA296632 AU137857
		AW467027 AI742080 AI624350 H58206 AA478518 AW439997 AW393555 AW393523 AI559753 AI808732 R66856 H01374 BI257369 BI259830
		AW960845 BM466252 AW956813 BE768647 AV658853 BM055248 BF372070 BF372055 BF372061 AA347852 AA905863 BG505078 AV654024
		BF093291 AW021929 H22650 AA459715 BG496341 BE697763 BI254209 BG499543 H42946 BI059780 BI086741 H87896 H87599 BF691752
		BE768511 BG940948 W37195 BF372041 BE883796 BF372082 BF367329 BF909744 AW966003 AV714014 BI492868 BI495144 AA921845
		AI693426 AI652147 AI435449 N47325 AI434429 AA573137 AI183429 AI829962 AI332526 BF513937 AI189561 AI221962 AI378034 AW118897
		AW665247 AW340077 N41605 AA478519 AA463875 AI858260 AA463379 AI292305 BE045947 AA971089 AI125820 BG940947 AI080245
35		AA884954 AI125702 AI382934 AA931835 AI358631 AW439905 AI027833 AI399648 AI014533 AA347851 AA738261 N67374 N69081 AI768687
		AA948472 AI819214 AA293133 AI186725 AA889214 AI222635 BI495143 N29605 N48812 AA769041 AI492769 D56771 AA095911 BE222062
		D56772 AW372265 BM054985 D12465 BG534562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 BI255749 BI492848
		HI6217 H21980 H22651 H88179 H87354 H44052 H25165 H44128
40	437866	U52054 AL581000 AA156850 AW293839 BI335865 AA024963 BF149420 BE073977 AW602574 BE164012 BE163992 BE163974 AW402161
	34267_1	BM194134 AW966609 W84374 BF916380 AA385173 W84366 AA383743 BF903598 AA043776 W84421 AA778446 AW444904 BF446960
		AA837481 AV755539 AW468444 AW468002 AA811830 AA581806 AI866686 AI572124 AA687333 D20160 AA812489 AU185248 AU186004
		AA156781 AI536733 BM144850 AI471883 AA40926 BF507639 AA043777 AW874142 BE832523 BE163972 BI022546 BI021204
		AI000341 AI766341 AW873274
45	458332	AV704062 BE162284 AI032946 BF360636
459513	417837_1	AI884781 AI652306 AI651694 AI638744 AI962493
449328	3030726_1	M18728
406685	0_0	BG116781 BI914326 BI030196 N58885 N63406 AV683374 N58892 BG110501 AA333708 AA359583 AW963123 N95562 N95696 N95587
417258	400835_1	AK074291 AW293424 BE676135 AI832125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28618 BF924261
447881	44623_1	AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119
		AW814195 BE879126 AI697928 BF594155 BE205787 BF063513 N35828 AI948557 AI433839 AI379679 BG056182 AI589094 N23123 AA588805
		AW316581 AI080272 AI421980 AI493318 BF194830 N87590 AA495993 N32996 AA699844 H96845 H95592 N28741 BI035539 BF747723
		BF171066 W01350 H05495 AI243785 Z39622 AA887432 AI350659 R46102
55	425481	AL520496 AW978162 AI610475 AI688890 AW470054 AA609426 AI167391 AA815231 AA358241
440838	371165_1	BG009500 AI376551 AA897445 T87714
442495	928718_1	AI184717 AW518883 AF121173
416311	1280744_1	AA179446 AA357794 D81719 D80529 C14833
431926	1237041_1	AW972724 AA877998 AA522631 AU185388
435154	126605_1	AW972063 AA668764 AA804491 AW665688 AA765069
60	437908	AI740586 AA771806 BE500996 AW204531 AI082424 AI033879 BF093176 AA771764 D38676

TABLE 33C:

65

Pkey:

Ref:

Strand:

Nt_position:

Unique number corresponding to an Eos probe set

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

70

Pkey	Ref	Strand	Nt_position
401403	7710966	Plus	146180-146294
406387	9256180	Plus	116229-116371,117512-117651
405268	4156151	Minus	24404-24521
406122	9144087	Minus	30940-31386
402550	7652009	Minus	80413-80673

75

80 TABLE 34A: About 703 genes upregulated in idiopathic pulmonary fibrosis relative to hypersensitivity pneumonitis or non-specific interstitial pneumonitis

Pkey:	Unique Eos probe set identifier number
ExAccn:	Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number					
Unigene Title: Unigene gene title					
R1: 90th percentile of IPF AIs divided by 90th percentile of HP AIs, where the minimum value for the numerator and denominator was set to 50					
R2: 90th percentile of IPF AIs divided by 90th percentile of NSIP AIs, where the minimum value for the numerator and denominator was set to 50					
5	Pkey	ExAcn	UnigeneID	Unigene Title	R1 R2
10	405443			Target Exon	9.66 7.50
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.23 3.66
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.63 3.03
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	4.84 2.81
15	406964	M21305		FGENES predicted novel secreted protein	4.73 5.69
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.34 4.34
	407244	M10014		fibrinogen, gamma polypeptide	4.14 5.88
	421823	N40850	Hs.28625	ESTs	4.12 1.80
20	419875	AA853410	Hs.93557	proenkephalin	3.90 2.01
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.88 2.90
	418310	AA814100	Hs.86693	ESTs	3.66 2.84
	442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	3.60 3.13
25	438315	R56795	Hs.82419	ESTs	3.49 3.70
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.47 1.38
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	3.46 3.46
	434233	AF119903	Hs.138453	hypothetical protein PRO2834	3.28 2.51
30	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	3.26 3.26
	447033	AJ357412	Hs.157601	Predicted gene: Eos cloned; secreted w/V	3.19 2.12
	420185	AL044056	Hs.251385	ESTs	3.18 3.01
	420195	N44348		Homo sapiens cDNA FLJ11177 fis, clone PL	3.16 3.16
35	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	3.08 3.18
	408221	AA912183	Hs.47447	ESTs	3.07 1.98
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.02 2.36
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.98 1.72
40	422163	AF027208	Hs.112360	prominin (mouse)-like 1	2.87 1.48
	422404	AL133571	Hs.336189	Homo sapiens mRNA; cDNA DKFZp434F1135 (f	2.80 2.66
	445745	AB007924	Hs.13245	KIAA0455 gene product	2.78 1.65
	407938	AA905097	Hs.85050	phospholamban	2.78 2.46
45	423575	C18663	Hs.163443	intron of periostin (OSF-2os)	2.78 1.55
	446659	AJ335361	Hs.226376	ESTs	2.74 1.56
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-like	2.74 1.85
	437620	AW976830		ESTs	2.72 2.72
50	414591	AJ888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.67 2.05
	416585	X54162	Hs.79386	leiomodulin 1, smooth muscle (LMOD1) (Thy	2.66 1.47
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.66 2.66
	430712	AW044647		ESTs	2.62 2.62
55	453111	AB014598	Hs.31720	hephaestin	2.61 1.72
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.59 1.27
	414290	AJ568801	Hs.71721	ESTs	2.59 1.23
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	2.58 2.58
60	412639	AW961284	Hs.203838	ESTs	2.58 2.29
	423720	AL044191	Hs.23388	hypothetical protein DKFZp434F0318	2.57 1.74
	429757	AW452355	Hs.256037	ESTs	2.57 1.60
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	2.57 1.00
65	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.56 1.12
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.56 1.25
	411880	AW872477		gb:hm30f03.x1 NCL CGAP_Thy4 Homo sapiens	2.54 2.54
	401645			C16001440*:g[12330704]gb[AA652890.1]AF3	2.53 3.38
70	401673			C16001416*:g[12743112]ref[XP_010131.2]	2.47 2.83
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	2.46 1.18
	416316	H58721	Hs.271628	ESTs	2.42 3.44
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.40 1.69
75	451149	AL047586		RNA binding motif protein 8B	2.40 1.95
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	2.40 1.61
	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	2.40 2.40
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	2.39 1.27
80	405120			C4001445:g[12697999]dbj[BAB21818.1] (AB	2.38 2.38
	432224	AW189460	Hs.208358	ESTs	2.38 2.00
	418663	AK001100	Hs.41690	desmocollin 3	2.38 2.38
	412622	AW664708	Hs.171959	ESTs	2.37 1.63
85	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.37 1.52
	442767	AL017208	Hs.131149	ESTs	2.36 1.22
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	2.35 1.79
	411800	N39342	Hs.103042	microtubule-associated protein 1B	2.35 1.18
90	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	2.34 2.34
	444009	AJ380792	Hs.135104	ESTs	2.34 2.07
	435143	R12375	Hs.194600	ESTs	2.33 1.68
	402333			Target Exon	2.33 3.15
95	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	2.33 1.10
	454078	AA501518	Hs.22209	secreted modular calcium-binding protein	2.32 1.30
	452242	R50956	Hs.159993	glycosyltransferase	2.32 1.45
	418693	AJ750878	Hs.87409	thrombospondin 1	2.32 2.32
100	428411	AW291464	Hs.10338	ESTs	2.32 1.54
	459702	AJ204995		gb:an03c03.x1 Stratagene schizo brain S1	2.31 1.98
	428839	AJ767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.31 2.49
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.31 1.32

5	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	2.30	2.30
	456536	AW135986	Hs.257859	ESTs	2.28	2.28
	428166	AA423849	Hs.79530	MS-14 protein	2.27	1.88
	456936	M81349	Hs.1955	serum amyloid A4, constitutive	2.25	2.16
	417728	AW138437	Hs.24790	KIAA1573 protein	2.25	1.37
10	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	2.24	2.42
	409159	AW673312	Hs.50848	hypothetical protein FLJ20331	2.24	2.24
	404942			splicing factor, arginine/serine-rich 9	2.24	2.64
	410286	AJ739159	Hs.61898	DKFZP586N2124 protein	2.24	2.46
	440516	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	2.24	1.94
15	421574	AJ000152	Hs.105924	defensin, beta 2	2.23	1.36
	418005	AJ186220	Hs.83164	collagen, type XV, alpha 1	2.22	1.37
	421948	L42583	Hs.334309	keratin 6A	2.20	2.20
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.19	1.61
	417563	AA203701		gb:zx52a10.r1 Soares_fetal_liver_spleen_	2.18	2.40
20	431089	BE041395		ESTs, Weakly similar to unknown protein	2.16	2.46
	447333	BE090580	Hs.70704	hypothetical protein DJ61688.3	2.16	2.00
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.16	1.26
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.16	1.99
	403362			NM_001615*:Homo sapiens actin, gamma 2,	2.16	1.61
25	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	2.15	2.11
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.15	2.24
	402641			C1002296:gi 6677817 ref NP_033126.1 rep	2.14	2.14
	418236	AW994005	Hs.337534	ESTs	2.14	2.14
	413059	BE151498		gb:RCO-HT0295-291199-031-E11 HT0295 Homo	2.14	2.14
30	432437	W07088	Hs.293685	ESTs	2.14	2.14
	428398	AJ249368	Hs.98558	ESTs	2.14	2.14
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.12	1.43
	421853	AL117472	Hs.108924	SH3-domain protein 5 (ponsin)	2.12	1.93
	436391	AJ227892	Hs.146274	ESTs	2.12	2.12
35	417430	AA984546		gb:am88e08.s1 Stratagene schizo brain S1	2.11	2.17
	407443	AF227138		gb:Homo sapiens candidate taste receptor	2.11	2.36
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.10	1.29
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.10	2.10
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	2.10	2.00
40	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.10	1.37
	450271	AI693900	Hs.200920	ESTs	2.09	2.34
	432222	AI204995		gb:am03c03.x1 Stratagene schizo brain S1	2.09	1.40
	458208	AI380016		ESTs, Weakly similar to T4S4_HUMAN TRANS	2.08	2.00
	405600			C12001673:gi 9631264 ref NP_048045.1 or	2.07	1.97
45	434654	AI825942	Hs.139366	Homo sapiens clone L5 polyadenylated HER	2.07	2.52
	439261	AI126020	Hs.145574	basic transcription factor 3	2.05	1.45
	421515	Y11339	Hs.105352	GaINAc alpha-2, 6-sialyltransferase I, I	2.04	2.04
	457741	BE044740		gb:hnm55g10.x1 NCL CGAP_RDF1 Homo sapiens	2.04	2.04
	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	2.02	1.33
50	412505	AA974491	Hs.21734	ESTs	2.02	2.02
	443180	R15875	Hs.258576	claudin 12	2.02	2.02
	431605	AW972407	Hs.124370	gb:EST384498 MAGE resequences, MAGL Homo	2.02	2.02
	416938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	2.02	2.17
	452571	W31518	Hs.34665	ESTs	2.02	2.09
55	405061			Target Exon	2.01	2.52
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	2.01	2.41
	402327			Target Exon	2.00	2.44
	418786	AJ796317	Hs.203594	Homo sapiens uncharacterized gastric pro	2.00	2.00
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.00	2.00
60	438634	AW340400	Hs.126728	ESTs	1.99	2.43
	416127	N49843	Hs.79022	GTP-binding protein overexpressed in ske	1.97	1.41
	423961	D13666	Hs.136348	perforin (OSF-2os)	1.96	1.48
	430397	AI924533	Hs.105607	bicarbonate transporter related protein	1.96	1.31
	411010	AW813339		gb:MR3-ST0192-101299-013-c05 ST0192 Homo	1.96	2.73
65	439828	W81007	Hs.58628	ESTs	1.96	1.28
	444301	AK000136	Hs.10760	asporin (LRR class 1)	1.96	1.58
	431726	NM_015361	Hs.268053	KIAA0029 protein	1.95	1.72
	410418	D31382	Hs.63325	transmembrane protease, serine 4	1.95	1.87
	452814	AI092790	Hs.334703	hypothetical protein FLJ14529	1.95	1.06
70	417562	AW888754	Hs.134126	crystallin, gamma S	1.95	2.14
	424480	AA341442	Hs.205299	ESTs	1.94	1.94
	404342			C7002192*:gi 7299207 gb AAFS4404.1 (AE0	1.92	1.32
	443320	AI051607	Hs.16335	ESTs	1.91	2.18
	449780	AA443241		ribosomal protein L44	1.90	1.76
75	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	1.89	2.16
	434416	AA805903	Hs.59498	cell division cycle 2-like 5 (chollineste	1.89	2.04
	457505	AL044659	Hs.43791	ESTs	1.89	2.34
	425912	AL137629	Hs.162189	serine/threonine kinase with Dbp- and pl	1.88	1.26
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	1.88	1.88
80	428231	U17989	Hs.183105	nuclear autoantigen	1.88	1.88
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	1.88	1.88
	404429			Target Exon	1.88	2.18
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	1.88	3.04
	406641	AJ235667		gb:Homo sapiens mRNA for immunoglobulin	1.86	2.57
	417059	AL037672	Hs.81071	extracellular matrix protein 1	1.86	1.48
	454565	BE141231		gb:MR0-HT0075-081199-003-a09 HT0075 Homo	1.86	1.21
	415115	AA214228	Hs.127751	hypothetical protein	1.85	1.23

	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	1.85	1.45
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	1.84	1.44
	403344			NM_000341:Homo sapiens solute carrier fa	1.84	1.84
	447245	AK001713	Hs.17860	hypothetical protein FLJ10851	1.84	2.33
5	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	1.84	2.02
	401593			Target Exon	1.83	2.34
	434392	AW983709	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	1.83	2.12
	405461			hypothetical protein, clone 24751	1.83	2.01
10	455657	BE065209		gb:RC1-BT0314-310300-015-b12 BT0314 Homo	1.83	1.26
	400609			C10001147:gij12698926[gib]AAK01739.1jAF33	1.82	2.08
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	1.81	1.14
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.81	1.22
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	1.81	2.10
	426521	AF161445	Hs.170219	hypothetical protein	1.81	2.08
15	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.81	1.64
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	1.80	1.34
	439606	W79123	Hs.58561	G protein-coupled receptor 87	1.80	1.80
	459189	AI909090		gb:IL-BT198-010499-007 BT198 Homo sapien	1.80	1.80
	412429	AV650262	Hs.75765	GRO2 oncogene	1.80	2.55
20	402674			Target Exon	1.80	3.41
	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	1.79	1.57
	454824	AW633646		gb:QV4-TT0008-161199-033-d09 TT0008 Homo	1.78	1.94
	401677			BAI1-associated protein 3	1.78	2.28
	426291	U58913	Hs.169191	small inducible cytokine subfamily A [Cy	1.78	1.53
25	430028	BE564110	Hs.227750	Target CAT	1.78	1.59
	445988	BE007663	Hs.13503	inactivation escape 2	1.78	2.10
	452272	AW292249	Hs.252739	hypothetical protein DKFZp434P0316	1.78	2.08
	418205	L21715	Hs.83760	troponin I, skeletal, fast	1.78	2.70
	400425	AY004252	Hs.287385	PR domain containing 12	1.77	2.02
30	400419	AF084545		Target	1.77	2.67
	447169	AI989803	Hs.157289	ESTs	1.77	2.21
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	1.77	2.12
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	1.76	2.54
	432808	NM_015985	Hs.278973	angiotensin-3	1.76	1.76
35	437400	AB011542	Hs.55599	EGF-like-domain, multiple 5	1.75	2.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	1.75	1.47
	444986	AI204197		ESTs	1.75	2.48
	451027	AW519204	Hs.40808	Homo sapiens, Similar to RIKEN cDNA 2810	1.74	1.69
40	413524	BE145837		gb:MR0-HT0208-101299-202-c07 HT0208 Homo	1.74	1.74
	409099	AK000725	Hs.50579	hypothetical protein FLJ20718	1.74	2.26
	405579			C22000151:gij16806921[ref]NP_004165.1j so	1.74	2.12
	405797			CX001015:gij11322384[emb]CAC16687.1j (AJ	1.73	2.66
	405159			ENSP00000243337*:CDNA FLJ13984 fis, clon	1.73	2.01
	450569	AW192334	Hs.38218	ESTs	1.73	2.08
45	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	1.73	1.24
	445261	T79759	Hs.250651	ESTs, Weakly similar to I38022 hypothe	1.73	2.52
	454231	AW450669	Hs.45068	hypothetical protein DKFZp434I143	1.73	1.64
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxicin)	1.72	1.37
	422259	AA307584		gb:EST178498 Colon carcinoma (HCC) cell	1.72	1.72
50	456034	AW450979		gb:U1-H-B13-ata-a-12-0-U1.s1 NC1_CGAP_Su	1.72	1.34
	451862	H09260	Hs.32333	ESTs	1.71	2.16
	403520			Target Exon	1.71	1.39
	456596	AA291834	Hs.78950	branched chain keto acid dehydrogenase E	1.71	2.26
55	426603	AA382291		gb:EST95683 Testis 1 Homo sapiens cDNA 5	1.70	1.70
	418387	R18085	Hs.22279	gb:yg16b12.r1 Soares infant brain 1N1B H	1.70	1.70
	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	1.70	1.87
	402538			C1001634:gij12621136[ref]NP_075245.1j Ba	1.69	1.57
	414844	AA296874	Hs.77494	deoxyguanosine kinase	1.69	2.06
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	1.69	1.63
60	446553	AB021179	Hs.15299	HMBP-inducible	1.68	2.02
	456235	AA203637		gb:zx58b12.r1 Soares fetal_liver_spleen_	1.68	2.12
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	1.68	2.03
	433930	AA620338		ESTs	1.68	2.28
	404151			Target Exon	1.68	1.80
65	429392	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN	1.67	2.18
	430070	AF197927	Hs.231967	ALL1 fused gene from Sq31	1.66	2.16
	400496			ENSP00000224716*:GTP-binding protein SAR	1.66	2.13
	413464	AL121500		ESTs	1.66	2.03
70	411188	BE161168		gb:PMO-HT0425-170100-002-a10 HT0425 Homo	1.66	2.12
	446281	H69416	Hs.14606	hypothetical protein FLJ20271	1.65	2.28
	443282	T47764	Hs.132917	ESTs	1.65	2.04
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.65	1.67
	453355	AW295374	Hs.31412	myopodin	1.65	1.66
	432375	BE538069	Hs.2962	S100 calcium-binding protein P	1.65	1.54
75	437929	T09353	Hs.106642	ESTs, Weakly similar to T09052 hypothe	1.65	2.04
	410295	AA741357		nidogen (enactin)	1.64	2.30
	437767	AA830103	Hs.293331	ESTs	1.64	1.26
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	1.64	3.38
	450795	AW173371	Hs.60435	ESTs	1.64	1.64
80	421847	NM_014717	Hs.108984	KIAA0390 gene product	1.64	2.75
	403010			C21000152:gij6226483[sp]Q52118[YM03_ERWS	1.64	2.03
	406387			Target Exon	1.64	1.78
	440423	AW293995	Hs.192277	ESTs	1.63	2.05

	444381	BE387335	Hs.283713	hypothetical protein BC014245	1.63	2.07
	442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.63	1.65
	442424	AJ342715	Hs.129569	ESTs, Moderately similar to B34087 hypot	1.62	2.40
	402885			Target Exon	1.62	1.18
5	408786	AA773187	Hs.294027	ESTs	1.62	1.59
	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	1.62	1.63
	414684	AW630023	Hs.76893	3-hydroxybutyrate dehydrogenase (heart,	1.62	2.10
	406838	AA827569	Hs.153	ribosomal protein L7	1.61	1.41
10	441600	AA939347	Hs.127223	Homo sapiens cysteine knot protein (ZSIG	1.61	2.32
	420693	NM_001972	Hs.99863	elastase 2, neutrophil	1.60	2.37
	412649	NM_002206	Hs.74369	integrin, alpha 7	1.60	1.23
	432331	W37862	Hs.274368	MSTP032 protein	1.60	1.23
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.60	1.69
	400279			NM_004581*:Homo sapiens Rab geranylgeran	1.60	1.56
15	437865	AJ472305	Hs.19565	ESTs	1.60	2.42
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	1.60	1.29
	442993	BE018682	Hs.166196	ATPase, Class I, type 8B, member 1	1.60	2.11
	410684	AA088500	Hs.170298	ESTs	1.59	1.46
20	433149	BE257672	Hs.42949	hypothetical protein HES6	1.59	2.22
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	1.59	1.41
	426457	AW894667	Hs.22660	chimerin (chimaerin) 1	1.59	1.26
	427654	AA410183	Hs.137475	ESTs	1.59	2.83
	411662	D60541	Hs.285519	Homo sapiens cDNA FLJ11904 fis, clone HE	1.59	2.18
25	440383	AA884208	Hs.30484	ESTs	1.58	2.19
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	1.58	1.58
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.58	1.47
	407857	A1928445	Hs.92254	synaptotagmin-like 2	1.58	1.51
	411573	AB029000	Hs.70823	KIAA1077 protein	1.57	1.29
30	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	1.57	1.17
	428471	X57348	Hs.184510	stratifin	1.57	1.55
	429249	X81479	Hs.2375	egf-like module containing, mucin-like,	1.57	1.19
	407966	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	1.57	2.12
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	1.57	1.05
35	430469	AW603667	Hs.288742	Homo sapiens cDNA: FLJ22712 fis, clone H	1.56	1.56
	445511	AA846512		Homo sapiens cDNA FLJ14459 fis, clone HE	1.55	2.08
	404501			nucleoside phosphorylase	1.55	2.54
	429107	AJ470451	Hs.99075	ESTs	1.55	2.05
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	1.55	1.45
40	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	1.54	2.61
	458091	AF150286		gb:AF150286 Human mRNA from cd34 stem ce	1.54	1.54
	439280	AI125436	Hs.123654	ESTs	1.54	2.06
	428096	AW291771	Hs.42239	Homo sapiens, clone IMAGE:3868989, mRNA,	1.53	1.55
	414221	AW450979		gb:U1-H-B13-ata-a-12-O-ULs1 NCL CGAP_Su	1.53	1.39
45	451712	AA019290	Hs.110489	ESTs	1.53	1.99
	402487			Target Exon	1.53	2.02
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.53	1.29
	452887	AJ702223	Hs.107253	hypothetical protein DKFZp761F241	1.53	1.21
50	410253	T51823		ESTs	1.52	2.03
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	1.52	1.37
	432985	T92363	Hs.178703	ESTs	1.51	1.48
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	1.51	1.15
	429259	AA420450	Hs.292911	Plakophilin	1.51	1.31
55	429289	AI400746	Hs.62187	phosphatidylinositol glycan, class K	1.51	1.19
	441457	AW996651	Hs.43838	ESTs	1.51	2.08
	433365	AF026944	Hs.293797	ESTs	1.51	2.74
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	1.51	1.21
	424386	BE146577	Hs.285132	ESTs	1.50	1.53
60	429655	U48969	Hs.211582	myosin, light polypeptide kinase	1.50	1.29
	442391	AW450544	Hs.220751	ESTs	1.50	1.65
	414341	D80004	Hs.75309	KIAA0182 protein	1.50	2.10
	436222	AI208737	Hs.122810	Homo sapiens cDNA FLJ11489 fis, clone HE	1.50	2.16
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.50	1.50
65	443878	AW292499	Hs.139709	hypothetical protein FLJ12572	1.50	1.37
	430152	AB001325	Hs.234642	aquaporin 3	1.50	1.43
	447752	M73700	Hs.105938	lactotransferrin	1.49	0.91
	404455			opioid receptor, kappa 1	1.49	1.36
	424106	AA412442	Hs.98132	ESTs	1.49	1.30
70	433095	AK001092	Hs.302480	Homo sapiens cDNA FLJ10230 fis, clone HE	1.49	2.02
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	1.48	1.50
	456256	AB000450	Hs.82771	vaccinia related kinase 2	1.48	1.42
	439310	AF086120	Hs.102793	ESTs	1.48	1.48
	407102	AA007629		glycerol-3-phosphate dehydrogenase 1 (so	1.48	1.15
75	437981	AA774445	Hs.145365	ESTs, Weakly similar to KIAA1397 protein	1.48	2.36
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	1.47	1.21
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	1.47	1.25
	453864	AW021407	Hs.21068	hypothetical protein	1.47	2.18
	401067			ENSP00000252105*:cDNA FLJ12240 fis, clon	1.47	1.81
80	456054	BE313241		gb:601151545F1 NIH_MGC_19 Homo sapiens c	1.47	1.99
	402324			C19001982:gl 3043638 dbj BAA25483.1 (AB	1.47	2.03
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	1.47	1.29
	457734	BE394365	Hs.38750	hypothetical protein FLJ11526	1.47	2.26
	402013			Target Exon	1.46	2.42
	429295	AA682377	Hs.99216	ESTs, Moderately similar to ALU8_HUMAN A	1.46	2.09

5	430920	U96402	Hs.248132	goosecoid-like	1.46	2.46
	409368	AA071059		gb:zm66a10.r1 Stratagene neuroepithelium	1.46	2.02
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta)	1.46	1.43
	427719	AI393122	Hs.134726	ESTs	1.46	1.46
	433430	AI863735		ESTs	1.46	1.15
10	423790	BE152393		gb:CM2-HT0323-171199-033-a08 HT0323 Homo	1.46	2.36
	444083	AI123195		gb:oo17a10.x1 Soares NSF_F8_9W_OT_PA_P_S	1.45	2.29
	433256	AW604447	Hs.339408	ESTs, Weakly similar to S26689 hypotheti	1.45	1.50
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	1.45	1.17
	456654	AW963354	Hs.334409	metallothionein 1G	1.45	2.20
15	438158	AI796556	Hs.187884	ESTs	1.45	1.18
	409883	AW452419	Hs.296098	ESTs	1.45	2.00
	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	1.45	1.27
	413048	M93221	Hs.75182	mannose receptor, C type 1	1.45	1.36
	457462	AL133573	Hs.272312	Homo sapiens mRNA: cDNA DKFZp434J2235 (f	1.44	2.08
20	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	1.44	1.28
	401116			Target Exon	1.44	2.19
	419618	AA528295		gb:nh26e06.s1 NCL_CGAP_Pr3 Homo sapiens	1.44	2.30
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	1.44	2.03
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	1.43	1.48
25	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	1.43	1.51
	418742	AW451197	Hs.113418	ESTs	1.43	1.24
	418335	R63267	Hs.28399	ESTs	1.43	1.14
	408404	AW192518		gb:x45h08.x1 NCL_CGAP_Pan1 Homo sapiens	1.43	2.08
	448175	BE296174	Hs.225160	hypothetical protein FLJ13102	1.43	2.29
30	431846	BE019924	Hs.271580	uropod protein 1B	1.43	2.12
	459557	N58315		gb:yv68g06.s1 Soares fetal liver spleen	1.43	2.00
	449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	1.43	1.33
	442321	AF207664	Hs.8230	a disintegrin-like and metalloprotease (1.43	1.10
	454843	AW834536	Hs.268549	gb:MR2-TT0014-241199-012-006 TT0014 Homo	1.43	1.55
35	410281	AF076612	Hs.166186	Homo sapiens clone 23928 mRNA sequence	1.43	1.38
	402998			NM_002463*:Homo sapiens myxovirus (infl	1.42	2.16
	443709	AI082692	Hs.134662	ESTs	1.42	2.22
	435259	AA152106	Hs.4859	cyclin L ania-6a	1.42	2.01
	454407	AW578420	Hs.118843	gb:RC1-CT0249-120100-022-b04 CT0249 Homo	1.42	1.76
40	453359	AA448787	Hs.24872	ESTs	1.42	1.33
	434128	AI138589	Hs.118206	ESTs	1.41	2.06
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	1.41	1.46
	442316	Z75331	Hs.8217	stromal antigen 2	1.41	2.20
	438330	AW450572	Hs.257316	ESTs	1.41	2.02
45	410935	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	1.41	1.33
	455985	BE153524		gb:PMO-HT0339-241199-002-C03 HT0339 Homo	1.41	1.24
	405550			C7001981*:gij565157[gb]AAB31881.1 T-cal	1.41	1.99
	451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	1.40	2.64
	424925	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	1.40	1.26
50	431022	AA490815	Hs.208351	ESTs	1.40	2.72
	439781	AA845538		glial cells missing (Drosophila) homolog	1.40	1.05
	429379	NM_014840	Hs.200598	KIAA0537 gene product	1.40	1.26
	435310	AA705075	Hs.169536	Rhesus blood group-associated glycoprote	1.39	1.18
	430702	U56979	Hs.278568	H factor 1 (complement)	1.39	1.26
55	451331	AK002039		Homo sapiens cDNA FLJ11177 fis, clone PL	1.39	1.22
	459198	AI086347	Hs.151138	ESTs	1.39	1.35
	442344	AI022925	Hs.79368	epithelial membrane protein 1	1.39	1.44
	402917			ENSP00000202587*:Bicarbonate transporter	1.39	2.08
	418211	BE244746	Hs.247474	hypothetical protein FLJ21032	1.38	2.07
60	437158	AW090198		KIAA1150 protein	1.38	1.24
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	1.38	2.15
	433911	AI923092	Hs.8899	ESTs	1.38	1.38
	402504			C1003823*:gij4826521[emb]CAB42853.1 (AL	1.37	2.22
	409465	AW393810	Hs.78054	gb:QV4-TT0006-251099-016-e11 TT0008 Homo	1.37	2.38
65	449426	T92251	Hs.198882	ESTs	1.37	2.74
	405491			Target Exon	1.37	1.34
	406685	M18728		gb:Human nonspecific crossreacting antig	1.37	1.56
	442410	AW996503	Hs.197680	ESTs	1.36	2.02
	407701	AW375009	Hs.164407	ESTs	1.36	2.10
70	400818			Target Exon	1.36	2.78
	406475			C15000508*:gij2558825[gb]AAC53387.1 (AF	1.36	1.41
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	1.36	2.20
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	1.35	0.94
	444195	AB002351	Hs.10587	KIAA0353 protein	1.35	1.22
75	447918	AI129320	Hs.115175	ESTs, Highly similar to JCS818 gamma-act	1.35	1.40
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:418312, mRNA,	1.35	1.24
	412992	AI423369	Hs.75111	protease, serine, 11 (IGF binding)	1.35	1.30
	401025			NM_004055*:Homo sapiens calpain 5 (CAPN5	1.34	2.12
	452862	AW378055	Hs.8687	ADAMTS2 (a disintegrin-like and metallo	1.34	1.02
80	425308	M97639	Hs.155585	receptor tyrosine kinase-like orphan rec	1.34	1.21
	402308			Target Exon	1.34	1.40
	428415	AA337211	Hs.184222	Down syndrome critical region gene 1	1.34	1.22
	407242	M18728		gb:Human nonspecific crossreacting antig	1.34	2.05
	410741	Z11695	Hs.324473	mitogen-activated protein kinase 1	1.34	1.12
	439335	AA742697	Hs.62492	NM_052863*:Homo sapiens secretoglobulin, fa	1.33	1.21
	431254	NM_006069	Hs.251385	murine retrovirus integration site 1 hom	1.33	2.03
	405213			Target Exon	1.33	

5	447990	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy	1.33	1.05
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synthase	1.33	2.09
	453914	NM_000507	Hs.574	fructose-1,6-bisphosphatase 1	1.33	1.32
	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	1.33	1.18
	430385	AA113437		N-myc downstream-regulated gene 3	1.32	1.48
10	447731	AA373527	Hs.19385	CGI-58 protein	1.32	2.22
	400740			hypothetical protein FLJ14280	1.32	2.01
	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	1.32	1.32
	440274	R24595	Hs.7122	scrapie responsive protein 1	1.32	1.32
	406867	AA157857	Hs.182265	keratin 19	1.32	1.42
15	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Drosophila)	1.32	2.30
	443144	BE246335		hypothetical protein MGC14797	1.32	2.03
	432810	AA863400		ESTs	1.32	4.01
	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	1.31	1.24
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	1.31	2.17
20	440099	AL080058	Hs.6909	DNFZP564G202 protein	1.31	1.53
	428957	NM_003881	Hs.194879	WNT1 inducible signaling pathway protein	1.31	1.31
	438874	H02780		gb:Y41a11.1.1 Soares placenta Nb2HP Homo	1.31	2.03
	402825			Target Exon	1.31	1.24
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danlos)	1.31	1.45
25	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	1.31	1.19
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	1.31	1.12
	436027	AB64053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	1.30	2.06
	407409	AF060168		gb:Homo sapiens AS10 protein mRNA, partial	1.30	2.16
	400221			NM_002082: Homo sapiens G protein-coupled	1.30	2.02
30	437751	AA767373		ESTs, Moderately similar to ALU1_HUMAN A	1.30	2.44
	450008	H52970	Hs.36688	WAP four-disulfide core domain 1	1.30	1.19
	441591	AF055992	Hs.183	Duffy blood group	1.29	1.03
	405973			Target Exon	1.29	1.32
	424604	AW865388	Hs.151076	KIAA1243 protein	1.29	0.92
35	410899	AW809716		gb:MR4-ST0124-241199-026-h09 ST0124 Homo	1.29	2.06
	405818			CX001073:gi4176497 emb CAA20116.1 (AL0	1.29	2.05
	402621			Target Exon	1.29	3.06
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	1.28	2.35
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subunit)	1.28	1.44
40	453331	AJ240665		ESTs	1.28	2.36
	439791	H77774	Hs.35755	ESTs	1.28	2.00
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.28	3.00
	407265	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	1.28	1.28
	446526	H89616		Homo sapiens cDNA FLJ13357 (is, clone PL	1.28	1.28
45	455577	BE006341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	1.28	1.28
	418863	AL135743	Hs.25566	ESTs, Weakly similar to 2004399A chromos	1.28	2.10
	407711	AI085846	Hs.25522	KIAA1808 protein	1.28	1.23
	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	1.28	1.19
	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	1.27	1.24
50	418203	X54942	Hs.83758	CDC28 protein kinase 2	1.27	2.08
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	1.27	2.05
	444418	AL034417	Hs.11169	Gene 33/Mig-6	1.27	1.98
	427809	M26380	Hs.180878	lipoprotein lipase	1.27	1.09
	414890	BE410103	Hs.12313	hypothetical protein FLJ14566	1.27	1.36
55	439919	AA970710	Hs.128064	ESTs	1.27	2.28
	401311			Target Exon	1.27	2.05
	444235	AW207346	Hs.143202	ESTs	1.27	2.00
	430858	AF007190		Homo sapiens SIB 297 intestinal mucin (M	1.26	1.23
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 (is, clone NT	1.26	2.40
60	400161			Eos Control	1.26	1.33
	444239	R57988	Hs.10706	epithelial protein lost in neoplasm beta	1.26	1.20
	438369	T77886	Hs.83428	nuclear factor of kappa light polypeptide	1.26	1.26
	441944	AW855861	Hs.8025	Homo sapiens clone 23767 and 23782 mRNA	1.26	1.12
	431142	AA852596	Hs.250641	tropomyosin 4	1.26	1.23
65	434229	R56378	Hs.181223	hypothetical protein PRO2801	1.26	2.04
	406733	AA976565	Hs.297753	vimentin	1.26	1.29
	422292	AJ815733	Hs.114360	transforming growth factor beta-stimulat	1.25	1.16
	424137	AA335769	Hs.16262	ESTs	1.25	1.27
	434868	R50032	Hs.159263	collagen, type VI, alpha 2	1.24	1.50
70	424408	AJ754813	Hs.146428	collagen, type V, alpha 1	1.24	1.29
	433750	H15448	Hs.31330	Homo sapiens clone HQ0319	1.24	1.27
	447299	AF043897	Hs.18075	chromosome 9 open reading frame 3	1.24	1.13
	438357	AJ042101	Hs.294107	ESTs	1.24	2.04
	409959	BE349470		mucin 6, gastric	1.23	2.22
75	439897	NM_015310	Hs.6763	KIAA0942 protein	1.23	2.44
	421982	AF206019	Hs.110347	REV1 (yeast homolog)-like	1.23	2.14
	407207	T03651	Hs.336780	tubulin, beta polypeptide	1.23	1.32
	416956	AA810664	Hs.101660	hypothetical protein MGC5391	1.23	2.39
	413624	BE177019	Hs.75445	SPARC-like 1 (mats, hev)	1.23	1.06
80	442941	AJ076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	1.23	1.51
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.23	1.01
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	1.22	1.41
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.22	1.17
	421341	AJ243212		deleted in malignant brain tumors 1	1.22	1.09
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	1.22	1.52
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 (is, clone L	1.22	2.55
	423189	M59371	Hs.171596	EphA2	1.22	1.15

	401899		Target Exon	1.22	1.22	
	403579		Target Exon	1.22	2.34	
	415954	AA171850	Hs.42251	ESTs	1.22	2.24
5	429171	A1743173	Hs.169095	ESTs, Weakly similar to ARL2_HUMAN ADP-R	1.21	1.14
	444071	A1627808	Hs.110524	ESTs	1.21	2.23
	424344	AF036973	Hs.145477	HCGIN-6 protein	1.21	2.15
	434051	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	1.21	1.25
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.21	1.39
10	404600			Target Exon	1.21	1.29
	429751	M55210	Hs.214982	laminin, gamma 1 (formerly LAMB2)	1.21	1.03
	430392	NM_000627	Hs.241257	latent transforming growth factor beta b	1.21	1.21
	422687	AW068823	Hs.119206	insulin-like growth factor binding prote	1.21	1.23
	424855	AW204725	Hs.25560	ESTs	1.20	1.98
15	418890	AA232134	Hs.190028	ESTs	1.20	1.33
	413232	BE073258	Hs.133988	hypothetical protein FKSG28	1.20	2.18
	414154	AW205314	Hs.323060	ESTs	1.20	1.34
	416784	AA334592	Hs.79914	lumican	1.20	1.27
	410933	C15974		gb:C15974 Clontech human aorta polyA mRN	1.19	2.05
20	415388	AF018081	Hs.78409	collagen, type XVIII, alpha 1	1.19	1.11
	406731	A1559131		gb:tg31g07.x1 NCL_CGAP_UI1 Homo sapiens	1.19	1.19
	447563	BE536115	Hs.160983	EST	1.19	1.14
	405531			Target Exon	1.19	2.02
25	400363	NM_001403		eukaryotic translation elongation factor	1.19	1.21
	426611	BE178050	Hs.171271	catenin (cadherin-associated protein), b	1.19	1.18
	427676	AA394062	Hs.300772	tropomyosin 2 (beta)	1.18	1.16
	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	1.18	1.20
	413856	D13639	Hs.75586	cyclin D2	1.18	1.20
	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	1.18	1.12
30	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	1.18	1.05
	412758	Y07818	Hs.74566	dihydropyrimidinase-like 3(UUP)	1.18	1.06
	446868	AV680737		ESTs	1.18	1.18
	417613	AV654351	Hs.82306	desmin (actin depolymerizing factor)	1.18	1.17
	405542			Target Exon	1.18	1.98
35	419908	AW971327	Hs.293315	ESTs	1.17	2.02
	434095	AA011117	Hs.3745	milk fat globule-EGF factor 8 protein	1.17	1.19
	407230	AA157857	Hs.182265	keratin 19	1.17	1.35
	448413	A1745379	Hs.42911	ESTs	1.17	2.87
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	1.17	1.39
40	424572	M19650	Hs.179600	2',3'-cyclic nucleotide 3' phosphodiester	1.17	2.08
	440109	AK001138	Hs.333149	hypothetical protein FLJ10276	1.17	1.06
	405131			C1002509:gil938010[ref]NP_064684.1[odo	1.17	2.22
	422354	U20982	Hs.1516	insulin-like growth factor-binding prote	1.17	1.19
	442124	R66412	Hs.129013	Homo sapiens cDNA FLJ14309 fis, clone PL	1.17	1.11
45	400080			Eos Control	1.16	2.53
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	1.16	2.00
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	1.16	1.30
	429207	AA447941	Hs.123423	ESTs	1.16	1.27
	415149	X12451	Hs.78056	cathepsin L	1.16	1.12
50	400231			Eos Control	1.16	1.17
	416553	AA768553	Hs.193145	metallothionein 1E (functional)	1.16	1.16
	422813	AV656571	Hs.121068	transmembrane 4 superfamily member 6	1.16	1.10
	439318	AW837046	Hs.6527	G protein-coupled receptor 55	1.16	1.15
	422424	A186431	Hs.296638	prostate differentiation factor	1.16	1.21
55	432745	A1821928		gb:nt178105.x5 NCL_CGAP_Pr3 Homo sapiens	1.15	2.00
	412477	AA150864		microsomal glutathione S-transferase 1	1.15	1.23
	430361	A0333965	Hs.239926	sterol-C4-methyl oxidase-like	1.15	2.31
	424512	X53002	Hs.149846	integrin, beta 5	1.15	1.15
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	1.15	1.24
60	414682	AL021154	Hs.76884	Inhibitor of DNA binding 3, dominant neg	1.15	1.07
	456076	BE243877		ATPase, Na ⁺ transporting, beta 3 polypep	1.15	2.00
	403026			Target Exon	1.15	2.32
	422545	X02761	Hs.287820	fibronectin 1	1.15	1.17
	412719	AW016610	Hs.816	ESTs	1.15	1.05
65	421848	X15880	Hs.108885	collagen, type VI, alpha 1	1.15	1.14
	422087	X58968	Hs.111301	matrix metalloproteinase 2 (gelatinase A	1.15	1.16
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	1.14	1.13
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	1.14	2.07
	430202	T85775		gb:yd60g02.r1 Soares fetal liver spleen	1.14	1.14
70	418806	AA485970	Hs.191718	ESTs	1.14	2.14
	424017	AA333789		gb:EST37925 Embryo, 9 week Homo sapiens	1.14	2.16
	422003	AA361760	Hs.296326	ESTs	1.14	1.17
	437272	AW975957		gb:EST388066 MAGE resequences, MAGN Homo	1.14	2.17
	438367	N79688	Hs.204354	ras homolog gene family, member B	1.14	1.23
75	453152	AK001933	Hs.31945	hypothetical protein FLJ11071	1.13	2.36
	406849	AA454809	Hs.172928	collagen, type I, alpha 1	1.13	1.33
	422110	A1376736	Hs.111779	secreted protein, acidic, cysteine-rich	1.13	1.05
	425335	BE394327	Hs.296267	folistatin-like 1	1.13	1.08
	434795	BE620794	Hs.4147	transferring chain-associating membrane	1.13	1.08
80	417426	NM_002291	Hs.82124	laminin, beta 1	1.13	1.11
	452924	AW580939	Hs.97199	complement component C1q receptor	1.13	1.01
	416379	N38857	Hs.34145	ESTs	1.12	1.12
	421464	AA291553	Hs.190086	ESTs	1.12	2.01
	442420	A024834	Hs.131729	ESTs	1.12	1.15

	405369			NM_005569: Homo sapiens LIM domain knas	1.12	1.99
	421730	AW449808	Hs.334534	glucosamine (N-acetyl)-6-sulfatase [Sanf	1.12	2.08
	405932			C15000305:gi3806122[gb]AAC69198.1] (AF0	1.11	2.01
5	453542	AW836724		Homo sapiens mRNA expressed only in plac	1.11	2.00
	437585	AW976857		ESTs	1.11	2.01
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	1.11	1.05
	449931	AW875786	Hs.25734	ESTs, Weakly similar to BING1 [Hsapiens	1.11	1.03
	407085	Z70759		gb:Hsapiens mitochondrial 16S rRNA gene	1.10	1.12
10	447191	NM_014521	Hs.17667	SH3-domain binding protein 4	1.10	1.04
	406713	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.10	1.07
	432675	AJ791855	Hs.105884	ESTs	1.10	2.30
	432731	R31178	Hs.287820	fibronectin 1	1.09	2.12
	430763	AA485468		DNA fragmentation factor, 45 kD, alpha p	1.09	2.10
15	438855	AW946276	Hs.6441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr	1.09	1.04
	405156			NM_003213*: Homo sapiens TEA domain famil	1.09	2.19
	409031	AA376836		ESTs	1.09	2.22
	422608	AW160644	Hs.118695	potassium voltage-gated channel, subfam	1.09	2.26
	440704	M69241	Hs.162	insulin-like growth factor binding prote	1.09	1.28
	410577	X91911	Hs.64639	glioma pathogenesis-related protein	1.08	2.64
20	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	1.07	1.02
	452219	AA024860	Hs.61224	ESTs	1.07	2.08
	430108	AA465294		ESTs	1.07	2.11
	402174			Target Exon	1.07	2.11
25	416952	AJ767736	Hs.290070	gelsolin (amyloidosis, Finnish type)	1.07	1.00
	410199	AW377424	Hs.205126	Homo sapiens cDNA: FLJ22667 fis, clone H	1.07	1.13
	442670	BE410050	Hs.11859	hypothetical protein FLJ13188	1.07	2.21
	442310	AF033199	Hs.8198	zinc finger protein 204	1.06	2.04
	405536			NM_005805: Homo sapiens 26S proteasome-as	1.06	2.20
30	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	1.06	1.06
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	1.06	1.06
	425371	O49441	Hs.155981	mesothelin	1.06	1.27
	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	1.06	2.37
	406711	N25514	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.06	1.05
35	409407	AW987370	Hs.342655	Homo sapiens cDNA FLJ13289 fis, clone OV	1.05	2.00
	406109			Target Exon	1.05	2.04
	418597	AK001678	Hs.86337	similar to DNA-directed RNA polymerase I	1.05	2.67
	403162			C2000231*:gi3802031[gb]AAF95597.1[AF239	1.05	2.07
40	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	1.05	1.07
	407225	J04617		eukaryotic translation elongation factor	1.05	1.02
	416955	AW889150	Hs.80595	NM_004552*: Homo sapiens NADH dehydrogena	1.05	1.10
	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	1.04	2.12
	410276	AJ554545		angiotensin-2	1.04	1.04
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.04	1.04
45	406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.03	1.05
	406773	AA812424	Hs.76067	heat shock 27kD protein 1	1.03	1.10
	452082	N51905	Hs.125133	hypothetical protein FLJ22501	1.03	2.01
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	1.03	2.24
	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	1.02	1.00
50	408339	R97502	Hs.30443	senb1n/SUMO-specific protease	1.02	2.19
	400247			Eos Control	1.02	2.04
	430030	BE300094	Hs.227751	lectin, galactoside-binding, soluble, 1	1.01	1.01
	442275	AW449467	Hs.54795	ESTs	1.01	1.04
	406786	AW161678	Hs.111334	ferritin, light polypeptide	1.01	1.06
55	439403	BE265745		ESTs, Weakly similar to ALUC_HUMAN!!!!	1.01	2.11
	428043	T92248	Hs.2240	uteroglobin	1.00	1.06
	406722	H27498	Hs.283441	Homo sapiens SNC73 protein (SNC73) mRNA,	1.00	1.02
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.00	2.16
	450724	R55428		gb:Y79b05.r1 Soares breast 2NbHst Homo	1.00	0.99
60	424125	M31669	Hs.1735	Inhibin, beta B (activin AB beta polypep	1.00	1.08
	432077	AL134685		gb:DKFZp547M126_r1 547 (synonym: hibr1)	1.00	2.05
	427687	AW003867	Hs.1570	histamine receptor H1	1.00	1.00
	435256	AF193766	Hs.13872	cytokine-like protein C17	1.00	1.00
	420026	AJ831190	Hs.166676	ESTs	1.00	1.00
65	455128	AW861555	Hs.314372	EST	1.00	1.00
	410685	AA497117	Hs.58893	ESTs, Moderately similar to ALU1_HUMAN A	1.00	1.00
	401404			Target Exon	1.00	1.00
	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	1.00	1.00
70	443458	R05385	Hs.143509	hypothetical protein FLJ21924	1.00	1.00
	452744	AJ267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	1.00	1.00
	418355	L42563	Hs.1165	ATPase, H7 transporting, nongastric, alp	1.00	1.00
	447947	N33033	Hs.270215	ESTs	1.00	1.00
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	1.00	1.00
	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	1.00	1.00
75	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	1.00	1.00
	444963	AJ916973	Hs.213603	ESTs	1.00	1.00
	410934	AW811114		gb:MR2-ST0131-111199-018-a04 ST0131 Homo	1.00	1.00
	442849	R10099	Hs.269805	ESTs	1.00	1.00
	420407	AA814732	Hs.145010	Epipolysaccharide-specific response 5-II	1.00	1.00
80	454500	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	1.00	1.00
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	1.00	1.00
	459045	N69101	Hs.40730	ESTs	1.00	1.00
	455500	AW963582		gb:EST375655 MAGE resequences, MAGH Homo	1.00	1.00
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	1.00	1.00

	429932	AI095005	Hs.21586	ESTs	1.00	1.00
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	1.00	1.00
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-1	1.00	1.00
5	431374	BE258532	Hs.251871	CTP synthase	1.00	1.00
	443162	T49951	Hs.9029	DKFZP434G032 protein	1.00	1.00
	432128	AA127221	Hs.296502	ESTs	0.99	2.33
	451838	AW005866	Hs.193969	ESTs	0.98	3.26
	438414	AA806794	Hs.131511	ESTs	0.97	3.61
	435872	AA701357	Hs.192759	ESTs	0.97	0.96
10	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	0.97	1.08
	424001	W67883	Hs.137476	paternally expressed 10	0.96	2.25
	418869	AW516565	Hs.332520	gb:xx01d05.x1 Soares_NHCEC_cervical_tumo	0.96	2.07
	458659	AW749895	Hs.85226	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	0.94	2.18
	418458	AA332941	Hs.278721	lipase A, lysosomal acid, cholesterol es	0.94	1.31
15	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	0.94	2.12
	432093	H28383		gb:y152c03.r1 Soares breast 3NbHBst Homo	0.94	2.19
	452239	AW379378		protein tyrosine phosphatase, receptor t	0.94	0.79
	403167			Target Exon	0.94	2.06
	402209			Target Exon	0.92	2.04
20	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	0.92	0.74
	424090	X99699	Hs.139262	XIAP associated factor-1	0.91	2.11
	432816	N38913	Hs.221575	ESTs	0.91	2.15
	451779	AW566616	Hs.296234	ESTs, Weakly similar to T31613 hypotheti	0.91	2.14
	406851	AA609784		major histocompatibility complex, class	0.89	1.04
25	427698	AW972594	Hs.335499	ESTs	0.89	0.90
	440006	AK000517	Hs.5844	NALP2 protein; PYRIN-Containing APAF1-li	0.88	2.42
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.87	1.14
	426024	Z43405	Hs.75668	Homo sapiens, Similar to RIKEN cDNA 1700	0.87	2.04
	400986			NM_024085: Homo sapiens hypothetical pro	0.87	2.10
30	430353	AW952337		citrate synthase	0.86	2.28
	404975			uncharacterized hypothalamus protein HTO	0.86	2.50
	406673	M34996	Hs.198253	major histocompatibility complex, class	0.86	1.94
	431323	AW970623		gb:EST382705 MAGE resequences, MAGK Homo	0.80	2.08
	404926			Target Exon	0.79	2.01
35	432297	AW663632	Hs.285625	Homo sapiens mRNA; cDNA DKFZp434A119 (fr	0.77	0.86
	437601	AA761546	Hs.248844	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	2.10
	421568	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	0.76	2.66
	406646	M33600	Hs.308026	major histocompatibility complex, class	0.76	1.09
	442195	NM_001430		endothelial PAS domain protein 1	0.76	2.00
40	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.76	0.78
	413916	N49813	Hs.75615	apolipoprotein C-II	0.73	2.06
	453716	AA037675	Hs.152675	ESTs	0.73	2.10
	437802	AI475995	Hs.122910	ESTs	0.70	2.08
	422282	AF019225	Hs.114309	apolipoprotein L	0.68	2.95
45	410361	BE391804	Hs.62651	guanylate binding protein 1, interferon-	0.54	2.11
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	0.53	0.53

TABLE 34B:

50	Pkey: CAT number: Accession:	Unique Eos probeset identifier number Gene cluster number Genbank accession numbers	
55	Pkey	CAT Number	Accession
	442006	1239046_1	AW975183 AA973583 AI365103 AI699495 AI301787
	420195	28714_1	AK002039 AL117524 AV714494 AW954901 AL045243 BF955185 AU137860 AW880615 AW880496 AA256290 BE767078 N44348 AI886676
			AA455877 N66571 AA999864 AU157344 AI817146 R54821 BE223107 AA455880 AI355752 BF589210 N63487 AI924033 AI923020 AI306145
			AI919421 AI584169 AI250173 AI440227 AA669696 AW244040 AI358104 AI570333 AI418315 N94787 R72348 N94780 BF944396 BF754698
60			AW005707 N98831 BF001047 BF588691 AA318076 AW601474 AW883910 H10056 N63481 BE838574 BF909132 BI084973 BG257295 BG818471
			BE348449 AI420623 AW271213 BE048764 W44682 AI887849 AW903942 AA975919 AA312915 BF948057 R55120 H10110 BI045196 AW880645
	437620	9575_20	AW976930 AW292808 AW451796 BF514112 AI806378 AI658903 AI769457 AW593455 AI625525 AI538551 AI660509 AA761825 AA973287
			AA861483 W73065 AI735361 W60499 W76653 BG959557
	430712	301999_1	AW044647 AI670953 AI656180 AA484715 AI659205 BF923472
65	411880	1139083_1	BE088101 T05990 AW872477
	451149	4941_2	AF231512 AW300273 BG779015 AW510935 AI898816 AA137069 AI748876 AW150861 AI862628 AI805872 AI675382 BE855437 AW044703
			AI677769 AA886718 AI753144 AA626885 AI018092 AI263010 AW026173 BE221138 AA256268 AW571932 AW276137 AI634216 AW256259
			AA977716 AI302589 AA348340 AI720838 AI311733 AA015867 N73713 AL047586 AW840354 AA256196 AW840357 AW840504 T35664 Z36755
			AW954421 AA247424 AI056930 T31380 BI910428 H88489 BG675223 AA443427 BE879501 AA478530 R72977 AA298568 BF792417 AA356982
70			BF922499 BE764808 BE565636 BF903986 BF331881 N42207 BG623760 BG611090 BF735387 BE697757 BE697755 BE718853 N78560 AI984095
			AA137140 AA053711 N59865 AI078134 AA643796 T57803 AA018642 N66799 AI004600 BG896323 BF895104 N73684 N73806 N73811 AW900287
			AA018641
	459702	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
	417563	2243443_1	AA203701 R68895
75	431089	125941_2	BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA521946 AA491826
	455797	1511159_1	BE091833 BE091874 BE091871
	413059	1488711_1	BE063078 BE151503 BE151498
	417430	40161_2	AW872732 AW827432 AA199662 AA610519 R54983
	432222	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
80	458208	45807_4	AI990640 AI380016 BM273298 BM273060
	457741	120741_1	BI017968 BE044740 BI017768 AW827360 BF380597 BI017970 BF746974 BF380582 BF380592 BF908552 BF907924 BF380784 BF380651
			BF380634 BE166581 BE161439 BF908606 BI017961 BE044718 AW827623 BF907758 BI017967 AW827621 AA653908 BI017765 BI017955
			BI017960 BI017798

411010	1066474_1	AW813381 AW816094 AW813357 AW814469 AW813293 AW816099 AW813295 AW813425 AW813331 AW813325 AW813351 AW813427 AW813339
449780	31099_2	BG721806 BG623574 AA367501 BG436403 BG619828 BG570704 BF086115 BF086118 R78932 BG620860 BG571920 BF997723 AA368244 BG620631 BG621967 BG435818 BG620442 BG621518 H12650 BG573175 H61600 R67494 H01715 D78811 BG435953 BF107266 D79043 R67255 H01310 BG570941 BG570693 R21776 AA327133 R32578 R30775 BG570963 T86946 H61601 W86279 BF991104 R21732 BF990905 BG622861 BE929694 A1090290 BE929277 BE929284 AA367783 AA082581 D78639 H78318 N91085 BE929344 D63217 BE929334 H53536 R80360 H54070 C17064 AW962470 R00900 BG619698 BG623946 H94918 BE929345 AA004267 BF957177 BG620685 BF086421 T87029 C17044 H60972 BG573514 AA131924 D78838 BG003560 C18615 W86323 R09737 R02529 AA367502
406641	0_0	AJ235667 AJ235668 AJ235669 AJ235670
454565	1061836_1	BE141160 BE141231 BE141793 BE141791 BE141167 BE141807 BE141806 BE141805 AW807591 AW807590 AW807586 AW807583 BE141803 AW845918 BE141207 BE141158
455657	1490185_1	BE065209 BE065364 BE065110 BE065111
459189	MH1945_5	AV683451 AK057494 BG718853 BM152866 BG390826 BE709644 A1864727 B1045181 B1459637 A1909102 A1909090 BG722507 B1023834
454824	1073655_1	AW833783 AW833646 AW833525 AW833351 AW833526 AW833825
444986	704733_1	AW268472 A1204197 AW592537
413524	1518859_1	BE145894 BE145837 BM263472
422259	140437_1	BF821471 AW785791 BF844843 BF821371 AA307584 AW795790 BF833724 BE154067 BE084709
456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
426603	1299162_1	AA994657 AA382291
456235	1979764_1	AA203637 AA832266 H67452
433330	19851_15	AW873618 AA620338
411464	415532_1	AL527514 A1732432 AA133309 A1225224 AV700997 BF589361 AW291763 AL121500 AA129708
411188	1072487_1	AW821260 BE162466 BE161168
410295	2817_1	BG402852 BG545066 AA150252 AL036760 AA452480 A1033256 W68776 W93372 N31248 A1052219 A1367635 W69374 N88610 R58194 B1524854 B1497111 BF940043 A1129268 A1359798 A1056480 AA121421 A1042150 AW449003 A1418180 A1419420 A1356058 BF832243 A1349330 A1359448 W76647 BF477170 A1099163 BF994549 AW608256 AA045418 H03770 AL574791 AW069455 BE302148 AW022281 AW960273 AA121268 A1336371 A1989381 A131425 A1147483 A1311537 AW338638 A1141649 AA709414 A1817177 AA780884 A1333805 AA045312 A1623918 A1349421 W63753 W70299 AA557276 AA299007 N98212 W74064 N24823 T54892 AA054724 W73059 A1869152 N93462 N71889 A1537432 R71628 AA303089 A1498550 T60941 AV706417 AW067848 A1150677 AW338118 A1336313 AA826256 A1139518 AA662948 AA902723 A1970175 W68682 A1089380 A1148372 H99951 AW183001 A1270317 AA532767 AA044727 AA931652 R82469 AA150261 W67788 H67495 R80715 AW149812 N78914 A1862034 W61122 AW023118 W69375 T88917 T47984 N21531 R35646 AA055544 H15534 AA688295 AA090586 AA044764 BF994641 R79547 N21313 BF674610 H02874 AW975323 R16904 AA328030 AA054671 R79546 BF832310 A1249109 Y08200 NM_004581 BC003093 BE733834 B1753321 BG773890 BF091906 B1917541 A1023762 AA587230 BF435086 A1264262 A1687392 A1810536 AW588866 A1244419 A749261 AA535435 AW205689 A1765770 A1765431 C02465 AW305347 A1818456 AA322111 AW381845 AW381829 AV749407 AA811636 AU159893 AA603065 AA652542 A1468678 RA9616 AW381863 BE389867 BE182387 BF087771 AA527551 AA134051 AA831504 AA134052 A1871759 AW089048 B1913532 AA367709 BG828155 BF093014 BM471219 BE093160 BG171761 B1254009 A1905474 AA453162 AA829759 A1086559 AA776022 A1377446 BF589018 AA452822 AW614566 AA443880 AA476733 AW970674 A1393291 AA988283 A1905528 AW384956 D78656 AF150286 AV739062 AA835857 AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945 AA774785 AA584875 AA577705 AA683178 AA083204 AW362057 T82332 T51823 T02858 AA083375 T92381 AW945170 BF930905 F33652 BG057818 A1368018 A1421485 A1300352 A1378525 A1264177 A1276281 A1245302 A1281050 A190036 AW451438 AW242903 A910870 F22289 F19647 F22375 F22376 F22377 F22378 BF445785 AA774528 F33447 C01077 AW772227 F17769 H42812 R09701 AA349096 R48772 H42892 H42537 R47898 N28263 H25721 F32386 H43971 R48205 F21390 H45809 AA007629 R47897 R83734 H45844 AW983653 H43970 H42538 H24495 R48875 H42961 H22079 R86018 BF314481 BE313241 B1196333 BE383148 AA071059 AA085201 AA085020 AA961586 A1863735 AA588325 BE152393 AA330984 BE073904 BF176271 B1836699 A1123195 BG168298 AA247945 AA528295 AW971284 BF308896 BE298629 BE298765 AW192518 BE299614 BE300025 BF307463 BG623239 N58315 A1524952 BE153524 BE153576 BE153583 AA019761 AA017658 AA017374 AA845538 AA890229 AK002039 A117524 AV714494 AW954901 AL045243 BF955185 AU137860 AW880615 AW880496 AA256290 BE767078 N44348 A1866676 AA455877 N66571 AA999864 AU157344 A1817146 R54821 BE223107 AA455880 A1355752 BF589210 N63487 A1924033 A1923020 A1308145 A1919421 A1584169 A1250173 A1440227 AA669696 AW244040 A1358104 A1570333 A1418315 N94787 R72348 N94780 BF944396 BF754698 AW005707 N98831 BF001047 BF588691 AA318076 AW601474 AW883910 H10056 N63481 BE839574 BF909132 B1084973 BG257295 BG818471 BE348449 A1420623 AW271213 BE048764 W44682 A1887849 AW903942 AA975919 AA312915 BF948057 R55120 H10110 B1045196 AW880645 AL050068 AA160485 AW173544 AW296506 AW439880 A1521563 A1702529 A1393606 A1713823 AA570109 H18504 BM021968 BF063327 BF593552 AA630766 A1597717 A1807128 AA523012 A1356250 AW451857 AA974203 A1762577 BF512552 AW007307 BE675286 AW450602 AA962057 AW516069 A1582546 BF221924 BF222543 A1801808 AW468599 AW000736 A1866625 AW235356 BM021837 AA911956 A1680606 W85516 T03370 AW611634 A141653 A1468349 H19588 AW090198 AW043993 R39847 M18728 NM_032013 AB044943 AF308609 B1769254 A1819262 AA845639 A1289073 BE670187 AA207127 T33098 AA633492 BE328324 A1083620 A1204945 AA903471 A1372602 A1049836 A1049737 BF000101 A1866167 BF435896 A1659189 T32971 AA311302 AW733149 A1435981 T03438 AA879206 A1972177 T33083 AA613910 A1971019 A1027140 AA853739 A1620528 A1637519 A1972307 BF054681 AK027665 BF082751 A1598127 T33663 AA204743 BE086660 F12132 T26372 BF765338 AA323106 AA322907 B1037062 BE315235 AV722868 BE254381 T66212 BE566142 T09034 AA406202 BF843940 A1743855 AA113358 BG990683 BE086729 BE535539 AB058726 A1651414 BE245990 BE245765 BF439734 AA648422 AA040639 A1340155 AA255928 AA278365 BE766296 AA280771 AL555562 A1474638 A1863068 B1260946 AK027039 BG615852 A1698039 AA252016 AA258886 BE905205 AW501167 BF514117 B1857400 AW297001 A1624923 A1125900 AW272165 AA1190967 AA280729 AA035532 AW129692 AA125899 BG528645 BE614599 BE464693 A1560128 AA551511 A1351149 AL555561 BG292389 C06094 A1668930 A1045434 AA310513 AA830127 AW134897 AA046953 AW965490 A1810530 BF092924 AA334151 AA334725 D31302 R20723 AA263003 B1824635 A1276287 A1684428 A1524234 A1335035 AW014704 A1911443 AA972102 A1367512 A1126670 AW016017 A1268003 A1147163 AA626033 A1539156 AA555542 A1094253 AW512612 BE889628 AA744752 BE646308 AW471324 AA999975 AA863400 H17550 A1991439 R46187 BE929954 AA333976 D63102 BF744491 AF075017 R66779 R22463 M02780 NM_002082 L16862 BG828886 BE795217 BE904064 BE294526 BE297283 BE394617 BE935127 BE935106 F12351 BG823182 H16710 AW978796 AA767373 AW173343 AA863163 N27563 AA905328 R97032

410899	1063474_1	BF374577 AW809840 AW809996 AW809798 AW809695 AW809646 AW809738 BF374582 AW809716 AW809826 AW809802 AW809747
453331	16559_1	AW810152 BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999
5		T49904 R75732 B1057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190933 H01642 BF510304 AA626915 AA746952 A1161014 AA095554 BG572534 A1803329 A1809932 A1808765 AA411449 A1378760 AA976929 A1378620 AA909584 R75632 A1360919 A1350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 A1240665 BF989591 B1056086 BG001590 BF107035 AK023419 BE464935 BE221668 A1148885 B1859909 A1374780 AA766892 A1347967 A1582917 AA477117 AA229236 AA652637 AA636109 AU134580 F21298 BF802607 BE769124 AV658891 H89616 AV659853 BE008307 BE006341 BE006311 AF007190 AW820705 BE168488 AF007192 BF753303 BG978971 BG978568 U44839 NM_004651 BC000350 A158316 AU117940 BG759024 BG749694 BE799505 BG831537 A1816335 AA325352 A1547005 AW157038 A1859331 A1816186 AU150786 AL043549 AW162880 AU159233 A143169 T03478 BE727648 AA764725 BE206603 A1369814 A1984369 AW157545 BE221486 H99016 AU159025 A1074496 A1494516 BE245950 AA704385 AA280862 A1479595 A1369776 BE671398 T05538 AA682249 B1677303 BE645335 A1359434 H92868 D52599 D53609 D54715 T06015 BE222174 A1954706 D53218 D53787 R68889 W68896 A1497670 R70771 BF309414 BE620147 BG910697 AW964958 BE836120 AL579715 H56512 D55956 B1044097 AL555239 BF220278 AA081891 A1819544 AW001573 AW131600 A1858764 D52367 W22034 BG818979 BG024561 BE702779 B1458863 B1910399 BG707755 BF348284 H10055 B1086315 BE620574 H41088 BG119517 W23267 W21941 AA328817 AW513804 BE179199 BE179195 BE179198 BE179204 BE162586 NM_007329 AF159456 AJ243212 AJ297935 AA295769 NM_017579 AJ243224 A1492875 A1796676 A1749838 AA918144 A1814590 A1923531 BF513992 A1720725 A1150879 A1279072 AW612904 A1921004 A1284510 A1141231 A613554 AW662148 AW769047 AA565885 AW612888 AU100513 BG955586 BG955588 AA295763 BE829414 BF706645 BG954398 AA295332 AA295795 BE932867 AW769569 T89953 BE934311 AF116622 A1114507 AA640834 BF111602 AA377959 C16024 C15974 AW811056 AW811052 AW811020 A1559131 AK074473 BC017997 B1831060 BF971101 A1886394 A1082824 AV708785 W86073 W07772 AV660737 A1816793 R52250 BG183529 AA633473 A191256 RA4763 R19947 BF571346 W86257 BC013310 AF261085 BC004109 AY007133 BC008081 BC001601 NM_002046 M33197 BC020308 J02642 M36184 BE794233 AV721080 BE255459 BG926429 BG389312 BG477333 A10331799 BF763443 B1260432 AA989106 AV728576 B1091380 AA402499 A1200513 A1284734 A1223995 A1289749 BG263291 BM013814 AW438544 BM450203 F35345 F33262 BE890852 AA401181 BG939668 F35525 B1088182 F34674 F33506 BM471326 F34677 AW276712 AA187508 F34866 AA114245 AA522581 N23935 A1076923 A1018505 BE879774 BM465637 A1733078 BG222159 AA595947 BF970917 B1094125 AA719841 BE893087 BG775178 BE793983 BE797071 BF339134 BE409272 BE266456 BE796770 BE745957 BG755835 BE266758 BE259342 BM450181 BG748174 BE298322 BM423587 BM467637 BM452667 BM479516 BM452420 BE273297 BM466364 BM450640 BM478743 BM459094 BM455306 BM472001 BM478247 BM478771 BM480379 BM459071 BM450106 BM467584 BM464548 BM465044 BM450176 BF563599 BM462924 BM455329 BM471815 B1862301 BG331736 H04903 AA374894 BE902964 AA658826 A1821926 A1791191 AA635129 AA564492 A1220117 A1857837 A1218371 BM091400 A1304964 A1198508 A1400738 AW571549 AW950042 A1089943 AA437280 AU150878 BF197070 A1267984 BF594181 BF196688 A1433152 A138921 A1620364 A1280197 AA652531 A1674938 A1342447 A1620350 A1281295 A1148621 N54787 A1338121 A1281153 N51899 A1087072 AA954788 AW069054 A1346309 BG529629 A1340135 BF083036 A1167365 AW819557 AA935468 A1467868 AW148701 A1383720 BE047685 AW015498 AA937149 AA708346 AW771478 AW802508 H53334 AW389204 AW798230 A1553922 A1560688 AW950043 A1961682 AV706506 R01853 AA126514 N62757 A1536893 A1926052 A1418720 N99964 A1568933 A1915737 A1080691 A1185358 N48996 N68575 H82824 H60037 A1247247 T95684 BF593863 A1749537 AW088541 AA991294 AA887452 A1037326 AA633132 AA629674 AA629649 AA629656 AA578595 A168758 AA804572 A1085786 AA994396 AA991209 AA948563 AA929054 AA927852 T87001 AA928210 AA629296 AW802267 AW384129 BF744400 AA194110 A1382839 AA194837 AA406284 A1250750 R37035 A1525586 W01244 BG210376 BG217800 BE925778 W39114 BG682395 N70644 BE709097 AW275615 BC001469 A1564888 A1088126 AW003852 BF792438 AA161295 AW970131 A1127310 AW029307 AW192534 AA843144 AW606235 BE221641 AW008111 AA224203 AA604507 AW794761 AA134005 AA126850 N99165 AW769391 AW818302 A1269871 BE503027 AW401627 AA486231 AA486417 AA191542 AA028128 AA159991 A1498090 A1241024 BM145449 AA774661 A1262021 C18261 BE185811 AA291517 N38896 N59222 A1245611 AA169207 A1298572 AA169585 A1131139 A157960 A1439983 A1208276 A936061 W67305 AW337587 A1357055 W04739 A1214517 AA617789 AW241277 A1088023 A1582789 A143996 BE814848 N49964 A193622 A1817819 F09976 AA039349 AW805002 T35117 N94388 A1699530 AW384573 AW384555 AW384539 AW384473 A129709 AW384466 BG194342 BG204579 BG027536 AL578075 AA399553 AW794949 T88866 AW511211 R26588 R36111 BG170598 BE937009 BG678833 AA862899 H96612 H02273 A1768487 BF211173 N32570 AA088287 R68451 AA297563 H16847 R06665 AA421891 W69402 R28379 R64119 R70109 R77661 R67963 BG701844 H68670 AA169664 AA114111 BE715243 R69317 BE715252 BE713804 BG336586 NM_001679 BC011835 U51478 BM463117 AU119746 B1462090 B1227086 BG706303 BF059073 BG706532 B1544716 A1568735 BE858747 AU122881 AU126210 A1186547 AU134705 BE281323 A1147220 BE263820 AW973937 BG281863 BE858367 BE278941 A1262814 A1001194 A1391616 A1200862 N32564 A1161064 A1089818 BF514359 A1370916 A1341797 BE263168 A1218415 A131098 A1285310 A1928440 A1066642 A1375442 AW028327 A1217792 A1161020 A1342854 A1221544 A1304700 A1343005 BM148839 AA831536 AW074258 BF940589 A1149876 A1914574 AA298442 A1241343 AA668985 AW272172 A1160537 BG209220 AA028152 AA025989 AW968345 AA468998 T85775 AW966107 AA334317 AA333789 AB075828 BG107783 AW021313 B1492345 AW385707 AW580860 AW296117 BE072066 AW580775 BF679498 AW580828 BE003666 BE003672 AW580851 AW580908 B1037146 AW580894 AW580864 H17858 N50343 N54223 F05579 F07386 F05578 AA773248 AA354359 AA330257 C20685 BE548300 AW588728 AW968554 AA777644 AA706896 AA682517 AA832267 BF165087 N51087 N51567 R95837 B1256603 W89042 R95836 R97364 AW975957 AA747943 AA811289 BF568186 BF899745 AW835724 BE243668 AW976857 A1809001 AA769369 AW102732 AA761235 AL578301 A1337389 A1671302 AA978185 BF591738 A1765912 BF036043 AW190446 BG194731 AW682036 AA45021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 A1270167 A1857345 AA937302 AW818444 BE929780 BG498678 BF155010 B1598271 B1599811 BE161728 AW578737 AW763711 AW379707 AW381918 BG506608 AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 A1018009 N42850 AW573242 A1417258 AA463483 A1676131 A1167170 AA836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW474332 B1043239 AW474342 BG708553 AW362423 BF090028 BE827258 R16550 R39478 R39479 R4368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AW966405 AW994425 D81879 BE093545 AW901107 AA383529 B1021552 R56420 N39976 AA573281 H82595 AA234955 BE093539 AW367006 BF358697 BF366318 AA663856 BE702099 BF035869 A1267384 A1267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53704 AW954476 AW954472 AA376836 AV724531 D53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 A118798 BM128728 AA193411 AW444709 AW952455 A1887612 BF431948 B1496876 A1264159 BM128481 A1624657 A1689301 A1969467 AA861685 AA251595 AA625761 AA872090 A1826790 AA328366 BE827416 R75951 D56918 R68122 BE827384 A118797 A1184164 A1164411 B1495332 BE858113 A1863860 H00660 T69849 AW780389 C14667 BE934995 B1018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302 AA928810 AW968393 AA465294 AA811301 AA083514 A1554545 AW169852 A1363822 A1633826 A1656026 A1765624 AA147545 AA147552 BC022339 BC009610 BC010537 X79805 NM_006713 U12979 BM467814 BM450743 AU132951 AU137129 BG493425 AV758819 BG708412 BG705885 BG702217 AV716638 BG777009 B1545689 B1552153 BM476712 BG770858 BG527656 BG528277 BG391388 AV716861 B1602926
430108	1233254_1	
410276	641443_1	
400247	2764_1	

5				BG290073 BI667399 BM451469 BI667173 BI602139 BG532171 BI669216 BI544727 BG721852 AV716503 AV701327 BM090738 BI492000 AI308856 BI544904 AL599813 AV715829 AV716505 AV714587 AV717902 BF668072 AV716385 BI461927 BM090954 AV717826 BG503676 AV647719 BG501392 BG428433 BE895629 BM313117 AW021050 BG435032 BM152910 AA313503 AA872377 BG574714 AV712054 AV732696 AA252476 AV712759 AL599643 BE790872 BG654930 W73337 AW675377 AV760378 AV725139 AV716379 AA887165 BEB30003 AW023796 AL599291 AI902948 BG944042 F00781 AA352483 BG217897 N33888 AW581924 BG654730 D31410 AA353088 D31288 AA295029 H95170 BE935104 AU139980 BG772963 BG776470 BG532512 BG105449 BI545421 AV715456 AW386083 BG659714 AL535832 AL514940 BG190861 BG210593 AW999254 H95138 AA353863 BE764809 N50375 BE091363 BG701255 BI860846 BI832485 BG168150 BG028647 BE546301 BG900321 BI909737 BG702363 BG614141 BG611137 BG700121 BF031492 N85802 AV715940 N51590 BG993478 BE172016 AW893622 AK056692 AF086220 AI375066 AA284293 W32566 AW797961 AA960897 AA504145 BF060834 BI019048 AW862002 AK056737 AA429538 AW063311 AW440655 AW231970 AA428584 AA995028 AW854593 AA984131 AA552874 AA564758 AA528743 BG927275 BE045117 AW975234 AA664937 BF749390 BG928948 AA984546 BE009153 AV732487 BE078167 AW872716 AW063245 AA578441 AI820704 AI732283 R55428 BF999154 BF880485 AL134685 AW972760 AA525319 AA526644 AA525342 AA526632 AA525296 AV739423 AW972755 BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360 AW852530 AW852526 AW852527 AL597969 AW811114 AW811095 AW811094 AW811124 AW811157 AW811054 AW811087 AW810001 BF374633 AW809694 AW809672 BF374748 BF374562 AW810209 AW810092 AW809786 AW810428 AW810429 AW809884 BF374650 BF374641 BF374764 BF374744 AW810552 BF374678 BF374653 BF374579 AW810168 AW810170 BF374611 BF374676 BF374667 AW810353 BF374682 AW810154 BF374688 BF374565 BF374757 BF374637 BF374743 BF374719 AW809664 BF374643 BF374680 BF374714 BF374708 BF374716 AW810432 BF374691 BF358066 AW810006 AW810345 AW809960 AW963582 BE064192 BE064169 BE152580 AW963587 AV704306 BF368780 AW867826 AW855986 AA229762 AA230035 AW972670 AA525808 H28359 H28383 BG034853 AW173315 AW303375 BG190225 BG939153 BF057308 AA600738 AI751258 AI090486 BE939504 AW631492 AI768270 AI862133 AA417652 BE378218 AA599207 AW794702 AA024968 AA446024 AI148235 AI191710 BI493797 AI272646 BI493796 AA634323 AI754332 AA258414 C05155 AI218226 AI039656 AI350380 AI084698 AI764989 AI673545 AI432010 AI751035 AA375571 AA446297 BG216743 AA609784 R97304 BG010106 AL560652 AU133296 AU133086 BE268567 BE268523 BI544879 BE398161 BG473088 BI544445 BE258021 BE296339 BE255040 BE263020 BG706790 AL598627 AW952337 BG758113 AW512753 BE267666 BE253415 BI225718 BE268350 BE258245 BI224965 AW772605 BG723903 BE397282 BI196341 BG702880 AI878949 AL600437 AA416759 BE259917 AI031582 BF512142 AI088248 BE560328 AI802623 AI288613 AL597585 AW768553 AI816352 BF732831 BI225687 AA833686 AA722593 AA807750 AW068064 AA405187 AI923238 N51593 AL527710 BG282576 AL525927 AL525971 BI869547 AI064725 R91856 H46814 H20112 W01682 AW848870 AW848585 AW376662 AW848985 AW848937 AW848862 AW848581 AW848512 AW848176 AW752623 AW752618 AW376822 AW376821 AW376684 AW376623 AW376622 BE706047 AW752602 AW752691 AW752674 AW752652 AA379167 AW752610 AW752684 AW752613 AW752660 AW848709 AW848576 AW849155 AW848981 AW848980 AW848979 AW848978 AW848973 AW848916 AW848713 AW848708 AW848642 AW848641 AW848539 AW848573 AW848493 AW848492 AW848489 AW848488 AW848487 AW848353 AW848352 AW848220 AW752698 AW752697 AW752682 AW752681 AW752680 AW752679 AW752664 AW752651 AW752638 AW752637 AW752636 AW752628 AW752626 AW752624 AW752619 AW752596 AW752608 AL582019 BE875587 AL529175 AW965868 BG686208 AA259073 BE696973 AA459543 AA358314 W40564 BF926427 AW849000 AW848718 AW848515 AW848507 AW848444 AW848440 AW848232 AW848222 AW752657 AW376786 AW376781 AW376615 AW376614 BI752581 AA534520 AI748906 AAD47799 AI014753 AL514460 AL581982 BG743146 W24171 H20102 H11227 AW752607 AW006596 AW130378 BE716519 AW752661 AW848289 BF349557 AW752612 AW752632 AW848910 NM_004077 AF047042 AL560606 BI765896 BI196831 BI855656 BE906674 BG749937 BE535486 BE019810 AA313713 AA992542 AA332541 AA682985 AA356125 BE140478 BG750945 BI457548 BG025661 BF325302 AA325019 BG980676 AA337465 AA321974 BG949285 BG427585 R23979 BG611485 BE560678 W16977 N50379 BG824101 BG471750 BI463171 W04691 AU099360 BG471590 BM011999 BE262945 BE555801 BF756438 BE881957 BE314546 BG911831 BG150811 BG112017 AA157518 T92368 AW752620 AW970623 AA502839 AA502819 U81984 NM_001430 BE907085 BI333232 AI021986 AU138476 C18601 U51626 AU100517 BI054387 AU076970 BE786454 BG010080 AW377189 BF998789 AA368139 R11396 T83613 BG006324 BI012404 BG001643 BF757957 AL549361 AL544018 BE002870 BE929314 BE090199 AL046650 BI053717 BE929315 BI054967 BF960055 BF925432 R05421 BF922073 T70331 BI004403
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TABLE 34C:

55	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
60	NL_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	NL_position
	405443	7408143	Plus	90716-90887,101420-101577
	401645	7657839	Minus	34986-35133
	401673	7689903	Minus	122587-122705,122765-123047
65	405120	8099940	Plus	140176-140340
	401785	7249190	Minus	185776-165996,166189-166314,166408-16656
	402333	8844110	Minus	165693-165856
	404942	7382153	Plus	92095-92252
	403362	8571772	Plus	64099-64260
70	402641	9958129	Minus	122596-125136
	405600	5923640	Plus	26662-27225
	405081	7656744	Minus	132492-132932
	402327	7656695	Minus	108675-108770,109801-109910
	404342	9838093	Plus	115854-116033
75	404429	7407979	Plus	31352-31498
	403344	6697726	Plus	70823-70990
	401593	7230957	Plus	10368-10572,11293-12356
	406461	9756020	Minus	158842-159136
	400609	9887671	Minus	92037-92247
80	402674	8077108	Minus	39290-39502
	401677	9965537	Minus	62856-63086,63603-63884
	405579	6456174	Plus	100996-101542
	405797	1934909	Minus	5599-5681,5821-6104

5	405159	9966252	Plus	79659-79804
	403520	7684483	Minus	97621-98084
	402538	9801137	Minus	96314-96539
	404151	7534014	Minus	69038-69399
	400496	9743564	Plus	41515-41695
	403010	3132346	Plus	78385-79052
	405387	9256180	Plus	116229-116371,117512-117651
	402885	9926751	Plus	71919-72049
10	404501	7229859	Minus	37270-37526
	402487	9797538	Plus	75677-75843
	404455	7677926	Minus	26927-27611
	401067	5764724	Minus	153366-153509
	402324	7630361	Plus	26052-26803
15	402013	7407997	Plus	174540-174634,175449-175568
	401116	9966569	Plus	123579-124447
	402998	2996643	Minus	17175-17373
	405550	1552494	Plus	91720-92115
	402917	7406502	Minus	1034-1177,3143-3266
20	402504	9797871	Plus	12366-12614
	405491	5801645	Plus	81857-82045
	400818	8569994	Plus	172644-172765,173085-173200
	406475	9797684	Plus	125417-125563,128052-128180
	401025	8117518	Minus	179287-179483,181044-181166,181844-18203
25	402308	7340295	Minus	92080-93638
	405213	6692345	Minus	50267-51151
	400740	7329267	Minus	79920-80510,80576-80746
	402825	6165330	Minus	78572-78807
	405973	8247789	Plus	103859-104254
30	405818	4071056	Plus	29055-29196
	402621	9930950	Plus	130806-131036
	401311	9212516	Minus	180124-180754
	401899	7230209	Minus	155620-155815
	403579	8101179	Minus	36167-36365
35	404500	8705107	Plus	118354-118444,118649-118792
	405531	9665194	Plus	35602-35803
	405542	9857564	Plus	71331-72183
	405131	8516051	Minus	136764-137594
	403026	7670575	Plus	56521-56840
40	405369	2078469	Minus	34183-34357,35686-35751
	405932	7767812	Minus	123525-123713
	405156	9966228	Plus	146733-146860,147899-147961,153127-15325
	402174	8575912	Plus	253499-253674
	405536	9795661	Plus	164091-164162,164397-164516,166720-16679
45	406109	9127147	Minus	58328-58485
	403162	9838085	Plus	82652-83613
	401404	7710968	Plus	136474-136646
	403167	9838127	Plus	162599-162935
	402209	8576119	Minus	53315-53472
50	400986	8085497	Minus	63140-63319
	404975	3419864	Minus	86096-86605
	404926	7341919	Minus	150411-151484

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TABLE 35A: About 323 genes upregulated in hypersensitivity pneumonitis relative to idiopathic pulmonary fibrosis or non-specific interstitial pneumonitis

60	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UnigeneID:	Unigene number				
	Unigene Title:	Unigene gene title				
	R1:	90th percentile of HP AIs divided by 90th percentile of IPF AIs, where 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator. The minimum value for the numerator and denominator was set to 50.				
65	R2:	90th percentile of HP AIs divided by the median of IPF AIs, where the minimum value for the numerator and denominator was set to 50.				
	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
70	402550			Target Exon	4.03	4.70
	421563	NM_006433	Hs.105806	granulysin	3.37	2.70
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	3.31	2.42
	417967	BE244373	Hs.11119	nuclear receptor subfamily 4, group A, m	3.09	1.51
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	2.99	1.28
75	416350	AF188625	Hs.189507	phospholipase A2, group IID	2.71	1.43
	406654	M90686	Hs.73885	HLA-G histocompatibility antigen, class	2.70	1.53
	459705	BE082764	Hs.270252	ESTs, Weakly similar to androgen recepto	2.70	1.14
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	2.69	2.99
	452194	AI694413		olfactory receptor, family 2, subfamily	2.63	2.67
80	447709	U97145	Hs.19317	GDNF family receptor alpha 2	2.63	1.52
	410910	AW810204		gb:MR4-ST0125-021199-017-d08 ST0125 Homo	2.59	1.00
	454671	AW812929	Hs.336908	ESTs	2.50	2.34
	441859	AW194364	Hs.94814	Interleukin-4 induced gene-1 protein (FI	2.45	1.90
	422398	AI476149	Hs.334469	hypothetical protein FLJ21992	2.45	1.36
	403244			C2002870-gj[82698]pir[juQ0985 hydroxypr	2.40	1.53

	415462	R52692	Hs.12698	ESTs	2.40	1.00
	447028	AI973128	Hs.167257	brain link protein-1	2.33	1.64
	412394	AW984150		gb:PM2-HN0008-170300-001-h09 HN0008 Homo	2.32	1.00
5	450165	AA007235	Hs.63931	ESTs	2.32	1.32
	431093	AB031038	Hs.301704	eomesodemin (Xenopus laevis) homolog	2.30	1.81
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	2.28	1.69
	413682	BE156991		gb:RC3-HT0371-290100-013-e02 HT0371 Homo	2.27	1.59
	441320	AI768724		fibulin 1	2.27	1.87
10	456766	R87310	Hs.7740	oxysterol binding protein-like 1	2.27	1.36
	420340	NM_000734	Hs.97087	CD32 antigen, zeta polypeptide (TIT3 com	2.26	1.98
	459721	AI299050	Hs.143835	gb:qn14d12.x1 NCI_CGAP_Lu5 Homo sapiens	2.25	1.82
	405452			Target Exon	2.25	1.29
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	2.25	5.80
	401447			Target Exon	2.25	1.55
15	423066	Y18264	Hs.123094	sal (Drosophila)-like 1	2.24	1.51
	441704	AI458766	Hs.192125	ESTs	2.24	1.00
	405097			ENSP00000175238*:A disintegrin and metal	2.24	1.00
	408544	AW293825		ESTs	2.22	1.95
20	413454	BE141162		gb:MR0-HT0076-021299-001-d03 HT0076 Homo	2.20	2.26
	444404	M31525		major histocompatibility complex, class	2.20	1.37
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.19	2.88
	436063	AK000028		ribosomal protein S24	2.19	1.42
	429212	NM_001504	Hs.198252	G protein-coupled receptor 9	2.18	1.22
25	400712			Target Exon	2.18	1.00
	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	2.17	1.79
	403478			NM_022342:Homo sapiens kinase protein 9	2.17	1.80
	418747	AJ249977	Hs.88049	protein kinase, AMP-activated, gamma 3 n	2.17	1.76
	429712	AW245825	Hs.211914	ENSP00000233627*:NADH-ubiquinone oxidore	2.16	1.44
30	451668	Z43948	Hs.326444	cartilage acidic protein 1	2.16	2.12
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	2.15	2.88
	456057	AA947457	Hs.135560	ESTs, Weakly similar to T43458 hypothe	2.15	2.50
	444346	AI142274		ESTs	2.15	2.38
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	2.14	1.93
35	451318	AA029888	Hs.95071	ESTs	2.14	1.16
	458935	Y16521	Hs.24812	CDP-diacylglycerol synthase (phosphatida	2.13	1.52
	417105	X60992	Hs.81226	CD6 antigen	2.13	2.61
	408219	BE061111	Hs.254211	gb:QV0-BT0041-011199-039-f02 BT0041 Homo	2.13	1.94
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	2.11	2.66
40	443711	N67861	Hs.49390	ESTs	2.10	1.00
	423234	AA323534	Hs.296162	AD037 protein	2.10	1.52
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	2.09	3.74
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	2.08	1.84
	405827			Target Exon	2.08	1.00
45	406909	L20777	Hs.73885	gb:Human MHC class I HLA-G gene (HLA-A33	2.08	2.29
	437285	AW779318	Hs.88417	ESTs	2.07	1.72
	424281	AA766243		gb:oa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	2.07	1.00
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.07	2.16
	423901	AA333006		gb:EST37064 Embryo, 8 week I Homo sapien	2.07	1.50
50	405075			Target Exon	2.07	1.15
	457423	AK000642	Hs.265018	hypothetical protein FLJ20635	2.07	2.67
	406267			Target Exon	2.07	1.30
	423365	AA324992	Hs.257168	ESTs	2.06	1.70
	449970	AI678068	Hs.201227	ESTs	2.06	2.48
55	430733	AW975920	Hs.121036	ESTs	2.06	1.00
	446323	AI288274	Hs.345792	ESTs	2.06	1.00
	402240			Target Exon	2.05	1.94
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypothe	2.05	1.44
	424463	AW195353	Hs.119903	ESTs	2.04	1.32
60	400107			Eos Control	2.04	2.42
	404811			NM_021096:Homo sapiens calcium channel,	2.03	2.18
	403589			Target Exon	2.03	1.57
	404088			Target Exon	2.03	1.00
	414991	C17898		gb:C17898 Human placenta cDNA (TFujiwara	2.03	2.04
65	429073	AA446167	Hs.47385	ESTs	2.03	3.10
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfam	2.02	1.92
	401897			C17001987:gi73033380[gb]AAF58438.1] (AE0	2.02	1.55
	431094	AW972276	Hs.116195	ESTs	2.02	1.00
	424899	AL119387	Hs.119062	ESTs	2.01	2.41
70	419711	C02621	Hs.159282	ESTs	2.01	1.92
	459019	AA017156	Hs.40719	hypothetical protein KIAA1164	2.01	1.76
	405453			NM_005748*:Homo sapiens YY1-associated f	2.01	1.24
	402516			Target Exon	2.01	1.00
	457365	AA577297	Hs.303249	EST	2.01	2.36
75	407928	NM_002262	Hs.41682	killer cell lectin-like receptor subfam	2.01	2.62
	436553	AW407157	Hs.8997	immunoglobulin lambda locus	2.00	1.64
	406266			Target Exon	2.00	2.46
	419409	AW297831	Hs.143792	hypothetical protein MGC2656	2.00	1.60
80	435028	AW193035	Hs.187370	ESTs	2.00	1.55
	404696			NM_013443:Homo sapiens CMP-NeuAC:(beta)-	2.00	1.21
	403533			Target Exon	2.00	1.17
	411673	BE064863		gb:RC1-BT0313-110300-015-f06 BT0313 Homo	2.00	1.00
	424148	BE242274	Hs.1741	Integrin, beta 7	1.99	3.66
	419833	AA251131	Hs.220697	ESTs	1.99	1.69

5	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	1.99	1.84
	426416	AW612744	Hs.169824	killer cell lectin-like receptor subfami	1.98	2.56
	449317	AW293413	Hs.132906	19A24 protein	1.98	2.44
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	1.97	2.51
	422109	S73265	Hs.1473	gastrin-releasing peptide	1.97	3.32
10	424218	AF031824	Hs.143212	cystatin F (leukocystatin)	1.96	1.86
	406303			C16000922gij7499103 pir T20903 hypothe	1.96	2.16
	438676	AA813745	Hs.123446	ESTs	1.95	3.62
	404240			NM_018950:Homo sapiens major histocompat	1.95	2.06
	404056			Target Exon	1.94	2.60
15	425508	AA991551	Hs.97013	Homo sapiens, Similar to RIKEN cDNA 2310	1.93	3.24
	429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	1.93	2.35
	416941	BE000150	Hs.48778	niban protein	1.92	2.24
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.92	5.44
	409153	W03754	Hs.50813	hypothetical protein FLJ20022	1.92	6.08
20	419490	NM_008144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	1.90	5.52
	446608	N75217	Hs.257846	ESTs	1.90	4.63
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	1.89	1.50
	414812	X72755	Hs.77367	monokine induced by gamma interferon	1.89	4.93
	422994	AW891802	Hs.296276	ESTs	1.88	3.30
25	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	1.88	2.17
	433671	AW138797	Hs.132906	19A24 protein	1.88	1.83
	412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymph	1.86	3.12
	447656	NM_003726	Hs.19126	src kinase-associated phosphoprotein of	1.86	1.88
	432468	AW402155	Hs.3003	CD3E antigen, epsilon polypeptide (TIT3	1.84	1.65
30	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	1.83	2.46
	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	1.82	2.07
	431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	1.82	2.63
	436485	X59135	Hs.156110	immunoglobulin kappa constant	1.82	2.75
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	1.81	4.56
35	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.80	5.10
	448569	BE382657	Hs.21486	signal transducer and activator of trans	1.79	1.89
	429670	L01087	Hs.211593	protein kinase C, theta	1.78	3.34
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	1.78	3.55
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	1.78	1.97
40	406672	M26041	Hs.198253	major histocompatibility complex, class	1.76	2.12
	452203	X57522		transporter 1, ATP-binding cassette, sub	1.75	1.55
	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	1.73	2.04
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (lazarus	1.73	1.56
	414512	AL044336	Hs.6831	golgi phosphoprotein 1	1.73	2.00
45	426752	X69490	Hs.172004	titin	1.73	2.62
	444793	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	1.72	2.30
	452334	D60471	Hs.13390	gb:HUM111D09B Clontech human fetal brain	1.72	2.12
	446227	AI281459	Hs.270114	ESTs	1.72	2.48
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	1.72	2.72
50	423799	AW026300	Hs.132906	19A24 protein	1.71	2.40
	458332	AI000341		ESTs	1.70	3.71
	408380	AF123050	Hs.44532	diubiquitin	1.70	2.71
	437644	AA748575	Hs.136748	lectin-like NK cell receptor	1.70	2.58
	402736			NM_024852:Homo sapiens hypothetical prot	1.69	2.10
55	438866	U44385	Hs.325495	tissue inhibitor of metalloproteinase 2	1.69	1.39
	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	1.68	2.02
	426202	BE266484	Hs.82916	chaperonin containing TCP1, subunit 6A (1.68	2.14
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	1.68	3.30
	420440	NM_002407	Hs.97644	mammaglobin 2	1.67	2.42
60	416967	BE616731	Hs.80645	interferon regulatory factor 1	1.67	1.49
	415823	R81864	Hs.205103	ESTs	1.65	2.18
	421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	1.65	1.58
	427307	AF117947	Hs.174785	PDZ domain-containing guanine nucleotide	1.63	1.94
	444929	AI685841	Hs.161354	ESTs	1.63	2.16
65	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	1.63	1.74
	418196	AI745649	Hs.26549	KIAA1708 protein	1.62	2.76
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	1.62	4.42
	438568	R98865	Hs.11135	major histocompatibility complex, class	1.62	1.74
	430308	BE540865	Hs.238990	cyclin-dependent kinase inhibitor 1B (p2	1.62	1.85
70	433934	AW273261	Hs.216292	ESTs	1.62	2.00
	443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	1.61	2.00
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	1.61	1.46
	415349	AI766697	Hs.13231	ESTs	1.60	2.00
	406656	M16714	Hs.89643	major histocompatibility complex, class	1.60	1.47
75	456974	M12529	Hs.169401	apolipoprotein E	1.60	1.63
	416401	N80139	Hs.268916	ESTs	1.59	1.68
	439372	AF088033	Hs.159225	ESTs	1.59	2.04
	434666	AF151103	Hs.112259	T cell receptor gamma locus	1.59	4.08
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	1.58	3.06
80	417427	M80391	Hs.82127	interleukin 16 (lymphocyte chemoattracta	1.58	2.37
	431903	AB029488	Hs.272100	SMS3 protein	1.57	2.14
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	1.57	2.28
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	1.56	1.46
	412472	AW975398	Hs.293836	ESTs	1.56	2.26
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	1.56	2.38
	412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.55	1.67
	449835	AW979300	Hs.293813	ESTs	1.55	2.16

	405545		Target Exon	1.55	2.64	
	435299	AI745458	Hs.343026	ESTs, Weakly similar to T20593 hypotheti	1.55	3.81
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.54	2.14
5	424243	AI949359	Hs.143600	ESTs, Highly similar to cdc Golgi-locali	1.53	2.62
	457500	NM_002759	Hs.274382	protein kinase, Interferon-inducible dou	1.53	2.04
	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	1.53	2.00
	439039	AI656707	Hs.48713	ESTs	1.53	2.38
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	1.52	2.65
10	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.52	2.06
	415198	AW009480	Hs.943	natural killer cell transcript 4	1.52	1.40
	431594	AI823999		ESTs	1.52	2.12
	432656	NM_000246	Hs.3076	MHC class II transactivator	1.52	2.20
	422426	W79117	Hs.58559	ESTs	1.52	2.22
15	414372	AA143654		gb:zo65a02r1 Stratagene pancreas (93720	1.51	2.80
	427247	AW504221	Hs.174103	Integrin, alpha L (antigen CD11A (p180),	1.50	1.67
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.49	3.12
	406621	X57809	Hs.8997	immunoglobulin lambda locus	1.49	1.78
	419166	AA234638	Hs.293584	ESTs	1.49	2.10
20	418323	NM_002118	Hs.1162	major histocompatibility complex, class	1.49	1.47
	435304	H10709	Hs.269524	ESTs	1.48	2.96
	452834	AI638627	Hs.105685	KIAA1688 protein	1.48	2.14
	446616	R65964	Hs.334873	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.48	1.38
	429272	W25140	Hs.110667	ESTs	1.48	3.19
25	428379	X06026	Hs.2259	CD3G antigen, gamma polypeptide (TIT3 co	1.48	1.66
	433231	AB040926	Hs.143552	KIAA1493 protein	1.47	2.16
	408847	AW290997	Hs.30348	ESTs	1.46	2.08
	405441			Target Exon	1.46	2.99
30	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	1.45	1.56
	458644	AW197203		gb:xm38b01.x1 NCL CGAP_GC6 Homo sapiens	1.45	2.44
	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	1.45	1.70
	422934	BE244189	Hs.122492	hypothetical protein	1.44	1.27
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	1.44	3.46
	406698	X03068	Hs.73931	major histocompatibility complex, class	1.44	1.71
35	421407	T82331	Hs.182278	ESTs, Weakly similar to CGHU6C collagen	1.43	1.56
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	1.43	1.25
	400269			Eos Control	1.43	2.02
	420973	AA743415	Hs.291368	ESTs	1.42	2.08
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	1.42	2.20
40	430015	AW768399		ESTs	1.41	2.06
	427648	AI376722	Hs.180062	proteasome (prosome, macropain) subunit,	1.41	1.31
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	1.40	1.72
	437479	R61866	Hs.101277	ESTs	1.40	2.52
	425345	AU077297	Hs.155894	protein tyrosine phosphatase, non-recept	1.40	2.17
45	416030	H15261	Hs.21948	ESTs	1.40	2.62
	419886	AA251562	Hs.146168	ESTs, Weakly similar to AF118023 1 SH3 d	1.40	1.68
	443951	F13272		ferritin, light polypeptide	1.40	1.64
	414875	H42679	Hs.77522	major histocompatibility complex, class	1.40	1.42
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet	1.40	1.34
50	428782	X12830	Hs.193400	Interleukin 6 receptor	1.40	2.30
	400680			NM_014207:Homo sapiens CD5 antigen (p56-	1.39	1.93
	428289	M26301	Hs.2253	complement component 2	1.39	1.39
	441410	AA932689	Hs.233304	ESTs, Weakly similar to I38022 hypotheti	1.39	1.42
	406645	M57466	Hs.814	major histocompatibility complex, class	1.39	1.45
55	441379	AW175787	Hs.334841	selenium binding protein 1	1.38	1.32
	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	1.38	2.04
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	1.38	1.35
	423526	AB011086	Hs.129739	KIAA0514 gene product	1.37	1.41
	424168	L29277	Hs.321677	signal transducer and activator of trans	1.37	1.33
60	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.37	1.74
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	1.35	1.38
	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	1.35	1.54
	452353	C18825	Hs.29191	epithelial membrane protein 2	1.34	1.47
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (tr	1.31	1.77
65	435106	AA100847	Hs.5978	ESTs, Highly similar to AF174600 1 F-box	1.31	1.53
	444633	AF111713	Hs.286218	junctional adhesion molecule 1	1.30	1.37
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	1.29	1.49
	419092	J05581	Hs.89603	mucin 1, transmembrane	1.28	1.36
	451864	N20370	Hs.69547	ESTs	1.28	1.42
70	421140	AA298741	Hs.102135	signal sequence receptor, delta (translo	1.28	1.31
	412790	NM_014767	Hs.74583	KIAA0275 gene product	1.28	1.63
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	1.28	1.38
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	1.28	1.36
	435822	T95594	Hs.187435	ESTs	1.27	1.82
75	455863	AA907305	Hs.36475	ESTs	1.27	1.36
	404277			NM_019111:Homo sapiens major histocompa	1.27	1.52
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	1.27	1.54
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	1.27	1.53
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	1.26	1.27
80	434747	AA837085		ESTs	1.26	1.60
	425320	U29344	Hs.83190	fatty acid synthase	1.25	1.35
	452363	AI582743	Hs.94953	Homo sapiens, Similar to complement comp	1.25	1.41
	434644	H98071	Hs.4055	chromosome 21 open reading frame 50	1.25	1.30
	404854			Target Exon	1.25	1.57

5	406973	M34996	Hs.198253	major histocompatibility complex, class	1.25	1.57
	421071	AI311238	Hs.104476	ESTs, Weakly similar to CGHUIE collagen	1.24	1.26
	431779	AW971178	Hs.268571	apolipoprotein C-I	1.24	1.39
	416047	BE439894	Hs.78991	DNA segment, numerous copies, expressed	1.23	2.08
	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	1.23	1.20
10	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (a	1.22	1.24
	415661	AF057307	Hs.78575	prosaposin (variant Gaucher disease and	1.22	1.16
	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	1.22	1.17
	420679	X57152	Hs.99853	fibrillarin	1.22	1.30
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	1.21	1.58
15	418090	U57059	Hs.83429	tumor necrosis factor (ligand) superfamily	1.21	1.33
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	1.21	1.60
	406825	AI982529	Hs.84298	CD74 antigen (invariant polypeptide of m	1.20	1.20
	436906	H95990	Hs.181244	major histocompatibility complex, class	1.19	1.27
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	1.19	1.62
20	408279	AF216965	Hs.44095	Homo sapiens, clone MGC:12617, mRNA, com	1.18	1.25
	411372	AI147861	Hs.213289	low density lipoprotein receptor (famili	1.17	1.33
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	1.16	1.49
	406906	Z25424		gb:H.sapiens protein-serine/threonine ki	1.16	1.15
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	1.16	1.38
25	432805	X94630	Hs.3107	CD97 antigen	1.16	1.22
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	1.16	1.41
	438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group 1, m	1.16	1.36
	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	1.15	1.27
	429832	AW293301	Hs.288472	ESTs, Weakly similar to UBPF_HUMAN UBQU	1.15	1.72
30	438183	BE263252	Hs.6101	hypothetical protein MGC3178	1.15	1.21
	432680	T47364	Hs.278613	interferon, alpha-inducible protein 27	1.14	1.21
	406782	AA430373		gb:zw20f11.s1 Soares ovary tumor NbHOT H	1.14	1.41
	414662	AL036058	Hs.76807	major histocompatibility complex, class	1.12	1.25
	452547	AA335295	Hs.74120	adipose specific 2	1.11	1.39
35	414803	X03100	Hs.914	Human mRNA for SB classII histocompatibi	1.11	1.22
	430280	AA361258	Hs.237868	interleukin 7 receptor	1.10	1.73
	441384	AA447849	Hs.288660	retinoic acid induced 3	1.09	1.22
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibitor	1.09	1.14
	419200	AW968405		EST	1.08	1.64
40	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	1.08	1.18
	409428	M33680	Hs.54457	CD81 antigen (target of antiproliferativ	1.07	1.12
	447023	AA356764	Hs.17109	integral membrane protein 2A	1.07	1.71
	421481	AW391972	Hs.104696	KIAA1324 protein	1.07	1.58
	408868	AA505445	Hs.300697	Immunoglobulin heavy constant gamma 3 (G	1.07	1.23
45	412819	T25829	Hs.24048	FK506 binding protein precursor	1.06	1.45
	418253	AA215539	Hs.283643	Homo sapiens cDNA FLJ11606 fis, clone HE	1.06	1.24
	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	1.05	1.17
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	1.04	1.21
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	1.04	9.14
50	418156	W17056	Hs.83523	nuclear receptor subfamily 1, group 1, m	1.03	6.65
	438089	W05391		nuclear receptor subfamily 1, group 1, m	1.03	8.00
	429615	AF258627	Hs.211562	ATP-binding cassette, sub-family A (ABC1	1.01	1.25
	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	1.00	1.18
	438091	AW373062		nuclear receptor subfamily 1, group 1, m	0.99	12.84
55	407018	U49869		NM_018955:Homo sapiens ubiquitin B (UBB)	0.99	1.07
	412896	AW804157	Hs.308026	major histocompatibility complex, class	0.98	1.57
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	0.97	1.40
	426530	U24578	Hs.278625	complement component 4A	0.96	1.28
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	0.96	1.29
60	407241	M34516		gb:Human omega light chain protein 14.1	0.94	1.11
	425371	D49441	Hs.155981	mesothelin	0.92	1.45
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (0.91	1.28

60 TABLE 35B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

65	Pkey	CAT Number	Accession
	411089	5597_6	BI009308 BI009893 BF922023 BF922909 BF922913 BF922086 BF957733 BE701791 AA456454 AA579876 BF933710 AA091294 BI007291 AW906577 AW975593 AA713730 AW836781 AA666384 AA551106 BF594606 AI082382 AI955808 AI679895 AI679386 BF435555 AA586369 AA551351 AA595822 AA565188 BF808855 AA584921 N86077 AA601031 AA633188 AA514764 AA454562 AA551297 AA936109 BI009389 AW897806 BE815442 BF739374 BI009310 BF925422 BF933709 BF922034 BF925465 BI009680
70	452194	90339_1	AI694413 AW994700 AI912946 N73548 AI082035 AW271652 W24189 W24182 AI719718 AA024658 AW810120 AW015394 T79755 AA988043 AI709339
	410910	1063929_1	AW810196 AW810555 AW810507 AW810204 AW810619 AW810534
75	412394	1174616_1	AW947794 AW947793 AW947802 AW947798 AW947792 AW984150 AW984166 AW984167 AW984168 AW984179 AW984134 AW984160 AW984180 AW984194 AW984202 AW984190
	413682	1527038_1	BE156943 BE157375 BE156965 BE156949 BE156956
80	441320	58978_5	AJ346734 AI377971 BG193341 BG548376 AA928353 AI768724 BG215700 AA449370 BI462157 BI060283 BG677508 AA318802 BG719160
	408544	683260_1	AW293825 AW235391
	413454	1515217_1	BE141291 BE141306 BE141288 BE141283 BE141162 BE141168 BE141290 BE141161 BE141165
	444404	16136_1	BC013183 AW408658 NM_002119 M31525 M29039 BM456399 BF732381 BM152457 AW407685 BM193161 AW407778 BI819141 AA702254 BF855074 BI761232

436063	5483_1	AK000028 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 NA0094 N28596 AA884747 AA512890 BG436593 AI147991 AI142274 AI198553 AA338252 AA338213 AW962691 AA333006 AA332289 D78831 C17898 D78863 BF330730 BF350539 BE153665 BE065062 BE064650 BE064863 BF330763 BE153820 BE064737 BE155079 BE064651 AW856751 AW856622 BE064691 BE153674 BE153698 BE064730 BE153536 BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL564623 AL560492 AL566882 AL541576 AL550654 B1823519 B1770023 AL554969 B1489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073295 AI361433 AA564644 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI23422 AU158860 BE300655 AW170777 AA586956 AL571889 AL556850 AL576404 AL582800 B1258544 BF342301 BG875994 AA054458 AA353161 AJ940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG757203 BG764420 BG775028 BG824418 AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601 AA678742 AL566474 AA135770 BE774050 BF914200 H88457 AA627746 B1560216 B1753586 AI000341 AI766341 AW873274 AI823999 AA970060 AA508176 AW972585 AJ873427 AW972389 BI083452 AW970865 BG118285 AA569075 AA492132 AW753140 AA213770 AA143654 W03900 AW197203 AW753300 X65018 BC022318 NM_003019 BE465060 AI732255 BF446634 AI820677 AI002217 AI924488 B1821373 B1770406 B1823937 B1820255 B1489632 BG482911 AA617783 AI807697 AW205576 T94427 AA487101 T94513 B1819407 B1822450 B1820618 B1824619 BG542824 BG537862 BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA663876 AI375927 AA648810 AA948193 AA490916 AI459893 AA58188 AI240408 AI191843 AI131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 B1198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE660537 BE903782 BE732947 B1227204 BG761305 BE262642 BE391848 BE382475 BG008258 B1547991 B1459099 BE391391 BE259420 BE298109 AW245422 AI423847 AI914618 H80534 BE301004 AL531791 AA35581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI369493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 B1041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 B1091658 N72512 W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 B1262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA756606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA898120 AA746235 AW028983 AA789102 AU185751 AW971465 AA499681 AW971893 AW612086 BE077936 B1860809 BE002760 BG746251 BE982912 BM454584 AL134894 BF104082 H80591 AI334106 R63583 AI028079 AI140098 AI911625 AI890637 F34815 T65959 N40935 W52768 AA854747 AA861945 AA878472 AA778270 W32249 AA026061 W52662 W15352 W79670 W85384 T94283 AA002155 R82052 BE825493 BE825520 BE177661 H06215 BE144709 BE144829 AW976537 AI033582 AA837085 AA745261 AA648395 AA430373 AA968771 BF036043 AW190446 BG194731 AW662036 AI445021 BE937550 AW818972 AW393132 AA834685 BF112058 AW721682 H16423 AI270167 AI857345 AA937302 AW818444 BE929780 BG498678 BF155010 B1598271 B1599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608 AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 AI018009 N42850 AW537324 AI417258 AA463483 AI676131 AI167170 AA836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW474332 B1043239 AW474342 BG708553 AW362423 BF090028 BE827256 B16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AW966405 AW994425 D81879 BE093545 AW901107 AA383529 B1021552 R56420 N39976 AA573281 H82595 AA234955 BE093539 AW367006 BF358697 BF366318 AA663856 BE702099 BF035969 AI267384 AI267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836 AV724531 D53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 AI118798 BM128728 AA193411 AW444709 AW952455 AI887612 BF431948 B1496876 AI264159 BM128481 AI624657 AI689301 AI969467 AA861685 AA251695 AA625761 AA872090 AI826790 AA328366 BE827416 R75961 D56918 R68122 BE827384 AL118797 AI184164 AA164411 B1495332 BE858113 AI863860 H00660 T69849 AW780389 C14667 BE934995 B1018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302 BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AI185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344846 BE009112 BG899664 H91240 R60548 N41701 AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE500772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 B1003244 AI299190 AW40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955538 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 B1039626 B1037700 R00353 BF155184 N98343 N79072 H01812 T55581
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TABLE 35C:

75

Pkey:

Ref:

Strand:

Nt_position:

Unique number corresponding to an Eos probe set

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

80

Pkey	Ref	Strand	Nt_position
402550	7652009	Minus	80413-80673
403244	7637828	Plus	175792-176144
405452	7656638	Minus	93876-94275

5	401447	8574299	Minus	65053-65283
	405097	8072599	Plus	171191-171360
	400712	8118874	Plus	36087-36268
	403478	9958258	Plus	116458-116564
	405827	7109593	Plus	10279-10972
	405075	7770506	Minus	124680-125321
	406267	7528342	Minus	2570-2731
	402240	7690131	Plus	104382-104527,106136-106372
10	404811	3702428	Plus	26424-26596,28854-28987
	403589	8101229	Plus	5-330
	404088	9958257	Plus	184131-184295
	401897	8569218	Plus	604-767
	405453	7656675	Minus	83710-83980
	402516	9798099	Minus	195342-195511
15	406266	7528342	Minus	2365-2518
	404696	9800109	Minus	60037-60144,62675-63081
	403533	8076874	Plus	162922-163658
	406303	8575868	Plus	173622-173786
20	404240	5002624	Minus	116132-116407,116653-116922
	404056	3548785	Plus	75843-76980,77146-78263
	402736	9212044	Minus	66876-67010
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	405441	7408124	Plus	100952-101283
25	400680	8118752	Plus	118343-118684,120720-121013
	404277	1834458	Minus	91665-91946
	404854	7143420	Plus	14260-14537

30 TABLE 36A: About 52 genes upregulated in non-specific interstitial pneumonitis relative to hypersensitivity pneumonitis or idiopathic pulmonary fibrosis

	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
35	Unigene Title:	Unigene gene title			
	R1:	90th percentile of NSIP AIs divided by 90th percentile of HP AIs, where the minimum value for the numerator and denominator was set to 50.			
	R2:	90th percentile of NSIP AIs divided by 90th percentile of IPF AIs, where the minimum value for the numerator and denominator was set to 50.			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1 R2
40	435140	AA668123	Hs.134170	ESTs	2.76 2.76
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	2.57 1.00
	435375	AI733610		ESTs	2.55 2.55
	420813	X51501	Hs.99949	prolactin-induced protein	2.55 1.35
45	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.52 0.73
	421296	NM_002666	Hs.103253	perilipin	2.50 2.45
	419290	AI128114	Hs.112885	spinal cord-derived growth factor-B	2.43 1.79
	408882	H12084	Hs.31110	ESTs, Weakly similar to MAGE-B4 [H.sapi	2.42 1.77
	437318	AW362939	Hs.120721	ESTs	2.36 1.61
50	421823	N40850	Hs.28625	ESTs	2.29 0.56
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.28 0.89
	430536	AI809163	Hs.9908	nitrogen fixation cluster-like	2.25 2.80
	414009	R67516		ESTs	2.19 1.86
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	2.19 0.33
55	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	2.18 1.24
	413722	BE247354	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	2.14 1.95
	433874	AW204429	Hs.155033	ESTs	2.13 1.72
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	2.12 0.91
	414290	AI568801	Hs.71721	ESTs	2.11 0.81
60	451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.11 1.01
	406785	AA588061		gbnkl10d03.s1 NCI_CGAP_Co2 Homo sapiens	2.10 1.61
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	2.08 0.85
	444179	W35132	Hs.267442	ESTs	2.08 1.13
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.05 0.80
65	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.04 0.79
	439134	AA830599		ESTs	2.04 1.89
	418512	AW498974		diacylglycerol kinase, zeta (104kD)	2.02 2.02
	457311	AI497811	Hs.172753	Homo sapiens chromosome 19, BAC 41195 (C	2.00 1.45
	402274			C[9000498~gll4567179]gb AAD23607.1 AC00	1.88 2.24
70	453222	AA033929	Hs.19156	ESTs	1.77 2.00
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	1.73 2.02
	427297	AW292593	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com	1.69 1.69
	406714	AI219304	Hs.266959	hemoglobin, gamma G	1.62 2.47
	418333	W92113		gb:zh48e01.r1 Soares_fetal_liver_spleen_	1.59 2.04
75	404090			Target Exon	1.48 2.03
	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fs, clone K	1.39 2.06
	414386	X00442	Hs.75990	haploglobin	1.09 1.44
	439372	AF088033	Hs.159225	ESTs	1.05 2.13
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	1.01 2.08
80	412472	AW975398	Hs.293836	ESTs	1.00 2.26
	432894	AW167668	Hs.279772	brain specific protein	0.97 1.19
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	0.96 2.06
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, pro	0.95 1.08

5	424310	AA338648	Hs.50334	testes development-related NYD-SP22	0.93	1.47
	422109	S73265	Hs.1473	gastrin-releasing peptide	0.92	3.05
	420440	NM_002407	Hs.97644	mammaglobin 2	0.91	2.11
	418196	AI745649	Hs.26549	KIAA1708 protein	0.90	2.25
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	0.89	1.11
	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypothetl	0.85	1.74
	446608	N75217	Hs.257846	ESTs	0.82	2.10
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	0.73	1.32
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas)	0.70	1.76

TABLE 36B:

15	Pkey: Unique Eos probeset identifier number					
	CAT number: Gene cluster number					
	Accession: Genbank accession numbers					
	Pkey	CAT Number	Accession			
	435375	130020_1	AI733610 AI049989 AA678769			
	414009	438978_1	BE221268 R87515 AV730582 R67516			
	406785	0_0	AA588061			
	439134	2581476_1	AA830599 AA970659 AA883802			
	418512	12225_6	BM046773 AA224297 T33786 T08951 T09274 T08592 T30936 AA350905			
	418333	73080_1	AF264624 AW668618 AV731446 R93353 AA584550 AV732728 BF802614 BF434359 AA077092 BI027317 AA199812 AW629027 AAB31618 AI124782			
25			AA765804 AA055698 AA677404 AA065366 AA889402 AA765530 BE503126 BE467367 AW139964 W81697 AI887846 W81696 AA447817 AA447667			
			F13631 BF055573 AW268271 AW088477 BF677839 AL601859 AW502118 AW502624 AA574189 BI020104			

TABLE 36C:

35	Pkey: Unique number corresponding to an Eos probeset			
	Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.			
	Strand: Indicates DNA strand from which exons were predicted.			
	NL_position: Indicates nucleotide positions of predicted exons.			
	Pkey	Ref	Strand	NL_position
	402274	2935596	Plus	5604-6527
	404090	9967460	Minus	100815-100966

TABLE 37A: About 206 genes downregulated in lung fibrosis relative to normal lung

50	Pkey: Unique Eos probeset identifier number			
	ExAccn: Exemplar Accession number, Genbank accession number			
	UnigenelD: Unigene number			
	Unigene Title: Unigene gene title			
	R1: 90th percentile of normal lung AIs divided by the median of IPF AIs, where the minimum value for the numerator and denominator was set to 50.			
	Pkey	ExAccn	UnigenelD	Unigene Title
				R1
	454229	AW957744	Hs.278469	lacrimal proline rich protein
	432128	AA127221	Hs.296502	ESTs
60	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte
	420958	AA309431	Hs.66	Interleukin 1 receptor-like 1
	402608			Homo sapiens defensin, alpha 1, myeloid-
	406714	AI219304	Hs.266959	hemoglobin, gamma G
	406673	M34996	Hs.198253	major histocompatibility complex, class
	416539	Y07909	Hs.79368	epithelial membrane protein 1
	418021	M15881	Hs.1137	uromodulin (uromucoid, Tamm-Horsfall gly
	409385	AA071267		gb:zmf1g01.r1 Stratagene fibroblast (937
	450847	NM_003155	Hs.25590	stanniocalcin 1
70	404518			CD83 antigen (activated B lymphocytes, i
	413951	AW051200	Hs.75640	natriferic peptide precursor A
	407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran
	429509	AW614420	Hs.204354	ras homolog gene family, member B
	445769	AI741471	Hs.23666	ESTs
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h
	425571	AJ007292	Hs.158306	ephrin-A2
	423168	R34385	Hs.124940	GTP-binding protein
	401234			mitogen-activated protein kinase 8 inter
80	402181			Target Exon
	403479			NM_007064:Homo sapiens serine/threonine
	435424	AW083883	Hs.37696	Homo sapiens cDNA FLJ13510 fis, clone PL
	402911			NM_021158*:Homo sapiens protein kinase d
	442195	NM_001430		endothelial PAS domain protein 1
	400089			Eos Control
				3.60

	413948	C05145	Hs.75636	myosin light chain 2a	3.56
	438564	AA381553	Hs.198253	major histocompatibility complex, class	3.54
	413956	AJ821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.54
	431319	AA873350	Hs.302232	ESTs	3.52
5	434292	AF124368	Hs.306551	Homo sapiens IMAGE Consortium ID 839832,	3.48
	401540			NM_002675:Homo sapiens promyelocytic leu	3.46
	426477	AA379464	Hs.154073	gb:EST92386 Skin tumor I Homo sapiens cD	3.43
	402328			Target Exon	3.42
	401590			Target Exon	3.42
10	403645			NM_024513*:Homo sapiens FYVE and coiled-	3.37
	403376			Target Exon	3.36
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.35
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	3.28
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	3.27
15	401126			NM_006856*:Homo sapiens activating trans	3.27
	408243	Y00787	Hs.624	interleukin 8	3.23
	412429	AV650262	Hs.75765	GRO2 oncogene	3.22
	426420	BE383808	Hs.322430	NDRG family, member 4	3.21
	449338	H73444	Hs.394	adrenomedullin	3.19
20	401904			Target Exon	3.16
	401919			NM_012448*:Homo sapiens signal transduce	3.14
	406443			ENSP00000236574*:Hypothetical 21.8 kDa p	3.14
	458232	BE217872	Hs.279537	ESTs	3.12
	406016			Target Exon	3.12
25	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	3.11
	451831	NM_001674	Hs.460	activating transcription factor 3	3.08
	450562	AW136468	Hs.202199	ESTs	3.07
	405938			Target Exon	3.04
	451029	AA852097	Hs.25829	ras-related protein	3.02
30	421201	AW241940	Hs.102500	hypothetical protein FLJ20481	2.98
	439839	AA889354		ESTs	2.98
	439891	AL389940	Hs.109968	ESTs	2.96
	418935	T28499	Hs.89485	carbonic anhydrase IV	2.95
	418853	NM_005236	Hs.89296	excision repair cross-complementing rode	2.95
35	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.94
	410326	AI368909	Hs.47650	ESTs	2.88
	407244	M10014		fibrinogen, gamma polypeptide	2.85
	459721	AI299050	Hs.143835	gb:qn14d12.x1 NCI_CGAP_Lu5 Homo sapiens	2.84
	416212	R40290	Hs.124685	ESTs	2.84
40	428688	AA431801	Hs.98764	ESTs, Weakly similar to A29861 actin gam	2.83
	437508	AI204354	Hs.121347	ESTs	2.82
	437990	AI686579	Hs.121784	ESTs	2.82
	443709	AI082692	Hs.134662	ESTs	2.81
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor I	2.80
45	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	2.79
	404231			Target Exon	2.78
	434305	AI018280	Hs.130189	ESTs	2.77
	445493	AI915771		metallothionein 1E (functional)	2.76
	418056	AA524886		gb:nh34f02.s1 NCI_CGAP_Pr3 Homo sapiens	2.76
50	404102			Target Exon	2.75
	440206	AI762232	Hs.46794	ESTs	2.75
	403031			cathepsin D (lysosomal aspartyl protease	2.75
	413164	BE068494		gb:MR1-BT0371-050500-009-a12 BT0371 Homo	2.74
	459330	C16931		gb:C16931 Clontech human aorta polyA mRNA	2.74
55	456967	AW004056	Hs.168357	T-box 2	2.74
	427602	AI375258	Hs.98005	ESTs	2.74
	431367	Z20964	Hs.323817	DKFZP547E1010 protein	2.72
	406059			Target Exon	2.71
	420575	BE263301	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	2.71
60	457275	AA463422	Hs.209431	ESTs	2.71
	432559	AW452948	Hs.257631	ESTs	2.71
	402483			NM_020389:Homo sapiens putative capacita	2.70
	416069	R37101	Hs.20982	ESTs	2.70
	445445	AF238870	Hs.275706	Homo sapiens clone GLSH-3 similar to gli	2.69
65	436232	AA707006	Hs.187863	ESTs	2.68
	418773	T39748	Hs.325474	Target CAT	2.67
	434038	AA622104		ESTs	2.67
	405448			Homo sapiens mRNA; cDNA DKFZp586i2022 (f	2.66
	404439			ENSP00000067222*:Mitochondrial 28S ribos	2.65
70	435724	N39308	Hs.117898	ESTs	2.65
	404026			Target Exon	2.65
	400881			NM_025080:Homo sapiens hypothetical prot	2.64
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	2.62
	405429			Target Exon	2.62
75	402642			C1002296:gij6677817[ref]NP_033126.1[rep	2.61
	438575	BE304709	Hs.146550	myosin, heavy polypeptide 9, non-muscle	2.61
	449293	AA001088	Hs.29739	ESTs, Weakly similar to C34323 GTP-bind	2.61
	416157	NM_003243	Hs.342874	transforming growth factor, beta recepto	2.60
	446122	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.59
80	433291	AF007191		gb:Homo sapiens SIB 276 intestinal mucin	2.59
	426795	AI810474	Hs.196945	ESTs	2.58
	423503	M92843	Hs.343586	zinc finger protein homologous to Zip-36	2.58
	430768	AB030207	Hs.247888	guanine nucleotide binding protein 13, g	2.58

	423387	AJ012074		vasoactive intestinal peptide receptor 1	2.57
	442681	AI809182	Hs.130907	ESTs	2.57
	408652	R43409	Hs.6829	Homo sapiens mRNA for KIAA1644 protein,	2.56
5	402217			C19001662:g[6753872ref]NP_034345.1	2.56
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	2.56
	455674	BE065941		gb:RC3-BT0319-100100-012-d12 BT0319 Homo	2.56
	457831	AA706937	Hs.120802	ESTs, Moderately similar to A26641 Na7ex	2.56
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	2.55
10	458648	AW444551	Hs.35380	x 001 protein	2.55
	456653	BE251104	Hs.113052	RNA cyclase homolog	2.54
	440178	AW502463	Hs.196521	ESTs	2.53
	457139	AI557280	Hs.184270	capping protein (actin filament) muscle	2.52
	405857			Target Exon	2.51
15	410204	AJ243425	Hs.326035	early growth response 1	2.50
	412851	AI826502	Hs.97269	ESTs	2.49
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	2.49
	409209	AA460160	Hs.73217	ESTs	2.49
	447173	AW449385	Hs.157294	ESTs	2.48
20	440034	AI908639	Hs.246781	ESTs	2.44
	418168	R85350	Hs.101368	ESTs	2.43
	417285	AW993524	Hs.43148	epithelial membrane protein 1	2.43
	406305			transcriptional adaptor 3 (ADA3, yeast h	2.42
	427886	AA417083	Hs.104789	ESTs	2.42
25	436409	AJ238982	Hs.183656	VNN3 protein	2.42
	413861	BE175424		gb:RC4-HT0578-170300-012-d01 HT0578 Homo	2.40
	403605			C3000142:g[4503015ref]NP_003900.1 co	2.37
	402594			C1002603:g[9887091]gb AAG01738.1 AF248	2.37
	402803			NM_001397:Homo sapiens endothelin conver	2.37
30	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.36
	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	2.36
	442630	AW572938	Hs.130580	ESTs	2.35
	409368	AA071059		gb:zm66a10.r1 Stralagene neuroepithelium	2.33
	405156			NM_003213*:Homo sapiens TEA domain famil	2.31
35	448162	AL039531	Hs.323363	hypothetical protein FLJ22169	2.31
	403591			Target Exon	2.31
	406193			Target Exon	2.30
	420813	X51501	Hs.99949	prolactin-induced protein	2.30
40	442941	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	2.28
	400703			C11001794:g[10946612ref]NP_067286.1	2.27
	415026	AA159356	Hs.72308	ESTs	2.25
	400334	Y13187		Homo sapiens dmd gene, intron 11	2.18
	445878	AI262974	Hs.145587	ESTs	2.18
	404975			uncharacterized hypothalamus protein HT0	2.18
45	436370	R01220	Hs.185679	ESTs	2.17
	400513			Target Exon	2.16
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	2.15
	415405	R59141		gb:yg96d11.r1 Soares infant brain 1N1B H	2.15
	407612	U26403	Hs.37142	ephrin-A5	2.12
50	409837	AW501504		gb:UI-HF-BP0p-ajd-h-04-0-UI.r1 NIH_MGC_5	2.08
	458637	AV657446		gb:AV657446 GLC Homo sapiens cDNA clone	2.07
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	2.00
	418922	AW956580	Hs.42699	ESTs	1.98
	402404			NM_024967*:Homo sapiens hypothetical pro	1.98
55	421893	R22497	Hs.110571	growth arrest and DNA-damage-inducible,	1.98
	413731	BE243845	Hs.75511	connective tissue growth factor	1.96
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	1.96
	428193	NM_004235		Kruppel-like factor 4 (gut)	1.93
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	1.92
60	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	1.92
	433883	AI925688	Hs.222312	ESTs	1.91
	406564			msh (Drosophila) homeo box homolog 2	1.91
	403581			Target Exon	1.90
	403716			Target Exon	1.90
	404758			Target Exon	1.90
65	439500	W73158	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	1.89
	448793	AI864581		ESTs	1.84
	435857	AF253468	Hs.3736	delta-like 4 homolog (Drosophila)	1.83
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	1.82
	402051			Target Exon	1.81
70	409859	AW501926		gb:UI-HF-BR0p-ejp-f-08-0-UI.r1 NIH_MGC_5	1.78
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	1.78
	405063			Target Exon	1.78
	405163			C5000561:g[7513700]pir T14151 Inv pro	1.75
75	402386			Target Exon	1.73
	406755	N80129	Hs.199263	metallothionein 1L	1.73
	409811	AW500896		gb:UI-HF-BP0p-ajr-a-03-0-UI.r1 NIH_MGC_5	1.70
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.70
	400489			Target Exon	1.70
80	428704	AA432007	Hs.192090	ESTs	1.69
	429307	AU076592	Hs.198951	Jun B proto-oncogene	1.67
	400116			Eos Control	1.65
	404795			Target Exon	1.65
	408053	AW139474	Hs.246862	ESTs	1.65

5	414580	BE386918		gb:01275386F1 NIH_MGC_20 Homo sapiens c	1.63
	428800	M57627	Hs.193717	Interleukin 10	1.63
	451676	R84770	Hs.33538	ESTs, Weakly similar to oxygen-regulated	1.62
	402394			Target Exon	1.61
	404818			Target Exon	1.60
	436364	X06096		gb:Human macrophage alpha1-antitrypsin c	1.55
	420369	U96769	Hs.97220	chondroadherin	1.54
	405590			CX001497:gi 4557543 ref NP_001384.1 ex	1.54
	402448			Target Exon	1.53
10	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	1.51
	409020	AA062549	Hs.21162	retbindin	1.51
	405443			Target Exon	1.12

TABLE 37B:

15	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
20	Pkey	CAT Number	Accession	
	409385	110758_1	T65940 T64515 AA071267 AA071334	
	442195	15007_1	U81984 NM_001430 BE907085 BI333232 AK021986 AU138476 C18601 U51626 AU100517 BI054387 AU076970 BE786454 BG010080 AW377189	
25			BF998789 AA368139 R11396 T83613 BG006324 BI012404 BG001643 BF757957 AL549361 AL544018 BE002870 BE929314 BE090199 AL046650	
			BI053717 BE929315 BI054967 BF960055 BF925432 R05421 BF922073 T70331 BI004403	
	439839	2594580_1	AK023587 AA893354 AA846791	
	445493	423456_1	AV711317 AI809938 AI808768 AJ240593 AI915771	
	418056	286199_1	AW971347 AA524886 AA211537 BF903005 BF357120	
30	413164	1492512_1	BE068758 BE068745 BE068689 BE068778 BE068529 BE068683 BE068445 BE068392 BE068719 BE068473 BE068521 BE068628 BE068422	
			BE068618 BE068354 BE068390 BE068414 BE068433 BE068369 BE068384 BE068661 BE068324 BE068301 BE068436 BE068754 BE068329	
			BE068672 BE068494 BE068596 BE068332 BE068347 BE068588 BE068328 BE068493 BE068740 BE068685 BE068759 BE068307 BE068429	
			BE068303 BE068693 BE068374 BE068295 BE068625 BE068302 BE068663 BE068675 BE068579 BE068311 BE068674 BE068547 BE068602	
			BE068605 BE068352 BE068308 BE068401 BE068537 BE068552 BE068450 BE068723 BE068393 BE068671 BE068748 BE068317 BE068447	
			BE068568 BE068632 BE068357 BE068330 BE068498 BE068631 BE068540 BE068410 BE068626 BE068591 BE068522 BE068676 BE068499	
35			BE068361 BE068598 BE068350 BE068299 BE068580 BE068567 BE068692 BE068321 BE068327 BE068739 BE068526 BE068538 BE068765	
			BE068340 BE068733 BE068293 BE068565 BE068480 BE068476 BE068761 BE068712 BE068706 BE068549 BE068419 BE068383 BE068434	
			BE068418 BE068525 BE068543 BE068752 BE068550 BE068623 BE068470	
	459330	105725_1	BG563152 BF846777 BF849354 BF849359 BF846636 BF849201 BF849356 C16931 AA056717 AW864542 AW882724 AA056567	
	434038	630986_1	AI910738 AW139227 AA932891 AA622104	
40	433291	73706_1	AF007191 AW820706 BG978594 BF872238	
	423387	2612_2	L13288 AA928785 AI608912 AW872978 AA565655 AU022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805 R46356	
			AA18798 BM129553 BM129126 BM129292 BM128865 AI808418 AI689932 AI806573 BF431808 AW872985 AW166269 H73241 T16182 AI264547	
			R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449838 R73300 NM_004624 AT979007 BE045543 BF110021 BF754250 T83923	
			AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902 BI763932 BI910138	
45	455674	1490762_1	BE065941 BE065997 BE066003 BE066070 BE066098	
	413861	1561647_1	BF352282 BE175424 BE175418 BE175383	
	409368	110612_1	AA071059 AA085201 AA085020	
	415405	1872126_1	W18191 R59141 R54142 R12130 F11362 Z42794 F08242 F07925 H21084 R54090 R59142	
	409837	915621_1	AW501504 AW501656 AW503048 AW502449 AW502098	
50	458637	395206_1	AF657752 AF657446	
	428193	430_1	AF105036 U70663 NM_004235 AF022184 AU141767 AU141110 AL040569 D44830 BI011351 AL575805 AI290876 AI014784 AI393429 AI266211	
			AW074303 AA620711 BF197792 AW008768 D25944 AI687397 AA621680 AV714408 BF446905 BM314505 BF514079 BM314197 AA845201	
			AW874084 BE720622 AI127241 AA236239 AI679709 AI679135 AI572470 AA573434 AI568487 BE049325 AA687950 BG925989 AI338031	
			AI365073 AI024576 AA298805 H04001 H45668 BG682146 AL552388 BI462361 BG547513 BG896863 BI256661	
55	448793	3006936_1	AI936948 AI864581 AI570641	
	409859	916430_1	AW501926 AW502568 AW501927	
	409811	58948_2	AK057581 AW500962 AW500896 AW501105	
	400116	5269_1	D42041 NM_014610 AJ000332 BI758702 BG720650 AU141129 AU130711 AU141380 AU132402 BM048556 AU127520 BE259984 AU128952	
60			BE614151 AL601516 BM146777 AU128103 BM194094 BE937951 BE596396 AK026997 AK026567 BF969293 BE798100 BI086881 BG166248	
			BE877845 BG385414 AW886747 BF093789 AW390159 BF820311 AA421676 AW880845 AW404827 BF726465 BE161190 BE254102 AW406002	
			BE161223 AI912055 BF930228 AW374357 AW794531 BE720524 BE933982 BE933658 BE933694 BE933978 BE933654 BE933583 BE166557	
			BE933874 BE933641 BE933859 BE933626 BE933866 BE933633 BE933864 BE933631 BE933867 BE933634 BE933857 BE933624 BE933683	
			BE933650 BE720491 AA420426 BE720410 BE720458 BE720444 BE720411 AW368748 BF874616 BE933498 BE835979 BF926667 AW849921	
65			AW850026 AW850022 AW849977 AW849900 BG250251 W87689 AI192825 AI692824 AA426263 AI090315 AI309537 AA877437 AA478438	
			AI538868 AW276162 AI279916 AA600318 AI188838 AW662284 AI262619 AA293457 BF347442 AA421677 AA659063 AA565510 AA937060	
			AI142684 AA788940 AA827426 AU152614 AI342784 AU148738 AA219664 AA047835 H99450 AA018563 AI073634 BM475120 BG875251	
			BG248778 U46372 AA383858 AU140356 BG821891 BF935049 BI760656 BI054103 BF982309 BE872215 BI257291 AU158469 AU160599	
			AU152469 AU152375 AU152059 AU148575 N32267 AU149554 AI627459 AI719840 AW779017 AI291493 AW304181 AW70005 AI086491	
70			AI311387 AI634232 AI151241 AI288848 AW050588 AW558580 AI241353 AI880219 AA039309 AA028517 AA016238 AA013444 H86822 R87530	
			AA058462 N27082 Z39679 BE544309 W52619 AA018076 AI813568 AW189907 AI418104 AU159878 AU150087 R21754 AA015932 H67274	
			AU153097 AI961344 AA018208 W32429 R45344 R77453 BM470129 AU130415 BI227374 BE298179 AW844963 AW844983 AI904066 AA379006	
			BF850571 AA355641 BG747156 AL547262 AW367941 BE560004 BI116081 BG899031 BE560318 BF174177 BI051456 BE001967 BE386446	
			BF969326 BF808765 BF684480 BG421617 AI940607 AW875483 BE789632 BF808711 BI192691 AW904249 BI911430 BE265407 BE730343	
			BE397808 BI226516	
75	414580	623093_1	BG333973 BE385437 BE408833 BE387650	
	436364	1414_37	X06826 X06096 BG468890 AW951851 W23562 T28392 H56742 H58030 T69205	

TABLE 37C:

80	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		

Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
5	402608	9910096	Plus	37495-37669
	404518	8151988	Plus	84494-84603
	401234	9929642	Plus	120173-120337
	402181	8575912	Plus	449746-450040
10	403479	7329292	Minus	148369-148533,150678-150809
	402911	7263904	Plus	142689-142979
	401540	8072433	Plus	105838-107310
	402328	4464283	Minus	13758-13922,14558-14752
	401590	9966320	Minus	33547-33649
	403645	8699714	Minus	4433-4582
15	403376	9369545	Minus	108698-108830
	401126	8699701	Minus	68290-68487
	401904	8671966	Plus	60959-61603,62670-62890,63778-63838
	401919	9502466	Plus	67536-67666
20	406443	9280765	Plus	85951-87327
	406016	8272661	Plus	41341-41940
	405938	6758795	Minus	166871-167411
	404231	8218035	Minus	61077-61322
	404102	7229900	Plus	97685-98018
	403031	7768597	Minus	1308-1416
25	406059	9103984	Minus	13856-14004
	402483	7574980	Minus	65578-66119
	405448	7582529	Plus	136347-136532
	404439	7139680	Plus	55316-55585
	404026	7582549	Minus	79674-79968
30	400881	2842777	Minus	91446-91603,92123-92265
	405429	7321905	Minus	51577-51723
	402642	9958129	Minus	125599-125756
	402217	9795981	Minus	21521-21757
	405857	6758728	Plus	26564-26819
35	406305	8575869	Plus	108239-108386,112216-112378,115388-11557
	403605	6862654	Plus	91614-91718
	402594	7705170	Plus	103082-103414
	402803	3287156	Minus	55923-56033
40	405156	9966228	Plus	146733-146860,147899-147961,153127-15325
	403591	8101229	Plus	4201-4833
	406193	7289992	Plus	30183-30662
	400703	8118859	Plus	63657-63857,64802-64905
	404975	3419864	Minus	86096-86605
45	400513	9796593	Plus	74613-74823
	402404	3970932	Plus	53154-53280
	406564	7711604	Minus	52788-53013
	403581	8101182	Plus	6794-7396
	403716	7239669	Plus	86899-87122
50	404758	7706327	Minus	130204-130806
	402051	8082020	Minus	19346-19480,20041-20119
	405063	7658414	Minus	111047-111666
	405163	9966267	Minus	161171-161299
	402386	9799769	Plus	22069-22303
55	400489	8954013	Plus	131475-131652
	404795	4826439	Plus	147501-147780
	402394	9929690	Plus	33308-33482
	404818	2769655	Plus	33671-33839
	405590	6960456	Plus	90492-90818
60	402448	9796640	Plus	112942-113069,114303-114521
	405443	7408143	Plus	90716-90887,101420-101577

65 TABLE 38A: About 207 genes upregulated in lung fibrosis relative to normal tissues

70	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	90th percentile of lung fibrosis AIs divided by 70th percentile of normal tissue AIs, where the minimum value for the numerator and denominator was set to 50.			
75	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	437275	AW976035	Hs.292396	ESTs, Weakly similar to A47582 B-cell gr	4.28
	407891	AA486620	Hs.41135	endomucin-2	4.14
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.07
	410219	T98226	Hs.171952	occludin	3.96
80	434666	AF151103	Hs.112259	T cell receptor gamma locus	3.88
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	3.87
	406617			Target Exon	3.76
	420568	F09247	Hs.247735	protocadherin alpha 10	3.70
	425873	NM_013390	Hs.160417	transmembrane protein 2	3.69

	438797	C16181	Hs.283040	hypothetical protein PRO2543	3.68
	410315	A1638871	Hs.152519	Homo sapiens cDNA: FLJ22524 fis, clone H	3.65
	446714	W73818	Hs.110028	ESTs	3.64
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	3.61
5	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	3.58
	412790	NM_014767	Hs.74583	KIAA0275 gene product	3.56
	424338	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-	3.56
	412654	A1093480		hypothetical protein FLJ11896	3.56
10	414386	X00442	Hs.75990	haploglobin	3.54
	451035	AU076785	Hs.430	plastin 1 (I isoform)	3.52
	436473	A1193122	Hs.132275	ESTs	3.51
	406714	A1219304	Hs.266959	hemoglobin, gamma G	3.46
	414586	AA306160	Hs.16488	lymphocyte cytosolic protein 1 (L-plasti	3.45
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	3.45
15	427527	A1809057	Hs.153261	immunoglobulin heavy constant mu	3.39
	452813	U54727	Hs.191445	ESTs	3.36
	442831	A1798959	Hs.131686	ESTs	3.35
	427774	AA278583	Hs.180737	Homo sapiens clone 23664 and 23905 mRNA	3.34
	445330	R52656	Hs.21691	ESTs	3.31
20	436001	AW903849	Hs.173840	HUEL (C4orf1)-interacting protein	3.31
	431681	AK000378	Hs.267566	hypothetical protein FLJ20371	3.29
	432314	AA533447	Hs.312989	ESTs	3.28
	436129	A1381659	Hs.267086	ESTs	3.28
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	3.24
25	422607	Z45471	Hs.118684	stromal cell-derived factor 2	3.21
	421205	AL137540	Hs.102541	netrin 4	3.20
	428582	BE336699	Hs.185055	BENE protein	3.20
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	3.19
30	424880	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator	3.17
	421233	AA209534	Hs.284243	tetraspan NET-6 protein	3.17
	429350	A1754634	Hs.131987	ESTs	3.16
	428727	AF078847	Hs.191356	general transcription factor IIH, polype	3.16
	434850	Z43161	Hs.283714	30 kDa protein	3.13
35	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	3.12
	446506	A1123118	Hs.15159	chemokine-like factor, alternatively spl	3.11
	416114	A1695549	Hs.183868	glucuronidase, beta	3.10
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	3.09
	444212	AW503976	Hs.10649	basement membrane-induced gene	3.08
40	422442	AA324998	Hs.147086	signal transducer and activator of trans	3.08
	442870	N45018	Hs.8769	hypothetical protein DKFZp761J17121	3.08
	424456	AA341017	Hs.25549	hypothetical protein FLJ20898	3.07
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	3.07
	445107	AL208121	Hs.147313	ESTs, Weakly similar to I38022 hypotheti	3.06
45	438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	3.04
	428106	BE620016	Hs.182470	PTD010 protein	3.04
	428403	A1393048	Hs.326159	leucine rich repeat (in FLJ1) interactin	3.04
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.03
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmib	3.02
50	423067	AA321355	Hs.285401	colony stimulating factor 2 receptor, be	3.01
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	2.96
	415000	AW025529	Hs.239812	Homo sapiens serologically defined breas	2.96
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	2.96
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	2.96
55	419660	BE280337	Hs.194693	solute carrier family 7 (cationic amino	2.96
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.95
	414493	AL133921	Hs.76272	retinoblastoma-binding protein 2	2.94
	416883	AW140128	Hs.184902	ESTs	2.92
	417675	A1808607	Hs.3781	similar to murine leucine-rich repeat pr	2.92
60	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	2.92
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	2.92
	429640	U83508	Hs.2463	angiotensin 1	2.91
	449843	R85337	Hs.24030	solute carrier family 31 (copper transpo	2.91
	401958			Target Exon	2.90
65	416926	H03109	Hs.263395	HT018 protein	2.90
	433691	AA605012		ESTs	2.88
	441892	AB028981	Hs.8021	KIAA1058 protein	2.87
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.87
	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	2.87
70	414291	A1289619	Hs.13040	G protein-coupled receptor 86	2.87
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	2.87
	435913	W95006	Hs.269559	ESTs, Weakly similar to S65657 alpha-1C-	2.86
	422050	AA302741	Hs.25786	ESTs, Moderately similar to JCS238 galac	2.85
	451356	AA748418	Hs.164577	ESTs	2.85
75	442085	AA975688	Hs.159955	ESTs	2.84
	427704	AW971053	Hs.292882	ESTs	2.83
	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11A (p180),	2.83
	441965	AA972712	Hs.269737	ESTs	2.82
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	2.82
80	450056	BE047394	Hs.8208	ESTs, Weakly similar to S71512 hypotheti	2.80
	407245	X90568	Hs.172004	titin	2.80
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	2.80
	446601	A1312783	Hs.155772	Homo sapiens thymic stromal co-transport	2.80
	432195	AJ243669	Hs.8127	KIAA0144 gene product	2.80

	449088	AI654048	Hs.196556	ESTs	2.80
	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	2.80
	406648	AA563730	Hs.277477	major histocompatibility complex, class	2.79
5	412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymph	2.78
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	2.78
	440255	AI932285	Hs.160569	ESTs	2.78
	410057	R66834	Hs.268107	multimerin	2.77
	417497	AW402482	Hs.82212	CD53 antigen	2.77
	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega	2.76
10	431884	AA521246	Hs.210792	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.75
	409969	AW514668	Hs.194258	ESTs, Moderately similar to ALU5_HUMAN A	2.75
	436729	BE621807		transmembrane 4 superfamily member 1	2.75
	431451	AA761378	Hs.192013	ESTs	2.74
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypothe	2.74
15	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	2.74
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	2.74
	424673	AA345051	Hs.294092	ESTs, Weakly similar to I38022 hypothe	2.74
	443194	AI954968		matrix Gla protein	2.71
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypothe	2.71
20	452870	AW502761	Hs.30909	KIAA0430 gene product	2.70
	430334	AI824719	Hs.143251	ESTs	2.70
	437187	AL080208	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	2.70
	432279	N95104	Hs.274260	ATP-binding cassette, sub-family C (CFTR	2.70
	413950	AA249096	Hs.32793	ESTs	2.70
25	430016	NM_004736	Hs.227656	xenotropic and polytropic retrovirus rec	2.70
	431710	AI735482		ESTs	2.70
	448749	AW859679	Hs.21902	Homo sapiens clone 25237 mRNA sequence	2.69
	451154	AA015879	Hs.33536	ESTs	2.69
30	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	2.69
	446899	NM_005397	Hs.16426	podocalyxin-like	2.68
	418031	AA648744	Hs.269493	ESTs	2.68
	453902	BE502341	Hs.3402	ESTs	2.68
	405121			mitogen-activated protein kinase 8 Inter	2.68
35	410163	AF151977	Hs.59260	NTT5 protein	2.67
	429632	AW195336	Hs.148910	ESTs	2.67
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	2.67
	455004	AW850303		gb:IL3-CT0219-191199-030-F09 CT0219 Homo	2.67
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	2.67
40	401113			solute carrier family 22 (organic cation	2.66
	419462	AF071076	Hs.112255	nucleoporin 98kD	2.66
	407635	AW370213	Hs.295232	ESTs, Moderately similar to A46010 X-fin	2.66
	419175	AW270037		KIAA0779 protein	2.66
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	2.66
45	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	2.66
	430592	AJ224864	Hs.9688	leukocyte membrane antigen (IRC1)	2.65
	446830	BE179030		Human DNA sequence from clone RPS-1174N9	2.64
	433327	AI674779	Hs.126744	ESTs	2.64
	424868	AJ568170	Hs.96886	ESTs	2.64
50	429854	R55508	Hs.99472	ESTs	2.63
	427080	AW068287	Hs.301175	ras-related C3 botulinum toxin substrate	2.63
	456711	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	2.63
	419777	D60134	Hs.270975	ESTs	2.63
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	2.62
55	427596	AA449506	Hs.270143	extracellular glycoprotein EMILIN-2 prec	2.62
	452445	AB002438	Hs.29596	Homo sapiens mRNA from chromosome 5q21-2	2.62
	447482	AB033059	Hs.18705	KIAA1233 protein	2.62
	419110	AA234171	Hs.187626	ESTs	2.62
	450353	AJ244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	2.62
60	419828	T81422	Hs.14922	ESTs	2.62
	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	2.62
	412491	W31589	Hs.73957	RAB5A, member RAS oncogene family	2.61
	436496	AA281959	Hs.5210	glia maturation factor, gamma	2.61
	435053	AW629386		ESTs	2.61
65	435029	AF167706	Hs.19280	cysteine-rich motor neuron 1	2.61
	425976	C75094	Hs.334514	NG22 protein	2.60
	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	2.60
	430539	AK001489		ADP-ribosylation factor-like 1	2.60
	419825	AI754011	Hs.7326	ESTs	2.59
70	412577	Z22968	Hs.74076	CD163 antigen	2.58
	425894	AW954011	Hs.180711	ESTs	2.58
	410883	D43767	Hs.66742	CCL17 chemokine (TARC) (SCYA17)	2.58
	441028	AI333660	Hs.17558	Homo sapiens cDNA FLJ14446 fis, clone HE	2.58
	413949	AA316077	Hs.75639	Human TB1 gene mRNA, 3' end	2.58
	434943	AJ929819	Hs.92909	chromosome 21 open reading frame 50	2.58
75	443605	H06865	Hs.134131	ESTs	2.57
	425017	AL119305	Hs.26409	ESTs	2.57
	440334	BE276112	Hs.7165	zinc finger protein 259	2.56
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	2.56
80	425345	AU077297	Hs.155894	protein tyrosine phosphatase, non-recept	2.56
	407174	T79938	Hs.77062	leukocyte immunoglobulin-like receptor,	2.56
	443834	AI741510	Hs.173548	ESTs	2.55
	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	2.55
	420539	AA282735	Hs.44004	AD031 protein	2.55

5	421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFp586N0121 (f	2.54
	437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	2.54
	422994	AW891802	Hs.296276	ESTs	2.54
	411992	AW816214	Hs.143055	ESTs	2.54
	451180	H61899	Hs.171937	steroid dehydrogenase-like	2.53
10	415775	H00747	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	2.54
	429752	H52348	Hs.36636	ESTs	2.53
	414612	BE274552	Hs.76578	protein inhibitor of activated STAT3	2.53
	453329	T97205	Hs.193400	ESTs, Weakly similar to 2109260A B cell	2.53
	436503	AJ277750	Hs.183924	ubiquitin associated and SH3 domain cont	2.52
15	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	2.52
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.52
	435943	R60194	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	2.52
	452253	AA928891	Hs.28608	Homo sapiens cDNA: FLJ22115 fis, clone H	2.52
	442506	BE586411	Hs.41726	ESTs	2.52
20	419972	AL041465	Hs.182982	golgin-67	2.52
	431074	BE072772	Hs.8997	ESTs, Moderately similar to A46010 X-in	2.52
	449129	AI631602	Hs.258949	ESTs	2.51
	440524	R71264	Hs.16798	ESTs	2.51
	419203	AA488719	Hs.190151	ESTs	2.51
25	404370			Target Exon	2.51
	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	2.51
	439219	N33883	Hs.41322	ESTs	2.51
	428044	AA093322	Hs.301404	RNA binding motif protein 3	2.50
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.50
30	437644	AA748575	Hs.136748	lectin-like NK cell receptor	2.50
	442566	R37337	Hs.12111	ESTs	2.50
	409317	U20165	Hs.53250	bone morphogenetic protein receptor, typ	2.50
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	2.50
	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	2.50
35	415165	AW887604	Hs.78065	complement component 7	2.50
	435284	AA879470	Hs.96849	Homo sapiens cDNA FLJ11492 fis, clone HE	2.50
TABLE 38B:					
40	Pkey:	Unique Eos probeset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
45	Pkey	CAT Number	Accession		
	412654	1350_1	BG743181 AI830050 BE695688 AA126591 AI903503 R26045 N62894 N63950 AA131619 AI681480 N79626 AA461603 R78979 AW608865 N66622 BF448838 AA779000 AA460314 AI092721 AI870182 AI436284 AI494151 AI127704 AI127702 BE349350 AI093480 AA115264 AA131567 R26840 R78885		
	433691	2203511_1	AI223854 AI129852 AA605012		
50	436729	6624_1	X75684 AL573167 AA445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI965838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA708057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA577735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189368 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773484 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 BE773462 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI665439 AI918453 AI472527 AI446740 AA035576 AA191414 AW675302 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AI574095 AL576200 AL571074 AL574525 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AI574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI665912 AI925607 AI871950 AI093510 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI587995 W60075 BF941183 AI738844 BE811458 BE773481 AI282930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843997 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG505731 BC008442 BC010166 AL550134 AL553095 AL548700 AL550751 AL547978 AL545286 AI540643 AU118627 AL601379 BI259821 BG741788 BI888522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE19182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 BI754027 BF696071 AI351939 BG151298 AI919334 AI401620 BI770165 W72057 T96158 T29478 AA181252 BG927793 AA714431 AA600749 AA181247 AA614756 AA081092 H52207 BG926934 BF222579 BG899001 N64245 AA953040 AI832406 AA102441 BG928081 AA933445 AA916041 AA987847 AA983329 AA737219 AA916443 AW128994 AI492560 AI761847 BC005272 NM_000900 X53331 M58549 BI758966 AL598829 BI754530 BG699770 BE439699 BE440148 AV704365 AV733652 BG212015 BG184149 BG200180 BG212690 BI761222 BG182079 AW338822 AI925631 AI423041 AW071181 AI889836 AW129112 BG925339 AI017633 AA568964 BF725590 AI004210 AI809799 BE083097 BG896220 AW997681 BF668788 BE083134 AW631281 BE439998 AW023269 BE813871 AW999947 BE839108 AV707983 AA369722 AW796627 AW890608 AA836844 AA985478 AW082259 AI816747 AA502221 AA971294 BE327509 AI719562 BG576669 AI479382 BF824747 AI741800 BG982962 AI088473 AA916151 AW473324 BG901177 BE439998 AW023269 BE813871 AW999947 BE839108 AV707983 AA369722 AW796627 AW890608 AI341771 AA302459 BI493353 AA366332 AA371104 AA367277 AL547972 BG928011 AI678903 AI695886 AI956165 AA484893 AA643953 AW591063 BG203275 BG211093 AI334791 AA916589 AW058266 AI362370 AI143352 AA508721 AI928079 DS7214 BE045265 AA541785		

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- 406621; X57809; Hs.181125; immunoglobulin lambda locus; Ig,HSP70,Ppx-GppA;TM=M;SS=N; 14.36
 443709; AI082692; Hs.134662; ESTs; SNF,fn3,none; 14.05
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7tm_3;TM=Y;SS=M; 13.88
 457200; U33749; Hs.197764; thyroid transcription factor 1; homeobox;TM=M;SS=N; 13.86
 432519; AI221311; Hs.130704; ESTs, Weakly similar to BCHUA S-100 pro; none,none; 13.82
 422355; AW403724; Hs.300697; coagulation factor VII (serum prothrombin); none,Ig; 13.62
 430280; AA361258; Hs.237868; Interleukin 7 receptor; fn3,none; 13.47
 415457; AW081710; Hs.7369; Homo sapiens testes specific A2 homolog; MORN,sugar,Ir;TM=Y;SS=M; 13.35
 431164; AA493650; Hs.94367; thyroid transcription factor 1; none,homeobox; 13.32
 414998; NM_002543; Hs.77729; oxidized low density lipoprotein (lectin; lectin_c;TM=Y;SS=M; 12.83
 400269; ; Hs.253495; Eos Control; lectin_c,Collagen,Xlink; 12.30
 424310; AA338648; Hs.50334; testes development-related NYD-SP22; none;TM=M;SS=N; 11.81
 451558; NM_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1; ABC_tran,SRP54;TM=Y;SS=M; 11.79
 452304; AA025386; Hs.61311; ESTs, Weakly similar to S10590 cysteine; none,none; 11.68
 445537; AJ245671; Hs.12844; EGF-like domain, multiple 6; EGF,MAM; 11.56
 423778; Y09267; Hs.132821; flavin containing monooxygenase 2; FMO-like,pyr_redox;TM=Y;SS=M; 11.41
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 11.31
 430832; AI073913; Hs.100566; ESTs, Weakly similar to JE0350 Anterior; none,none; 11.25
 407910; AA650274; Hs.41298; fibronectin leucine rich transmembrane p; fn3,LRR,LRRCT,LRRNT;TM=Y;SS=M; 11.15
 451497; H83294; Hs.284122; Wnt inhibitory factor-1; EGF,WIF; 11.07
 430250; NM_016929; Hs.283021; chloride intracellular channel 5; none;TM=M;SS=N; 11.07
 411020; NM_007770; Hs.67726; macrophage receptor with collagenous str; SRCR,Collagen;TM=Y;SS=M; 11.05
 446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin; ; Osteopontin; 11.01
 438091; AW373062; Hs.351545; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 10.97
 413048; M93221; Hs.75182; mannose receptor, C type 1; fn2,lectin_c,Ricin_B_Lectin,Xlink;TM=Y;SS=M; 10.93
 432231; AA339977; Hs.274127; CLST 11240 protein; none;TM=M;SS=M; 10.81
 416402; NM_000715; Hs.1012; complement component 4-binding protein; ; sush1;TM=M;SS=M; 10.77
 418156; W17056; Hs.83623; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 10.63
 436553; AW407157; Hs.181125; immunoglobulin lambda locus; Ig,HSP70,Ppx-GppA;TM=M;SS=N; 10.58
 421071; AI311238; Hs.104476; ESTs, Weakly similar to CGHUIE collagen; none;TM=Y;SS=M; 10.57
 418007; M13509; Hs.83169; matrix metalloproteinase 1 (interstitial; hemopexin,Peptidase_M10,Astacin,PG_binding_1; 10.33
 419086; NM_000216; Hs.89591; Kallmann syndrome 1 sequence; fn3,wap; 10.30
 407786; AA687536; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 10.28
 441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3,none; 10.26
 453914; NM_000507; Hs.574; fructose-1,6-bisphosphatase 1; FBPase;TM=M;SS=N; 10.22
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 10.09
 423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alpha; vwa,CACHE;TM=M;SS=N; 10.03
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3,TPR;TM=M;SS=N; 10.02
 408562; AI436323; Hs.31141; roundabout (axon guidance receptor, Dros; Ig,fn3;TM=M;SS=N; 10.02
 448782; AL050295; Hs.362806; KIAA0758 protein; 7tm_2,Ig,GPS,SEA;TM=Y;SS=N; 9.86
 419235; AW470411; Hs.288433; neurotrophin; none,none; 9.79
 415992; C05837; Hs.145807; hypothetical protein FLJ13593; none;TM=Y;SS=M; 9.74
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos;TM=M;SS=M; 9.70
 439018; AW300887; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 9.69
 442652; AI005163; Hs.201378; Homo sapiens cDNA FLJ40427 fis; none;TM=M;SS=N; 9.68
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT;TM=M;SS=Y; 9.64
 408380; AF123050; Hs.44532; diubiquitin; ubiquitin;TM=M;SS=N; 9.54
 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 9.52
 449494; AW237014; Hs.315369; aquaporin 4; MIP,none; 9.51
 456082; AI866286; Hs.71952; ESTs, Weakly similar to B36298 prolif-r; none,none; 9.42
 446428; AW082270; Hs.12458; ESTs, Weakly similar to ALUA_HUMAN ALU S; none,none; 9.41
 421952; AA300900; Hs.98849; dynein light chain 2B (DNLC2B); none,none; 9.19
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell; Ribosomal_S14,ank,kinase,death,none; 9.16
 456034; AW450979; ; gb:UH-BI3-ala-a-12-O-Ul.s1 NCL_CGAP_Sur; none,none; 9.15
 407788; BE514982; Hs.38991; S100 calcium-binding protein A2; ehand,S_100,S_100,ehand; 9.15
 416955; N26223; Hs.160436; MDAC1; none;NA;NA; 9.03
 443324; R44013; Hs.164225; ESTs; none,none; 9.03
 435575; AF213457; Hs.44234; triggering receptor expressed on myeloid; Ig;TM=Y;SS=M; 9.00
 440273; AI805392; Hs.325335; Homo sapiens cDNA: FLJ23523 fis, clone L; none,none; 8.99
 424527; AW138558; Hs.334873; ESTs, Weakly similar to I54374 gene NF2; Zn_carboPept,none; 8.80
 409203; AA780473; Hs.687; cytochrome P450, subfamily IVB, polypept; p450;TM=M;SS=Y; 8.76
 423387; AJ012074; Hs.348500; vasoactive intestinal peptide receptor 1; 7tm_2,HRM,CSD;TM=Y;SS=M; 8.74
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none;TM=M;SS=Y; 8.73
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 8.68
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell; Ig;TM=Y;SS=M; 8.56
 421563; NM_006433; Hs.105806; granulysin; none; 8.55
 450726; AW204600; Hs.355462; HUMSPSPA Human pulmonary surfactant-asso; SAPA,Surfactant_B,none; 8.51
 419693; AA133749; Hs.301350; FXD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 8.51
 424450; AL137526; Hs.374425; dynein intermediate chain 2; WD40; 8.42
 402474; ; NM_004079;Homo sapiens cathepsin S (CTSS; Peptidase_C1; 8.41
 458079; AI796870; Hs.54277; Homo sapiens similar to RIKEN cDNA 28100; none;TM=M;SS=N; 8.40
 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 8.36
 453310; X70697; Hs.553; solute carrier family 6 (neurotransmitter; SNF,SHT_transporter;TM=Y;SS=N; 8.34
 448140; AF145761; Hs.20450; BCM-like membrane protein precursor; Ig;TM=Y;SS=N; 8.33
 404240; ; NM_018950;Homo sapiens major histocompat; Ig,MHC_1;TM=Y;SS=M; 8.28
 459702; AI204955; ; gb:an03c03.x1 Stratagene schizo brain S1; none,none; 8.17
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 8.17
 442994; AI026718; Hs.16954; ESTs; ank,kinase,death,Ribosomal_S14; 8.12
 446998; N99013; Hs.278966; Homo sapiens mRNA; cDNA DKFZp564B2062 (f; PMP22_Claudin,none; 8.07
 420137; AA306478; Hs.95327; CD3D antigen, delta polypeptide (TIT3 co; ITAM;TM=Y;SS=M; 8.01
 435472; AW972330; Hs.283022; triggering receptor expressed on myeloid; Ig;TM=M;SS=M; 7.99
 432441; AW292425; Hs.163484; Intron of hepatocyte nuclear factor-3 at; Fork_head,none; 7.99
 409208; Y00093; Hs.172631; Integrin, alpha X (antigen CD11C (p150); vwa,FG-GAP,Integrin_A,vwa,Integrin_A,FG-GAP; 7.94

- 432606; NM_002104; Hs.3066; granzyme K (serine protease, granzyme 3; trypsin; TM=Y; SS=M; 7.92
 442832; AW206560; Hs.253569; ESTs; none, none; 7.90
 412104; AW205197; Hs.240951; Homo sapiens, Similar to RIKEN cDNA 2210; none; TM=M; SS=N; 7.89
 427337; Z46223; Hs.176683; Fc fragment of IgG, low affinity IIb, r; Ig; TM=Y; SS=M; 7.86
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22_Claudin, none; 7.84
 418299; AA279530; Hs.83968; Integrin, beta 2 (antigen CD18 (p95), ly; Integrin_B, EGF, PSI; TM=Y; SS=M; 7.79
 447131; NM_004585; Hs.17466; retinoic acid receptor responder (tazarot; none; TM=Y; SS=N; 7.78
 423961; D13666; Hs.136348; perostin (OSF-2os); Fasciclin; TM=M; SS=M; 7.73
 424917; A1636208; Hs.96901; hypothetical protein FLJ23049; none; TM=M; SS=N; 7.72
 438564; AA381553; Hs.198253; major histocompatibility complex, class I; IgMHC_II_alpha, none; 7.65
 456672; AK002016; Hs.114727; Homo sapiens, clone MGC:16327, mRNA, cont; none, PK, PK_C, myosin_head, RhoGAP; 7.64
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily; SRP14, TNFR_c6; 7.63
 436954; AA740151; Hs.130425; ESTs; none, none; 7.58
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain; SH2; 7.56
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC; TM=Y; SS=M; 7.55
 417105; X60992; Hs.81226; CD6 antigen; SRCR; TM=Y; SS=M; 7.51
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; Ig; TM=Y; SS=M; 7.46
 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen; TM=M; SS=M; 7.40
 432222; A1204995; g; gb:an03c03.x1 Stratagene schizo brain S1; none, none; 7.38
 422667; H25642; Hs.132821; ESTs; FMO-like, FMO-like; 7.37
 444527; NM_005408; Hs.11383; small inducible cytokine subfamily A (C; IL8; 7.36
 457411; AW085961; Hs.130093; Iroquois-class homeobox protein IRX2; none, none; 7.32
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, kinase, Recep_L_domain, YLP, none; 7.32
 419231; A1046294; Hs.136245; ESTs, Weakly similar to T17227 hypothet; none, none; 7.30
 438873; A1302471; Hs.124292; Homo sapiens cDNA: FLJ23123 fis, clone L; none, none; 7.27
 424027; AW337575; Hs.201591; ESTs; 7tm_2_HRM, none; 7.26
 428927; AA441837; Hs.90250; Homo sapiens hypothetical protein FLJ231; none, none; 7.24
 432435; BE218886; Hs.282070; ESTs; none, none; 7.22
 428467; AK002121; Hs.184465; hypothetical protein FLJ11259; none; TM=Y; SS=M; 7.21
 416030; H15261; Hs.21948; ESTs; none, none; 7.20
 433293; AF007835; Hs.32417; hypothetical protein MGC2742; none; TM=M; SS=N; 7.18
 418741; H83265; Hs.8881; ESTs, Weakly similar to S41044 chromosome; kinase, Activin_rec, kinase, Activin_rec; 7.16
 420656; AA279098; Hs.187636; ESTs; none, none; 7.14
 427698; AW972594; Hs.335499; ESTs; none, none; 7.11
 432268; BE311856; Hs.274230; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase, ATP-sulfurylase; TM=M; SS=N; 7.06
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kin; SAM_PNT, none; 7.04
 430413; AW842182; Hs.241392; small inducible cytokine A5 (RANTES); IL8; TM=M; SS=Y; 7.04
 452363; A1582743; Hs.94953; Homo sapiens, Similar to complement comp; C1q, Collagen; 7.03
 421481; AW391972; Hs.104696; KIAA1324 protein; none; TM=M; SS=M; 7.01
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase, PLAT; TM=M; SS=N; 6.97
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGFb_propeptide, TGF-beta, none; 6.96
 458124; AW005548; Hs.124590; ESTs; none, none; 6.94
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kd, chr; SH3, PX; TM=M; SS=N; 6.93
 411027; AF072099; Hs.87846; leukocyte immunoglobulin-like receptor, ; Inositol_P, Ig; TM=M; SS=N; 6.92
 428820; AA435187; Hs.172631; Integrin, alpha M (complement component; vva, Integrin_A, FG-GAP; TM=Y; SS=M; 6.90
 423575; C18863; Hs.163443; intron of perostin (OSF-2os); Fasciclin, none; 6.89
 419490; NM_006144; Hs.90708; granzyme A (granzyme 1, cytotoxic T-lymp; trypsin; TM=M; SS=M; 6.89
 450954; A1904740; Hs.25691; receptor (calcitonin) activity modifying; none; TM=Y; SS=M; 6.87
 425976; C75094; Hs.334514; NG22 protein; voltage, CLC; TM=Y; SS=M; 6.84
 425555; AA359291; Hs.130767; Homo sapiens cDNA: FLJ23553 fis, clone L; LRR; TM=M; SS=N; 6.81
 414991; C17898; ; Homo sapiens up-regulated by BCG-CWS (LO; Zip, none; 6.80
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, rec; ITAM; TM=Y; SS=M; 6.80
 422163; AF027208; Hs.112360; prominin (mouse)-like 1; none; TM=Y; SS=M; 6.79
 445885; A1734009; Hs.127699; KIAA1603 protein; none, none; 6.77
 436576; A1458213; Hs.77542; ESTs; 7tm_1, DnaJ; 6.77
 417079; U65580; Hs.81134; interleukin 1 receptor antagonist; IL1; 6.76
 424711; NM_005795; Hs.152175; calcitonin receptor-like; 7tm_2_HRM; TM=Y; SS=M; 6.75
 418847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3; TM=M; SS=N; 6.73
 426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54); Ig, ICAM_N; TM=M; SS=M; 6.71
 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain; Ig, abhydrolase; 6.70
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none, lectin_c; 6.70
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (C; IL8; TM=M; SS=Y; 6.68
 421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; Ion_trans, K_letra, asp; 6.65
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C, IMPDH_N, CBS, integrin_B, Ricin_B, lectin; 6.62
 428582; BE336699; Hs.185055; BENE protein; none; TM=Y; SS=M; 6.60
 453142; AA033648; Hs.7473; Homo sapiens gap junction protein, alpha; connexin; TM=Y; SS=M; 6.60
 432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 fis, clone PL; none, none; 6.58
 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2, STAT, STAT_bind, STAT_prot; TM=M; SS=N; 6.54
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2, SH3, kinase; TM=M; SS=N; 6.51
 446932; AA961459; Hs.125644; ESTs; none, LRR, LRRNT; 6.50
 427247; AW504221; Hs.174103; Integrin, alpha L (antigen CD11A (p180); vva, Integrin_A, FG-GAP; TM=Y; SS=M; 6.48
 425998; AU076629; Hs.165950; fibroblast growth factor receptor 4; Ig, kinase; TM=M; SS=M; 6.47
 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; none; TM=M; SS=M; 6.46
 431745; AW972448; Hs.163425; Novel FGENSESH predicted cadherin repeat; none, none; 6.43
 417370; T28651; Hs.374466; tryptophanyl-tRNA synthetase; WHEP-TRS, tRNA-syn_1b; 6.41
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin, In3, Y_phosphatase; TM=M; SS=N; 6.40
 429610; AB024937; Hs.211092; LUNX protein; PLUNC (palate lung and nas; none; 6.39
 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, P13, P14_kinase, FAT, FATC, BoA, RUN; TM=M; SS=N; 6.37
 413385; M34455; Hs.840; indoleamine-pyrrole 2,3 dioxygenase; IDO; TM=M; SS=N; 6.36
 451820; AW058357; Hs.199248; ESTs; 7tm_1; TM=Y; SS=M; 6.34
 408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+pep; PTR2; TM=Y; SS=N; 6.32
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys, Jg, FAD_Synth, Idh, Idh_C, kinase; 6.32

- 444090; S69115; Hs.10308; natural killer cell group 7 sequence; PMP22_Claudin; TM=Y; SS=M; 6.31
- 416819; U77735; Hs.80205; pim-2 oncogene; pkinase; 6.30
- 421659; NM_014459; Hs.106511; protocadherin 17; cadherin; TM=M; SS=M; 6.27
- 415198; AW009480; Hs.943; natural killer cell transcript 4; none; TM=M; SS=N; 6.26
- 5 424273; W40460; Hs.144442; phospholipase A2, group X; phospho; TM=M; SS=Y; 6.24
- 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2; TM=M; SS=N; 6.23
- 452194; A1694413; Hs.373599; olfactory receptor, family 2, subfamily ; none, none; 6.22
- 424144; AA454033; Hs.41644; AKAP-associated sperm protein; Rila; 6.21
- 10 414142; AW368397; Hs.334485; hemiscentin (fibulin 6); EGF, Ig, Isp, 1, hormone4, squash, TIL, Adeno_E3_CR1; TM=M; SS=M; 6.21
- 442006; AW975183; Hs.372210; ESTs, Weakly similar to S72482 hypotheti; none, none; 6.20
- 420256; U84722; Hs.76206; cadherin 5, type 2, VE-cadherin (vascula; cadherin, Cadherin_C_term; TM=Y; SS=M; 6.19
- 421379; Y15221; Hs.103982; small inducible cytokine subfamily 8 (C); IL8; TM=M; SS=Y; 6.17
- 440452; A1925136; Hs.55150; ESTs, Weakly similar to CAYP_HUMAN CALCY; none; NA; NA; 6.17
- 15 421462; AF016495; Hs.104624; aquaporin 9; MIP; TM=Y; SS=M; 6.16
- 452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor t; Y_phosphatase; none; 6.15
- 410361; BE391804; Hs.62661; guanylate binding protein 1, interferon-; GBP, GBP_C; TM=Y; SS=M; 6.13
- 415765; NM_005424; Hs.78824; tyrosine kinase with immunoglobulin and ; EGF, fn3, Ig, pkinase, laminin_EGF; TM=M; SS=Y; 6.12
- 430478; NM_014349; Hs.241535; apolipoprotein L 3; MoLA_ExtB; TM=Y; SS=M; 6.12
- 20 413869; NM_000878; Hs.75596; Interleukin 2 receptor, beta; none; TM=Y; SS=M; 6.09
- 446608; N75217; Hs.175622; ESTs; Armadillo_seg, HEAT_PBS; TM=M; SS=M; 6.08
- 430378; Z29572; Hs.2556; tumor necrosis factor receptor superfamily; IL2; 6.08
- 426116; AA868729; Hs.144694; ESTs; none, none; 6.06
- 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 6.05
- 25 425721; AA383588; Hs.288545; ESTs, Weakly similar to T29012 hypotheti; zf-C2H2; TM=M; SS=N; 6.05
- 429228; A1553633; Hs.356828; ESTs; none, none; 6.05
- 421757; Z20897; Hs.296259; paraoxonase 3; Arylesterase; 6.04
- 437669; A1358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA; none, pkinase, pkinase_C; 6.03
- 419608; AW997938; Hs.30786; ATP-binding cassette, sub-family C (CFTR; ABC_tran, ABC_membrane; TM=Y; SS=M; 6.02
- 30 428667; A1375550; Hs.346868; nucleolar protein p40; homolog of yeast ; none, none; 6.01
- 432731; R31178; Hs.287820; fibronectin 1; fn1, fn2, fn3, none; 6.95
- 446568; H95741; Hs.17914; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 5.95
- 450656; AA010539; Hs.18912; unnamed protein product; zf-C2H2; 5.94
- 35 418460; M26315; Hs.85258; CD8 antigen, alpha polypeptide (p32); Ig; TM=Y; SS=M; 5.94
- 424054; AA334511; Hs.26638; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 5.94
- 408048; NM_007203; Hs.42322; A kinase (PRKA) anchor protein 2; Paralemin; TM=M; SS=N; 5.94
- 438670; A1275803; Hs.123428; ESTs; none; NA; NA; 5.91
- 424238; AA337401; Hs.137635; ESTs; none; TM=M; SS=M; 5.90
- 444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2, none; 5.89
- 40 423690; AA329648; Hs.23804; ESTs, Weakly similar to PN0099 son3 prot; ion_trans, IQ, none; 5.88
- 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase; TM=M; SS=N; 5.81
- 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor ; Ig; TM=Y; SS=M; 5.81
- 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none; TM=Y; SS=M; 5.80
- 420340; NM_000734; Hs.97087; CD32 antigen, zeta polypeptide (TIT3 com; ITAM; TM=M; SS=M; 5.79
- 45 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar_tr; TM=Y; SS=N; 5.79
- 413441; A1929374; Hs.75367; Src-like-adaptor; SH2, SH3; TM=M; SS=N; 5.79
- 443257; A1334040; Hs.11614; HSPC065 protein; trypsin; TM=M; SS=N; 5.76
- 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, re; Ig; TM=Y; SS=N; 5.70
- 435299; A1745458; Hs.343026; ESTs, Weakly similar to T20583 hypotheti; none; NA; NA; 5.69
- 50 415995; NM_004573; Hs.355888; phospholipase C, beta 2; C2, PI-PLC-Y, PI-PLC-X; TM=M; SS=N; 5.67
- 436772; AW975688; Hs.348918; metallothionein 1E (functional); 7tm_2, HRM, none; 5.67
- 431385; BE178536; Hs.11090; membrane-spanning 4-domains, subfamily A; none, none; 5.66
- 419833; AA251131; Hs.220697; Homo sapiens tryptophanyl-HRNA synthetas; WHEP-TRS, tRNA-synt_1b, none; 5.66
- 421859; AA356620; Hs.108947; KIAA0050 gene product; ank, PH, ArtGap; 5.64
- 55 407756; AA116021; Hs.38260; ubiquitin specific protease 18; UCH-1, UCH-2; 5.63
- 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1; TM=Y; SS=M; 5.63
- 423533; NM_014339; Hs.129751; interleukin 17 receptor; none; TM=Y; SS=M; 5.63
- 419577; L36531; Hs.91296; integrin, alpha 8; integrin_A, FG-GAP; TM=Y; SS=N; 5.61
- 452561; A1692181; Hs.49169; KIAA1634 protein; TPR, PDZ, WW, Guanylate_kin; TM=M; SS=N; 5.61
- 60 426577; A1657119; Hs.351582; troponin I, cardiac; none; TM=M; SS=N; 5.60
- 425509; AF079363; Hs.158213; sperm associated antigen 6; Armadillo_seg, HEAT_PBS; TM=M; SS=N; 5.58
- 453852; AW961818; Hs.211592; MUM2 protein; pkinase, DAG_PE-bind, C2, pkinase_C, none; 5.57
- 421924; BE514514; Hs.109606; coronin, actin-binding protein, 1A; WD40, Ikh_C; TM=M; SS=N; 5.57
- 448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 5.55
- 65 431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha ; FG-GAP, Rhabd_glycop, integrin_A; TM=Y; SS=M; 5.53
- 410257; BE244044; Hs.61469; hypothetical protein; none, none; 5.53
- 441965; AA972712; Hs.269737; ESTs; pkinase, Activin_recpt, TSPN, Collagen; 5.52
- 413934; U03056; Hs.75619; hyaluronoglucosaminidase 1; integrin_B, Glyco_hydro_56; 5.52
- 424517; A1539443; Hs.137447; Homo sapiens cDNA FLJ12169 fls, clone MA; SH2, STAT, STAT_bnd, STAT_prot, none; 5.50
- 70 447357; A1375922; Hs.132821; ESTs; FMO-like, FMO-like; 5.46
- 422109; S73265; Hs.1473; gastrin-releasing peptide; Bombesin, Defensin_propept; TM=M; SS=M; 5.46
- 447033; A1357412; Hs.157601; Predicted gene: Eos cloned; secreted w/v; none, none; 5.45
- 417412; X16896; Hs.82112; interleukin 1 receptor, type I; Ig, TIR; TM=M; SS=M; 5.45
- 436057; AJ004832; Hs.5038; neuropathy target esterase; cNMP_binding, Ion_trans, Patatin; TM=Y; SS=M; 5.41
- 75 417497; AW402482; Hs.82212; CD53 antigen; transmembrane4; TM=Y; SS=M; 5.41
- 439285; AL133916; Hs.47860; hypothetical protein FLJ20093; Ig, pkinase, LRR, LRRNT, LRRCT, none; 5.40
- 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1; TM=Y; SS=M; 5.40
- 443623; AA345519; Hs.9641; complement component 1, q subcomponent ; C1q, Collagen; 5.40
- 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrat; SH3, HS1_rep; TM=M; SS=N; 5.38
- 437275; AW976035; Hs.292396; ESTs, Weakly similar to A47582 B-cell gr; none, Frizzled, Fz; 5.37
- 80 419650; BE280337; Hs.194693; solute carrier family 7 (cationic amino ; aa_permeases; TM=Y; SS=M; 5.37
- 449853; AF006823; Hs.24040; potassium channel, subfamily K, member 3; ion_trans; TM=Y; SS=M; 5.36
- 442434; AA995787; Hs.129583; ESTs; IRK, none; 5.36
- 428065; A1634046; Hs.157313; ESTs; ICE_p20, DED, ICE_p10, ICE_p20, DED; 5.36

- 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to; ras, arl, TK; 5.33
 425638; NM_012337; Hs.158450; nasopharyngeal epithelium specific probe; none; TM=M; SS=N; 5.32
 419034; NM_002110; Hs.89555; hamocytic cell kinase; SH2, SH3, pkinase; TM=M; SS=N; 5.32
 452416; AA026115; Hs.114777; ESTs; none; Porphobil deam; 5.29
 425205; NM_005854; Hs.155106; receptor (calcitonin) activity modifying; none; TM=Y; SS=N; 5.29
 440475; AI807671; Hs.24040; potassium channel, subfamily K, member 3; ion, trans, none; 5.28
 417355; D13166; Hs.82002; endothelin receptor type B; 7tm_1, zf-C3HC4, fn3, SPRY, KRAB, zf-C2H2, rve, zf-B_box; TM=Y; SS=M; 5.28
 436120; AI248193; Hs.119860; ESTs; hema_1, none; 5.27
 418307; U70867; Hs.83974; solute carrier family 21 (prostaglandin); OATP_N, OATP_C; TM=Y; SS=M; 5.27
 409745; AA077391; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7tm_1, zf-C3HC4, fn3, SPRY, KRAB, zf-C2H2, rve, zf-B_box; TM=Y; SS=M; 5.26
 421554; AW137676; Hs.97775; ESTs; none, none; 5.23
 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0462; none, none; 5.22
 410434; AF051152; Hs.63668; toll-like receptor 2; LRR, LRRCT, TIR; TM=M; SS=M; 5.21
 421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2 (7tm_1; TM=Y; SS=M; 5.19
 400261; Hs.1802; Eos Control; ig, MHC, IL_beta; TM=Y; SS=M; 5.19
 436856; AI469355; Hs.127310; ESTs; pkinase, rmt; TM=M; SS=N; 5.18
 408761; AA057264; Hs.238936; ESTs; Weakly similar to (define not ava; 7tm_1, none; 5.17
 425023; AW956889; Hs.154210; EDG-1 (endothelial differentiation, sph; 7tm_1; TM=Y; SS=M; 5.16
 452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, sub; ABC, tran, ABC, membrane, SRP54, Thymidylate_kin; TM=Y; SS=M; 5.16
 451220; AF124251; Hs.26054; novel SH2-containing protein 3; SH2; TM=M; SS=N; 5.15
 417771; AA804698; Hs.82547; retinoic acid receptor responder (lazarus; none, none; 5.14
 424925; NM_002432; Hs.153837; myeloid cell nuclear differentiation ant; PAAD, DAPIN, HIN; 5.14
 451099; RS2795; Hs.25954; interleukin 13 receptor, alpha 2; fn3; TM=Y; SS=M; 5.13
 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a; 7tm_1; TM=Y; SS=M; 5.12
 423196; AK001866; Hs.125139; hypothetical protein FLJ11004; none; TM=M; SS=N; 5.12
 433671; AW138797; Hs.132906; 19A24 protein; ig; TM=M; SS=M; 5.11
 426457; AW894667; Hs.380138; chimerin (chimaerin) 1; DAG, PE-bind, RhoGAP, SH2; TM=M; SS=N; 5.06
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit; vwa, Integrin_A, FG-GAP; TM=Y; SS=M; 5.05
 418185; AW958272; Hs.347326; intercellular adhesion molecule 2 (ICAM; none; TM=Y; SS=M; 5.05
 437352; AL335957; Hs.284181; hypothetical protein DKFZp434P0531; DUF221; TM=Y; SS=M; 5.03
 457918; AL359590; Hs.162604; hypothetical protein DKFZp762M186; PLDc; TM=M; SS=N; 5.02
 452924; AW580939; Hs.97199; complement component C1q receptor; EGF, lectin_c, Tissue_fac, Xlink, TIL; TM=Y; SS=M; 5.02
 426535; AU077012; Hs.288582; ESTs; Weakly similar to ubiquitous TPR m; Kunitz_BPTI, Kunitz_BPT1, 7tm_2, HRM; 4.99
 432805; X94630; Hs.3107; CD97 antigen; 7tm_2, EGF, GPS, FecCD; TM=Y; SS=M; 4.95
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; SH3, PH, WW, RhoGAP; 4.95
 414291; AD289619; Hs.13040; G protein-coupled receptor 86; 7tm_1; TM=Y; SS=M; 4.94
 428981; BE313077; Hs.93135; ESTs; Weakly similar to ALU2_HUMAN ALU S; none, rmt; 4.92
 451154; AA015879; Hs.33536; ESTs; TIMP; none; 4.92
 435730; AB020635; Hs.4984; KIAA0828 protein; AdoHcyase, TrkA-N, 2-Hacid_DH_C; TM=M; SS=N; 4.90
 413011; AW068115; Hs.821; biglycan; LRR, LRRNT; 4.90
 422732; AA577455; Hs.24937; transformer-2 alpha (htra-2 alpha); rmt, lg; 4.89
 417015; M83772; Hs.80876; flavin containing monooxygenase 3; FMO-like, pyr_redox; TM=Y; SS=M; 4.88
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII KAL OR; PLDc; TM=M; SS=N; 4.88
 439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein; 7tm_1, LRR; TM=Y; SS=N; 4.87
 405102; C15001220; gi|4469558|gb|AAD21311.1| (AF; DAG, PE-bind, PH, RhoGEF, DC1; 4.86
 422795; AB033109; Hs.375510; KIAA1283 protein; 7tm_1, kazal, A2M, A2M_N; TM=Y; SS=M; 4.84
 432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C; TM=M; SS=N; 4.83
 414936; C14774; gb:C14774 Clontech human aorta polyA mRNA; ank, pkinase, death; none; 4.82
 430152; AB001325; Hs.234642; aquaporin 3; MIP; TM=Y; SS=M; 4.82
 444838; AV651680; Hs.208558; ESTs; Integrin_A, FG-GAP; none; 4.81
 410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-recept; SH2, Y_phosphatase, DSPc; TM=M; SS=N; 4.81
 453107; NM_016113; Hs.279746; vanilloid receptor-like protein 1; ank, ion, trans; TM=Y; SS=N; 4.80
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD, ICE_p10, ICE_p20; 4.80
 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 tis, clone C; none, SDF, sugar_br; 4.78
 419542; AA366037; Hs.90911; solute carrier family 16 (monocarboxylic; none, none; 4.76
 438899; AF085833; Hs.135624; ESTs; none, PI3_P14_kinase, PI3Ka, PI3K_C2, PI3K_rbd, PI3K_p85B; 4.75
 427418; AA402587; Hs.356667; LAT1-3TM protein; none, none; 4.75
 431924; AK000850; Hs.272203; Homo sapiens cDNA FLJ20843 tis, clone AD; SH3; none; 4.73
 424218; AF031824; Hs.143212; cystatin F (leukocystatin); cystatin; 4.72
 414888; AL039185; Hs.77558; thyroid hormone receptor interactor 7; HMG14_17; none; 4.72
 416178; AJ808527; Hs.192822; serologically defined breast cancer ant; none; TM=M; SS=N; 4.71
 430037; BE409649; Hs.227789; mitogen-activated protein kinase-activat; pkinase; TM=M; SS=N; 4.71
 451527; AF022813; Hs.26518; transmembrane 4 superfamily member 7; none, none; 4.71
 453870; AW385001; Hs.8042; Homo sapiens cDNA: FLJ23173 tis, clone L; FG-GAP, Integrin_A, NIF; 4.71
 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 tis, clone A; 7tm_3; none; 4.70
 438543; AA810141; Hs.192182; ESTs; SH2, pkinase; none; 4.70
 424943; AU077260; Hs.153924; death-associated protein kinase 1; ank, pkinase, death, SPRY, SAP, Ribosomal_L24e, SRP54, dDENN, DENN_u, DENN; TM=M; SS=N; 4.70
 438113; AI467908; Hs.8882; ESTs; 7tm_1; none; 4.70
 422164; NM_014312; Hs.112377; cortic al thymocyte receptor (X. laevis; ig, Gemini_mov; TM=Y; SS=M; 4.69
 414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1; TM=Y; SS=M; 4.69
 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker; aldo, ka_red; none; 4.67
 432314; AA533447; Hs.285173; ESTs; Xlink; none; 4.66
 453518; AW503205; Hs.27268; gb:UL-HF-BN0-akt-g-03-0-ULr1 NIH_MGC_50; SH3, PH, RhoGEF; TM=M; SS=N; 4.66
 418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase; pkinase, CNH; TM=M; SS=N; 4.66
 446063; AJ720140; Hs.151079; ESTs; ISK_Channel; none; 4.65
 454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member; aldedh; 4.65
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC; TM=Y; SS=N; 4.65
 443402; U77846; Hs.9295; elastin (supraaortic stenosis; none, PDZ, LIM, pkinase; 4.65
 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA; TM=Y; SS=N; 4.64
 427535; R29543; Hs.2164; pro-platelet basic protein (includes pia; ILB; TM=M; SS=M; 4.64
 437119; AI379921; Hs.177043; XP_171387 similar to rhotekin; none, none; 4.63
 411779; AA292811; Hs.72050; non-metastatic cells 5, protein express; NDK; 4.63
 429784; M89796; Hs.30; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=N; 4.62

- 415934; NM_000928; Hs.992; phospholipase A2, group 1B (pancreas); phoslip; 4.61
 408873; AL046017; Hs.356216; calmodulin 2 (phosphorylase kinase, delta; none, none; 4.61
 426432; AF001601; Hs.169857; paraoxonase 2; Arylesterase; TM=M; SS=N; 4.59
 444805; AB007899; Hs.12017; homolog of yeast ubiquitin-protein ligase; WW, HECT, RNA_pol_A, none; 4.59
 5 408000; L11690; Hs.198589; bullous pemphigoid antigen 1 (230/240kD); efhand, spectrin, GAS2, SH3, Plectin, RA, Xylose_Isom, FliD, bZIP, Tropomyosin, Myc-LZ, M, Idh, C, CH, AIP3; TM=M; SS=N; 4.59
 431087; H12723; Hs.290791; ESTs; Ion_trans; none; 4.58
 425465; L18964; Hs.1904; protein kinase C, iota; pkinase, DAG, PE-bind, pkinase_C, OPR; TM=M; SS=N; 4.58
 10 422427; AA310514; Hs.96692; ESTs; PH, Els, CH, spectrin, Ca_channel_B, none; 4.57
 441527; W19504; Hs.7884; solute carrier family 21 (organic anion); OATP_N, OATP_C; TM=Y; SS=N; 4.56
 416464; NM_000132; Hs.79345; coagulation factor VIII, procoagulant co; Cu-oxidase, F5_F8_type_C; 4.56
 421233; AA209534; Hs.284243; tetraspan NET-6 protein; transmembrane4; TM=Y; SS=M; 4.56
 422311; AF073515; Hs.114948; cytokine receptor-like factor 1; fn3; TM=M; SS=N; 4.55
 15 444895; A1674383; Hs.22891; solute carrier family 7 (cationic amino); ASC, death, TNFR_c6; 4.55
 428141; D50402; Hs.182611; solute carrier family 11 (proton-coupled); Nramp; TM=Y; SS=N; 4.55
 410290; AA02307; Hs.322844; hypothetical protein DKFZp564A176; Sema, PSI, TIG, integrin_B; TM=Y; SS=M; 4.54
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg, UQ_con, none; 4.54
 450086; AW016343; Hs.233301; ESTs; ank, death, ZU5, NMU, none; 4.54
 20 438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nuclear trans; HLH, PAS, IL8; TM=M; SS=N; 4.54
 414788; X78342; Hs.77313; cyclin-dependent kinase (CDC2-like) 10; pkinase; TM=M; SS=N; 4.53
 429109; AL008637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3, OPR, PX; TM=M; SS=N; 4.53
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6, ET, PLA2_inh; 4.53
 411213; AA676939; Hs.69285; neuropilin 1; MAM, F5_F8_type_C, CUB, CUB, MAM, F5_F8_type_C; 4.53
 25 434158; T86534; Hs.14372; ESTs; adenylate kinase, none; 4.52
 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fls, clone CO; pkinase, Furin-like, Recep_L_domain, none; 4.52
 447341; AF106941; Hs.18142; arrestin, beta 2; arrestin, arrestin_C, PX, PH, PLDc; 4.52
 447656; NM_003726; Hs.19126; src kinase-associated phosphoprotein of; SH3, PH; TM=M; SS=N; 4.51
 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related; SH2, SH3, pkinase; TM=M; SS=N; 4.51
 30 422893; X98411; Hs.380077; myosin IF; SH3, myosin_head, IQ; TM=M; SS=N; 4.51
 407202; N58172; Hs.109370; ESTs; F5_F8_type_C, pkinase, Els, none; 4.51
 447079; AA280057; Hs.105280; ESTs; Weakly similar to dJ963K23.2 [Hs]; zf-C2H2, zf-C3HC4, UIM; TM=M; SS=N; 4.51
 450747; AL064821; Hs.129953; ESTs; Highly similar to 1818357A EWS gen; rrm, zf-RanBP, GAS2; 4.50
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig, pkinase; TM=Y; SS=M; 4.50
 35 453856; AA804769; Hs.379109; PDZ-LIM protein mystique; LIM, PDZ; TM=M; SS=N; 4.49
 432744; AA988835; Hs.38664; ESTs; none, none; 4.49
 419032; W81330; Hs.99877; ESTs; Highly similar to JAK3B [Hs]; pkinase, SH2, Insulin, pkinase, SH2; 4.48
 444009; AJ380792; Hs.135104; ESTs; TNFR_c6, TIL, none; 4.48
 426416; AW612744; Hs.169824; killer cell lectin-like receptor subfamily; lectin_c; TM=Y; SS=M; 4.48
 412802; U41518; Hs.74602; aquaporin 1 (channel-forming integral pr; MIP; TM=Y; SS=M; 4.48
 40 447217; BE465754; Hs.17778; neuropilin 2; CUB, MAM, F5_F8_type_C; TM=M; SS=M; 4.47
 408771; AW732573; Hs.47584; potassium voltage-gated channel, delayed; efhand, Ion_trans, K_tetra, none; 4.47
 435049; AL122067; Hs.4746; hypothetical protein FLJ21324; none; TM=M; SS=N; 4.46
 413276; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin; 4.45
 423804; AW403448; Hs.1706; interferon-stimulated transcription factor; IRF, zf-C3HC4, IIR, zf-RanBP; TM=M; SS=N; 4.45
 45 434308; N51517; Hs.47282; ESTs; pkinase, pkinase_C, none; 4.45
 434448; W26667; Hs.184581; Homo sapiens cDNA FLJ14821 fls, clone OV; pkinase, pkinase_C; 4.45
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF, laminin_Nterm, integrin_B; 4.44
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN, MK; TM=M; SS=Y; 4.44
 430259; BE550182; Hs.375142; RalGEF-like protein 3, mouse homolog; fn3, RA, RasGEF; TM=M; SS=M; 4.44
 50 436001; AW903849; Hs.173840; HUEL (C4orf1)-interacting protein; ig; TM=M; SS=M; 4.44
 452355; N54926; Hs.29202; G protein-coupled receptor 34; 7tm_1, OATP_C; TM=Y; SS=N; 4.43
 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory su; SH2, none; 4.43
 410068; A1633888; Hs.58435; FYN-binding protein (FYB-120/130); SH3; TM=M; SS=N; 4.43
 449961; AW265634; Hs.133100; ESTs; pkinase, Furin-like, Recep_L_domain, none; 4.42
 55 451734; NM_006176; Hs.26944; neurogranin (protein kinase C substrate); IQ, 7tm_1; TM=M; SS=N; 4.42
 410598; AB17130; Hs.9195; Homo sapiens cDNA FLJ13698 fls, clone PL; RasGEF, PRK; 4.42
 439411; AA044876; Hs.58043; ESTs; Weakly similar to CYA2_HUMAN ADENY; guanylate_cyc; TM=Y; SS=M; 4.42
 433179; AW362945; Hs.162459; ESTs; Armadillo_seg, none; 4.42
 414849; AW372721; Hs.291623; ESTs; Weakly similar to unnamed protein; pkinase, none; 4.42
 60 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD, helicase_C, CARD; TM=M; SS=N; 4.41
 445903; AJ347487; Hs.132781; class I cytokine receptor; fn3; TM=Y; SS=N; 4.41
 438507; AA809052; Hs.356627; ESTs; none, none; 4.41
 409524; AW402151; Hs.54673; tumor necrosis factor (ligand) superfamily; TNF; TM=Y; SS=M; 4.40
 453037; AA045175; Hs.17914; ESTs; none; TM=Y; SS=M; 4.40
 65 412228; AW503785; Hs.73792; complement component (3d/Epstein Barr vt; sush2; TM=Y; SS=M; 4.40
 451035; AL076785; Hs.430; plastin 1 (I isoform); efhand, CH, Adaplin_N; 4.40
 415149; X12451; Hs.78056; cathepsin L; Peptidase_C1; 4.39
 408105; AW152207; Hs.270977; ESTs; Weakly similar to I38022 hypotheti; Y_phosphatase, carb_anhydrase, DSPc; none; 4.39
 70 423099; NM_002837; Hs.123641; protein tyrosine phosphatase, receptor t; fn3, Y_phosphatase, DSPc, COX6C; TM=M; SS=M; 4.39
 436330; AW450572; Hs.257316; ESTs; pkinase, zf-C4, ERM, CNH, none; 4.39
 433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE_p10, ICE_p20; 4.39
 429747; M87507; Hs.2480; caspase 1, apoptosis-related cysteine pr; CARD, ICE_p10, ICE_p20; 4.39
 426410; BE298446; Hs.305890; BCL2-like 1; Bcl-2, BH4, none; 4.38
 434511; R28982; Hs.18106; ESTs; pkinase, Glyco_hydro_39; 4.38
 75 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M; SS=N; 4.37
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor t; fn3, Y_phosphatase, MAM; TM=Y; SS=M; 4.36
 432583; AW023624; Hs.162282; potassium channel TASK-4; potassium chan; Ion_trans_X; TM=Y; SS=M; 4.36
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high aff; SDF; TM=Y; SS=M; 4.36
 426828; NM_000020; Hs.172670; activin A receptor type II-like 1; pkinase, Activin_rec; TM=M; SS=M; 4.36
 80 448444; AW818436; Hs.351305; solute carrier family 16 (monocarboxylic; none; TM=Y; SS=M; 4.36
 437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbon; HCO3_cotransp; TM=Y; SS=N; 4.36
 429670; L01087; Hs.211593; protein kinase C, theta; DAG, PE-bind, pkinase, pkinase_C, DNA_pol_viral_N, PHD, DC1; TM=M; SS=N; 4.35
 421195; BE464560; Hs.133017; ESTs; none, none; 4.35

- 415758; BE270465; Hs.78793; protein kinase C, zeta; pkinase,DAG_PE-bind,pkinase_C,OPR; 4.35
 457001; J03258; Hs.2062; vitamin D (1,25-dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metallothio_5;TM=M;SS=N; 4.34
 419150; T29618; Hs.89640; TEK tyrosine kinase, endothelial (venous); EGF,fn3,pkinase,ig,laminin_EGF,DSL;TM=Y;SS=M; 4.34
 440675; AWO05054; Hs.279788; ESTs, Weakly similar to KCC1_HUMAN CALCI; pkinase,none; 4.34
 429557; D13526; Hs.2465; KIAA0001 gene product; putative G-protein; 7tm_1;TM=Y;SS=M; 4.34
 414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antigen); transmembrane4;TM=Y;SS=M; 4.34
 425771; BE561776; Hs.159494; Bruton agammaglobulinemia tyrosine kinase; SH2,SH3,pkinase,PH,BTK;TM=M;SS=N; 4.34
 452124; AA454220; Hs.61170; ESTs; pkinase,none; 4.33
 407775; NM_004914; Hs.38772; RAB36, member RAS oncogene family; ras,arf;TM=M;SS=N; 4.33
 452688; AA721140; Hs.49930; ESTs, Weakly similar to putative p150 [H; SH3,none; 4.33
 434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase;TM=M;SS=N; 4.32
 445330; R52656; Hs.21691; ESTs; 7tm_1,none; 4.32
 437527; A1241019; Hs.145644; ESTs; PIP5K,none; 4.32
 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1; TIMP,pkinase,DAG_PE-bind,RBD; 4.31
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated); Ig,ITAM,Zn_cus;TM=Y;SS=M; 4.31
 416269; AA177138; Hs.161671; ESTs; pkinase,DAG_PE-bind,RBD,none; 4.30
 425458; H89317; Hs.182889; ESTs; lon_trans,none; 4.30
 424206; NM_003734; Hs.198241; amine oxidase, copper containing 3 (vasc; Cu_amine_oxid,Cu_amine_oxidN2,Cu_amine_oxidN3;TM=M;SS=M; 4.29
 451876; T63141; ; gbyy99a12.s1 Stratagene lung (937210) H; SH3,none; 4.29
 417801; AA417383; Hs.82582; integrin, beta-like 1 (with EGF-like rep; EGF; 4.29
 435240; A1025435; Hs.117532; ESTs; GHMP_kinases,none; 4.27
 444051; N48373; Hs.10247; activated leucocyte cell adhesion molecu; none,none; 4.26
 423523; AW299828; Hs.193580; ESTs; none,none; 4.26
 426274; D38122; Hs.2007; tumor necrosis factor (ligand) superfamily; TNF;TM=Y;SS=N; 4.26
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 14; Exo_endo_phos,SH2;TM=M;SS=N; 4.26
 448386; AB037750; Hs.21061; KIAA1329 protein; PKD,BNR;TM=Y;SS=M; 4.26
 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4;TM=Y;SS=M; 4.26
 427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, for; ig,pkinase;TM=Y;SS=M; 4.26
 416602; NM_006159; Hs.367895; Protein kinase C-binding protein NELL2; EGF,wc,TSPN; 4.25
 436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.25
 436494; AA720997; Hs.128295; ESTs; none,CAP_GLY,HCO3_cotransp,Glyco_hydro_63,PH; 4.24
 439668; A1091277; Hs.302634; frizzled (Drosophila) homolog 8; Frizzled,Fz,7tm_2,toxin_2;TM=Y;SS=M; 4.24
 418255; AW135405; Hs.37251; ESTs; pkinase,none; 4.24
 400328; X87344; ; transporter 2, ATP-binding cassette, sub; none;TM=Y;SS=N; 4.24
 405121; ; mitogen-activated protein kinase 8 inter; Cys_knot,TGF-beta,vwa,wc,wild,TIL,DUF139; 4.24
 425795; AJ000479; Hs.159543; EDG-6 (endothelial differentiation, G-p; 7tm_1;TM=Y;SS=M; 4.23
 406786; AW161678; Hs.111334; ferritin, light polypeptide; ferritin;TM=M;SS=N; 4.23
 449843; R85337; Hs.24030; solute carrier family 31 (copper transpo; none;TM=Y;SS=M; 4.23
 445657; AW612141; Hs.279575; Homo sapiens G-protein coupled receptor ; 7tm_1;TM=Y;SS=M; 4.23
 413795; AL040178; Hs.142003; ESTs; none,pkinase,LRR,LRRCT; 4.22
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran,M,SMC_N,SMC_C,DUF164,none; 4.22
 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M;SS=N; 4.22
 417318; AW953937; Hs.240845; ESTs; SH3,PH,RhoGEF; 4.21
 424291; AL120051; Hs.144700; ephrin-B1; Ephrin;TM=Y;SS=M; 4.21
 408279; AF216965; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, com; none,none; 4.20
 432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 4.20
 424618; L29472; Hs.1802; major histocompatibility complex, class ; Ig,MHC_II_beta;TM=Y;SS=M; 4.19
 445633; A145338; Hs.17287; ESTs, Weakly similar to S26689 hypotheli; IRK,none; 4.19
 432882; NM_013257; Hs.279696; serum/glucocorticoid regulated kinase-II; pkinase,PX,pkinase_C; 4.19
 425481; AW978162; Hs.372811; ESTs; none,Oxysterol_BP; 4.19
 429061; Y14039; Hs.195175; CASP8 and FADD-like apoptosis regulator; ICE_p20,DED;TM=M;SS=N; 4.18
 401083; ; NM_016582; Homo sapiens peptide transpo; PTR2;TM=Y;SS=M; 4.18
 420676; AA34780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG_PE-bind,none; 4.18
 424377; AF081675; Hs.146322; killer cell lectin-like receptor subfamily; lectin_c;TM=Y;SS=M; 4.17
 424148; BE242274; Hs.1741; Integrin, beta 7; Integrin_B,EGF,metalthio,PSI;TM=Y;SS=M; 4.17
 421391; AW304350; Hs.191958; immunoglobulin superfamily receptor tran; ig,none; 4.17
 452100; A168668; Hs.379032; inositol polyphosphate-5-phosphatase, 75; Exo_endo_phos,RhoGAP,none; 4.17
 413969; X14034; Hs.75648; phospholipase C, gamma 2 (phosphatidylin; SH2,SH3,C2,PH,PI-PLC-Y,PI-PLC-X,PDGF; 4.17
 422310; AA136622; Hs.98370; cytochrome P450, subfamily IIS, polypept none,pkinase,fn3,ig; 4.17
 444034; AL161957; Hs.10177; pleckstrin homology domain interacting p; E1-
 E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase,Ribosomal_S15,bromodomain,WD40;TM=M;SS=N; 4.16
 450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypotheli; ABC_tran,ABC_membrane,ig,MHC_II_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 4.16
 407245; X90568; Hs.172004; titin; fn3,ig,SGXXSG,pkinase;TM=M;SS=N; 4.16
 418962; AA714835; Hs.271863; ESTs; RhoGAP,SH2,pkinase,POLO_box,none; 4.15
 410590; BE615216; Hs.64746; chloride intracellular channel 3; none;TM=M;SS=N; 4.15
 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 4.15
 446967; A1699629; Hs.156781; ESTs; none,none; 4.14
 432176; AW090386; Hs.112276; arrestin, beta 1; arrestin,arrestin_C,none; 4.14
 452571; W31518; Hs.34665; ESTs; none;TM=M;SS=N; 4.14
 425421; L11669; Hs.157145; tetracycline transporter-like protein; sugar_tr;TM=Y;SS=M; 4.14
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase; 4.14
 417871; AA521368; Hs.24252; ESTs; IBB,Armadillo_seg,none; 4.13
 429819; AL133011; Hs.253920; Homo sapiens mRNA; cDNA DKFZp434P201 (fr; none,none; 4.12
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C; 4.12
 429623; NM_005308; Hs.211569; G protein-coupled receptor kinase 5; pkinase,RGS;TM=M;SS=N; 4.12
 413019; BE281604; Hs.75140; low density lipoprotein-related protein-; none;TM=M;SS=Y; 4.12
 434071; AF116653; Hs.34192; Homo sapiens PRO0823 mRNA, complete cds; none;TM=M;SS=N; 4.11
 434779; AF153815; Hs.50151; potassium inwardly-rectifying channel, s; IRK;TM=Y;SS=N; 4.11
 449656; AA002008; Hs.188633; ESTs; PIP5K,none; 4.11
 406403; ; NM_002162; Homo sapiens intercellular ad; ig;TM=Y;SS=M; 4.10
 427732; NM_002980; Hs.2199; secretin receptor; 7tm_2,HRM;TM=M;SS=M; 4.10
 437608; AA761605; Hs.292308; ESTs, Weakly similar to ALU1_HUMAN ALU S; pkinase,RIO1,none; 4.10
 432885; AA595607; Hs.368129; ESTs, Weakly similar to ALU1_HUMAN ALU S; pkinase,pkinase_C,none; 4.10

- 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase, pkinase_C, HR1; TM=M; SS=N; 4.10
 418342; BE002723; Hs.334330; lepin receptor; ICE_p20, DED, ICE_p10, ICE_p20, DED; 4.10
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese; 4.10
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3, RhoGAP, FCH; TM=M; SS=N; 4.10
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz, Frizzled, 7tm_2; TM=Y; SS=M; 4.10
 437952; D63209; Hs.5944; solute carrier family 11 (proton-coupled; none; TM=Y; SS=M; 4.10
 432827; Z68128; Hs.3109; Rho GTPase activating protein 4; FCH, RhoGAP, SH3; TM=M; SS=N; 4.09
 435140; AA668123; Hs.134170; ESTs; none, none; 4.09
 422627; BE336857; Hs.116787; transforming growth factor, beta-induced; Fasciclin, ABC_tran, ABC_membrane, GTP_EFTU; TM=M; SS=M; 4.08
 428483; AI908539; Hs.184592; KIAA0344 gene product; none, none; 4.08
 446232; AI281848; Hs.194691; retinoic acid induced 3; 7tm_3, none; 4.07
 431674; AA089001; Hs.301642; G-protein coupled receptor; none, GCV_H; 4.07
 409686; AK000002; Hs.55879; Homo sapiens mRNA; cDNA DKFZp434L0827 (f; ABC_tran, ABC_membrane; TM=M; SS=M; 4.07
 441518; AW161697; Hs.294150; ESTs; Y_phosphatase, DSPc, none; 4.07
 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3, ank; TM=M; SS=N; 4.06
 436982; AB018305; Hs.5378; spondin 1, (f-spondin) extracellular mat; lsp_1, Reeler; 4.05
 420361; N92054; Hs.194718; zinc finger protein 265; zf-RanBP, 7tm_1; 4.05
 439549; AW937885; Hs.137314; ESTs; SH2, none; 4.04
 419981; AA897581; Hs.128773; ESTs; pkinase, DAG_PE-bind, pkinase_C, OPR, none; 4.04
 418836; AI655499; Hs.161712; ESTs; pkinase, Activin_recpt, PDZ, ZU5, death; 4.04
 408806; AW847814; Hs.75608; Homo sapiens cDNA; FLJ21532 f1s, clone C; SH3, PDZ, Guanylate_kin, none; 4.04
 432106; N58323; Hs.269098; ESTs; Weakly similar to RETROVIRUS-RELAT; SH3, PDZ, Guanylate_kin, none; 4.03
 426086; T94907; Hs.188572; ESTs; PH, Ets, CH, spectrin, Ca_channel_B, none; 4.03
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 4.03
 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha, arf; TM=M; SS=N; 4.03
 416350; AF188625; Hs.189507; phospholipase A2, group IID; phospholip; TM=M; SS=Y; 4.02
 434457; AF141332; Hs.200333; apolipoprotein B48 receptor; none; TM=M; SS=N; 4.02
 414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain, PHD, PWWP, zf-MYND; TM=M; SS=N; 4.02
 425694; U51333; Hs.159237; hexokinase 3 (white cell); hexokinase, hexokinase_2; TM=M; SS=N; 4.02
 449943; AF104266; Hs.24212; latrophilin; 7tm_2, GPS, Gal_Lectin, OLF, Latrophilin, HRM; TM=Y; SS=M; 4.01
 408938; AA059013; Hs.22607; ESTs; fn3_Y_phosphatase, carb_anhydase, none; 4.01
 426839; M74782; Hs.172689; interleukin 3 receptor, alpha (low affin; none; TM=M; SS=M; 4.00
 422282; AF019225; Hs.114309; apolipoprotein L; MotA_ExcB; TM=Y; SS=M; 4.00
 410726; AI623859; Hs.15936; ESTs; pkinase, pro_isomerase, none; 4.00
 428318; BE300110; Hs.183842; ubiquitin B; lipocalin, aldedh, ubiquitin, IRK; 4.00
 440188; AK001812; Hs.7036; N-Acetylglucosamine kinase; ROK; TM=M; SS=N; 3.99
 429952; AF080158; Hs.226573; inhibitor of kappa light polypeptide gen; pkinase, ubiquitin, Enterotoxin_A, PHO4, pkinase, ubiquitin; 3.99
 414700; H63202; Hs.38163; ESTs; 7tm_1; TM=Y; SS=M; 3.99
 432269; NM_002447; Hs.2942; macrophage stimulating 1 receptor (c-met; pkinase, Sema, PSI, TIG, A4_EXTRA; TM=M; SS=M; 3.99
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none; TM=M; SS=N; 3.98
 427541; AI798983; Hs.375835; solute carrier family 35 (CMP-sialic acid; none, none; 3.98
 440248; AA876138; Hs.369458; ESTs; SH2, none; 3.98
 437400; AB011542; Hs.5599; EGF-like-domain, multiple 5; TNFR_c6, laminin_EGF; TM=Y; SS=N; 3.98
 425262; D87119; Hs.155418; GS3955 protein; pkinase; 3.98
 420166; AW732276; Hs.95583; transmembrane 4 superfamily member (tet; transmembrane4; TM=Y; SS=M; 3.98
 437151; AA745618; Hs.380121; BNP homolog, SMAR1 homolog; none, none; 3.98
 443574; U83993; Hs.321709; purinergic receptor P2X, ligand-gated ion; P2X_receptor; TM=Y; SS=M; 3.97
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49, EGF, ig, Neuregulin; TM=M; SS=N; 3.97
 411574; BE242842; Hs.6780; protein tyrosine kinase 9-like (A6-relat; LRR, LRRCT, TIR, cofilin_ADF; TM=M; SS=N; 3.97
 432639; AW973785; gb:EST385886 MAGE resequences, MAGM Homo; none, IRK; 3.97
 457675; AF119917; Hs.306574; Homo sapiens PRO3098 mRNA, complete cds; none; 3.97
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; SH2, PH; TM=M; SS=N; 3.96
 437157; BE048860; Hs.17287; ESTs; IRK, none; 3.96
 453641; AA444140; Hs.90960; ESTs; Cbl_N, Cbl_N2, Cbl_N3, UBA, zf-C3HC4, none; 3.96
 446714; W73818; Hs.110028; ESTs; 7tm_1, 7tm_1; 3.96
 427648; AI376722; Hs.180062; proteasome (prosome, macropain) subunit; proteasome; 3.96
 453686; AL110326; Hs.304679; ESTs, Moderately similar to Z195_HUMAN Z; none, lectin_c, Ig_chan; 3.96
 457718; F18572; Hs.22978; ESTs, Weakly similar to ALU4_HUMAN ALU S; pkinase, pkinase; 3.95
 428727; AF078847; Hs.78452; general transcription factor IIH, polype; PHO4, LIM; TM=M; SS=N; 3.95
 435411; AW444619; Hs.138211; ESTs; none, pkinase; 3.94
 440209; H05049; Hs.247837; neurexin 3; laminin_G, EGF, none; 3.94
 416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic; none, none; 3.94
 435272; AA906415; Hs.110041; ESTs; none, pkinase; 3.93
 402550; ; Target Exon; none, none; 3.93
 425233; Z17861; Hs.155218; E1B-55kDa-associated protein 5; SPRY, SAP, pkinase, fn3, ig; 3.93
 410073; AW408163; Hs.58488; catenin (cadherin-associated protein), alpha; Stathmin, Vinculin; 3.92
 453548; AL079983; Hs.116774; Integrin, alpha 1; none, vwa, FG-GAP, Integrin_A; 3.92
 417226; AW505054; Hs.4283; ESTs; pkinase, RGS, PH, myosin_head, Myosin_tail; 3.92
 446755; AW451473; Hs.16134; serine/threonine kinase 10; pkinase, TYA; TM=M; SS=N; 3.92
 452344; AI264357; Hs.55405; hypothetical protein MGC16212; Sulfate_transp, STAS; 3.92
 418516; NM_006218; Hs.85701; phospholipase-3-kinase, catalytic, at; PI3_P14_kinase, PI3Ka, PI3K_C2, PI3K_rbd, PI3K_p85B, none; 3.91
 423069; W15613; Hs.1613; adenosine A2a receptor; 7tm_1; TM=Y; SS=M; 3.91
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor; ig, pkinase; TM=Y; SS=N; 3.91
 434392; AW983709; Hs.250824; Homo sapiens cDNA: FLJ23435 f1s, clone H; pkinase, none; 3.91
 428615; AF258627; Hs.211562; ATP-binding cassette, sub-family A (ABC1; ABC_tran; TM=Y; SS=M; 3.91
 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle, trypsin, plant_thionins; 3.91
 442831; AI798959; Hs.131686; ESTs; ABC_tran, PRK, ABC_tran; 3.91
 441657; BE314696; Hs.7936; BAI1-associated protein 2; SH3; TM=M; SS=N; 3.91
 438698; AW297855; Hs.361171; ESTs, Weakly similar to I38022 hypothet; lipoxigenase, PLAT, none; 3.90
 447560; AF065214; Hs.18858; phospholipase A2, group IVC (cytosolic; PLA2_B; TM=M; SS=N; 3.90
 437897; AA770561; Hs.146170; hypothetical protein FLJ22963; zf-DHHC, none; 3.89
 429379; NM_014840; Hs.200598; KIAA0537 gene product; pkinase, RIO1; TM=M; SS=N; 3.89
 410179; W27273; Hs.59498; cell division cycle 2-like 5 (cholinester; pkinase; 3.89

- 428713; AA432067; Hs.268551; ESTs, Moderately similar to CYA4 RAT ADE; pkinase;; 3.89
 456629; AW891955; Hs.367942; histone deacetylase 3; HSP90,HATPase_c,zf-C2H2,PHD:none; 3.89
 425190; AW028302; Hs.155079; protein phosphatase 2, regulatory subunit B56; TM=M;SS=N; 3.89
 426752; X69490; Hs.172004; titin; tn3,jg,pkinase,SGXXSG;TM=M;SS=N; 3.89
 417767; BE242241; Hs.82542; acylcoyl hydrolase (neutrophil); Lipase_GDSL;TM=M;SS=M; 3.88
 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dep; Man-6-P_recep;TM=M;SS=M; 3.88
 416140; AJ918035; Hs.301198; roundabout (axon guidance receptor, Dros; none:none; 3.88
 434224; AA380731; Hs.84; interleukin 2 receptor, gamma (severa co; tn3;TM=Y;SS=M; 3.88
 410011; AB020641; Hs.57856; PFTAIRe protein kinase 1; pkinase;TM=M;SS=N; 3.87
 406908; Z25437;; gb:H.sapiens protein-tyrosine kinase gen; none:none; 3.87
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN;; 3.87
 441859; AW194364; Hs.9877; Interleukin-4 induced gene-1 protein (FI; Amino_oxidase,FAD_binding_3,TBC;TM=M;SS=N; 3.87
 439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triph; Ham1p_like;TM=M;SS=N; 3.87
 415392; Z44067; Hs.10957; ESTs; PIP5K;none; 3.86
 416033; NM_012201; Hs.78979; Golgi apparatus protein 1; cys_rich_FGFR;TM=Y;SS=M; 3.86
 414649; AJ672727; Hs.76753; endoglin (CD105 antigen) (ENG); none;TM=Y;SS=M; 3.85
 425729; L22647; Hs.159360; prostaglandin E receptor 1 (subtype EP1); 7tm_1;TM=Y;SS=M; 3.85
 414496; W73853; Hs.355424; ESTs; pkinase,F5_F8_type_C,adh_short;none; 3.84
 412204; AJ125507; Hs.24937; ESTs; tg,rmn;none; 3.84
 434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase,ATP-sulfurylase,PRK,Thymidylate_kin;; 3.84
 444981; AW855398; Hs.12210; hypothetical protein FLJ13732 similar to; SH2;TM=M;SS=N; 3.84
 412309; M23892; Hs.73809; arachidonate 15-lipoxygenase; lipoxygenase,PLAT;; 3.84
 405545;; Target Exon; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 3.84
 407143; C14076; Hs.332329; EST; none;TM=Y;SS=M; 3.84
 420593; AA280356; Hs.187634; ESTs; B56;none; 3.84
 413420; AW410235; Hs.75348; proteasome (prosome, macropain) activator; PA28_alpha,PA28_beta,bioplerin_H;; 3.83
 448253; H25899; Hs.201591; ESTs; 7tm_2,HRM;none; 3.83
 444042; NM_004915; Hs.10237; ATP-binding cassette, sub-family G (WHIT; ABC_tran,PRK,GBP;TM=Y;SS=N; 3.83
 430397; AJ924533; Hs.105607; bicarbonate transporter related protein ; HCO3_cotransp;TM=Y;SS=N; 3.83
 423067; AA321355; Hs.285401; colony stimulating factor 2 receptor, bc; tn3;TM=Y;SS=M; 3.83
 458188; AW297226; Hs.137840; ESTs, Moderately similar to SIX4_HUMAN H; pkinase,WD40; 3.82
 426486; BE178285; Hs.170056; Homo sapiens mRNA; cDNA DKFZp56880220 (f; pkinase;none; 3.82
 428791; AA435661; Hs.264750; ESTs; zf-C3HC4;none; 3.82
 438068; AJ927209; Hs.306210; Homo sapiens cDNA: FLJ23133 fis, clone L; NusG;; 3.82
 453370; AJ470523; Hs.139336; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=N; 3.82
 419250; AW770185; Hs.356066; U5 snRNP-specific protein, 116 kD; 7tm_1,BAH,zf-CXXC,DNA_methylase; 3.82
 410017; AW952426; Hs.109438; Homo sapiens clone 24775 mRNA sequence; none;none; 3.82
 420679; X57152; Hs.165843; fibrillarin; CK_II_beta,Fibrillarin,WD40;TM=M;SS=N; 3.82
 417916; NM_006416; Hs.82921; solute carrier family 35 (CMP-sialic acid; DUF6;TM=Y;SS=M; 3.81
 425923; NM_005026; Hs.162808; phosphoinositide-3-kinase, catalytic, de; none;none; 3.81
 417365; D50583; Hs.82028; transforming growth factor, beta receptor; pkinase,WD40;TM=Y;SS=N; 3.64
 414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigen; DAN;TM=M;SS=M; 3.52
 422398; AJ476149; Hs.334489; hypothetical protein FLJ21992; SH2,SH3;; 3.51
 418432; M14156; Hs.85112; insulin-like growth factor 1 (somatomedin; Insulin;; 3.50
 459705; BE082764; Hs.270252; ESTs, Weakly similar to androgen receptor; none,C2,WW,HECT; 3.48
 425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor t; tn3,jg,Y_phosphatase,MAM;TM=Y;SS=M; 3.38
 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-t; tn3,Y_phosphatase,carb_anhydrase;TM=Y;SS=M; 3.37
 433336; AF017986; Hs.31386; secreted frizzled-related protein 2 (str; Fz,NTR;; 3.24
 426125; X87241; Hs.166994; FAT tumor suppressor (Drosophila) homolog; EGF,cadherin,laminin_G;TM=Y;SS=M; 3.11
 419721; NM_001650; Hs.315369; aquaporin 4; MIP;none; 2.99
 433147; AF091434; Hs.43080; platelet derived growth factor C; PDGF,CUB;; 2.91
 417976; BE565892; Hs.83077; Interleukin 18 (interferon-gamma-inducin; none;TM=M;SS=N; 2.89
 439180; AJ393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.69
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.23
 411089; AA458454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none;none; 2.07
 428800; M57627; Hs.193717; Interleukin 10; IL10;; 1.10

TABLE 40B

60	Pkey:	Unique Eos probe set identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
65	Pkey	CAT Number Accession
	456034	685586_1 AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	459702	539529_1 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
	432222	539529_1 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
70	414991	1785136_1 D78831 C17898 D78863
	409745	MH1944_5 BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625
		BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377
		AA150780 BI033518 BI027818 BG015789 BI033607 AA341445
	414936	1782849_1 C14774 C17911 D79033
75	451876	2328579_1 T63141 AI821021 BF370092 BF370127 BF370060 T62998
	432639	1237887_1 AW973785 H60163 AA557608

TABLE 40C

80	Pkey:	Unique number corresponding to an Eos probe set
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	NL_position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
5	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	404240	5002624	Minus	116132-116407,116653-116922
	405102	8076881	Minus	120922-121296
	405121	8102330	Minus	35816-36004,36587-36684
10	401083	3242744	Plus	33192-33360
	406403	9256305	Minus	151426-151680
	402550	7652009	Minus	80413-80673
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182

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TABLE 41A: 556 GENES UP-REGULATED IN PANCREATIC TUMORS OR PANCREATITIS RELATIVE TO NORMAL TISSUES

Table 41A lists about 556 genes up-regulated in pancreatic tumors or pancreatitis relative to normal tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

20	Hu03 Genechip array.				
	Pkey:	Unique Eos probe identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	90th percentile of pancreatic cancer/median of normal pancreas			
25	Pkey	ExAccn	UnigeneID	Unigene Title	R1
30	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	7.25
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	1.64
	444995	AJ272265	Hs.12230	secreted phosphoprotein 2, 24kD	3.58
	453953	X02544	Hs.572	orosomucoid 1	114.18
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	922.40
35	421344	AW631030	Hs.103665	villin-like	2.19
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	61.10
	438091	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m	607.40
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	228.20
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	4.97
40	443162	T49951	Hs.9029	DKFZP434G032 protein	38.01
	423096	AA732684	Hs.278428	progesterin induced protein	189.60
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	11.06
	448243	AW369771	Hs.52620	integrin, beta 8	116.90
	421044	AF061871	Hs.311736	Human DNA sequence from clone RP1-238D15	21.52
45	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	8.74
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (COM	3.11
	432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	307.70
	457059	BE561665	Hs.177677	exosome component Rrp40	33.60
	451945	BE504055	Hs.211420	ESTs	7.31
50	453354	W56946	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HE	133.70
	443247	BE614387	Hs.333893	c-Myc target JPO1	349.10
	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	330.00
	416984	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5	3.78
	413835	AI272727	Hs.249163	fatty acid hydroxylase	3.53
55	433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	73.90
	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.39
	410639	BE269047	Hs.65234	hypothetical protein FLJ20596	1.72
	410541	AA065003	Hs.64179	syntenin-2 protein	10.29
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	6.79
60	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	4.62
	407604	AW191962	Hs.249239	collagen, type VIII, alpha 2	366.30
	431193	AW749505	Hs.296770	KIAA1719 protein	6.99
	442080	AW444761	Hs.44565	ESTs	118.00
	427670	BE612888	Hs.180224	myosin regulatory light chain	2.73
65	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	647.30
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	738.90
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	68.43
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	3.03
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	7.73
70	416913	AW934714	Hs.164021	gb:RC1-DT0001-031299-011-a11 DT0001 Homo	227.30
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	115.60
	452355	N54926	Hs.29202	G protein-coupled receptor 34	192.20
	419481	AI879195	Hs.90606	15 kDa selenoprotein	119.90
	407230	AA157857	Hs.182265	keratin 19	12.11
75	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	6.63
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	592.10
	411498	NM_014210	Hs.70499	ecotropic viral integration site 2A	120.40
	445517	AF208855	Hs.12830	hypothetical protein	117.40
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.25
80	428385	AF112213	Hs.184052	putative Rab5-interacting protein	3.12
	448663	BE614599	Hs.106823	hypothetical protein MGC14797	135.20
	406867	AA157857	Hs.182265	keratin 19	11.32
	417426	NM_002291	Hs.82124	laminin, beta 1	406.20

	406366	AF026692	Hs.105700	secreted frizzled-related protein 4	0.62
	401201	#(NOCAT)		Target Exon	0.75
	420767	AF072711	Hs.99918	carboxyl ester lipase (bile salt-stimula	0.63
5	405556	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	0.75
	442776	AW959498	Hs.8709	chymotrypsin C (caldecrin)	0.67
	405555	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	0.83
	403207	#(NOCAT)		C2000960:gi131432 sp P23132 LUTH_BOVIN	0.80
	427858	NM_001971	Hs.21	elastase 1, pancreatic	0.98
10	426004	AW600300	Hs.124123	ESTs, Moderately similar to SYNLRAT SYN	0.88
	401541	NA		Target Exon	0.91
	429793	AJ417638	Hs.114648	estrogen regulated gene 1	0.85
	423068	M25629	Hs.123107	kallikrein 1, renal/pancreas/salivary	0.81
	433110	D58494	Hs.3191	rat regenerating islet-derived-like, hum	0.72
	425988	BE045897	Hs.274454	ESTs, Weakly similar to I38022 hypotheli	0.95
15	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	0.87
	412470	M93283	Hs.73923	pancreatic lipase-related protein 1	0.89
	431969	AA366217	Hs.2879	carboxypeptidase A1 (pancreatic)	0.97
	419219	AW583139	Hs.89717	carboxypeptidase A2 (pancreatic)	0.95
20	412688	AW583062	Hs.74502	chymotrypsinogen B1	0.95
	427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	1.07
	420937	AW966719	Hs.1340	colipase, pancreatic	0.99
	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUS protein d	1.02
	410839	NM_006849	Hs.66581	protein disulfide isomerase	1.00
	437986	AA774575	Hs.121776	testis expressed sequence 11	1.02
25	415934	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)	1.06
	427965	D00306	Hs.181289	elastase 3, pancreatic (protease E)	1.22
	406399	#(NOCAT)		NM_003122::Homo sapiens serine protease	1.08
	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.11
30	414061	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	1.22
	421243	AW873803	Hs.102876	pancreatic lipase	1.13
	419263	AW583874	Hs.89832	insulin	1.12
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	1.13
	408983	NM_000492	Hs.663	cystic fibrosis transmembrane conductanc	1.32
35	436217	T53925	Hs.107	fibrinogen-like 1	1.72
	435975	AL118990	Hs.41997	alpha-1-B glycoprotein	1.60
	431330	X69532	Hs.2777	inter-alpha (globulin) inhibitor, H1 pol	2.02
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	1.82
	415003	M11437	Hs.77741	kininogen	3.83
40	422281	M36803	Hs.1504	hemopexin	2.14
	414910	X12662	Hs.289057	arginase, liver	97.90
	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	236.70
	400836	#(NOCAT)		Target Exon	2.47
	452983	L32140	Hs.531	afamin	117.10
45	419768	T72104	Hs.93194	apolipoprotein A-I	4.87
	413841	M34276	Hs.75576	plasminogen	374.00
	400560	#(NOCAT)		NM_030878::Homo sapiens cytochrome P450,	144.50
	419502	AU076704	Hs.90765	fibrinogen, A alpha polypeptide	266.50
50	425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acyl	77.80
	426205	D63521	Hs.167877	leukocyte cell-derived chemotaxin 2	169.80
	414590	NM_000506	Hs.76530	coagulation factor II (thrombin)	3.60
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	400.40
	429023	NM_000312	Hs.2351	protein C (inactivator of coagulation fa	4.72
55	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	5.26
	425260	L47726	Hs.1870	phenylalanine hydroxylase	73.78
	443316	AJ478463	Hs.18443	aldehyde dehydrogenase 8 family, member	182.20
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	335.00
	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	173.40
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	565.30
60	407731	NM_000066	Hs.38069	complement component 8, beta polypeptide	86.20
	413585	AJ133452	Hs.75431	fibrinogen, gamma polypeptide	477.20
	452624	AU076606	Hs.30054	coagulation factor V (proaccelerin, labi	201.50
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	426.10
	425573	AB006423	Hs.158308	serine (or cysteine) proteinase inhibito	1.10
65	421905	AJ660247	Hs.32699	ESTs, Weakly similar to LJV-1 protein [H	0.62
	406672	M26041	Hs.198253	major histocompatibility complex, class	4.02
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (5.34
	421712	AK000140	Hs.107139	hypothetical protein	5.62
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	8.85
70	442896	R37725	Hs.261108	ESTs	157.70
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	137.70
	428486	AW583497	Hs.184604	pancreatic polypeptide	2.59
	457489	AJ693815	Hs.127179	cryptic gene	3.23
	404866	NA		ENSP00000251112::Sodium/potassium-transp	2.84
75	432874	W94322	Hs.279651	melanoma inhibitory activity	2.48
	445891	AW391342	Hs.199460	ESTs	70.38
	404682	NA		CS001188::gi12738842 ref NP_073725.1 p	1.38
	429547	AW009168	Hs.99376	ESTs	6.85
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	5.21
80	422397	AJ223366	Hs.116051	Homo sapiens cDNA: FLJ22495 fis, clone H	1.74
	446868	AV660737	Hs.135100	ESTs	102.10
	404287	NA		C6001909:gi704441 dbj BAA18909.1 (D298	242.70
	443267	AW450630	Hs.133851	ESTs	98.90
	451635	AA018899	Hs.127179	cryptic gene	2.16

	417801	AA417383	Hs.82582	Integrin, beta-like 1 (with EGF-like rep	131.70
	414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	128.70
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter	92.90
	410309	BE043077	Hs.278153	ESTs	108.80
5	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	170.10
	431938	AA938471	Hs.54431	specific granule protein (28 kDa); cyste	75.70
	449592	AI655494	Hs.195718	ESTs	4.58
	414259	W44633	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, clone L	188.50
10	406685	M18728		gb:Human nonspecific crossreacting antg	1123.60
	411573	AB029000	Hs.70823	KIAA1077 protein	995.60
	429201	X03178	Hs.198246	group-specific component (vitamin D bind	11.32
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	8.38
	428698	AA852773	Hs.334838	KIAA1866 protein	662.00
15	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	4.00
	432596	AJ224741	Hs.278461	matrilin 3	283.50
	428824	W23624	Hs.173059	ESTs	4.65
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.01
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.21
20	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	4.80
	448844	AI581519	Hs.177164	ESTs	362.80
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	133.90
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil doma	128.20
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	13.83
25	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	316.00
	452571	W31518	Hs.34655	ESTs	245.50
	443646	AI085198	Hs.164226	ESTs	189.40
	436032	AA150797	Hs.109276	laxin protein	291.10
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	252.20
30	422109	S73265	Hs.1473	gastrin-releasing peptide	278.20
	430407	H23551	Hs.30974	ESTs	6.20
	419235	AW470411	Hs.288433	neurotrophin	423.50
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.01
	444301	AK000136	Hs.10760	asporin (LRR class 1)	499.90
35	427333	AF067797	Hs.176658	aquaporin 8	1.05
	417931	W95642	Hs.82951	trefoll factor 3 (intestinal)	4.33
	407777	AA161071	Hs.71465	squalene epoxidase	3.64
	435652	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	1.47
	421341	AJ243212	Hs.279611	deleted in malignant brain tumors 1	3.98
40	453935	AI633770	Hs.42572	ESTs	2.08
	431629	AU077025	Hs.265827	Interferon, alpha-inducible protein (clo	3.84
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	14.21
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	315.70
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.53
45	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	3.13
	410310	J02931	Hs.52192	coagulation factor III (thromboplastin,	9.33
	440484	BE328156	Hs.150356	ESTs	1.03
	447395	AI418412	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	1.09
50	440099	AL080058	Hs.6909	DKFZP564G202 protein	14.74
	434665	AA642125	Hs.332649	gb:n60c01.s1 NC1_CGAP_Lym3 Homo sapiens	0.98
	452194	AI694413	Hs.48950	olfactory receptor, family 2, subfamily	2.23
	408915	NM_016651	Hs.146549	heptacellular carcinoma novel gene-3 pro	329.40
	424411	NM_005209	Hs.170808	crystallin, beta A2	1.71
55	426575	M74826	Hs.12680	glutamate decarboxylase 2 (pancreatic is	2.69
	445417	AK001058	Hs.2012	Homo sapiens cDNA FLJ10196 fis, clone HE	1.70
	426322	J05068	Hs.194725	transcobalamin I (vitamin B12 binding pr	3.19
	429010	Y18198	Hs.76095	one cut domain, family member 2	1.96
	414420	AA043424	Hs.118400	Immediate early response 3	2.54
	422565	BE259035	Hs.7155	singed (Drosophila)-like (sea urchin fas	3.30
60	414004	AA737033	Hs.7782	ESTs, Moderately similar to 2115357A TYK	312.80
	441350	AB020690		paraneoplastic antigen MA2	177.80
	406173	#(NOCAT)		ENSP00000250148*:Growth hormone variant	1.46
	403776	#(NOCAT)		ENSP00000226542*:Small Inducible cytolin	121.80
	403574	NA		Target Exon	16.12
65	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	3.94
	458449	H04482	Hs.29019	ESTs	71.60
	409958	NM_001523	Hs.57697	hyaluronan synthase 1	1.77
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	3.13
	451181	AI796330	Hs.207461	ESTs	68.00
70	440508	BE267911	Hs.196970	ESTs	38.00
	429636	AA456692	Hs.163232	ESTs	30.70
	419570	W68738		gb:zd37g06.s1 Soares_fetal_heart_NbH19W	1.02
	431779	AW971178	Hs.268571	apolipoprotein C-I	3.36
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	10.20
75	428330	L22524	Hs.2256	matrix metalloproteinase 7 (MMP7; uterin	3.94
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fascioli	1171.10
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	809.50
	440482	AA866558	Hs.50873	ESTs	9.95
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	30.70
80	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	82.90
	452239	AW379378	Hs.170121	protein tyrosine phosphatase, receptor I	26.01
	433364	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	5.38
	409335	NM_001502	Hs.53985	glycoprotein 2 (zymogen granule membrane	0.54
	420876	AA918425	Hs.177744	ESTs	0.89

	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibitor	0.94
	401732	#(NOCAT)		NM_001176:Homo sapiens Rho GDP dissociation	1.13
	404142	NA		Target Exon	1.33
5	424165	AW582904	Hs.142255	islet amyloid polypeptide	2.95
	413880	AI660842	Hs.110915	interleukin 22 receptor	1.34
	407007	U22961		gb+human mRNA clone with similarity to L	1.57
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	1.48
	432855	AF017988	Hs.279565	secreted frizzled-related protein 5	1.28
10	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.31
	445730	AI624342	Hs.170042	ESTs	2.14
	406666	V00495	Hs.184411	albumin	2.95
	435849	BE305242	Hs.16098	claudin 2	1.96
	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	2.49
	430272	X04898	Hs.237658	apolipoprotein A-II	3.29
15	412374	X01388	Hs.73849	apolipoprotein C-III	2.42
	419276	BE165909	Hs.306881	MSTP043 protein	83.40
	415448	T68645	Hs.952	solute carrier family 10 (sodium/bile ac	3.52
	423541	AA296922	Hs.129778	gastrointestinal peptide	3.16
20	428355	BE256452	Hs.2257	vitronectin (serum spreading factor, som	6.24
	425551	AA359252	Hs.126485	hypothetical protein FLJ12604; KIAA1692	14.67
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	4.30
	428786	Y16577	Hs.2314	mannose-binding lectin (protein C) 2, so	92.10
	420726	K02402	Hs.1330	coagulation factor IX (plasma thrombopla	203.30
25	451253	H48299	Hs.26126	claudin 10	1.37
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	3.38
	413881	L00190	Hs.75599	serine (or cysteine) proteinase inhibitor	7.04
	431930	AB035301	Hs.272211	cadherin 7, type 2	5.84
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.65
30	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	9.28
	422237	M13149	Hs.1498	histidine-rich glycoprotein	34.26
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	1.92
	414386	X00442	Hs.75390	haptoglobin	8.32
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (MMP11; stro	1.74
35	452689	F33868	Hs.284176	transferrin	6.51
	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	35.08
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	170.30
	428874	W32133	Hs.194366	transferrin (prealbumin, amyloidosis t	2.34
	405849	#(NOCAT)		Target Exon	103.10
40	405281	#(NOCAT)		NM_002864:Homo sapiens pregnancy-zone pr	31.20
	419078	M93119	Hs.89584	insulinoma-associated 1	6.28
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	2.89
	425834	NM_001639	Hs.1957	amyloid P component, serum	3.80
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.82
45	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	13.15
	450400	AI694722	Hs.279744	ESTs	5.22
	413916	N49813	Hs.75615	apolipoprotein C-II	8.60
	444632	AI184027	Hs.146986	ESTs, Weakly similar to FATH_HUMAN CADHE	71.30
	415906	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	1.70
50	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	4.65
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	3.01
	436961	AW375974	Hs.156704	ESTs	164.60
	446319	AW207590	Hs.160711	ESTs	1.88
	427899	AA829286	Hs.332053	serum amyloid A1	6.98
55	419092	J05581	Hs.89603	mucin 1, transmembrane	2.12
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase 1, I	132.20
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.23
	406319	NA		CX000780:g[6679197]ref[NP_032800.1] pol	51.50
	404286	NA		C6001909:g[704441]dbj[BAA18909.1] (D298	1.75
60	419183	U60669	Hs.89663	cytochrome P450, subfamily X0V (vitamin	52.90
	406293	NA		Target Exon	68.30
	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	102.43
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	208.30
	425200	BE255203	Hs.155101	ATP synthase, H transporting, mitochondr	5.78
65	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	200.10
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	97.70
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	3.96
	428921	AA526911	Hs.82772	collagen, type XI, alpha 1	30.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	4.66
70	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp56482062 (f	193.80
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.05
	420001	J05064	Hs.1282	complement component 6	159.00
	449038	AL133084	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f	39.10
	423184	NM_004428	Hs.1624	ephrin-A1	2.39
75	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	327.90
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	90.50
	445593	AW203963	Hs.150896	ESTs	49.20
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	3.12
	424420	BE614743	Hs.146688	prostaglandin E synthase	1.93
80	408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferri	39.90
	417940	R28205	Hs.24230	ESTs	57.20
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen I	2.51
	439920	H05430	Hs.288433	neurotrophin	1.91
	432542	AW083920	Hs.16098	claudin 2	3.47

	410418	D31382	Hs.63325	transmembrane protease, serine 4	3.82
	415989	AI267700	Hs.317584	ESTs	182.50
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.84
	400024			AFFX control - HUMRGE/M10098_5	4.82
5	418067	AI127958	Hs.83393	cystatin E/M	4.19
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.92
	405909	NA		Target Exon	71.80
	448811	AI590371	Hs.174759	ESTs	6.74
10	430044	AA464510	Hs.152812	ESTs	14.91
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	757.80
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	1.65
	423733	AA330281		gb:EST33985 Embryo, 12 week II Homo sapi	104.70
	450154	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	143.00
15	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	311.80
	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, ty	63.00
	422330	D30783	Hs.115263	epiregulin	141.70
	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	2.59
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	181.90
20	430691	C14187	Hs.103538	ESTs	95.80
	401682	NA		Target Exon	6.17
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	318.60
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.51
	442560	AA365042	Hs.228598	ESTs, Weakly similar to 2004399A chromos	3.90
25	414812	X72755	Hs.77367	monokine induced by gamma interferon	434.60
	425211	M18667	Hs.1867	progastricin (pepsinogen C)	6.58
	421430	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 fis, clone L	35.10
	419693	AA133749	Hs.301350	FXD domain-containing ion transport reg	2.45
	409420	Z15008	Hs.54451	laminin, gamma 2 (niclin (100kD), kalini	8.56
30	448437	AW470125		gb:cxw60c04.x1 NCL CGAP_Pan1 Homo sapiens	79.80
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	147.30
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	30.07
	424586	NM_003401	Hs.150930	X-ray repair complementing defective rep	55.10
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (CX	405.20
35	438746	AI885815	Hs.184727	ESTs	3.57
	456032	AW957446	Hs.301711	ESTs	136.80
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	36.10
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	9.93
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	146.40
40	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	20.60
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	1.58
	437157	BE048860	Hs.120655	ESTs	91.80
	404285	NA		C6001909:gi 704441 tbl BAA18909.1 (D298	123.80
	424036	AA770888	Hs.28777	H2A histone family, member L	5.26
45	422026	U80736	Hs.110826	trinucleotide repeat containing 9	130.40
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	48.80
	437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	3.15
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	253.20
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	80.00
50	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	3.05
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.66
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	23.02
	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	78.10
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	1.74
55	421298	AW172431	Hs.13012	ESTs	133.10
	422424	AI186431	Hs.296638	prostate differentiation factor	2.65
	421582	AI910275	Hs.1406	trefol factor 1 (pS2)	5.17
	401480	NA		Target Exon	73.70
60	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	137.70
	409757	NM_001898	Hs.123114	cystatin SN	9.36
	449722	BE260074	Hs.23960	cyclin B1	162.70
	452240	AI591147	Hs.61232	ESTs	151.90
	415165	AW887604	Hs.78065	complement component 7	2.85
65	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	290.30
	428450	NM_014791	Hs.184339	KIAA0175 gene product	6.89
	409041	AB033025	Hs.50081	KIAA1199 protein	334.10
	453331	AI240665	Hs.8895	ESTs	12.85
	400288	X06258	Hs.149609	integrin, alpha 5 (fibronectin receptor,	12.42
70	453160	AI263307	Hs.239884	H2B histone family, member L	156.40
	444015	AI472865	Hs.135634	ESTs	14.60
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	87.20
	448045	AJ297436	Hs.20166	prostate stem cell antigen	526.20
	422426	W79117	Hs.58559	ESTs	58.30
75	450737	AW007152	Hs.203330	ESTs	281.00
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	31.25
	456553	AA721325	Hs.189058	ESTs, Highly similar to Similar to a C.e	78.00
	413281	AA881271	Hs.222024	transcription factor BMAL2	212.10
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	3.40
80	431630	NM_002204	Hs.265829	Integrin, alpha 3 (antigen CD49C, alpha	3.48
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	281.50
	431753	X76029	Hs.2841	neuromedin U	60.50
	428651	AF196478	Hs.188401	annexin A10	508.30
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	85.80
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	55.30

	435039	AW043921	Hs.130526	ESTs	64.00
	447033	AK57412	Hs.157601	ESTs	123.20
	433578	BE336888	Hs.3416	adipose differentiation-related protein	9.22
	422511	AJ076442	Hs.117938	collagen, type XVII, alpha 1	525.70
5	411274	NM_002776	Hs.69423	kallikrein 10 (KLK10) (PRSSL1) (nes1)	44.36
	452705	H49805	Hs.246005	ESTs	120.10
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	92.30
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	29.37
	422562	AJ962060	Hs.118397	AE-binding protein 1	3.84
10	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	27.80
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholestergic	4.09
	440868	R79707	Hs.263339	ESTs, Moderately similar to I38022 hypot	76.30
	421493	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	2.37
	410199	AW377424	Hs.205126	Homo sapiens cDNA: FLJ22667 fis, clone H	3.44
15	426320	W47595	Hs.169300	transforming growth factor, beta 2	138.10
	419290	AI128114	Hs.112885	spinal cord-derived growth factor-B	3.45
	459309	AA040620	Hs.5672	hypothetical protein AF140225	127.80
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	361.20
20	422553	AI697720	Hs.171455	ESTs, Weakly similar to T31613 hypotheti	136.60
	423275	BE536069	Hs.2962	S100 calcium-binding protein P	6.87
	400534	#(NOCAT)		C22000015:gij12741327[refXP_008833.2] z	89.00
	428970	BE276891	Hs.194691	retinoic acid induced 3	4.78
	423739	AA398155	Hs.97600	ESTs	135.60
25	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	148.50
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	87.70
	407001	U12471	Hs.247954	Human thrombospondin-1 gene, partial cds	76.80
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	110.60
	419948	AB041035	Hs.93847	NM_016931:Homo sapiens NADPH oxidase 4 (234.60
30	428471	X57348	Hs.184510	stratfin	3.72
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	437.90
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	219.20
	419842	AA765489	Hs.104350	ESTs	3.80
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (MMP1; inters	606.80
35	444207	AI565004	Hs.79572	cathepsin D (lysosomal aspartyl) protease	2.62
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	258.70
	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin	304.80
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	8.78
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	10.95
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	199.70
40	438199	AW016531	Hs.122147	ESTs	67.70
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily	107.20
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	3.59
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	3.45
	421937	AJ878857	Hs.109706	hematological and neurological expressed	3.17
45	427961	AW293165	Hs.143134	ESTs	109.30
	422043	AL133649	Hs.110953	retinoic acid induced 1	2.98
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	276.50
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	5.28
50	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	27.85
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	342.30
	424086	AI351010	Hs.102267	lysyl oxidase	213.50
	432731	R31178	Hs.287820	fibronectin 1	185.10
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	106.10
55	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	2.27
	417308	H60720	Hs.81892	KIAA0101 gene product	405.30
	438146	Z36842	Hs.57548	ESTs	8.38
	424800	AL035588	Hs.153203	MyoD family inhibitor	172.10
	416143	AI956650	Hs.79033	glutamyl-peptide cyclotransferase (glu	45.70
60	408380	AF123050	Hs.44532	ubiquitin	11.18
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakines	149.10
	422963	M79141	Hs.13234	ESTs	33.60
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	6.73
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	8.96
65	424897	D63216	Hs.153684	frizzled-related protein	312.40
	421110	AJ250717	Hs.1355	cathepsin E	790.80
	411789	AF245505	Hs.72157	DKFZP564I1922 protein	3.17
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	8.62
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	558.00
70	406837	R70292	Hs.156110	immunoglobulin kappa constant	4.36
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	2.83
	421470	R27496	Hs.1378	annexin A3	242.90
	407242	M18728		gh:Human nonspecific crossreacting anti	36.91
	432101	AI918950	Hs.123642	EphA3	221.60
75	406687	M31126	Hs.272620	matrix metalloproteinase 11 (MMP11; stro	5.34
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	292.00
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	184.90
	435202	AI971313	Hs.170204	KIAA0551 protein	64.80
	407216	N91773	Hs.102267	lysyl oxidase	73.70
80	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	3.20
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	288.70
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	502.60
	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	6.13
	441020	W79283	Hs.35962	ESTs	178.90

	453857	AL080235	Hs.35861	DKFZP586E1621 protein	504.30
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	242.10
	413435	X51405	Hs.75360	carboxypeptidase E	7.30
	436476	AA326108	Hs.33829	bHLH protein DEC2	247.20
5	406747	AJ925153	Hs.217493	annexin A2	110.00
	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	112.10
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	583.90
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	6.56
10	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	460.90
	444655	BE613126	Hs.47783	B aggressive lymphoma gene	204.40
	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	7.75
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	14.61
	424560	AA158727	Hs.150555	protein predicted by clone Z3733	99.80
15	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	242.20
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	17.88
	410668	BE379794	Hs.65403	hypothetical protein	4.18
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	116.40
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	60.30
20	442577	AA292998	Hs.163900	ESTs	4.18
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	334.20
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	8.16
	451277	AK001123	Hs.26176	hypothetical protein FLJ10251	375.30
	445133	AW157646	Hs.153506	ESTs	292.40
25	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	4.38
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam	89.00
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	322.10
	410687	U24389	Hs.65436	lysyl oxidase-like 1	9.10
	417409	BE272506	Hs.82109	syndecan 1	4.05
30	426471	M22440	Hs.170009	transforming growth factor, alpha	138.60
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	250.50
	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	4.89
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	11.76
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.79
35	408491	AI088063	Hs.7882	ESTs	8.25
	437802	AI475995	Hs.122910	ESTs	4.54
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	175.10
	421155	H87879	Hs.102267	lysyl oxidase	170.10
40	451310	AW250651	Hs.26213	Human DNA sequence from clone RP3-447F3	2.91
	439867	AA847510	Hs.161292	ESTs	261.60
	417771	AA804698	Hs.82547	retinoic acid receptor responder (lazar	723.00
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	251.70
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	155.50
	457180	R26022	Hs.194652	calponin 3, acidic	68.00
45	424408	AI754813	Hs.146428	collagen, type V, alpha 1	17.19
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induc	5.32
	425139	AW630488	Hs.325820	protease, serine, 23	371.90
	432978	AF126743	Hs.279884	DNAJ domain-containing	7.27
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	19.30
50	421891	NM_014918	Hs.110488	KIAA0990 protein	190.50
	421814	L12350	Hs.108623	thrombospondin 2	15.02
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	28.57
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	519.20
	413048	M93221	Hs.75182	mannose receptor, C type 1	240.60
55	404210	#(NOCAT)		NM_005936:Homo sapiens myeloid/lymphoid	404.60
	452862	AW378065	Hs.8687	ESTs	364.20
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	226.20
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	4.31
60	427390	AI432163	Hs.268231	Homo sapiens cDNA: FLJ23111 fis, clone L	10.41
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	22.46
	451295	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene	23.74
	448569	BE382657	Hs.21486	signal transducer and activator of trans	5.68
	417148	AA359896	Hs.293885	hypothetical protein FLJ14902	190.80
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	230.50
65	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	361.90
	422545	X02761	Hs.287820	fibronectin 1	8.81
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	7.30
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	267.20
	422110	AI376736	Hs.111779	secreted protein, acidic, cysteine-rich	5.07
70	431512	BE270734	Hs.2795	lactate dehydrogenase A	270.10
	417433	BE270265	Hs.82128	5T4 oncofetal trophoblast glycoprotein	504.60
	426369	AF134157	Hs.169487	Kreiser (mouse) mal-related leucine zip	10.62
	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	2.80
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	14.01
75	428797	AA496205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586I0324 (f	9.15
	434423	NM_006769	Hs.3844	LIM domain only 4	297.30
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	486.20
	422573	AW297985	Hs.295726	integrin, alpha V (vitronectin receptor	9.73
	421552	AF026592	Hs.105700	secreted frizzled-related protein 4	762.90
80	424730	NM_003358	Hs.23703	ESTs, Moderately similar to CEGT_HUMAN C	7.81
	400133	NA		Eos Control	357.00
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheri	1150.30
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.50
	446019	AI362520	Hs.279789	histone deacetylase 3	11.26

426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	459.50
422687	AW068823	Hs.119206	Insulin-like growth factor binding prote	2.68
432401	NM_013330	Hs.274479	NME7	4.99
437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	7.65

Table 41B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
419570	1860604_1	W68738 W68831
423733	231476_1	AA330281 QAA330232 AW962521
434665	390530_1	AA642125 AA654516
448437	763310_1	AW470125 A1734872 A1749559 AW856504 A1583942 AW779036 AW843429 AW844876 A1520713 AW847236

Table 41C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400534	6981826	Minus	278637-279292
400560	9843598	Plus	94182-94323,97056-97243,101095-101236,102824-103005
400836	8954179	Plus	677-1188
401201	9743387	Minus	138534-138629,139234-139294,140121-140335,142033-142479
401480	7321503	Plus	166120-166347,166451-166557,169651-169832
401541	8072607	Minus	50018-50158
401682	4755167	Plus	13022-13473
401732	1200312	Plus	19346-19525,19625-19708,19897-19973,20067-20130,20215-20414
403207	7630829	Plus	89914-90033,90729-90855,91131-91198
403574	8101156	Plus	5542-6176
403776	7770611	Minus	1414-1513,1624-1756
404142	9856692	Minus	80316-80459
404210	5006246	Plus	169926-170121
404285	2326514	Plus	32282-32416
404286	2326514	Plus	51086-51301
404287	2326514	Plus	53134-53281
404682	9797231	Minus	40977-41150
404866	9366919	Minus	11743-11929
405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
405849	7651817	Minus	17705-18287
405809	7705180	Minus	86985-87233
406173	7230224	Plus	12925-13213
406293	5686274	Minus	17646-17853
406319	9211730	Minus	82320-82561
406399	9256288	Minus	63448-63554

TABLE 42A: 574 genes upregulated in pancreatic cancer relative to normal body tissues

Table 42A lists about 574 genes upregulated in pancreatic cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccon: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.ProIDomains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1: 90th percentile of pancreatic cancer AIs divided by the 50th percentile of normal tissue AIs
 R2: 90th percentile of pancreatic cancer AIs divided by the 90th percentile of normal pancreas AIs, where the 15th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccon; UniGeneID; UniGene Title; Pred.ProIDomains; R1; R2

426230; AA367019; Hs.241395; protease, serine, 1 (trypsin 1); trypsin,loxin_4;SS=M; 107.29; 1.07
 415934; NM_000928; Hs.992; phospholipase A2, group 1B (pancreas); phospho;SS=M; 83.67; 1.06
 421996; AW583807; Hs.1460; glucagon; hormone;2;SS=M; 59.35; 1.61
 406399; ; NM_003122; Homo sapiens serine protease ; kazal;SS=M; 55.49; 1.08
 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen;TM=M;SS=M; 53.65; 43.61

- 406685; M18728; ; gb:Human nonspecific crossreacting antigen; Ig; TM=M; SS=M; 52.73; 22.83
- 428698; AA852773; Hs.334838; KIAA1866 protein; none; NA; NA; 32.44; 13.11
- 437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbonate; HCO₃ cotransp; TM=Y; 29.80; 1.46
- 428874; W32133; Hs.194366; transthyretin (prealbumin, amyloidosis t; Transthyretin; SS=M; 29.42; 1.94
- 444754; T83911; Hs.374341; transmembrane 4 superfamily member 4; none; TM=Y; SS=M; 28.78; 3.13
- 418058; AW971155; Hs.293902; ESTs, Weakly similar to ISHUS protein d; none; TM=M; SS=M; 28.61; 0.98
- 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group 1, m; hormone_rec.zf.C4; none; 25.38; 3.63
- 413719; BE439580; Hs.75498; small inducible cytokine subfamily A (C); IL8; SS=M; 24.64; 7.21
- 417771; AA804698; Hs.82547; retinoic acid receptor responder (Iazaro; none; none; 23.77; 6.74
- 414998; NM_002543; Hs.77729; oxidized low density lipoprotein (lectin; lectin_c; TM=Y; SS=M; 22.96; 4.57
- 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4; TM=Y; SS=M; 22.31; 5.42
- 425573; AB006423; Hs.158308; serine (or cysteine) proteinase inhibitor; serpin, GCV_H; TM=M; SS=M; 21.91; 1.03
- 433110; D56494; Hs.3191; rat regenerating islet-derived-like, hum; lectin_c; TM=M; SS=M; 21.90; 0.60
- 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; PAC; PAS; TM=M; 21.41; 19.89
- 453863; X02544; Hs.572; orosomucoid 1; lipocalin, aldehyd, ubiquitin, IRK; SS=M; 20.80; 8.12
- 421126; M74587; Hs.102122; insulin-like growth factor binding prote; thyroglobulin_1, IGFBP; SS=Y; 20.60; 8.48
- 451035; AU076785; Hs.430; plastin 1 (I isoform); ehand, CH, Adaptin_N; SS=M; 19.25; 3.53
- 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kinase; SAM_PNT; none; 18.38; 2.53
- 420332; NM_001756; Hs.1305; serine (or cysteine) proteinase inhibitor; serpin; TM=M; SS=M; 18.19; 2.29
- 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group 1, m; hormone_rec.zf.C4; none; 17.67; 4.80
- 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF, laminin_Niemn, Integrin_B; SS=M; 17.08; 6.37
- 427509; M62505; Hs.2161; complement component 5 receptor 1 (CSa t; 7tm_1; TM=Y; SS=M; 16.89; 7.15
- 441031; A110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen_C, G-alpha, arf; TM=M; SS=M; 16.59; 7.74
- 445033; AV652402; Hs.72801; cyclin-dependent kinase inhibitor 2B (p1; ank; 16.28; 9.22
- 431183; NM_005855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept; TM=M; SS=M; 15.96; 2.38
- 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodi; Somatomedin_B, Endonuclease, Phosphodiester; TM=Y; SS=M; 15.65; 1.33
- 408243; Y00787; Hs.624; interleukin 8; IL8, PAS, IL8; TM=M; 15.53; 4.34
- 419355; AA428520; Hs.90061; progesterone binding protein; hema_1; TM=Y; SS=M; 15.45; 10.50
- 426006; R49031; Hs.22627; ESTs; pkinase, TBC; 15.17; 0.58
- 433376; A1249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD, ICE_p10, ICE_p20; SS=M; 14.84; 3.04
- 422260; AA315993; Hs.105484; regenerating gene type IV; lectin_c; SS=M; 14.71; 2.89
- 430280; AA361258; Hs.237858; interleukin 7 receptor; fn3; none; 14.28; 11.47
- 406993; NM_000492; Hs.663; cystic fibrosis transmembrane conductanc; ABC_tran, ABC_membrane, PRK, Bac_export_3; TM=Y; 13.98; 1.18
- 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8; TM=M; SS=Y; 13.81; 7.69
- 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese, DSPc, Y_phosphatase, Ribosomal_S3_N; TM=M; 13.59; 2.24
- 425988; BE045897; Hs.53985; ESTs, Weakly similar to I38022 hypotheti; none; none; 13.54; 0.95
- 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD, helicase_C, CARD; TM=M; 13.48; 3.59
- 429556; AW139399; Hs.99988; ESTs; none; TM=M; 13.20; 1.18
- 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; SS=M; 12.83; 7.72
- 427286; AW732802; Hs.2132; epidermal growth factor receptor pathway; SH3, TonB_boxC; TM=M; 12.72; 9.01
- 431912; A160552; Hs.356183; ESTs, Weakly similar to A56154 Abl subst; none, Acyl-CoA_dh, Acyl-CoA_dh_M, Acyl-CoA_dh_N; 12.72; 6.72
- 412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymph; 7tm_1; TM=Y; SS=M; 12.71; 12.56
- 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB, DNA_topoisolv, HATPase_c; SS=M; 12.52; 4.92
- 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran, M, SMC_N, SMC_C, DUF164; none; 12.38; 7.59
- 428157; A1738719; Hs.198427; hexokinase 2; hexokinase, hexokinase2; none; 12.34; 11.53
- 424273; W40460; Hs.144442; phospholipase A2, group X; phospholip; TM=M; SS=Y; 12.32; 3.02
- 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; Ig; TM=Y; SS=M; 12.29; 2.21
- 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3, TPR; TM=M; 12.16; 4.14
- 427283; AL119796; Hs.174185; ectonucleotide pyrophosphatase/phosphodi; Sulfatase, Somatomedin_B, Phosphodiester, Endonuclease; TM=M; SS=Y; 11.97; 5.93
- 434779; AF153815; Hs.50151; potassium inwardly-rectifying channel, s; IRK; TM=Y; 11.76; 1.58
- 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1; TM=Y; SS=M; 11.75; 3.56
- 412228; AW503785; Hs.73792; complement component (3d/Epstein Barr vi; sushi; TM=Y; SS=M; 11.67; 3.77
- 450737; AW007152; Hs.63325; transmembrane protease, serine 4; trypsin, jld_recept, a; none; 11.65; 4.52
- 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C, IMPDH_N, CBS, Integrin_B, Ricin_B, Lectin; 11.56; 5.46
- 431512; BE270734; Hs.2795; lactate dehydrogenase A; ldh, ldh_C, SH3, pkinase, UBA; TM=M; 11.55; 5.11
- 429638; A1916862; Hs.211577; kinesin (kinesin receptor); bZIP, Tropomyosin, spectrin, LBP, BPI, CETP, B56_M, TM=Y; SS=M; 11.47; 4.65
- 445133; AW157646; Hs.198689; ESTs; ehand, spectrin, GAS2, SH3, Plectin, RA_Xylose_isom, FliD, bZIP, Tropomyosin, Myc-LZ, M, ldh_C, CH, AIP3; TM=M; 11.41; 12.62
- 411352; NM_002890; Hs.758; RAS p21 protein activator (GTPase activa; SH2, SH3, C2, PH, RasGAP; TM=M; SS=M; 11.24; 9.95
- 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none; none; 11.19; 4.16
- 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS, AIRS_C; TM=M; 11.17; 5.98
- 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin, fn3, Y_phosphatase; TM=M; 11.14; 9.09
- 440594; AW445167; Hs.126036; ESTs; none; none; 11.05; 16.45
- 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD, DAPN, HIN; SS=M; 11.05; 10.38
- 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese, DSPc; TM=M; 11.05; 4.70
- 448811; A1590371; Hs.199460; ESTs; none; TM=Y; 10.85; 9.69
- 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2, SH3, pkinase; TM=M; 10.72; 8.65
- 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2; TM=M; 10.51; 12.97
- 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys, Ig, FAD_Synth, ldh, ldh_C, pkinase; SS=M; 10.37; 6.35
- 436856; A1469355; Hs.127310; ESTs; pkinase, rrm; TM=M; 10.36; 2.74
- 427337; Z46223; Hs.176563; Fc fragment of IgG, low affinity IIb, r; Ig; TM=Y; SS=M; 10.34; 3.14
- 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related ; SH2, SH3, pkinase; TM=M; 10.34; 4.47
- 418299; AA279530; Hs.83968; Integrin, beta 2 (antigen CD18 (p95); ly; integrin_B, EGF, PSI; TM=Y; SS=M; 10.21; 4.58
- 415820; AW058357; Hs.199248; ESTs; 7tm_1; TM=Y; SS=M; 10.18; 2.67
- 413048; M93221; Hs.75182; mannose receptor, C type 1; fn2, lectin_c, Ricin_B, Lectin, Xlink; TM=Y; SS=M; 10.17; 8.35
- 429752; H52348; Hs.36636; ESTs; pkinase, pkinase; 10.13; 12.35
- 452721; A1269529; Hs.301871; solute carrier family 37 (glycerol-3-pho; MORN, sugar_Ir; TM=Y; SS=M; 10.08; 8.74
- 421462; AF016495; Hs.104624; aquaporin 9; MIP; TM=Y; SS=M; 10.05; 6.06
- 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1; TM=Y; SS=M; 9.98; 3.16
- 416389; AA180072; Hs.149846; Integrin, beta 5; integrin_B; none; 9.85; 9.59
- 421044; AF081671; Hs.101302; Human DNA sequence from clone RP1-238D15; fn3, vwa, Collagen, TSPN; TM=M; SS=M; 9.78; 5.96
- 446620; AA128808; Hs.179902; transporter-like protein; none; TM=Y; SS=M; 9.75; 2.64
- 405102; ; C15001220*gi4469558|gb|AAD21311.1| (AF; DAG_PE-bind, PH, RhoGEF, DC1; SS=M; 9.74; 1.88
- 418693; A1750878; Hs.87408; thrombospondin 1; EGF, tssp_1, vwc, TSPN, tssp_3; SS=M; 9.72; 6.94

- 426535; AU070712; Hs.288582; ESTs, Weakly similar to ubiquitous TPR m; Kunitz_BPT1,Kunitz_BPT1,7tm_2,HRM; 9.68; 10.58
 448105; AW591433; Hs.298241; Transmembrane protease, serine 3; Id1_receptL, trypsin; TM=Y; SS=M; 9.67; 4.06
 456266; L29073; Hs.198726; cold shock domain protein A; 7tm_2,HRM,CSD; TM=Y; SS=M; 9.62; 2.36
 410240; AL157424; Hs.61289; synaptotagmin 2; Exo_endo_phos,Syja_N,rm, Gram-ve porins; TM=M; 9.62; 3.77
 457001; JQ3258; Hs.2062; vitamin D (1,25-dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metallothio_S; TM=M; 9.60; 8.05
 456373; BE247706; Hs.89751; membrane-spanning 4-domains, subfamily A; none; TM=Y; 9.57; 3.77
 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3; TM=M; 9.56; 10.50
 437158; AW090198; Hs.348709; KIAA1150 protein; none; NA; NA; 9.55; 8.87
 426108; AA622037; Hs.166468; programmed cell death 5; DUF122; TM=M; 9.47; 5.67
 403344; ; NM_000341; Homo sapiens solute carrier fa; alpha-amylase; TM=Y; 9.47; 1.42
 449543; AF070632; Hs.23729; Homo sapiens clone 24405 mRNA sequence; K_tetra,ion_trans,none; 9.46; 3.12
 433233; AB040927; Hs.301804; KIAA1494 protein; SH3,zf-C3HC4; TM=M; 9.42; 4.01
 444838; AV651680; Hs.208558; ESTs; Integrin_A,FG-GAP,none; 9.42; 1.87
 439803; AA001021; Hs.6685; thyroid hormone receptor interactor 8; none,none; 9.41; 5.55
 426505; AL035461; Hs.2281; chromogranin B (secretogranin 1); Granin; SS=M; 9.40; 3.46
 411213; AA676939; Hs.69285; neuropilin 1; MAM,F5_F8_type_C,CUB,CUB,MAM,F5_F8_type_C; 9.38; 6.32
 432810; AA863400; Hs.374489; ESTs; none,Skp1,AAA; 9.38; 4.36
 427581; NM_014788; Hs.179703; KIAA0129 gene product; SPRY,zf-B_box; TM=M; 9.34; 8.26
 413109; AW389845; Hs.110855; ESTs, similar to leukemia virus receptor; PHO4,none; 9.34; 4.67
 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,kinase; TM=M; 9.31; 4.24
 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm_3,none; 9.24; 7.12
 448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 9.23; 6.03
 437672; AW748265; Hs.5741; flavohemoprotein b57; heme_1,NAD_binding,lipoxygenase,FAD_binding_6; TM=M; 9.22; 10.72
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans; TM=Y; SS=M; 9.20; 4.46
 409956; AW103364; Hs.727; inhibin, beta A (activin A, activin AB a; TGF-beta,TGFB_propeptide,tub; SS=M; 9.19; 16.46
 413095; AA494358; Hs.30715; potassium voltage-gated channel, Isk-rel; none,START; 9.15; 2.18
 418838; AW385224; Hs.35198; ecdonucleotide pyrophosphatase/phosphodi; Phosphodiect; TM=Y; SS=M; 9.14; 3.03
 452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor t Y_phosphatase,none; 9.14; 11.75
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; coilin_ADF; SS=M; 9.11; 4.29
 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG; TM=M; 9.06; 9.68
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome; TM=M; 9.05; 5.61
 413367; NM_005517; Hs.75317; solute carrier family 16 (monocarboxylic sugar_tr; TM=Y; 9.04; 5.79
 437296; AA350994; Hs.20281; KIAA1700; Rhodanese,DSPC; TM=M; 9.02; 5.75
 418888; AU076801; Hs.89436; cadherin 17, LI cadherin (liver-intestin; cadherin; TM=Y; SS=M; 8.94; 5.01
 446406; A0553681; Hs.348490; Arg/Abi-interacting protein ArgBP2; Sorb,none; 8.91; 1.77
 428820; AA436187; Hs.172631; Integrin, alpha M (complement component ; vwa,Integrin_A,FG-GAP; TM=Y; SS=M; 8.85; 4.74
 434398; AA121098; Hs.3838; serum-inducible kinase (SNK); pkinase,POLO_box; TM=M; 8.78; 4.54
 453902; BE502341; Hs.3402; ESTs; none,none; 8.72; 3.71
 433334; A1927208; Hs.231958; matrix metalloproteinase 28; Peptidase_M10,none; 8.71; 4.28
 446488; AB037782; Hs.15119; KIAA1361 protein; pkinase; SS=M; 8.70; 3.71
 450247; AF123303; Hs.24713; hypothetical protein; efhand,milo_cam; TM=Y; SS=M; 8.68; 3.40
 432101; A1918950; Hs.123642; EphA3; fn3,pkinase,SAM,EPH_tbd; TM=Y; SS=M; 8.62; 5.62
 410763; AF279145; Hs.8966; hypothetical protein FLJ21776; none,none; 8.61; 13.53
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2; TM=Y; SS=M; 8.55; 4.82
 425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR; TM=M; 8.50; 3.18
 419111; AA234172; Hs.137418; ESTs; none,IRK; 8.47; 7.51
 430024; A1808780; Hs.227730; Integrin, alpha 6; Integrin_A,FG-GAP; TM=Y; SS=M; 8.45; 3.46
 447574; AF162666; Hs.18895; tousel-like kinase 1; pkinase; TM=M; 8.45; 5.30
 447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5_F8_type_C; TM=M; SS=M; 8.44; 6.30
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase; TM=M; 8.43; 4.87
 405555; ; homeodomain-interacting protein kinase 3; trypsin; TM=M; 8.39; 0.68
 417412; X16896; Hs.82112; Interleukin 1 receptor, type I; ig,TIR; TM=M; SS=M; 8.35; 4.74
 405556; ; homeodomain-interacting protein kinase 3; trypsin; TM=M; 8.31; 0.87
 407687; AK002011; Hs.37658; hypothetical protein FLJ11149; lys,Ig,FAD_Synth,ldh,ldh_C,pkinase; SS=M; 8.28; 3.12
 408051; A1623351; Hs.172148; ESTs; PH,RhoGAP,none; 8.27; 5.65
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1; TM=Y; SS=M; 8.26; 5.49
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 dom; SH2; SS=M; 8.24; 8.91
 405204; ; NM_002086; Homo sapiens growth factor re; SH2,SH3; TM=M; 8.23; 6.43
 426806; T19228; Hs.172572; hypothetical protein FLJ20093; ank,pkinase,UPF0073; SS=M; 8.20; 6.11
 428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xa; pkinase; TM=M; 8.18; 8.37
 450375; AA009647; Hs.352537; a disintegrin and metalloproteinase dom; Reprolysin,Pep_M12B_propep,disintegrin,Reprolysin,Pep_M12B_propep,disintegrin; 8.17; 12.24
 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase,ICE_p10,ICE_p20; TM=M; SS=M; 8.15; 4.61
 413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent, catalytic; PKI; SS=M; 8.15; 11.12
 428513; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA sequence; PSI,none; 8.13; 13.28
 429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 8.13; 1.15
 425838; NM_014071; Hs.159613; nuclear receptor coactivator RAP250; per; none; TM=M; 8.12; 4.54
 425836; AW955696; Hs.90960; ESTs; Cbl_N,Cbl_N2,Cbl_N3,UBA,zf-C3HC4,none; 8.11; 7.47
 406366; ; secreted frizzled-related protein 4; trypsin; SS=M; 8.05; 0.69
 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic ; C2,PLA2_B; TM=M; 8.04; 5.20
 458946; AA009716; Hs.42311; ESTs; none,DSPC,Y_phosphatase; 8.02; 1.93
 425280; U31519; Hs.1872; phosphoenolpyruvate carboxykinase 1 (sol; PEPCK; TM=M; 7.97; 19.33
 445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase, ty; none,none; 7.90; 11.44
 449444; AW818438; Hs.351306; solute carrier family 16 (monocarboxylic; none; TM=Y; SS=M; 7.89; 7.00
 426167; AF039023; Hs.167496; RAN binding protein 6; Armadillo_seg,HEAT_PBS; 7.83; 11.16
 400408; S75765; ; Homo sapiens delta CCK-B gene, partial c; 7tm_1,none; 7.81; 0.78
 448362; AA641767; Hs.21015; hypothetical protein DKFZp564L0864 simil; sugar_tr; TM=Y; SS=M; 7.78; 7.02
 457670; AF119666; Hs.23449; insulin receptor tyrosine kinase substr; SH3; TM=M; 7.75; 2.63
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase; TM=M; 7.72; 2.68
 447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED; TM=M; 7.68; 2.40
 421684; BE281591; Hs.106768; hypothetical protein FLJ10511; Armadillo_seg; SS=M; 7.49; 6.57
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HE; Nucleoside_tra2,none; 7.47; 2.53
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule; EGF,lactin_c,sushi; TM=M; SS=M; 7.38; 5.60
 436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none; TM=Y; SS=M; 7.29; 5.78

- 428970; BE276891; Hs.194691; retinoic acid induced 3; 7tm_3; TM=Y; SS=M; 7.26; 11.00
 426761; A015709; Hs.172089; PORIMIN Pro-oncogenesis receptor inducing me; none; TM=Y; SS=M; 7.25; 7.22
 413880; A1660842; Hs.110915; Interleukin 22 receptor; Tissue_fac; TM=Y; SS=M; 7.24; 0.98
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase; PLAT; TM=M; 7.22; 6.45
 413441; A1929374; Hs.75367; Src-like-adaptor; SH2,SH3; TM=M; 7.20; 5.72
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like; pkinase; Recep_L_domain; Furin-like; pkinase; Recep_L_domain; Peptidase_M24; 7.13; 3.97
 428474; AB023182; Hs.184523; KIAA0965 protein; pkinase; TM=M; 7.13; 5.43
 421582; A1910275; Hs.350470; trefoil factor 1 (breast cancer, estrogen; trefoil; Gastrin; SS=M; 7.08; 21.61
 449843; R85337; Hs.24030; solute carrier family 31 (copper transp; none; TM=Y; SS=M; 7.07; 6.18
 452110; T47667; Hs.28005; Homo sapiens cDNA FLJ11309 fis, clone PL; pkinase; Activin_rec; none; 6.94; 4.82
 451295; A1557212; Hs.17132; ESTs, Moderately similar to I54374 gene; pkinase; DAG_PE-bind; pkinase_C; OPR; none; 6.92; 15.34
 430680; AW138724; Hs.168974; ESTs, Highly similar to ALU7_HUMAN ALU S; Y_phosphatase; Adaplin_N_Y_phosphatase; 6.88; 1.94
 441600; AA939347; Hs.127223; Homo sapiens cysteine knot protein (ZSIG; 7tm_1; Idl_recept_L; LRR; SS=M; 6.86; 0.97
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase; SS=M; 6.83; 7.24
 425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor t; fn3; Ig_Y_phosphatase; MAM; TM=Y; SS=M; 6.83; 11.43
 400539; ; Target Exon; none; TM=M; 6.70; 1.19
 431113; AK000673; Hs.274337; hypothetical protein FLJ20666; pkinase; TM=M; 6.65; 2.21
 445280; AW055063; Hs.343220; v-ck avian sarcoma virus CT10 oncogene; SH2,SH3; none; 6.61; 10.66
 425834; NM_001639; Hs.1957; amyloid P component, serum; pentaxin; TM=M; SS=M; 6.57; 2.20
 435706; W31254; Hs.7045; GL004 protein; PDEase; GAF; none; 6.55; 11.44
 415906; A1751357; Hs.288741; Homo sapiens cDNA: FLJ22256 fis, clone H; Ephrin; none; 6.45; 5.25
 408308; AL033377; Hs.44197; hypothetical protein DKFP564D0462; none; none; 6.42; 9.14
 432336; NM_002759; Hs.274382; protein kinase, interferon-inducible dou; dsrm; pkinase; TM=M; 6.42; 4.12
 417874; BE616160; Hs.62829; protein tyrosine phosphatase, non-recept; Y_phosphatase; TM=Y; 6.42; 2.26
 446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G-protein c; 7tm_1; TM=Y; SS=M; 6.41; 4.54
 444006; BE395085; Hs.10086; type I transmembrane protein Fn14; Idl_recept_L; PKD; MHC; 1; TM=M; SS=Y; 6.38; 3.55
 412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanese; DSPc; SS=M; 6.35; 4.95
 422583; AA110506; Hs.27973; KIAA0874 protein; ank, G-alpha; TM=M; 6.35; 3.56
 452355; NS4926; Hs.29202; G protein-coupled receptor 34; 7tm_1; OATP_C; TM=Y; 6.32; 11.02
 422282; AF019225; Hs.114309; apolipoprotein L; MoA_Extb; TM=Y; SS=M; 6.32; 5.15
 407235; D20569; Hs.169407; SAC2 (suppressor of actin mutations 2; y; none; Ribosomal_S13; Galactosyl_T; Zip; adh_short; zf-C3HC4; 6.30; 8.35
 428486; AW583497; Hs.184604; pancreatic polypeptide; hormone3; TM=M; SS=Y; 6.29; 3.51
 408847; AW290997; Hs.30348; ESTs; pkinase; Ig; none; 6.28; 3.63
 428179; A1127772; Hs.278696; serum/glucocorticoid regulated kinase-II; pkinase; PX; pkinase_C; SS=M; 6.28; 3.50
 443614; AV655386; Hs.7645; fibrinogen, B beta polypeptide; none; none; 6.26; 7.48
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1; TM=Y; SS=M; 6.25; 3.98
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M; 6.21; 4.10
 428180; A1129767; Hs.182874; guanine nucleotide binding protein (G pr; G-alpha; arf; TM=M; 6.18; 4.62
 409245; AA361037; Hs.356436; tRNA isopentenylpyrophosphate transferase; Armadillo_seg; TM=M; 6.17; 11.15
 417952; A192838; Hs.372643; dual-specificity tyrosine-(Y)-phosphoryl; pkinase; none; 6.17; 3.05
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; SH2,PH; TM=M; 6.16; 11.90
 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; none; TM=M; 6.10; 2.96
 426797; AW936328; Hs.342849; ADP-ribosylation factor-like 5; arf; Ca_channel_B; SH3; 6.03; 3.17
 408331; NM_007240; Hs.44229; dual specificity phosphatase 12; DSPc; TM=M; 5.99; 2.65
 441384; AA447849; Hs.288660; Homo sapiens cDNA: FLJ22182 fis, clone H; 7tm_3; none; 5.97; 13.12
 414217; A1309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none; NA; NA; 5.92; 6.47
 418506; AA084248; Hs.85339; Unknown protein for MGC:29643; none; none; 5.91; 1.94
 436345; AA873008; Hs.121572; ESTs; CARD; BIR_zf-C3HC4; CARD; BIR_zf-C3HC4; 5.90; 1.40
 414087; W19712; ; gbzb36d03.r1 Soares_papillary_thyroid_tumor_N; pkinase; none; 5.85; 0.90
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank; death_ZU5; EGF; kringle; trypsin; Nebulin; LIM; SS=M; 5.77; 1.24
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, subfamily A; none; none; 5.71; 4.00
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6; ET; PLA2_inh; SS=M; 5.71; 3.83
 414171; AA360328; Hs.865; RAP1A, member of RAS oncogene family; pkinase; DAG_PE-bind; RBD; ras; OC1; GFP; TM=M; 5.69; 3.07
 418870; AF147204; Hs.89414; chemokine (C-X-C motif); receptor 4 (fus; 7tm_1; 7tm_2; TM=Y; SS=M; 5.68; 12.92
 425317; AW205118; Hs.210546; interleukin 21 receptor; none; TM=Y; SS=M; 5.60; 5.45
 417863; AB000450; Hs.82771; vaccinia related kinase 2; pkinase; TM=M; 5.59; 4.19
 400151; ; Eos Control; AT_hook; DNA_mis_repair; HATPase_c; UQ_con; TM=M; 5.53; 8.13
 450139; AK001838; Hs.355608; serum/glucocorticoid regulated kinase; none; none; 5.52; 8.61
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 5.52; 10.04
 433556; W56321; Hs.111460; calcium/calmodulin-dependent protein kin; pkinase; none; 5.51; 6.75
 424701; NM_005923; Hs.151988; mitogen-activated protein kinase kinase; pkinase; TM=M; 5.47; 4.58
 415875; AA894876; Hs.5687; protein phosphatase 1B (formerly 2C); ma; PP2C; TM=M; 5.43; 5.30
 408761; AA057264; Hs.238936; ESTs, Weakly similar to (define not ava; 7tm_1; none; 5.42; 2.59
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphatase tran; PHO4; LIM; TM=M; 5.37; 8.69
 444184; T87841; Hs.282990; Human DNA sequence from clone RP1-28H20; pkinase; RIO1; APH; KOW; TM=M; 5.36; 3.32
 410434; AF051152; Hs.63668; toll-like receptor 2; LRR; LRRCT; TIR; TM=M; SS=M; 5.36; 3.94
 429023; NM_000312; Hs.2351; protein C (inactivator of coagulation fa; EGF; trypsin; gla; SS=M; 5.31; 4.30
 421559; NM_014720; Hs.105751; S1e20-related serine/threonine kinase; pkinase; UVR; TM=M; 5.31; 3.26
 429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone; TM=M; 5.27; 3.12
 440682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin; bZIP; TM=M; 5.26; 4.82
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A receptor; Neur_chan_LBD; Neur_chan_memb; TM=Y; SS=M; 5.25; 11.26
 428234; U93553; Hs.183123; nuclear receptor subfamily 5, group A, m; hormone_rec; zf-C4; SS=M; 5.20; 1.11
 408683; R58665; Hs.46847; TRAF and TNF receptor-associated protein; Exo_endo_phos; TM=M; 5.19; 6.25
 408657; AA782601; Hs.173328; ESTs; B56; none; 5.18; 5.47
 438746; A1885815; Hs.184727; Human melanoma-associated antigen p97 (nr transferrin; Guanylate_kin; PDZ; SH3; 5.17; 4.02
 438698; AW297855; Hs.361171; ESTs, Weakly similar to I38022 hypotheti; lipoxygenase; PLAT; none; 5.16; 2.91
 442200; AW590572; Hs.235768; ESTs; none; none; 5.11; 4.22
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none; none; 5.08; 2.71
 419088; A1538323; Hs.367688; integrin, beta 8; Integrin_B; none; 5.07; 3.53
 414555; N98569; Hs.76422; phospholipase A2, group IIA (platelets; ; phosph; TM=M; SS=Y; 5.05; 3.42
 408414; A114688; Hs.193400; ESTs, Weakly similar to 2109260A B cell; in3; Ig; TM=Y; SS=M; 5.05; 3.41
 430407; H23551; Hs.30974; ESTs; pkinase; PBD; none; 5.03; 1.63
 427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C; none; 5.00; 5.14

- 452194; A1694413; Hs.373599; Ubiquitin-like protein FAT10777 - diubiq; none; none; 4.98; 2.65
 410073; AW408163; Hs.58488; catenin (cadherin-associated protein), α ; Stathmin, Vinculin; SS=M; 4.97; 10.60
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc, Rhodanese; none; 4.96; 2.87
 432841; M93425; Hs.62; protein tyrosine phosphatase, non-recept; Y_phosphatase; SS=M; 4.88; 21.69
 433470; AW960564; Hs.351313; transmembrane 4 superfamily member 1; none; TM=Y; SS=M; 4.88; 4.60
 418529; AW005695; Hs.250897; TRK-fused gene; Band_41, ERM, pkinase, LRR, LRRCT, MAM, Nucleoplasmin, Tropomyosin, OPR, filament, bZIP, G-gamma, M, DUF164; TM=M; 4.79; 5.47
- 5
 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; efhand, kazal, arf, ras, 7tm_1; TM=M; 4.75; 5.41
 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese, DSPc, Y_phosphatase; TM=M; 4.74; 9.76
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); none; TM=M; SS=M; 4.73; 4.68
 430630; AW269920; Hs.2621; cystatin A (stafin A); cystatin; TM=M; 4.66; 5.61
 452239; AW379378; Hs.356289; protein tyrosine phosphatase, receptor t; none; none; 4.63; 6.62
 427333; AF067797; Hs.176658; aquaporin 8; MIP; TM=Y; SS=M; 4.63; 0.80
 431890; X17033; Hs.271986; Integrin, alpha 2 (CD49B, alpha 2 subunit); vwa, integrin_A, FG-GAP; TM=Y; SS=M; 4.58; 11.38
 428085; A1634046; Hs.157313; ESTs; ICE_p20, DED, ICE_p10, ICE_p20, DED; 4.55; 4.51
 428582; BE336699; Hs.185055; BENE protein; none; TM=Y; SS=M; 4.54; 8.76
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; efhand; SS=M; 4.54; 19.57
 450056; BE047394; Hs.8208; ESTs. Weakly similar to S71512 hypothetical; ABC_tran, ABC_membrane, Ig, MHC_II_beta, SRP54, proteasome, ABC_membrane, ABC_tran; 4.49; 10.47
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2; TM=M; 4.41; 7.27
 447232; AW498834; Hs.327; interleukin 10 receptor, alpha; none; TM=M; SS=M; 4.41; 10.25
 433208; AW002834; Hs.24095; ESTs; arf, Ca_channel_B, SH3; 4.39; 12.14
 403208; ; Target Exon; lectin_c; none; 4.37; 0.76
 440486; BE243513; Hs.7212; hypothetical protein PP1044; LRR, PAAD, DAPIN, AAA, CARD, NB-ARC; NA; NA; 4.36; 10.34
 414278; AA330116; Hs.355877; Human glucose transporter pseudogene; none; none; 4.35; 7.95
 424833; NM_003894; Hs.153405; period (Drosophila) homolog 2; PAS; SS=M; 4.34; 6.23
 422573; AW297985; Hs.295726; Integrin, alpha V (vitronectin receptor; FG-GAP integrin_A; none; 4.32; 5.85
 418721; NM_002731; Hs.87773; protein kinase, cAMP-dependent, catalytic; pkinase, pkinase_C; SS=M; 4.31; 3.09
 412330; NM_005100; Hs.788; A kinase (PRKA) anchor protein (gravin); none; TM=M; 4.25; 12.74
 421939; BE169531; Hs.109727; TAK1-binding protein 2; KIAA0733 protein; z-RanBP, CUE; TM=M; 4.25; 12.54
 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle, trypsin, plant, thionins; SS=M; 4.24; 6.91
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none; TM=Y; SS=M; 4.22; 5.27
 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, re; ig; TM=Y; 4.16; 7.22
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen, COLFI, TSPN, laminin_G, CorA; SS=M; 4.16; 9.27
 445496; AB007860; Hs.12802; development and differentiation enhancin; SH3, ank, PH, ArfGAP; TM=M; 4.15; 23.43
 436075; BE090176; Hs.179902; transporter-like protein; none; TM=Y; SS=M; 4.14; 3.76
 414462; BE622743; Hs.301064; arfaptin 1; none; none; 4.08; 13.43
 435730; AB020635; Hs.4984; KIAA0828 protein; AdoHcyase, TrkA-N, 2-Hacid_DH_C; TM=M; 4.06; 9.12
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar_tr; TM=Y; 4.04; 10.05
 429379; NM_014840; Hs.200598; KIAA0537 gene product; pkinase, RIO1; TM=M; 4.00; 6.35
 429061; Y14039; Hs.195175; CASP6 and FADD-like apoptosis regulator; ICE_p20, DED; TM=M; 3.98; 5.66
 405203; ; NM_002086; Homo sapiens growth factor re; SH2, SH3; TM=M; 3.95; 17.71
 409335; NM_001502; Hs.53985; glycoprotein 2 (zymogen granule membrane; zona_pellucida; TM=M; SS=M; 3.94; 0.58
 446008; NM_004403; Hs.13530; deafness, autosomal dominant 5; none; TM=M; SS=M; 3.89; 7.59
 413899; AF083892; Hs.75608; tight junction protein 2 (zona occludens; SH3, PDZ, Guanylate_kin; TM=M; 3.84; 8.89
 438000; A1825880; Hs.5985; non-kinase Cdc42 effector protein SPEC2; none; TM=M; 3.83; 4.22
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR, Lysyl_oxidase; TM=M; SS=M; 3.81; 6.45
 450285; AW383258; Hs.24752; spectrin SH3 domain binding protein 1; SH3; TM=M; 3.78; 8.49
 417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, α ; hormone_rec, rec-C4; SS=M; 3.77; 4.22
 456376; AA663904; Hs.89862; TNFRSF1A-associated via death domain; death; TM=M; 3.68; 4.92
 438113; A1467808; Hs.8882; ESTs; 7tm_1; none; 3.59; 12.12
 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS; 3.58; 10.93
 429952; AF080158; Hs.226573; Inhibitor of kappa light polypeptide gen; pkinase, ubiquitin, Enterotoxin_A, PHO4, pkinase, ubiquitin; 3.57; 5.10
 415088; A1077288; Hs.374374; serum/glucocorticoid regulated kinase; none; none; 3.56; 4.60
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank; 3.55; 4.52
 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2, STAT, STAT_bind, STAT_prot; TM=M; 3.54; 8.19
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none; TM=M; 3.52; 9.70
 400288; X06256; Hs.149609; Integrin, alpha 5 (fibronectin receptor; Integrin_A, FG-GAP; TM=Y; 3.45; 6.44
 445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase_2; TM=M; 3.41; 6.03
 418255; AW135405; Hs.37251; ESTs; pkinase; none; 3.41; 13.97
 408822; AW500715; Hs.57079; Homo sapiens cDNA FLJ13267 fis, clone OV; PIP5K; none; 3.40; 8.97
 426432; AF001601; Hs.169857; paraoxonase 2; Arylesterase; TM=M; 3.39; 11.24
 431628; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none; TM=M; SS=Y; 3.39; 5.10
 414291; A128619; Hs.13040; G protein-coupled receptor 86; 7tm_1; TM=Y; SS=M; 3.38; 10.25
 457329; A1634860; Hs.247043; type 1 tumor necrosis factor receptor sh; Peptidase_M1; SS=M; 3.38; 13.78
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none; TM=Y; SS=M; 3.36; 4.17
 443710; A1928136; Hs.9691; Homo sapiens cDNA: FLJ23249 fis, clone C; G-alpha; none; 3.32; 20.33
 454294; AB000734; Hs.50840; JAK binding protein; SH2; TM=M; 3.31; 6.94
 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo_seg; TM=M; SS=M; 3.29; 3.07
 426728; NM_007118; Hs.367689; triple functional domain (PTPRF interact; SH3, Ig, pkinase, PH, spectrin, RhoGEF; TM=M; 3.27; 14.90
 427202; BE272822; Hs.173936; Interleukin 10 receptor, beta; Tissue_fac; TM=Y; SS=M; 3.24; 4.49
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase; TM=M; 3.24; 12.27
 425976; C75094; Hs.334514; NG22 protein; voltage_CLC; TM=Y; SS=M; 3.23; 13.40
 417534; NM_004998; Hs.82251; myosin IE; SH3, myosin_head, IQ; TM=M; 3.21; 15.21
 458097; AW341135; Hs.58104; ESTs; none; SH3, PID; 3.21; 7.34
 437928; NM_005476; Hs.5920; UDP-N-acetylglucosamine-2-epimerase/N-ac; hexokinase, FGGY, ROK, Epimerase_2; SS=M; 3.20; 8.38
 425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none; SS=M; 3.19; 5.09
 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none; none; 3.18; 4.17
 453489; AA300067; Hs.102000; hypothetical protein DKFZp434N185; F5_F8_type_C, pkinase, Ets; 3.17; 7.88
 414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT, FATC, PI3_P14_kinase; TM=M; 3.16; 4.71
 412767; AA233808; Hs.286241; protein kinase, cAMP-dependent, regulator; SH3, 7tm_2, cadherin, GPS, laminin_G, EGF, laminin_EGF, Sulfate_transp, STAS, cNMP_binding, RIIa; 3.16; 7.19
- 5
 415662; AW972481; Hs.170610; ESTs, Highly similar to G01887 MEK kinas; pkinase; none; 3.16; 7.21
 407788; AA687538; Hs.38972; tetraspan 1; transmembrane4; TM=Y; SS=M; 3.15; 22.66

- 437175; AW968078; Hs.87773; protein kinase, cAMP-dependent, catalytic; pkinase, pkinase_C, none; 3.14; 11.72
 409270; BE090051; Hs.23120; PIST; In3, pkinase, PDZ, DUF139; TM=Y; SS=M; 3.09; 7.81
 419591; AF090900; Hs.91393; Homo sapiens cDNA: FLJ21887 f1s, clone H; PDZ, L27; TM=M; 3.06; 5.46
 447225; R62676; Hs.17820; Rho-associated, coiled-coil containing p; PH, pkinase, HR1, none; 3.04; 13.05
 412692; AF044288; Hs.74515; aryl hydrocarbon receptor nuclear trans; HLH, PAS, PAC; TM=M; 2.95; 12.28
 409274; NM_003930; Hs.52644; SKAP55 homologue; SH3, PH; SS=M; 2.90; 14.62
 417707; AL035786; Hs.82425; actin related protein 2/3 complex, subunit; none; TM=M; 2.90; 11.00
 427045; H86504; Hs.173328; protein phosphatase 2, regulatory subunit; B56; TM=M; 2.89; 6.12
 431177; NM_003304; Hs.250587; transient receptor potential channel 1; ion_trans, ank; TM=Y; 2.89; 6.53
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none; TM=M; 2.87; 9.18
 418546; AA224827; gbnc32g04.s1 NCL CGAP_P2 Homo sapiens; vwa, Integrin, AFG-GAP, none; 2.86; 9.94
 446568; W58353; Hs.285123; Homo sapiens mRNA full length insert cDN; NDK, PH, Oxysterol_BP; SS=M; 2.85; 14.25
 454080; A1193711; Hs.576; fucosidase, alpha-L-1, tissue; Alpha_L_fucos; TM=M; SS=Y; 2.80; 10.53
 432874; W94322; Hs.279651; melanoma inhibitory activity; SH3; TM=M; SS=Y; 2.80; 10.53
 433000; U26710; Hs.3144; Cas-Br-M (murine) ectropic retroviral tr; zfc3HC4, UBA, Cbl_N, Cbl_N2, Cbl_N3; 2.77; 10.93
 444488; AW192879; Hs.355660; ancient conserved domain protein 4; none, none; 2.77; 12.58
 417904; A1750762; Hs.82911; protein tyrosine phosphatase type IVA, m; Y_phosphatase, DSPC; TM=M; 2.76; 12.78
 425204; NM_002436; Hs.1861; membrane protein, palmitoylated 1 (55kD); SH3, PDZ, Guanylate_kin; SS=M; 2.74; 5.71
 419262; AA834664; Hs.29131; nuclear receptor coactivator 2; PAS, zfc2H2, SET; 2.73; 12.50
 410793; AW581906; Hs.66392; Intersectin 1 (SH3 domain protein); SH3, ehfand, C2, PH, RhoGEF, M; SS=M; 2.73; 9.84
 446081; AA972412; Hs.13755; t-box and WD-40 domain protein 2; WD40, F-box, Ribosomal_L14; TM=M; 2.71; 12.29
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor; ig, pkinase; TM=Y; 2.71; 10.53
 452683; A1089575; Hs.374574; progesterone membrane binding protein; homeobox, none; 2.69; 12.53
 423533; NM_014339; Hs.129751; interleukin 17 receptor; none; TM=Y; SS=M; 2.67; 8.59
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin, ABC_tran, ABC_membrane, GTP_EFTU; TM=M; SS=M; 2.67; 12.22
 453915; AA588721; Hs.12284; ribosomal protein L44; none, T-box; 2.65; 6.38
 416810; AF035606; Hs.80019; programmed cell death 6; ehfand; TM=M; 2.61; 13.89
 439658; AA332057; Hs.6639; hypothetical protein MGC15440; none; TM=M; SS=M; 2.58; 10.19
 449924; W30681; Hs.146233; Homo sapiens cDNA: FLJ22130 f1s, clone H; SH3, none; 2.56; 19.04
 412926; A1879076; Hs.75061; macrophage myristoylated alanine-rich C; MARCKS; SS=M; 2.55; 14.99
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, pkinase, Recep_L_domain, YLP, none; 2.52; 14.71
 409098; AA132672; Hs.7984; pleckstrin homology, Sec7 and coiled/coil; PH, Sec7; TM=M; 2.51; 14.51
 413040; AA193338; Hs.12321; sodium calcium exchanger; Na_Ca_Ex; TM=Y; SS=M; 2.49; 9.28
 422070; AF149785; Hs.111126; pituitary tumor-transforming 1 interact; TCTP; TM=M; SS=Y; 2.45; 12.49
 452289; BE568205; Hs.28827; mitogen-activated protein kinase kinase; pkinase; TM=M; 2.44; 6.68
 427657; AV652249; Hs.180107; polymerase (DNA directed), beta; none; TM=M; 2.43; 7.97
 446287; BE247683; Hs.14611; dual specificity phosphatase 11 (RNA/RNP); DSPC; SS=M; 2.41; 9.51
 410017; AW952426; Hs.109438; Homo sapiens clone 24775 mRNA sequence; none, none; 2.41; 14.01
 424756; AW504657; Hs.152931; lamin B receptor; ERG4_ERG24, FKBP; TM=Y; 2.40; 5.98
 447590; A1953360; Hs.88201; ESTs; none, none; 2.36; 11.63
 426276; AW881411; Hs.169078; hypothetical protein FLJ23018; hormone_rec, zfc4; TM=M; 2.34; 13.34
 424441; X14850; Hs.147097; H2A histone family, member X; histone, CBFD_NFYB_HMF; 2.33; 12.17
 429623; NM_005308; Hs.211569; G protein-coupled receptor kinase 5; pkinase, RGS; TM=M; 2.32; 15.80
 439866; AA280717; Hs.6727; Ras-GTPase activating protein SH3 domain; rrm, NTF2; TM=M; 2.32; 12.48
 453648; W21493; Hs.28329; hypothetical protein FLJ14005; none, none; 2.31; 13.19
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22, Claudin, none; 2.31; 8.51
 453327; AW500180; Hs.356109; tryptophanyl-tRNA synthetase; rrm, vwa, FG-GAP; 2.30; 13.02
 439256; AA322302; Hs.183302; PCTAIRE protein kinase 2; none, none; 2.26; 10.36
 424467; A1929392; Hs.350026; Dnal (Hsp40) homolog, subfamily B, member; Dnal, pkinase, UBA, pkinase_C; SS=M; 2.26; 11.82
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_tr; TM=Y; SS=M; 2.26; 12.54
 456607; A1680190; Hs.106070; cyclin-dependent kinase inhibitor 1C (p5; CDK; TM=M; 2.25; 13.11
 423960; AA164516; Hs.136309; SH3-containing protein SH3GLB1; SH3, none; 2.20; 20.05
 424058; AL121516; Hs.138617; thyroid hormone receptor interactor 12; HECT, WVE; TM=M; 2.20; 13.38
 446644; NM_003272; Hs.15791; transmembrane 7 superfamily member 1 (up; none; TM=Y; SS=M; 2.18; 15.68
 411218; H46440; Hs.180628; dynamin 1-like; dynamin_2, dynamin, GED, none; 2.18; 13.83
 414721; X90392; Hs.77091; ribosomal protein L10; Exo_endo_phos, Ribosomal_L10a, Acyltransferase, SCP; TM=M; SS=M; 2.14; 11.24
 421759; AA027968; Hs.107979; small membrane protein 1; none; TM=Y; SS=M; 2.14; 14.03
 416240; NM_001981; Hs.79095; epidermal growth factor receptor pathway; ehfand, DUF164; TM=M; 2.13; 12.86
 435521; W23814; Hs.6361; mitogen-activated protein kinase kinase; none, none; 2.12; 11.08
 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, P13_P14_kinase, FAT, FATC, BclA, RUN; TM=M; 2.12; 14.05
 453064; R40334; Hs.89463; potassium large conductance calcium-act; none, none; 2.12; 8.96
 409223; AA312572; Hs.362852; phosphoinositide-3-kinase, regulatory su; SH2, SH3, RhoGAP, none; 2.08; 11.60
 414482; S57498; Hs.78252; endothelin receptor type A; 7tm_1; TM=Y; SS=M; 2.06; 14.23
 414496; W73853; Hs.355424; ESTs; pkinase, F5_F8_type_C, adh_short, none; 2.05; 13.45
 450455; AL117424; Hs.25035; chloride intracellular channel 4; none, TNF; 2.05; 19.04
 449906; NM_005638; Hs.24167; synaptobrevin-like 1; synaptobrevin, NTF2; TM=Y; 2.04; 13.34
 422112; BE540240; Hs.111783; Lsm1 protein; Sm, BAG; SS=M; 2.03; 12.60
 434935; BE561824; Hs.273369; uncharacterized hematopoietic stem/proge; none; TM=M; 2.02; 10.52
 433427; A1816449; Hs.171889; cholinephosphotransferase 1; SH2, CDP-OH_P_transf; TM=M; 2.02; 16.87
 410850; AW362867; Hs.302738; Homo sapiens cDNA: FLJ21425 f1s, clone C; Sulfate_transp, STAS, HMG_box; 2.02; 9.37
 440481; AA182907; Hs.7200; Homo sapiens, clone MGC:16714, mRNA, cont; pkinase, RCC1; TM=M; 2.02; 12.31
 434645; AF255303; Hs.112227; membrane-associated nucleic acid binding; zfcCCH, gpdh, Adeno_E1B_55k, zfc3HC4; TM=M; 2.00; 9.15
 410113; AW996564; Hs.250824; Homo sapiens cDNA: FLJ23435 f1s, clone H; pkinase, none; 1.99; 10.64
 414636; AL120259; Hs.76691; stannin; none; TM=M; SS=Y; 1.95; 7.72
 408176; AK001553; Hs.43436; adenylate kinase 3 alpha like; adenylate kinase, none; 1.95; 14.95
 422690; AU077275; Hs.119222; suppression of tumorigenicity 13 (colon; TPR; TM=M; 1.94; 10.91
 427881; BE538296; Hs.323834; cytochrome c oxidase subunit Va; none, GKAP; 1.93; 20.57
 433387; L76628; Hs.3260; presenilin 1 (Alzheimer disease 3); Presenilin, 7tm_3, oxidored_q5_N; TM=Y; 1.92; 12.58
 453938; AF082569; Hs.36794; D-type cyclin-interacting protein 1; B56; TM=M; 1.90; 12.74
 433592; NM_004642; Hs.3436; deleted in oral cancer (mouse, homolog); none; TM=M; 1.89; 23.27
 447791; BE241859; Hs.19575; CGI-11 protein; V-ATPase_H, Armadillo_seg; TM=M; 1.88; 12.82
 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 f1s, clone H; adenylate kinase, none; 1.88; 14.95

- 432650; D00860; Hs.56; phosphoribosyl pyrophosphate synthetase ; none;none; 1.88; 12.70
 424250; AF073310; Hs.143648; Insulin receptor substrate 2; PHIRS;TM=M; 1.86; 19.50
 424482; BE268621; Hs.149155; voltage-dependent anion channel 1; Euk_porin;SS=M; 1.85; 11.29
 425335; BE394327; Hs.296267; follistatin-like 1; ehand,kazal,arf,ras,7tm_1;TM=M; 1.85; 13.62
 426122; NM_006925; Hs.166975; splicing factor, arginine/serine-rich 5; rrm;SS=M; 1.83; 10.88
 451579; AW607731; Hs.26670; Human PAC clone RP3-515N1 from 22q11.2-q; kingle;TM=Y;SS=M; 1.83; 20.35
 428901; A1929568; Hs.146668; KIAA1253 protein; 7tm_2,UFP0073,TMS,TDE;TM=Y;SS=M; 1.83; 19.00
 453963; AA040311; Hs.28959; ESTs; pkinase,Activin_rec;none; 1.82; 15.25
 417414; AA434589; Hs.367676; dUTP pyrophosphatase; dUTPase,KRAB; 1.81; 14.20
 414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigenit; DAN;TM=M;SS=M; 1.81; 22.29
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 14; Exo_endo_phos,SH2;TM=M; 1.80; 18.30
 417733; AL048678; Hs.82503; H.sapiens mRNA for 3'UTR of unknown prot; none;NA;NA; 1.80; 6.28
 424805; AF230904; Hs.153260; c-Cbl-interacting protein; SH3;TM=M; 1.80; 11.99
 420747; BE294407; Hs.99910; phosphofructokinase, platelet; PFK;TM=M; 1.79; 25.25
 416819; U77735; Hs.80205; pim-2 oncogene; pkinase;SS=M; 1.78; 15.25
 437708; AB033020; Hs.5801; KIAA1194 protein; LRR,Exo_endo_phos;TM=M; 1.77; 11.11
 439877; H39685; Hs.258730; tryptase beta 1; pkinase;SS=M; 1.77; 21.91
 440256; U23841; Hs.18851; hypothetical protein FLJ10875; none,UBA,UBX; 1.76; 12.95
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 1.76; 21.01
 414703; BE243877; Hs.374366; ATPase, Na7 transporting, beta 3 polypep; Na_K-ATPase;TM=Y;SS=M; 1.75; 20.03
 443693; AJ344782; Hs.349261; DnaJ (Hsp40) homolog, subfamily C, membe; rrm,DnaJ,TPR;TM=M; 1.75; 13.29
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (fr; ABC_tran,GTP_EFTU,ABC_membrane;none; 1.75; 8.75
 413796; AW408084; Hs.75545; Interleukin 4 receptor; fn3,granulin;TM=M;SS=M; 1.74; 14.73
 438438; AA257992; Hs.50651; Janus kinase 1 (a protein tyrosine kinase; pkinase,SH2,adenylatekinase;none; 1.73; 24.10
 429655; U48959; Hs.211582; myosin, light polypeptide kinase; pkinase,fn3,lg;none; 1.73; 31.59
 421456; AW579842; Hs.104557; hypothetical protein FLJ10697; zf-C2H2,DUF18,ehand,C2,PI-PLC-Y,PI-PLC-X;TM=M; 1.73; 16.87
 444252; R21135; Hs.54985; ESTs; none;none; 1.71; 10.40
 442819; BE622721; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; none,pkinase,PBD; 1.69; 14.02
 447918; AI129320; Hs.115175; ESTs, Highly similar to JC5818 gamma-act; pkinase,SAM;none; 1.69; 17.14
 429279; AB018271; Hs.198689; KIAA0728 protein; Myosin_tail,ehand,spectrin,GAS2,Myosin_tail; 1.68; 14.21
 450440; AB024334; Hs.25001; tyrosine 3-monooxygenase/tryptophan 5-mo; 14-3-3;TM=M; 1.67; 24.67
 413423; AU076684; Hs.75350; vinculin; Vinculin;none; 1.65; 29.28
 420972; AW814616; Hs.31431; hypothetical protein FLJ12171; Fructosamin_kin;SS=M; 1.65; 10.75
 416884; M60484; Hs.80350; protein phosphatase 2 (formerly 2A), cat; Metallophos;SS=M; 1.63; 24.55
 436719; Y11192; Hs.5299; aldehyde dehydrogenase 5 family, member ; lipocalin,aldedh,ubiquitin,IRK;SS=M; 1.61; 11.20
 419223; X60111; Hs.1244; CD9 antigen (p24); transmembrane4;TM=Y;SS=M; 1.61; 14.93
 414176; BE140638; Hs.75794; EDG-2 (endothelial differentiation, lys; 7tm_1,CRCB;TM=Y; 1.61; 8.03
 431476; BE612705; Hs.256697; histidine triad nucleotide-binding prote; HIT;SS=M; 1.60; 24.37
 412347; AW970026; Hs.73818; ubiquinol-cytochrome c reductase hinge p; UCR_hinge,G-alpha,arf;TM=M; 1.59; 18.09
 423804; AW403448; Hs.1706; interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M; 1.59; 10.99
 426552; BE297660; Hs.170328; moesin; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmn,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M; 1.58; 25.97
 428216; M18468; Hs.183037; protein kinase, cAMP-dependent, regulator; cNMP_binding,Rli;SS=M; 1.56; 10.58
 421251; Z28913; Hs.102948; enigma (LIM domain protein); LIM,PDZ;SS=M; 1.56; 13.51
 448581; NM_002709; Hs.21537; protein phosphatase 1, catalytic subunit; none;none; 1.55; 12.33
 417098; AB017365; Hs.173859; frizzled (Drosophila) homolog 7; Frizzled,Fz,7tm_2,toxin_2;TM=Y;SS=M; 1.55; 13.77
 437076; AA951260; Hs.5443; BCL2-associated athanogene 5; BAG,Hania_nucleocap;TM=M; 1.54; 10.93
 426653; AA530892; Hs.171695; dual specificity phosphatase 1; Rhodanese,DSPC,Y_phosphatase;TM=M; 1.54; 11.88
 421143; AB024536; Hs.102171; immunoglobulin superfamily containing la; lg,LRR,LRRNT,LRRCT;TM=M;SS=M; 1.53; 23.05
 414457; AW514320; Hs.76159; ATPase, H transporting, lysosomal (vacuo; pkinase,ATP-synt_C;none; 1.53; 32.59
 414382; AW380339; Hs.8058; hemolipetic PBX-interacting protein; M;TM=M; 1.52; 8.66
 450698; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; rrm;TM=M; 1.52; 11.74
 402705; ; activator of S phase kinase; AhpC-TSA;TM=M;SS=M; 1.51; 26.85
 426268; AF083420; Hs.168913; serine/threonine kinase 24 (Ste20, yeast; pkinase;SS=M; 1.50; 24.04
 414604; AU076649; Hs.76556; growth arrest and DNA-damage-inducible 3; none;TM=M; 1.50; 14.35
 445584; AF217518; Hs.8360; PTD012 protein; none;SS=M; 1.49; 12.00
 407232; X04526; ; gb;Human liver mRNA for beta-subunit sig; WD40;TM=M; 1.49; 19.32
 424208; NM_003734; Hs.198241; amine oxidase, copper containing 3 (vasc; Cu_amine_oxid,Cu_amine_oxidN2,Cu_amine_oxidN3;TM=M;SS=M; 1.48; 13.21
 458761; AF090922; Hs.152738; mitochondrial ribosomal protein L11; ER_Jumen_recept,Ribosomal_L11,Ribosomal_L11_N;TM=Y;SS=M; 1.48; 12.50
 426340; Z97989; Hs.169370; FYN oncogene related to SRC, FGR, YES; BNR,SH2,SH3,pkinase;TM=Y;SS=M; 1.48; 17.75
 414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD,helicase_C,rm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,Rita,abhydrolase,TGF-beta,DUF139,TPR,DSPC,isp_1,Ribosomal_S21,nvp;TM=M; 1.46; 20.47
 452516; AA058630; Hs.29759; RNA POLYMERASE I AND TRANSCRIPT RELEASE ; none;SS=M; 1.46; 12.72
 414240; AL046742; Hs.75842; dual-specificity tyrosine-(Y)-phosphoryl; pkinase;SS=M; 1.45; 14.38
 420532; AA248016; Hs.194110; hypothetical protein PRO2730; pkinase,WD40;SS=M; 1.43; 13.92
 402575; ; Rho GTPase activating protein 1; PAP2;TM=Y;SS=M; 1.43; 13.71
 414765; X07854; Hs.77269; guanine nucleotide binding protein (G pr; G-alpha,arf;TM=M; 1.41; 24.62
 448423; BE390905; Hs.21198; translocase of outer mitochondrial membr; TPR;TM=M;SS=M; 1.41; 10.70
 422587; AJ879352; Hs.118625; hexokinase 1; hexokinase,hexokinase2;TM=M; 1.41; 19.31
 415995; NM_004573; Hs.355888; phospholipase C, beta 2; C2,PI-PLC-Y,PI-PLC-X;TM=M; 1.40; 11.21
 446108; AL036596; Hs.42322; A kinase (PRKA) anchor protein 2; Paralamin;TM=M; 1.40; 13.98
 427721; A1582843; Hs.180455; RAD23 (S. cerevisiae) homolog A; ubiquitin,UBA,Integrin_B;SS=M; 1.39; 15.01
 417891; W79410; Hs.82887; protein phosphatase 1, regulatory (inhib; none;TM=M; 1.39; 15.97
 427373; AB007972; Hs.130760; myosin phosphatase, target subunit 2; ank;TM=M; 1.39; 14.49
 446334; U52427; Hs.14839; polymerase (RNA) II (DNA directed) polyp; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frizzled,cathectin,7tm_2,rrm,PAP_essoc;TM=Y;SS=M; 1.38; 12.58
 447042; AB035863; Hs.182217; succinate-CoA ligase, ADP-forming, beta; ligase-CoA,ATP-grasp,Zip,CPSase_L_D2,GARS_B;TM=Y;SS=M; 1.37; 11.37
 427705; AI870421; Hs.180394; signal recognition particle 14kD (homolo; SRP14,TNFR_c6;SS=M; 1.37; 22.05
 425969; AW576265; Hs.301763; KIAA0554 protein; SH3,FCH,HR1;TM=M; 1.37; 13.68
 433572; AL046859; Hs.3407; protein kinase (cAMP-dependent, catalyti; PKI;SS=M; 1.35; 12.43
 410597; W16518; Hs.279518; amyloid beta (A4) precursor-like protein; Kunitz_BPTLA4_EXTRA,Coprogen_oxidase;TM=Y;SS=M; 1.35; 22.54
 418424; Y13622; Hs.85087; latent transforming growth factor beta b; EGF,TB,spider toxin,granulin,ANF_receptor;SS=M; 1.34; 12.09
 442603; AI035719; Hs.303091; pleckstrin homology, Sec7 and coiled/coi; PH,Sec7;TM=M; 1.34; 11.40
 418043; AW377752; Hs.83341; AXI receptor tyrosine kinase; fn3,lg,pkinase;TM=Y;SS=M; 1.31; 10.79

439278; AF0707046; Hs.6518; ganglioside expression factor 2; MAP1_LC3,aminotran_3;TM=M; 1.31; 15.89
 425875; AU077333; Hs.160483; erythrocyte membrane protein band 7.2 (s; PBP,Band_7;TM=M; 1.31; 17.93
 407744; AB020629; Hs.38095; ATP-binding cassette, sub-family A (ABC1; ABC_tran,PRK;TM=Y;SS=M; 1.29; 10.95
 420679; X57152; Hs.99853; fibrillarin; CK_II_beta,Fibrillarin,WD40;TM=M; 1.29; 18.69
 427397; A1929685; Hs.177656; calmodulin 1 (phosphorylase kinase, delta; ehand,RmaAD;SS=M; 1.29; 15.68
 424661; M29551; Hs.151531; protein phosphatase 3 (formerly 2B), cat; Metallophos;TM=M; 1.28; 13.39
 428950; BE311879; Hs.194673; phosphoprotein enriched in astrocytes 15; DED;TM=M; 1.27; 11.15
 440820; AL031846; Hs.356416; plakophilin 4; none,none; 1.26; 10.65
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevisiae; NusG;SS=M; 1.25; 12.07
 447386; NM_006289; Hs.375001; KIAA1027 protein; Band_41,I_LWEQ,Apolipoprotein,IRS;SS=M; 1.22; 10.65
 433053; BE301909; Hs.279952; glutathione S-transferase subunit 13 hom; HCCA_isomerase;TM=M; 1.20; 15.78
 440708; AF038962; Hs.7381; voltage-dependent anion channel 3; Euk_porin,Enterotoxin_A,PHO4,none; 1.20; 14.06
 417069; AA442192; Hs.374980; cytochrome c oxidase subunit VIII; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Fritzzled,calreticulin,7tm_2,mm,PAP_assoc;TM=Y;SS=M; 1.18; 16.91
 402559; ; Rho GTPase activating protein 1; PAP2;TM=Y;SS=M; 1.16; 15.49
 426636; BE242634; Hs.2055; ubiquitin-activating enzyme E1 (A1S9T an; Thif,UBACT;TM=M; 1.14; 10.99
 428773; BE256238; Hs.193163; bridging integrator 1; BAR,SH3;SS=M; 1.14; 11.38
 406906; Z25424; ; gb:H.sapiens protein-serine/threonine ki; none,none; 1.13; 12.97
 443932; AW888222; Hs.9973; tensin; SH2,WW,PID,none; 1.07; 15.41
 421996; AW583807; Hs.1460; glucagon; hormone2;SS=M; 59.35; 1.61
 414998; NM_002543; Hs.77729; oxidized low density lipoprotein (lectin; lectin_c;TM=Y;SS=M; 22.96; 4.57
 442573; H93366; Hs.7567; branched chain aminotransferase 1, cytos; aminotran_4,none; 21.41; 1.15
 451035; AU076785; Hs.430; plastin 1 (I isoform); ehand,CH,Adaptin_N;SS=M; 19.25; 3.53
 408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M; 15.53; 4.34
 421340; F07783; Hs.1369; decay accelerating factor for complement; sushit;SS=M; 14.84; 19.59
 422260; AA315993; Hs.105484; regenerating gene type IV; lectin_c;SS=M; 14.71; 2.89
 430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 14.28; 11.47
 412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymph; 7tm_1;TM=Y;SS=M; 12.71; 12.56
 451820; AW058357; Hs.199248; ESTs; 7tm_1;TM=Y;SS=M; 10.18; 2.67
 418693; A1750878; Hs.87409; thrombospondin 1; EGF,isp_1,vwc,TSPN,isp_3;SS=M; 9.72; 6.94
 448105; AW591433; Hs.828241; Transmembrane protease, serine 3; ktl_recept_La,lypsin;TM=Y;SS=M; 9.67; 4.06
 456266; L29073; Hs.198726; cold shock domain protein A; 7tm_2,HRM,CSD;TM=Y;SS=M; 9.62; 2.36
 413095; AA494359; Hs.30715; potassium voltage-gated channel, Isk-rel; none,START; 9.15; 2.18
 417933; X02308; Hs.82962; thymidylate synthetase; thymidylat_synth,MR_MLE,MR_MLE_N;SS=M; 8.97; 5.01
 433334; A1927208; Hs.231958; matrix metalloproteinase 28; Peptidase_M10,none; 8.71; 4.28
 418030; BE207573; Hs.83321; neuromedin B; Bombesin;TM=M;SS=Y; 8.38; 1.55
 433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE_p10,ICE_p20;SS=M; 8.31; 4.23
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 8.28; 5.49
 428513; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA sequence; PSI,none; 8.13; 13.28
 449444; AW818436; Hs.351306; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 7.89; 7.00
 453459; BE047032; Hs.257789; ESTs; none,none; 7.40; 0.60
 436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 7.29; 5.78
 426761; A1015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing me; none;TM=Y;SS=M; 7.25; 7.22
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 7.13; 3.97
 419968; X04430; Hs.93913; interleukin 6 (interferon, beta 2); IL6;SS=Y; 6.93; 3.43
 457133; M54968; Hs.351221; v-Ki-ras2 Kirsten rat sarcoma 2 viral on; ras,Idh;SS=M; 6.90; 2.85
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 6.88; 3.10
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase;TM=Y; 6.42; 2.26
 427969; NM_001963; Hs.2230; epidermal growth factor (beta-urogastrin; EGF,Idl_recept_b,EB;TM=M;SS=M; 6.37; 1.07
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank,death,ZU5,EGF,kringle,lypsin,Nebulin,LIM;SS=M; 5.77; 1.24
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptio; UPAR_LY6,ET,PLA2_inh;SS=M; 5.71; 3.83
 418283; S79895; Hs.83942; cathepsin K (pseudosostosis); Peptidase_C1;SS=M; 5.59; 38.68
 458471; AV648609; Hs.194240; ESTs; none,none; 5.23; 1.05
 433470; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.88; 4.60
 433293; AF007835; Hs.32417; hypothetical protein MGC4309; none;TM=M; 4.56; 4.96
 410867; X63556; Hs.750; fibrillin 1 (Marfan syndrome); EGF,TB,wnt,EB,TIL;SS=M; 4.32; 26.87
 417512; X76534; Hs.82226; glycoprotein (transmembrane) mmb; PKD;TM=Y;SS=M; 4.26; 8.04
 414825; X06370; Hs.77432; epidermal growth factor receptor (avian ; Furin-like,pkinase,Recep_L_domain;TM=M;SS=M; 3.94; 1.16
 439180; A1393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 3.76; 2.21
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=M; 3.47; 2.24
 419749; X73608; Hs.93029; sparc/osteonectin, cwcv and kazal-like d; kazal,thyroglobulin_1;SS=M; 3.37; 7.10
 436576; A1458213; Hs.77542; ESTs; 7tm_1,DnaJ; 3.15; 3.27
 428093; AW594506; Hs.104830; ESTs; none,none; 2.81; 3.40
 459683; A1674906; Hs.199460; gb:wc73f02.x1 NCI_CGAP_Pan1 Homo sapiens; none;TM=Y; 2.77; 1.36
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor.; lg,pkinase;TM=Y; 2.71; 10.53
 430451; AAB36472; Hs.297939; cathepsin B; Peptidase_C1,pro_isomerase;SS=M; 2.28; 14.59
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfam; 60s_ribosomal,Ribosomal_L10,TNFR_c6,DEAD; 2.21; 6.33
 435496; AW840171; Hs.265398; PAR-6 beta; none,none; 2.17; 2.00
 418641; BE243136; Hs.86947; a disintegrin and metalloproteinase doma; disintegrin,Repolyisin,Pep_M12B_propep,EGF;TM=Y;SS=M; 1.91; 13.06
 414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigen; DAN;TM=M;SS=M; 1.81; 22.29
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pkinase;TM=Y;SS=M; 1.52; 6.40
 452795; AW392555; Hs.18878; hypothetical protein FLJ21620; 2OG-Fell_Oxy;TM=M; 1.49; 3.29
 432199; A1693815; Hs.127179; cryptic gene; none;TM=M;SS=M; 1.23; 1.60
 453966; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin,Idl_recept_a,none; 1.00; 3.92
 445416; AW139377; Hs.127179; cryptic gene; none,none; 1.00; 2.45
 451106; BE382701; Hs.25960; N-MYC oncogene; HLH,Myo_N_1erm;TM=M; 1.00; 1.87
 447993; AW139525; Hs.170362; ESTs; none,none; 1.00; 1.30

TABLE 42B

Key: Unique Eos probe identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
5	406685	0_0 M18728
	414087	1632850_1 W19712 BE247277
	400151	9575_21 BC006850 U07418 NM_000249 U07343 AL574783 BI090482 BG684481 AA385302 BG196167 BI091720 BG195132 AI680106 AI457552 AA02478
		BG249688 AA347119 BG755996 BG822578
	418546	242836_1 T59708 AA224827 T59843 BE156903

10 TABLE 42C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
20	406399	9256288	Minus 63448-63554
	405102	8076881	Minus 120922-121296
	403344	8569726	Plus 70823-70990
	405555	1552511	Plus 153405-153564,154623-154876,155272-15540
25	405556	1552511	Plus 163497-163623,164715-164968,165369-16550
	405204	7230116	Plus 126569-126754
	406366	9256126	Minus 10639-10800,10890-11023,11113-11293
	400539	7574902	Plus 8559-8721
	403208	7630829	Minus 147706-147903,148667-148804
	405203	7230116	Plus 125295-125463
30	402705	8782736	Plus 88961-90114,90773-90895,91131-91261
	402575	9884830	Minus 109742-109883
	402559	9864273	Plus 33539-33715

35

TABLE 43A: 43 genes upregulated in pancreatic cancer relative to normal body tissues

40 Table 43A lists about 43 genes upregulated in pancreatic cancer relative to normal body tissues that are likely to encode proteins particularly useful for diagnostic or prognostic applications. These genes were selected from 59680 probesets on the Eos/Arraymatrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion transporter). Certain predicted protein domains are noted.

45 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Prod.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 50 UniGene Title: UniGene gene title
 R1 90th percentile of pancreatic cancer AIs divided by the 50th percentile of normal tissue AIs
 R2 90th percentile of pancreatic cancer AIs divided by the 90th percentile of normal pancreas AIs, where the 15th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

55

Pkey; ExAccn; UniGeneID; Unigene Title; Pred.Prod.Domains; R1; R2

446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin); Osteopontin;SS=M; 44.95; 2.17
 421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz,NTR;SS=M; 35.40; 29.13
 411274; NM_002776; Hs.69423; kallikrein 10; trypsin;TM=M; 30.10; 13.59
 446921; AB012113; Hs.16530; small inducible cytokine subfamily A (Cy; IL8;SS=Y; 29.33; 16.08
 413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8;SS=M; 24.64; 7.21
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGF-beta,propeptide,TGF-beta,none; 23.81; 10.74
 407811; AW190902; Hs.40098; cysteine knot superfamily 1, BMP antagonist; TGF-beta,DAN;SS=Y; 22.33; 10.20
 404682; ; C9001188; gi12738842|ref|NP_073725.1| p; none;TM=M; 17.72; 1.40
 65 413554; AA319146; Hs.75426; secretogranin II (chromogranin C); Granin;TM=M;SS=Y; 17.36; 2.01
 428392; H10233; Hs.2265; secretory granule, neuroendocrine protet; none;TM=M;SS=M; 18.82; 1.70
 408243; Y00787; Hs.624; interleukin 8; IL8,PAS,IL8;TM=M; 15.53; 4.34
 419216; AU076718; Hs.164021; small inducible cytokine subfamily B (Cy; IL8;SS=M; 15.40; 3.70
 428242; H55709; Hs.2250; leukemia inhibitory factor (cholinergic); LIF_OSM;SS=M; 14.85; 6.58
 70 421340; F07783; Hs.1369; decay accelerating factor for complement; sush;SS=M; 14.84; 19.59
 409757; NM_001898; Hs.123114; cystatin SN; cystatin;SS=M; 14.61; 12.75
 425071; NM_013989; Hs.154424; deiodinase, iodothyronine, type II; T4_deiodinase;TM=M;SS=Y; 14.35; 17.22
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 13.81; 7.69
 409420; Z15008; Hs.54451; laminin, gamma 2 (nicotin (100kD), kalin; laminin_B,laminin_EGF;SS=M; 13.05; 7.72
 75 432596; AJ224741; Hs.278461; matrilin 3; EGF,vwa;SS=M; 12.80; 9.91
 422109; S73265; Hs.1473; gastrin-releasing peptide; Bombesin,Defensin_propept;TM=M;SS=M; 12.79; 4.69
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 11.36; 2.22
 429547; AW009166; Hs.99376; FGENSEH predicted novel secreted protein; none,none; 10.25; 5.62
 422424; AI186431; Hs.296638; prostate differentiation factor; TGF-beta;SS=M; 9.96; 1.88
 80 428505; AL035461; Hs.2281; chromogranin B (secretogranin 1); Granin;SS=M; 9.40; 3.46
 409956; AW103364; Hs.727; inhibin, beta A (activin A, activin AB a; TGF-beta,TGF-beta_propeptide,Tub;SS=M; 9.19; 16.46
 418030; BE207573; Hs.83321; neuromedin B; Bombesin;TM=M;SS=Y; 8.38; 1.55
 452401; NM_007115; Hs.29352; tumor necrosis factor, alpha-induced pro; Xlnk,CUB;SS=M; 7.48; 4.96

- 421582; A1910275; Hs.350470; trefol factor 1 (breast cancer, estroge; trefol, Gastrin; SS=M; 7.08; 21.61
 423634; AW959908; Hs.1690; heparin-binding growth factor binding pr; none; TM=M; SS=M; 6.78; 12.19
 428486; AW583497; Hs.184604; pancreatic polypeptide; hormone3; TM=M; SS=Y; 6.29; 3.51
 443646; A1085198; Hs.164226; ESTs; EGF, tsp_1, vwc, TSPN, tsp_3, none; 6.17; 4.25
 457489; A1693815; Hs.127179; cryptic gene; none; TM=M; SS=M; 5.19; 2.79
 450983; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; none; SS=M; 5.01; 7.43
 422867; L32137; Hs.1584; cartilage oligomeric matrix protein (pse; tsp_3, EGF; SS=M; 4.87; 9.40
 426322; J05068; Hs.2012; transcobalamin I (vitamin B12 binding pr; Cobalamin_bind; SS=M; 4.71; 11.74
 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle, trypsin, plant_thionins; SS=M; 4.24; 6.91
 428758; AA433988; Hs.98502; CA125 antigen; mucin 16; SEA; TM=Y; 3.52; 8.43
 422048; NM_012445; Hs.288126; spondin 2, extracellular matrix protein; tsp_1; TM=M; SS=M; 3.45; 7.69
 424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; tn2, hemopexin, Peptidase_M10; SS=M; 3.43; 10.37
 417931; W95842; Hs.82961; trefol factor 3 (intestinal); trefol; SS=M; 2.98; 9.65
 445417; AK001058; Hs.12680; Homo sapiens cDNA FLJ10196 fis, clone HE; tsp_1, Reprolysin, Pep_M12B_propep, none; 2.97; 5.74
 432874; W94322; Hs.279651; melanoma inhibitory activity; SH3; TM=M; SS=Y; 2.80; 10.53
 431462; AW583672; Hs.256311; granin-like neuroendocrine peptide precu; none, none; 2.70; 1.99

TABLE 43C

- 20 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 25 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
404682	9797231	Minus	40977-41150

TABLE 44A: 754 GENES UP-REGULATED IN RHEUMATOID ARTHRITIS COMPARED TO NORMAL BODY

- 35 Table 44A lists about 754 genes up-regulated in rheumatoid arthritis. These were selected from 35403 probesets on the Affymetrix/Eos Hu01 GeneChip.

- 40 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title

Pkey	ExAccn	UnigenelD	Unigene Title
100042	M10098		AFFX control - HUMRGE/M10098_3
101577	M34353	Hs.1041	v-ros avian UR2 sarcoma virus oncogene h
103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa
104743	AA021157	Hs.33619	Homo sapiens cDNA FLJ20096 fis, clone CO
104996	AA112307	Hs.105894	hypothetical protein FLJ21919
105437	AA252191	Hs.25199	hypothetical protein
108258	AA063269		gb:zm02a09.s1 Stratagene corneal stroma
109086	AA166695	Hs.270737	tumor necrosis factor (ligand) superfamily
109279	AA196625	Hs.86080	ESTs
109779	F10527	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucur
111794	R32647	Hs.23545	ESTs
112531	R69798	Hs.29036	ESTs
112784	R96306	Hs.191290	ESTs
113293	T67026	Hs.187403	ESTs
115416	AA283893	Hs.337079	ESTs
116548	D20433		gb:HUMGS01407 Human promyelocyte Homo sa
116565	D45533	Hs.129691	hypothetical protein FLJ21603
118104	N55332	Hs.39785	ESTs
119243	T12603		gb:CHR90123 Chromosome 9 exon II Homo sa
119336	T55340	Hs.208238	ESTs
120101	W95414	Hs.55497	EST
120715	AA292700		gb:zs59a06.s1 NCI_CGAP_GCB1 Homo sapiens
120872	AA357993	Hs.96996	ESTs
121010	AA398355	Hs.97330	ESTs
121509	AA412092	Hs.97888	ESTs
121722	AA419482	Hs.98874	similar to proline-rich protein 48
122265	AA436838	Hs.98906	EST
123206	AA489681	Hs.102248	Homo sapiens cDNA: FLJ22105 fis, clone H
123490	AA599723		gb:ag11c07.s1 Gessler Wilms tumor Homo s
124198	H53099	Hs.198271	NADH dehydrogenase (ubiquinone) 1 alpha
124294	H90573	Hs.102298	EST
125067	T86429	Hs.111725	ESTs
125153	W38294		ESTs
125330	AA401804	Hs.114574	hypothetical protein FLJ20619
125335	T86520	Hs.16230	ESTs
125361	T90348	Hs.183404	ESTs
125439	AA826305		gb:PMO-LT0017-031299-001-c07 LT0017 Homo
125535	R17430	Hs.22215	secretogranin III
125583	R22272	Hs.86022	ESTs
125590	R23658	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,
125742	H81181	Hs.261023	hypothetical protein FLJ20958

5	125795	T98190	Hs.7756	proteasome (prosome, macropain) 26S subu
	125858	H11549	Hs.31066	ESTs
	125865	H12876	Hs.283078	hOAT4
	126039	AA160575	Hs.181102	p30 DBC protein
	126143	N29315	Hs.266331	hypothetical protein MGC4595
	126177	H93164	Hs.129750	hypothetical protein FLJ10546
	126219	N36368	Hs.293483	ESTs, Weakly similar to similar to C. el
	126221	AI248169	Hs.172965	ESTs
10	126262	C75147	Hs.143764	ESTs, Weakly similar to unknown (H.sapi
	126277	N39132	Hs.15441	Crm (Cramped Drosophila)-like
	126292	AA491328		gb:aa65d09.r1 NC1_CGAP_GC81 Homo saplens
	126293	Z18870	Hs.248121	G protein-coupled receptor 22
	126353	AI243114	Hs.94031	ESTs
15	126556	AA491325	Hs.112227	membrane-associated nucleic acid binding
	126559	R15866	Hs.170263	tumor protein p53-binding protein, 1
	126609	W87435	Hs.186802	ESTs
	126616	AA348581	Hs.134605	ESTs
	126628	AI357886	Hs.170994	hypothetical protein MGC10946
20	126636	AA001527		gb:zf56g09.r1 Soares retina N2b4HR Homo
	126861	AA742428	Hs.144432	ESTs
	126990	AA215510	Hs.191650	ESTs
	127017	AA740146	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I
	127049	AA235966	Hs.291811	ESTs
25	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene fami
	127331	F20186		gb:HSPD05873 HM3 Homo sapiens cDNA clone
	127357	AA452788		gb:zv80d10.r1 Soares_total_fetus_Nb2HF8_
	127368	AA434362	Hs.193326	fibroblast growth factor receptor-like 1
	127374	AA448728	Hs.312110	ESTs, Weakly similar to I38022 hypothet
30	127429	AA961490	Hs.293751	ESTs, Moderately similar to TPTE_HUMAN P
	127490	W52891	Hs.7278	cryptochrome 2 (photolyase-like)
	127502	AA614422	Hs.183502	ESTs
	127647	AI087279	Hs.148410	ESTs
	127650	AA873776	Hs.261957	ESTs
35	127676	D31237	Hs.279938	HSPC067 protein
	127746	AI239495	Hs.120189	ESTs
	127812	AA749094	Hs.291434	ESTs
	127824	AI208365	Hs.127811	ESTs
40	127933	AA811102	Hs.303581	ESTs, Moderately similar to ALU1_HUMAN A
	128006	AA058693	Hs.129908	KIAA0591 protein
	128011	AI347067	Hs.124636	ESTs
	128038	AA868782	Hs.137024	ESTs
	128058	AI126617	Hs.132449	ESTs
	128199	AI073548	Hs.164597	ESTs
45	128308	AI079496	Hs.134169	ESTs
	128389	AI142639	Hs.146662	ESTs
	128410	AA452788		gb:zv80d10.r1 Soares_total_fetus_Nb2HF8_
	129199	H90914	Hs.200332	hypothetical protein FLJ20651
	130998	C00810	Hs.293981	guanine nucleotide binding protein (G pr
50	134409	AA281600	Hs.164915	small nuclear RNA activating complex, p
	134578	AA194724	Hs.224137	hypothetical protein
	134644	S83308	Hs.87224	SRV (sex determining region Y)-box 5
	100262	D38500	Hs.278468	postmeiotic segregation increased 2-like
	100676	HG3044-HT3742	Hs.287820	fibronectin 1
55	100704	HG3242-HT3419	Hs.166110	calcium channel, voltage-dependent, alph
	100787	HG3872-HT4142	Hs.302063	immunoglobulin heavy constant mu
	100873	HG4333-HT4603	Hs.17364	zinc finger protein 79 (p17)
	100943	HG880-HT880		gb:PMO-SN0019-280300-001-D11 SN0019 Homo
	100996	J03909	Hs.14623	interferon, gamma-inducible protein 30
60	101046	K01160		
	101371	M13232	Hs.36989	coagulation factor VII (serum prothrombi
	101461	M22430	Hs.76422	phospholipase A2, group IIA (platelets,
	101697	M64358		gb:Human rhom-3 gene, exon.
	101909	S69265		
65	102199	U21128	Hs.79914	lumican
	102275	U30998	Hs.17752	phosphatidylserine-specific phospholipas
	102295	U32581	Hs.168052	KIAA0421 protein
	102319	U34587	Hs.66578	corticotropin releasing hormone receptor
	102383	U40622	Hs.150930	X-ray repair complementing defective rep
70	102470	U49835	Hs.154138	chitinase 3-like 2
	102544	U57721	Hs.169139	chitinase 3-like 2
	102649	U68133		kynureninase (L-kynurenine hydrolase)
	102798	U88898		gb:U68133 Human cell line PCI-O6A Homo s
	102804	U89942		gb:Human endogenous retrovirus H proteas
75	102851	V00532	Hs.83354	lysyl oxidase-like 2
	102852	V00571	Hs.93907	interferon, alpha 14
	102860	X00368	Hs.75294	corticotropin releasing hormone
	103262	X78565	Hs.289114	gb:Human prolactin gene 5' region.
	103484	Y08374	Hs.75184	hexabrachion (tenascin C, cytolactin)
	103559	Z19585	Hs.75774	chitinase 3-like 1 (cartilage glycoprote
80	103658	Z74615	Hs.172928	thrombospondin 4
	103719	AA064109	Hs.4273	collagen, type I, alpha 1
	103876	AA226865	Hs.8203	hypothetical protein FLJ13159
	103897	AA248870	Hs.55058	endomembrane protein emp70 precursor iso
				EH-domain containing 4

5	103906	AA249437	Hs.317403	hypothetical protein MGC2744
	103985	AA313880	Hs.99872	fetal Alzheimer antigen
	104056	AA397529	Hs.58297	CLL8 protein
	104209	AB000221	Hs.16530	small inducible cytokine subfamily A (Cy
	104386	H41895	Hs.144164	ESTs, Moderately similar to ALU8_HUMAN A
10	104398	H53555	Hs.36790	ESTs, Weakly similar to putative p150 [H
	104422	H86858	Hs.132909	ESTs
	104561	R60100	Hs.323817	DKFZP547E1010 protein
	104593	R81267	Hs.98640	hypothetical protein FLJ21069
	104643	AA004701	Hs.18978	Homo sapiens cDNA: FLJ22822 fis, clone K
15	104673	AA007633	Hs.20010	ESTs
	104681	AA009832	Hs.34500	ESTs
	104711	AA017254	Hs.32794	ESTs
	104812	AA034111	Hs.124187	ESTs
	104877	AA047437	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se
20	104886	AA053348	Hs.339699	growth differentiation factor 11
	104924	AA058532	Hs.28774	ESTs, Weakly similar to I38022 hypothe
	105071	AA136532	Hs.29475	ESTs
	105105	AA151872	Hs.87016	hypothetical protein FLJ22938
	105203	AA195660	Hs.7882	ESTs
25	105317	AA233926	Hs.52620	integrin, beta 8
	105617	AA280687	Hs.4069	glucocorticoid modulatory element bindin
	105707	AA291012	Hs.37617	ESTs, Weakly similar to A53933 myosin I
	105754	AA302657	Hs.192028	ESTs
	105770	AA347954	Hs.269873	Homo sapiens clone IMAGE:297403, mRNA se
30	105882	AA400292	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
	105883	AA400490	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com
	105890	AA400766	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,
	106080	AA418046	Hs.35124	ESTs
	106090	AA418909	Hs.169333	hypothetical protein DKFZp761E2110
35	106096	AA419609	Hs.170121	protein tyrosine phosphatase, receptor 1
	106124	AA423987	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H
	106308	AA436186	Hs.30662	ESTs
	106438	AA449199	Hs.21342	ESTs
	106660	AA460936	Hs.27056	KIAA1284 protein
40	106731	AA465657	Hs.29205	alpha integrin binding protein 63
	106880	AA488889	Hs.32425	ESTs
	107055	AA600152	Hs.29419	ESTs
	107151	AA621169	Hs.8687	ESTs
	107183	C20974	Hs.12114	vanin 1
45	107231	D59299	Hs.34727	ESTs, Moderately similar to I38759 zinc
	107490	W74158	Hs.103189	lipopolysaccharide specific response-68
	107572	AA001903	Hs.59962	ESTs
	107620	AA005039	Hs.60171	ESTs
	107801	AA019433	Hs.285803	Homo sapiens cDNA FLJ10674 fis, clone NT
50	107817	AA020781	Hs.60847	ESTs
	107823	AA021057	Hs.60836	ESTs
	107857	AA024687	Hs.61208	ESTs
	107882	AA025630	Hs.231967	ALL1 fused gene from 5q31
	108005	AA037769	Hs.194293	ESTs, Weakly similar to I54374 gene NF2
55	108092	AA045951	Hs.184029	hypothetical protein DKFZp761A052
	108115	AA047291	Hs.165216	ESTs
	108214	AA058661	Hs.60764	ESTs
	108382	AA074885	Hs.67726	macrophage receptor with collagenous str
	108409	AA075578		gb:zm88h03.r1 Stratagene ovarian cancer
60	108436	AA078801		gb:zm94a09.s1 Stratagene colon HT29 (937
	108625	AA101983	Hs.283022	triggering receptor expressed on myeloid
	108631	AA102553	Hs.334337	ESTs
	108763	AA127539	Hs.281397	hypothetical protein AD034
	108852	AA133131		gb:zm25d03.s1 Stratagene pancreas (93720
65	108931	AA147188		gb:zo38d01.s1 Stratagene endothelial cel
	108976	AA151480	Hs.91202	ESTs
	109026	AA157811		gb:zo35d07.s1 Stratagene colon (937204)
	109170	AA180352	Hs.191472	ESTs, Weakly similar to ALU1_HUMAN ALU
	109303	AA206126	Hs.269291	ESTs
70	109326	AA210719		gb:zr88e04.s1 NCL CGAB1 Homo sapiens
	109345	AA213774	Hs.203396	ESTs
	109404	AA224594	Hs.86941	ESTs
	109473	AA233151	Hs.81796	ESTs
	109725	F10003	Hs.79658	casein kinase 1, epsilon
75	109794	F10684	Hs.23687	ESTs
	109835	H00615	Hs.170044	ESTs
	109896	H04794	Hs.30489	ESTs
	109918	H05641	Hs.216701	Homo sapiens mRNA; cDNA DKFZp564I0816 (f
	109950	H08200	Hs.268770	ESTs, Weakly similar to 2004399A chromos
80	110078	H15054	Hs.318773	KIAA1836 protein
	110182	H20402	Hs.31746	hypothetical protein DKFZp547F072
	110213	H23216	Hs.86905	ATPase, H+ transporting, lysosomal (vacu
	110310	H38209	Hs.32728	EST
	110354	H41280	Hs.22586	ESTs
	110413	H48124	Hs.279454	ESTs
	110422	H48467	Hs.36094	EST
	110433	H49425	Hs.301062	UDP-N-acetyl-alpha-D-galactosamine:polyp

	110434	H49446	Hs.26299	ESTs
	110553	H58934	Hs.124990	ESTs
	110750	N20522	Hs.30981	ESTs
5	110827	N30077	Hs.14855	ESTs
	110829	N30198	Hs.28625	ESTs
	110917	N46363	Hs.5170	ESTs
	111100	N62522	Hs.20450	BCAM-like membrane protein precursor
	111112	N63281	Hs.35452	ESTs
10	111179	N67239	Hs.10760	asporin (LRR class 1)
	111185	N67551	Hs.12844	EGF-like domain, multiple 6
	111223	N68921	Hs.334838	KIAA1866 protein
	111275	N70970	Hs.35006	ESTs
	111443	R01901		gb:Homo sapiens endogenous retrovirus W
15	111573	R10305	Hs.185683	ESTs
	111590	R11157	Hs.75425	ubiquitin associated protein
	111671	R19368	Hs.229084	Homo sapiens cDNA FLJ11666 fis, clone H
	111732	R25153	Hs.163813	ESTs
	111809	R33616	Hs.24688	EST
20	111829	R36070		gb:Homo sapiens full length insert cDNA
	111944	R40606	Hs.21263	suppressor of potassium transport defect
	112015	R42836	Hs.23198	ESTs
	112023	R43020	Hs.236223	EST
	112055	R43621	Hs.26139	ESTs
25	112334	R56239	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S
	112340	R56602	Hs.8904	Ig superfamily protein
	112353	R58986	Hs.26613	Homo sapiens mRNA; cDNA DKFZp586F1323 (f
	112467	R65706		gb:yl16g12.s1 Soares placenta Nb2HP Homo
	112478	R66067	Hs.28664	ESTs
30	112533	R69886		gb:yl47f03.s1 Soares placenta Nb2HP Homo
	112588	R77302		gb:yl5h08.s1 Soares placenta Nb2HP Homo
	112595	R77783	Hs.22404	protease, serine, 12 (neurotrypsin, moto
	112676	R86976	Hs.34060	ESTs
	112744	R93206	Hs.293762	ESTs, Weakly similar to I38022 hypothel
35	112777	R95869	Hs.35467	EST
	112817	R98491	Hs.14584	ESTs
	112902	T09262	Hs.129190	Human DNA sequence from clone RP5-1046G1
	113009	T23699	Hs.7246	ESTs
	113151	T51620	Hs.9326	EST
40	113297	T67161	Hs.13059	ESTs
	113398	T82280	Hs.87016	hypothetical protein FLJ22938
	113484	T87795	Hs.187543	ESTs
	113769	U55966	Hs.22985	alpha2,8-sialyltransferase
	113794	W37382	Hs.11090	membrane-spanning 4-domains, subfamily A
45	113971	W86760	Hs.269172	ESTs
	114066	Z38152	Hs.26920	ESTs
	114178	Z39063	Hs.17930	chromosome 6 open reading frame 11
	114206	Z39294	Hs.27339	EST
	114371	Z41835	Hs.27810	ESTs
50	114428	AA017130	Hs.84790	KIAA0225 protein
	114466	AA026970	Hs.135150	lung type-I cell membrane-associated gly
	114625	AA084362		gb:zn05b10.r1 Stratagene hNT neuron (937
	114862	AA235174	Hs.106432	Homo sapiens cDNA FLJ13410 fis, clone PL
	114908	AA236545	Hs.54973	cadherin-like protein VR20
55	114973	AA250845	Hs.87762	ESTs
	115009	AA251561	Hs.48689	ESTs
	115055	AA253005	Hs.61753	ESTs
	115098	AA256161	Hs.161729	ESTs
	115321	AA280805	Hs.191540	ESTs
60	115385	AA282540	Hs.109694	KIAA1451 protein
	115466	AA287008	Hs.285655	ESTs
	115479	AA287596	Hs.278188	ESTs, Moderately similar to I54374 gene
	115663	AA405838	Hs.40507	ESTs
	115689	AA410645	Hs.199014	ESTs, Moderately similar to ALU7_HUMAN A
	115748	AA418835	Hs.90286	ESTs
65	115810	AA426026	Hs.187615	ESTs
	115827	AA427890	Hs.83583	actin related protein 2/3 complex, subun
	115881	AA435577	Hs.184942	G protein-coupled receptor 64
	116148	AA460708	Hs.62905	hypothetical protein FLJ14834
	116257	AA481493	Hs.88537	ESTs
70	116365	AA521080	Hs.46765	ESTs
	116941	H77395	Hs.39749	ESTs
	116982	H81933	Hs.312582	ESTs
	116995	H83928		gb:ys64b03.s1 Soares retina N2b4HR Homo
75	116997	H84214	Hs.40594	ESTs
	117016	H87171	Hs.52170	ESTs
	117097	H93608	Hs.41919	EST
	117101	H94043	Hs.24341	transcriptional co-activator with PDZ-bl
	117238	N20815	Hs.173337	ESTs
80	117303	N22776	Hs.264079	ESTs
	117399	N26480	Hs.43805	lipoma HMGIC fusion partner-like 3
	117503	N31953	Hs.44286	ESTs
	117544	N33222	Hs.44451	ESTs
	117594	N34929	Hs.171984	ESTs

5	117627	N36113	Hs.44789	ESTs, Weakly similar to B34087 hypothet
	117653	N38970	Hs.194214	ESTs
	117695	N40953	Hs.45093	EST
	117697	N40976		gb:yy80b06.s1 Soares_multiple_sclerosis_
	117766	N47807	Hs.46767	EST
10	117807	N48701	Hs.46523	EST
	117816	N48872		gb:yy77a05.s1 Soares_multiple_sclerosis_
	117882	N50101	Hs.301406	hypothetical protein PP3501
	117987	N51935	Hs.47374	Homo sapiens cDNA FLJ13561 fis, clone PL
	118074	N54188	Hs.130323	Homo sapiens, clone IMAGE:3960432, mRNA
15	118114	N56875	Hs.143212	cystatin F (leukocystatin)
	118151	N58276	Hs.229119	EST
	118270	N62868	Hs.48653	ESTs
	118291	N63076	Hs.138746	EST
	118358	N64017	Hs.144633	hypothetical protein DKFZp434F2322
20	118383	N64529	Hs.49001	EST
	118412	N64856	Hs.97437	centrosomal protein 1
	118433	N66248	Hs.141609	EST
	118600	N69222	Hs.238936	ESTs, Weakly similar to (define not av
	118641	N70298	Hs.49829	ESTs
25	118643	N70324	Hs.49840	ESTs
	118695	N71781	Hs.50081	KIAA1199 protein
	118915	N91481	Hs.54713	ESTs
	119041	R02591	Hs.284294	Breakpoint cluster region protein, uteri
	119069	R27619	Hs.231046	EST
30	119105	R42357	Hs.91453	ESTs
	119154	R61293		gb:yh07a05.s1 Soares infant brain 1N1B H
	119241	T12559		gb:CHR90079 Chromosome 9 exon II Homo sa
	119269	T16367	Hs.65327	EST
	119310	T40427		gb:ya01a05.s2 Stratagene lung (937210) H
35	119345	T63474	Hs.90696	EST
	119353	T66867	Hs.187402	ESTs
	119390	T89122	Hs.249712	ESTs, Weakly similar to ALU1_HUMAN ALU
	119423	T99544	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU
	119428	W02129	Hs.55242	EST
40	119529	W38053		ESTs, Highly similar to S03917 fibronec
	119795	W73370	Hs.339722	ESTs
	119817	W74257	Hs.159690	DKFZP586L2024 protein
	119831	W78050	Hs.58419	hypocretin (orexin) receptor 2
	119930	W86471	Hs.151624	ESTs
45	120039	W92548	Hs.94985	hypothetical protein
	120256	AA169801	Hs.98710	gb:zp54e11.s1 Stratagene NT2 neuronal pr
	120284	AA182626		KIAA0627 protein; Drosophila multiple as
	120350	AA211300	Hs.108614	gb:DKFZp434B1822_r1 434 (synonym: hbas3)
	120379	AA227849		FSH primary response (LRPR1, rat) homolo
50	120383	AA228030	Hs.123122	spinal cord-derived growth factor-B
	120420	AA236031	Hs.112885	novel protein with MAM domain
	120437	AA243427	Hs.104311	ESTs
	120461	AA251301	Hs.293369	ring finger protein 10
	120594	AA282054	Hs.5094	homeo box A10
55	120611	AA284178	Hs.110637	EST
	120626	AA285064	Hs.104485	ESTs
	120696	AA291503	Hs.97249	ESTs
	120747	AA302976	Hs.96672	ESTs
	120749	AA303235		gb:EST14544 Testis tumor Homo sapiens cD
60	120752	AA311972	Hs.22895	hypothetical protein FLJ23548
	120851	AA349662	Hs.174248	ESTs
	120866	AA350718	Hs.291272	ESTs
	120949	AA397830	Hs.98347	ESTs, Weakly similar to JC5308 testis-sp
	120996	AA398281	Hs.308114	ESTs
65	121038	AA398536	Hs.97365	ESTs
	121065	AA398558	Hs.97300	ESTs
	121067	AA398662	Hs.97302	ESTs
	121071	AA398678	Hs.139355	ESTs
	121082	AA398722		gb:zt175h07.s1 Soares_testis_NHT Homo sap
70	121172	AA400013	Hs.97750	EST, Weakly similar to MPL3 RAT MICROTUB
	121191	AA400205	Hs.104447	ESTs
	121354	AA405384	Hs.193737	ESTs
	121393	AA405981	Hs.262643	ESTs
	121399	AA406059	Hs.332700	EST
75	121479	AA411911	Hs.98110	ESTs
	121498	AA412033	Hs.178045	ESTs
	121704	AA418743	Hs.98306	KIAA1862 protein
	121736	AA421131	Hs.148515	Human clone 23564 mRNA sequence
	122198	AA435892	Hs.97541	ESTs
80	122220	AA436011	Hs.98187	ESTs
	122250	AA436692	Hs.98892	EST
	122279	AA437209	Hs.234016	ESTs
	122286	AA437259	Hs.104944	ESTs
	122330	AA442870	Hs.98628	Homo sapiens, clone IMAGE:4214491, mRNA,
	122338	AA443311	Hs.98998	ESTs
	122355	AA443789	Hs.19978	CGI-30 protein
	122590	AA453264	Hs.99310	ESTs

5	122746	AA458791		gb:aa68c02.s1 Stratagene fetal retina 93
	122805	AA460702	Hs.82772	collagen, type XI, alpha 1
	122841	AA461536	Hs.288908	WAS protein family, member 2
	122899	AA469960	Hs.178420	ESTs, Highly similar to WASP interacting
	122933	AA476728	Hs.107537	chromosome 7 open reading frame 2
10	123005	AA479726	Hs.52620	integrin, beta 8
	123142	AA487504	Hs.105718	EST
	123153	AA488349	Hs.334808	hypothetical protein MGC4189
	123168	AA488881	Hs.105218	EST
	123188	AA489092	Hs.177726	ESTs
15	123276	AA491270	Hs.187946	ESTs
	123305	AA496133		gb:zv51e12.s1 Soares_testis_NHT Homo sap
	123328	AA496968		gb:aa42g03.s1 Soares_NhHMPu_S1 Homo sapi
	123450	AA598913	Hs.111207	ESTs
	123464	AA599014	Hs.153321	Homo sapiens cDNA FLJ10577 fis, clone NT
20	123550	AA609332	Hs.180698	ESTs
	123700	AA609606	Hs.191956	ESTs
	123858	AA620821	Hs.112911	EST
	123863	AA620873	Hs.112916	ESTs
	124046	F10243		gb:HSC3CC122 normalized infant brain cDN
25	124059	F13673	Hs.283713	ESTs, Weakly similar to S64054 hypothe
	124196	H52617	Hs.144167	ESTs
	124197	H52921		gb:yq76c09.s1 Soares fetal liver spleen
	124229	H62793	Hs.268945	ESTs
	124230	H63111	Hs.6655	Homo sapiens EST from clone 208499, full
30	124241	H65947	Hs.165355	ESTs, Moderately similar to ZN91_HUMAN Z
	124251	H68286	Hs.107924	ESTs
	124400	N30597	Hs.179152	loll-like receptor 7
	124416	N34042	Hs.271674	ESTs
	124570	N67117	Hs.102808	ESTs
35	124575	N68168		gb:za11c01.s1 Soares fetal liver spleen
	124588	N69197	Hs.191361	ESTs, Weakly similar to I38022 hypothe
	124598	N70294	Hs.269137	ESTs, Weakly similar to A56194 thromboxa
	124655	N93176	Hs.102914	ESTs
	124706	R07499	Hs.193612	ESTs, Weakly similar to ALU8_HUMAN ALU
40	124848	R60135	Hs.203498	EST
	124882	R74041	Hs.101539	ESTs
	124898	R82846	Hs.273789	ESTs
	125086	T91161	Hs.173880	Interleukin 1 receptor accessory protein
	125145	W38001		
45	125216	W73409	Hs.103185	ESTs
	125342	AJ055916	Hs.133552	ESTs
	125351	T96520	Hs.324746	alpha-2-HS-glycoprotein
	125419	AJ076822	Hs.134544	ESTs
	125424	T99667	Hs.18564	ESTs
50	125526	R14487	Hs.17110	Homo sapiens mRNA; cDNA DKFZp43C2016 (f
	125539	R17870	Hs.248120	G protein-coupled receptor 21
	125633	AA508225	Hs.15463	Homo sapiens, clone IMAGE:2959994, mRNA
	125689	R48940	Hs.108043	Friend leukemia virus integration 1
	125707	C14616	Hs.284122	Wnt inhibitory factor-1
55	125790	AA868325	Hs.99962	proteoglycan 2, bone marrow (natural kil
	125876	AA324967	Hs.7298	biphenyl hydrolase-like (serine hydrolas
	125969	R94247	Hs.88414	BTB and CNC homology 1, basic leucine zi
	125970	AI400964	Hs.177516	high density lipoprotein binding protein
	125975	AA495891	Hs.152290	ESTs, Highly similar to JC2463 vasoactiv
60	125985	H54857	Hs.35981	ESTs
	126018	H54866	Hs.167583	ESTs
	126032	H59735	Hs.269065	ESTs, Highly similar to KIAA0349 [H.sapi
	126059	H66582	Hs.308486	ESTs
	126107	H79155	Hs.93361	ESTs
65	126154	AI004105	Hs.190488	Homo sapiens, Similar to nuclear localiz
	126199	AI000492	Hs.125829	ESTs
	126207	W77936	Hs.83583	actin related protein 2/3 complex, subun
	126227	N27236	Hs.269034	ESTs
	126269	AA830432	Hs.44701	ESTs
70	126373	F11606	Hs.6079	B cell RAG associated protein
	126378	AA347842		gb:yy62e11.s1 Soares_multiple_sclerosis_
	126383	AA885594	Hs.6298	KIAA1151 protein
	126403	N73388	Hs.125978	ESTs, Weakly similar to S71949 metallopr
	126525	AA884833	Hs.166432	ESTs
75	126527	AA548559	Hs.103853	hypothetical protein FLJ20043
	126566	W67245	Hs.103142	ESTs
	126583	W92895	Hs.279746	vanilloid receptor-like protein 1
	126610	AA460338	Hs.191391	ESTs
	126622	AA699443	Hs.193213	ESTs
80	126633	AA206993	Hs.315367	Homo sapiens, Similar to hypothetical pr
	126727	AA037230	Hs.135084	cystatin C (amyloid angiopathy and cereb
	126762	AA064671		gb:zm13b04.s1 Stratagene pancreas (93720
	126775	S86382	Hs.957	putative opioid receptor, neuromedin K (
	126783	AA126047		gb:zn09d10.s1 Stratagene hNT neuron (937
	126882	AA761143	Hs.250581	SWI/SNF related, matrix associated, acti
	126945	R51877	Hs.25845	ESTs
	126968	AJ311457	Hs.99472	ESTs

5	127070	AA641812	Hs.190037	ESTs
	127087	AA380418	Hs.88012	SHP2 interacting transmembrane adaptor
	127187	AA297138	Hs.207422	ESTs, Weakly similar to S71949 metallopro
	127215	AI246377	Hs.127675	ceroid-lipofuscinosis, neuronal 8 (epile
	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of
10	127278	AA342715		gb:EST48309 Fetal spleen Homo sapiens cD
	127299	AA360710	Hs.158480	ESTs
	127325	AA393073	Hs.126099	ESTs
	127347	AA428350	Hs.58389	hypothetical protein MGC4090
	127401	AA921944	Hs.127639	ESTs
15	127420	AA699582	Hs.82171	Homo sapiens clone 19187 placenta expres
	127438	AI224421	Hs.77100	general transcription factor IIE, polype
	127441	AA835684	Hs.287601	Homo sapiens cDNA FLJ13830 fis, clone TH
	127449	AI421866	Hs.75722	ribophorin II
	127493	AA808081	Hs.291701	ESTs
20	127505	AA594244	Hs.292245	ESTs, Weakly similar to ALU1_HUMAN ALU S
	127620	AI025699	Hs.116200	ESTs
	127623	AA773234	Hs.271877	angiotensin-like 2
	127633	AI339609	Hs.268538	potassium voltage-gated channel, Isk-rel
	127701	AA935466		gb:zf84c06.s1 Soares_pineal_gland_N3HPG
25	127713	AA688322	Hs.150683	ESTs
	127722	AA700444	Hs.189186	ESTs, Weakly similar to ALUD_HUMAN IIII
	127733	AA704680	Hs.189005	ESTs
	127816	AA743646	Hs.120604	ESTs, Weakly similar to YA02_HUMAN HYPOT
	127966	AI493406	Hs.292514	ESTs
30	127973	AI336794	Hs.129117	ESTs
	127989	AA909267	Hs.132413	ESTs
	127997	AI281549	Hs.311054	Homo sapiens mRNA full length insert cDN
	128016	N92597	Hs.82689	tumor rejection antigen (gp96) 1
	128037	AA868394	Hs.181129	ESTs, Weakly similar to S18968 cyrtilesti
35	128053	T65805	Hs.65377	ESTs, Moderately similar to KIAA1399 pro
	128066	AA884838	Hs.189171	ESTs
	128071	AA889398	Hs.189241	ESTs
	128091	AA904559	Hs.129329	ESTs
	128113	AI341423	Hs.288433	neurotrimin
40	128145	AI498467	Hs.166669	solute carrier family 4, sodium bicarbon
	128167	AA932961	Hs.85752	uncharacterized hematopoietic stem/proge
	128195	AI143866	Hs.127778	ESTs
	128265	T95851	Hs.17691	ESTs
	128283	AI076570	Hs.134053	ESTs
45	128309	AI457235	Hs.166479	ESTs
	128313	AI051250	Hs.157775	ESTs
	128346	AI088907	Hs.160189	ESTs
	128359	AI096526	Hs.270244	ESTs, Weakly similar to I38022 hypotheti
	128369	F12681	Hs.30445	Homo sapiens cDNA FLJ14687 fis, clone NT
50	128371	H12876	Hs.283078	hOAT4
	128421	T77876	Hs.268589	ESTs
	128453	X02761	Hs.287820	fibronectin 1
	128496	T83496	Hs.32944	inositol polyphosphate-4-phosphatase, ty
	128514	H84261	Hs.301693	Homo sapiens, clone IMAGE:3638994, mRNA,
55	128551	H09058	Hs.278398	KIAA1117 protein
	128683	AA316862	Hs.9605	cleavage and polyadenylation specific fa
	128731	AF005271	Hs.104555	neuropeptide FF-amide peptide precursor
	128843	AA234141	Hs.275675	katanin p80 (WD40-containing) subunit B
	128988	AA411040	Hs.294140	ESTs
60	129016	W84524	Hs.184194	transmembrane 4 superfamily member 5
	129021	AA426406	Hs.173081	KIAA0530 protein
	129095	L12350	Hs.108623	thrombospondin 2
	129171	AA234048	Hs.7753	calumenin
	129188	M30257	Hs.109225	vascular cell adhesion molecule 1
65	129410	U25987	Hs.272620	pregnancy specific beta-1-glycoprotein 9
	129467	AA410311	Hs.44208	hypothetical protein FLJ23153
	129518	AA369807	Hs.112238	ESTs
	129534	R73640	Hs.11260	hypothetical protein FLJ11264
	129632	L27213	Hs.1176	solute carrier family 4, anion exchanger
70	129691	X06700	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl
	129881	AA458952	Hs.181406	hypothetical protein FLJ22301
	129990	N30316		gb:gw75b05.s1 Soares_placenta_8to9weeks_
	130049	V01515	Hs.1460	glucagon
	130171	AA454177	Hs.245257	ESTs, Weakly similar to A46010 X-linked
75	130411	AA505009	Hs.169910	KIAA0173 gene product
	130479	R41163	Hs.12457	hypothetical protein FLJ10814
	130511	L32137	Hs.1584	cartilage oligomeric matrix protein (pse
	130521	U92971	Hs.194351	coagulation factor II (thrombin) recepto
	130645	AA020942	Hs.17200	STAM-like protein containing SH3 and ITA
80	130655	N92934	Hs.17409	cysteine-rich protein 1 (intestinal)
	130656	Z20481	Hs.330988	Homo sapiens, Similar to Bicaudal D (Dro
	130889	D57622	Hs.20985	sin3-associated polypeptide, 30kD
	131064	AA598441	Hs.22583	DKFZP434K2235 protein
	131070	F13594	Hs.22607	ESTs
	131189	L16782	Hs.240	M-phase phosphoprotein 1
	131318	X51699	Hs.2558	bone gamma-carboxyglutamate (gla) protei
	131506	W47579	Hs.5801	KIAA1194 protein

5	131551	AA127867	Hs.28508	Homo sapiens cDNA: FLJ22115 fis, clone H
	131563	C20547	Hs.302810	Novel human gene mapping to chromosome 20
	131830	U33054	Hs.32959	G protein-coupled receptor kinase 2 (Dro
	131879	AA017161	Hs.33792	ESTs
	132017	W67251	Hs.267659	vav 3 oncogene
10	132025	U58516	Hs.3745	milk fat globulin-EGF factor 8 protein
	132096	AA131410	Hs.3964	Homo sapiens clone 24877 mRNA sequence
	132159	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophila)
	132164	U84573	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio
	132180	AA405569	Hs.418	fibroblast activation protein, alpha
15	132223	R77451	Hs.4245	chromosome 11 hypothetical protein ORF3
	132238	AA453446	Hs.42673	ESTs
	132406	F09979	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f
	132945	N40559	Hs.6129	ATP-binding cassette, sub-family B (MDR/
	133185	AA481404	Hs.6686	hypothetical protein DKFZp564O1664
20	133193	C14015	Hs.303075	EST
	133370	AA156897	Hs.72157	DKFZP564I1922 protein
	133406	U22172	Hs.179697	Human DNA damage repair and recombination
	133409	U65918	Hs.73078	deleted in azoospermia-like
	133591	T82292	Hs.75111	protease, serine, 11 (IGF binding)
25	133699	X00588	Hs.77432	epidermal growth factor receptor (avian
	134137	F10045	Hs.79347	KIAA0211 gene product
	134339	AA478971	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
	134421	AA122386	Hs.82985	collagen, type V, alpha 2
	134462	U11037	Hs.181300	sel-1 (suppressor of lin-12, C.elegans)-
30	134515	C20737	Hs.84469	ESTs
	134527	T40835	Hs.322978	EST
	134711	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro
	134824	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor
	134854	J03464	Hs.179573	collagen, type I, alpha 2
35	134921	W60186	Hs.125511	Homo sapiens mRNA; cDNA DKFZp434P1530 (f
	135003	H42527	Hs.26102	trichorhinophalangeal syndrome I
	135210	W90522	Hs.93589	hypothetical protein DKFZp564B1162
	135348	AA442054	Hs.268177	phospholipase C, gamma 1 (formerly subty
	100547	HG2149-HT2219		gb:Homo sapiens mucin (mucin) mRNA, part
40	100572	HG2271-HT2367	Hs.73995	flaggrin
	100587	HG3115-HT3291		gb:Human Golli-mbp gene, exon 2.
	100695	HG315-HT315	Hs.272620	pregnancy specific beta-1-glycoprotein 9
	101447	M21305		gb:Human alpha satellite and satellite 3
	102329	U35407	Hs.158084	peroxisome receptor 1
45	102892	X05232	Hs.83326	matrix metalloproteinase 3 (stromelysin
	103036	X54925	Hs.83169	matrix metalloproteinase 1 (interstitial
	103206	X72755	Hs.77367	monokine induced by gamma interferon
	103260	X78416	Hs.3155	casein, alpha
	103751	AA082824		gb:zo08b08.s1 Stratagene neuroepithelium
50	104113	AA427510	Hs.181202	hypothetical protein FLJ10038
	104316	D61871	Hs.330821	EST
	104453	M19169	Hs.123114	cystatin SN
	104568	AA007312		gb:EST376468 MAGE resequences, MAGH Homo
	104916	AA056588	Hs.155489	NS1-associated protein 1
55	106151	AA424958	Hs.294132	ESTs
	106899	AA490107	Hs.21753	JM5 protein
	107379	U93868	Hs.333861	polymerase (RNA) III (DNA directed) (32k
	107412	W26105	Hs.287797	integrin, beta 1 (fibronectin receptor,
	107652	AA010195	Hs.52642	ESTs, Weakly similar to ALLU_HUMAN IIII
60	107754	AA017462	Hs.269244	ESTs
	107897	AA026240		gb:zo77a05.s1 NCL_CGAP_AA1 Homo sapiens
	108238	AA059473	Hs.66783	EST
	108497	AA083070		gb:zm85a05.r1 Stratagene ovarian cancer
	108710	AA121960		gb:zm24g09.r1 Stratagene pancreas (93720
65	109012	AA156576	Hs.5947	mel transforming oncogene (derived from
	109043	AA159605	Hs.72580	ESTs
	109560	F01778	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H
	110572	H60523	Hs.37844	EST
	110687	H93005	Hs.177311	ESTs
70	111418	R01084	Hs.19081	ESTs
	111507	R07728	Hs.268668	ESTs
	111644	R16539	Hs.223649	EST, Moderately similar to Cd-7 Metallo
	111919	R39925	Hs.21031	ESTs, Weakly similar to I78885 serine/th
	112102	R44840	Hs.326475	ESTs
75	112229	R50938	Hs.24949	ESTs
	112309	R55021		gb:yf76d05.s1 Soares breast 2NbHst Homo
	112368	R59371	Hs.26653	ESTs
	112397	R60822	Hs.26805	ESTs, Weakly similar to putative p150 [
	112532	R69824	Hs.28313	ESTs
80	112858	T02963	Hs.4454	ESTs
	113170	T54342	Hs.270373	ESTs, Weakly similar to S65657 alpha-1C
	113321	T70580	Hs.13759	RAB3A interacting protein (rabin3)-like
	113404	T82323	Hs.70337	immunoglobulin superfamily, member 4
	113420	T83964	Hs.15400	ESTs, Weakly similar to S65824 reverse
	113613	T83337	Hs.17167	ESTs, Highly similar to LRR FLJ1 intera
	113663	T95909		gb:ye47g07.s1 Soares fetal liver spleen
	113790	W33178	Hs.26912	ESTs

5	113889	W72720		gbzdz61c03.s1 Soares_fetal_heart_NbHH19W
	114016	W90671	Hs.11087	ESTs
	114251	Z39898	Hs.21948	ESTs
	115187	AA261805	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,
	115722	AA417297	Hs.59609	ESTs
10	115775	AA424030	Hs.46627	ESTs
	116380	AA598455	Hs.66817	ESTs
	116551	D20458	Hs.229071	EST
	117009	H85422	Hs.108556	ESTs
	117329	N23680	Hs.93670	Homo sapiens cDNA: FLJ22664 fis, clone H
15	117523	N32626	Hs.145532	ESTs, Weakly similar to FV1 MOUSE FRIEND
	118387	N64579		gb:yz51d11.s1 Morton Fetal Cochlea Homo
	118456	N66580		gb:yy69f01.s1 Soares_multiple_sclerosis_
	118741	N74042	Hs.50421	KIAA0203 gene product
	118771	N74690	Hs.50547	ESTs
20	119075	R36451	Hs.287820	fibronectin 1
	119217	R95778	Hs.237309	EST
	119306	T26914	Hs.132785	EAP30 subunit of ELL complex
	119347	T64349		gb:yc10d08.s1 Stratagene lung (937210) H
	120006	W90108	Hs.10848	KIAA0187 gene product
25	120441	AA243588	Hs.190035	ESTs
	120651	AA287286	Hs.99657	ESTs
	120811	AA346854	Hs.52788	fragile X mental retardation, autosomal
	121186	AA400156	Hs.339808	hypothetical protein FLJ10120
	121599	AA416770	Hs.98255	EST
30	122146	AA435584	Hs.250173	hypothetical protein FLJ13158
	122261	AA436830	Hs.98902	ESTs
	122352	AA443725	Hs.159677	ESTs
	122433	AA447417	Hs.285491	ESTs
	122489	AA448342	Hs.178551	ribosomal protein L8
35	122554	AA451886	Hs.154654	cytochrome P450, subfamily I (dioxin-Ind
	122857	AA463879	Hs.99606	EST, Weakly similar to STK2_HUMAN SERIN
	122889	AA465704	Hs.287687	Homo sapiens cDNA: FLJ21960 fis, clone H
	123399	AA521274	Hs.105516	EST
	123662	AA609385	Hs.112703	ESTs, Moderately similar to AF171102 1 r
40	123762	AA610013		gb:af18d04.s1 Soares_testis_NHT Homo sap
	123792	AA620333	Hs.112857	ESTs
	123900	AA621223	Hs.112953	EST
	123981	C20787	Hs.95481	ESTs
	124126	H18517	Hs.164568	fibroblast growth factor 7 (keratinocyte
45	124404	N31998	Hs.164256	hypothetical protein FLJ20657
	124557	N66025	Hs.141604	ESTs, Moderately similar to ALU1_HUMAN A
	124703	R07294	Hs.300076	solute carrier family 22 (organic cation
	124867	R68971	Hs.168500	ESTs
	125092	T92544	Hs.137548	CD84 antigen (leukocyte antigen)
50	125111	T96240	Hs.178658	RAD23 (S. cerevisiae) homolog B
	125331	AI422996	Hs.161378	ESTs
	125349	T87826	Hs.164480	ESTs, Weakly similar to T50609 hypotheti
	125426	R43963	Hs.184029	hypothetical protein DKFZp761A052
	125436	R64472	Hs.16131	hypothetical protein FLJ12876
55	125465	AI375276	Hs.158732	ESTs
	125515	R13353		gb:yy76c04.r1 Soares infant brain 1NIB H
	125626	AI038854	Hs.180789	S164 protein
	125656	AA040118	Hs.78687	neutral sphingomyelinase (N-SMase) activ
	125743	H17151		gb:ym37e05.r1 Soares infant brain 1NIB H
60	125757	AI274906	Hs.166835	ESTs, Highly similar to 1814460A p53-ess
	125760	W03020	Hs.40300	calpain 3, (p94)
	125804	R79519	Hs.16899	ESTs
	125967	AI341206	Hs.173770	ESTs
	126068	AI190171	Hs.144413	ESTs
65	126081	AI346024	Hs.227835	KIAA1049 protein
	126150	AA018427	Hs.64616	chromosome 12 open reading frame 3
	126171	AA704771	Hs.191942	ESTs
	126198	AI469355	Hs.127310	ESTs
	126224	AI097280	Hs.44493	Human DNA sequence from clone 462023 on
70	126289	AA194803	Hs.73451	ESTs, Weakly similar to S55024 nebulin,
	126343	AA628890	Hs.158701	ESTs
	126406	AA034096		gb:yy41h02.r1 Soares fetal liver spleen
	126419	AA451775	Hs.129064	Homo sapiens chromosome 19, cosmid F2216
	126479	T78141	Hs.12285	ESTs, Weakly similar to I55214 salivary
75	126500	AA885306	Hs.184376	synaptosomal-associated protein, 23kD
	126520	AA292988	Hs.72071	hypothetical protein FLJ20038
	126701	AA515212	Hs.339670	ESTs, Weakly similar to AF147790 1 trans
	126718	AA322718	Hs.309435	ESTs, Weakly similar to KIAA0927 protein
	126739	AI160709	Hs.289047	Homo sapiens cDNA FLJ14059 fis, clone HE
80	126745	AA057506		gb:zf49g04.r1 Soares retina N2b4HR Homo
	126846	AA663527	Hs.116910	ESTs
	126872	AA136653		gb:U1-H-B13-ala-a-12-0-U1.s1 NCI_CGAP_Su
	126952	AA185575	Hs.85962	hyaluronan synthase 3
	127036	AI468598	Hs.276916	nuclear receptor subfamily 1, group D, m
	127039	AA233366	Hs.168103	prp28, U5 snRNP 100 kd protein
	127067	F06732		gb:HSC1JA051 normalized infant brain cDN
	127083	Z44079	Hs.91608	otoferrin

5	127116	AA278492	Hs.288304	Homo sapiens cDNA FLJ11529 fis, clone HE
	127282	AA347547	Hs.185780	ESTs
	127349	AA412108	Hs.269350	ESTs
	127352	AA416577	Hs.189105	ESTs, Weakly similar to NBR13 [Hsapiens
	127482	AI337294	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I
	127543	AI364367	Hs.157392	Homo sapiens cDNA FLJ20780 fis, clone CO
	127553	AA282433		gb:aa63g02.r1 NCI_CGAP_GCB1 Homo sapiens
10	127556	AA679831	Hs.190228	ESTs
	127859	AA806837	Hs.291559	ESTs
	127993	AA847856	Hs.124565	ESTs
	128277	AI018275	Hs.269791	ESTs
	128285	AA634569	Hs.13351	LanC (bacterial tauribiotic synthetase c
	128317	AI051960	Hs.303754	ESTs
15	128334	AI080130	Hs.134207	ESTs
	128428	AI185718	Hs.143900	ESTs
	128582	U22963	Hs.101840	major histocompatibility complex, class
	128592	AA470056	Hs.113994	Homo sapiens cDNA FLJ20796 fis, clone CO
	128751	AA442274	Hs.183176	ESTs
20	129105	AA224351	Hs.108681	Homo sapiens brain tumor associated prot
	129161	N27334	Hs.181780	hypothetical protein FLJ20241
	129246	N99174	Hs.206063	ESTs
	129361	X64229	Hs.110713	DEK oncogene (DNA binding)
25	129577	AA424952	Hs.82906	CDC20 (cell division cycle 20, S. cerevi
	129600	N78980	Hs.271599	hypothetical protein MGC10500
	129989	AF005887	Hs.247433	activating transcription factor 6
	130024	U15197	Hs.113271	ABO blood group (transferase A, alpha 1-
	130292	U70136	Hs.218791	proteoglycan 4, (megakaryocyte stimulat
	130589	AA234308	Hs.16441	DKFZP434H204 protein
30	130736	T99385		gb:ow69g07.s1 Soares_fetal_liver_spleen_
	131238	R82327	Hs.24625	ESTs
	131378	AA463886	Hs.203910	small glutamine-rich tetratricopeptide r
	131601	M31165	Hs.29352	tumor necrosis factor, alpha-induced pro
	131605	AA256220	Hs.29383	Homo sapiens mRNA; cDNA DKFZp434E2321 (f
35	131676	C20785	Hs.30514	ESTs
	131861	D11925	Hs.184245	KIAA0929 protein Msx2 interacting nuclea
	131873	H39997	Hs.166852	KIAA1683 protein
	132023	F01927	Hs.3743	matrix metalloproteinase 24 (membrane-in
	132273	AA489716	Hs.43658	DKFZP586L151 protein
40	132770	AA425647	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL
	132859	D20925	Hs.69235	transportin-SR
	133052	R40166	Hs.106826	KIAA1696 protein
	133373	S72487	Hs.73946	endothelial cell growth factor 1 (platelet
	133446	M25322	Hs.73800	selectin P (granule membrane protein 140
45	134693	N70361	Hs.8854	Human transcription unit PVT gene, exons
	134733	U03644	Hs.89421	CBF1 interacting corepressor
	134965	J05480	Hs.272458	protein phosphatase 3 (formerly 2B), cat
	135327	AA477989	Hs.98800	ESTs
	135377	C21382	Hs.99766	Homo sapiens mRNA; cDNA DKFZp564J0323 (f
50	135398	AA194075	Hs.287270	ret proto-oncogene (multiple endocrine

TABLE 44B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

60	Pkey	CAT number	Accessions
65	108497	110079_2	AA074897 AA113914 AA064871 AA079329 AA071309 AA084710 AA129030 AA075042 AA074794 AA071453 AA078803 AA148628 AA122204 AA074159 AA126185 AA079117 AA127089 AA070912 AA079280 AA131372 AA078833 AA071087 AA076131 AA071047 AA079401 AA083070 AA102076 AA115163 AA074198 AA134725 AA113889 AA121103 AA075041 AA065148 AA071310 AA101144 AA079659 AA078931 AA079209 AA070928 AA068994 AA069817 AA076187 AA069053 AA131489 AA071308 AA063317 AA070166 AA071430 AA076056 AA075684 AA070053 AA126283 AA126078 AA075895 AA079208 AA074583 AA071086 AA079623 AA070627 AA078802 AA076622 AA065051 AA079143 AA071110 AA079434 AA148748 AA079230 AA085188 AA074485 AA070580 AA076151 AA083166 AA085118 AA079450 AA085044 AA120938 AA079200 AA100188 AA081472 AA122355 AA129031 AA085362 AA069220 AA070940 AA075968 AA074563 AA084027 AA115929
70	107897	91776_1	AA604872 AA026240
	130736	611414_1	AI168326 T99385
	108710	133560_1	AA121959 AA121960
	100943	45976_1	AW864944 L07517 AW869606
75	124575	1666649_1	N68168 N69188 N90450
	125439	465590_1	AW835829 AA826305 R01759
	117697	499877_1	N40976 AA902795
	125615	181_2	R13353 R13890 H11359
	118387	65081_5	N64579
80	126292	327512_1	AA491328 N42312
	102798	34624_4	U88896 U88898 AA916056 T03285 AI341594 AI359534 AI634031 U88897
	126378	244444_1	N58924 AA347842
	125743	5025_5	H17151 H11956
	126406	95703_1	N76683 AA034096 AA034082

	127067	1534978_1	F06732 Z43705
	119243	1774795_1	T12603 T12604
	111443	31528_18	AF072503 AF208161 AA613238 H12439 N76991 D78692 BE019603 AA776439 R37932 T93615 AF072508 R00744 R01948 R68685
5			AI128496 AA865193 AI797629 H13302 AF072506 NM_014590 AF072505 R00743 T93661 T39519 R68740 H13097 N58614 N77302
			H01372 N41878 H04136 AA426511 AW971553 AW900030 R76136 T52094 AI598135 AA781423 R76086 R77278 AI393478 AA837267
			AI570707 R01901 R27412 N53177 AI379210 AI128526 AA250958 R79323 R27389 H01325 N55091 T69704 AA868777 T47345 R27591
			AA860368 AA729556 H04137 T87297 C17420 AA293243 AA419144
	127278	240640_1	AA342715 AA367634
10	103751	118557_1	AA131367 AA082824
	126636	80804_1	AA057531 AA001527
	127331	379388_1	F20186 AA622352
	127357	288073_1	AA424107 AA452788
	126745	104479_1	AA047854 AA057506 AA053841
	126762	110350_1	AA064613 AA064671
15	126783	113388_1	AA083531 AA126047 AA074915 AA148649
	112309	1576900_1	R55021 H26613
	126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
			BE011368 BE011362 BE011215 BE011365 BE011363
20	120284	158963_1	AA179656 AA182626 AA182603
	111829	46636_1	AF074991 R36070
	104668	82752_1	AW964385 AA007312 AI081711 AA318253 AW891655 T99192
	127553	202308_2	AA505046 AW969109 AA505047
	120379	34824_3	AL042725 BE063316 AW975610 AA457591 BE062092 AI655202 AA714296 AI267264 AI075321 AA223286 AA071122 AA227849
25			AA216700 AI696002 AA101667 AA099426 AA135997 AL041698 T02815 T51824 AA207189 T59230 T51868 AA663341 BE165757
			AW818104 AW392886 AA584918 AA099408 AW856396 AW861859 AA053045
	127701	405284_1	AA679064 AA935466
	128410	288073_1	AA424107 AA452788
	114625	111686_1	AA081507 AA070071 AA070840 AA084362
30	109026	150431_1	AA157811 AA836869
	108409	113869_1	AA075631 AA075578
	100687	ligr_HT3291	L18862
	109326	genbank_AA210719	AA210719
	123762	genbank_AA610013	AA610013
35	116548	genbank_D20433	D20433
	125145	entrez_W38001	W38001
	125153	entrez_W38294	W38294
	116995	genbank_H83928	H83928
	102649	genbank_U68133	U68133
40	118456	genbank_N66580	N66580
	102860	entrez_X00368	X00368
	120715	genbank_AA292700	AA292700
	120749	genbank_AA303235	AA303235
	113663	genbank_T95909	T95909
45	113889	genbank_W77270	W77270
	108258	genbank_AA063269	AA063269
	101046	entrez_K01160	K01160
	129990	genbank_N30316	N30316
	122746	genbank_AA458791	AA458791
50	124046	genbank_F10243	F10243
	108436	genbank_AA078801	AA078801
	124197	genbank_H52921	H52921
	101447	entrez_M21305	M21305
	108852	genbank_AA133131	AA133131
55	101697	entrez_M64358	M64358
	108931	genbank_AA147186	AA147186
	101909	entrez_S69265	S69265
	117816	genbank_N48872	N48872
	119154	genbank_R61293	R61293
60	119241	genbank_T12559	T12559
	119310	genbank_T40427	T40427
	119347	genbank_T64349	T64349
	119529	entrez_W38053	W38053
	112467	genbank_R65706	R65706
65	112533	genbank_R69886	R69886
	112588	genbank_R77302	R77302
	121082	genbank_AA398722	AA398722
	123305	genbank_AA496133	AA496133
	123328	genbank_AA496968	AA496968
70	100547	ligr_HT2219	M57417
	123490	genbank_AA599723	AA599723

75 TABLE 45A: 90 GENES DOWN-REGULATED IN RHEUMATOID ARTHRITIS COMPARED TO NORMAL BODY

Table 45A lists about 90 genes down-regulated in rheumatoid arthritis. These were selected from 35403 probesets on the Affymetrix/Eos Hu01 GeneChip.

80 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

	Pkey	ExAccn	UnigeneID	Unigene Title
5	100137	D13627	Hs.15071	chaperonin containing TCP1, subunit 8 (l
	100240	D31767	Hs.75416	DAZ associated protein 2
	100289	D45248	Hs.179774	proteasome (prosome, macropain) activato
	100658	HG2855-HT2995	Hs.75452	heat shock 70kD protein 2
	100763	HG3597-HT3800		gb:Human major histocompatibility comple
10	100779	HG3731-HT4001	Hs.302063	immunoglobulin heavy constant mu
	101091	L06132	Hs.149155	voltage-dependent anion channel 1
	101155	L13972	Hs.301698	slatyltransferase 4A (beta-galactosidase
	102223	U24685		gb:Homo sapiens immunoglobulin heavy cha
	102282	U31383	Hs.79126	guanine nucleotide binding protein 10
15	102378	U40369	Hs.28491	spermidine/spermine N1-acetyltransferase
	102386	U40998	Hs.81728	unc119 (C.elegans) homolog
	102389	U41371	Hs.75916	splicing factor 3b, subunit 2, 145kD
	102480	U50327	Hs.1432	protein kinase C substrate 80K-H
	102566	U59752	Hs.303091	pleckstrin homology, Sec7 and coiled/coi
20	102605	U64444	Hs.181369	ubiquitin fusion degradation 1-like
	102693	U73824	Hs.183684	eukaryotic translation initiation factor
	102710	U77827	Hs.113207	G protein-coupled receptor 30
	102920	X12451	Hs.78056	cathepsin L
	102929	X13238	Hs.74649	cytochrome c oxidase subunit VIc
25	103166	X67951	Hs.180909	peroxiredoxin 1
	103283	X80199	Hs.83422	MLN51 protein
	103463	Y00281	Hs.2280	ribophorin I
	103835	AA172215	Hs.93748	Homo sapiens cDNA FLJ14676 fis, clone NT
	104796	AA029368	Hs.33026	hypothetical protein PP2447
30	105714	AA281429	Hs.12211	GDP-fucose transporter 1
	105927	AA02968	Hs.332040	hypothetical protein MGC13010
	105945	AA04512	Hs.14453	interferon consensus sequence binding pr
	106001	AA410986	Hs.8963	Homo sapiens mRNA full length insert cDN
	106027	AA412119	Hs.234799	breakpoint cluster region
35	106227	AA429262	Hs.19613	ESTs
	106295	AA435664	Hs.8583	similar to APOBEC1
	106417	AA448008	Hs.261828	G protein-coupled receptor kinase 7
	107391	W02877	Hs.284294	Breakpoint cluster region protein, uteri
	109107	AA169180	Hs.269280	ESTs
40	109685	F09325	Hs.28102	ESTs
	110021	H11252	Hs.31037	ESTs
	110738	H99370	Hs.139648	kinesin family member 1C
	112746	R93237	Hs.74170	metallothionein 1E (functional)
	113059	T26925	Hs.172684	vesicle-associated membrane protein 8 (a
45	113822	W47350	Hs.17466	retinoic acid receptor responder (tazaro
	113859	W67225	Hs.13273	KIAA0592 protein
	113909	W78127	Hs.9956	hypothetical protein FLJ20259
	114693	AA122158	Hs.300683	Homo sapiens cDNA FLJ12825 fis, clone NT
	115399	AA283182	Hs.92023	core histone macroH2A2.2
50	116606	D80217	Hs.259842	protein kinase, AMP-activated, gamma 2 n
	116633	F02702	Hs.268726	ESTs, Highly similar to ZN91_HUMAN ZINC
	119254	T15837	Hs.279009	matrix Gla protein
	119493	W35384	Hs.50477	RAB27A, member RAS oncogene family
	120108	W95696	Hs.16803	LUC7 (S. cerevisiae)-like
55	120886	AA365566	Hs.301342	hypothetical protein MGC4342
	120953	AA397911	Hs.97499	ESTs, Weakly similar to unknown [H.sapi
	121303	AA402441	Hs.303197	B-cell CLL/lymphoma 7C
	121547	AA412448	Hs.104777	ESTs
	123495	AA599850	Hs.106747	serine carboxypeptidase 1 precursor prot
60	123608	AA609144	Hs.112651	ESTs
	123749	AA609949	Hs.112790	EST
	124763	R39610	Hs.76288	calpain 2, (mII) large subunit
	125366	H60192	Hs.76853	Homo sapiens mRNA; cDNA DKFZp434N1728 (f
	125657	AA481719	Hs.150540	Homo sapiens, clone IMAGE:3954961, mRNA,
65	125670	AI432621	Hs.82685	CD47 antigen (Rb-related antigen, integr
	125882	H45538	Hs.101448	metastasis associated 1
	126541	AA204913	Hs.7854	zinc/iron regulated transporter-like
	126715	R70160	Hs.241552	KIAA0268 protein
	126817	AA478642	Hs.291623	ESTs, Weakly similar to unnamed protein
70	127112	AI143906	Hs.125103	ESTs
	127273	AA335263	Hs.144950	ESTs
	127615	AA718919		gb:zv88a04.s1 Soares_NhHMPu_S1 Homo sapi
	127635	AA766903	Hs.116346	ESTs, Highly similar to A46297 beta-1,6-
	128528	R39234	Hs.251699	ESTs, Weakly similar to IDNA-GGTR14 [H.s
75	129398	AA437374	Hs.234573	Homo sapiens mRNA for TL132
	129621	AA489459	Hs.301005	purine-rich element binding protein B
	131037	AA256171	Hs.22391	chromosome 20open reading frame 3
	131328	V01512	Hs.25647	v-fos FBJ murine osteosarcoma viral onco
	131631	AA486868	Hs.29802	stit (Drosophila) homolog 2
80	132079	H67964	Hs.38694	ESTs
	132455	T15774	Hs.4892	Homo sapiens clone 24841 mRNA sequence
	132582	AA318547	Hs.278712	eukaryotic translation initiation factor
	132610	AA443114	Hs.5326	amino acid system N transporter 2; porcu
	132755	AA609201	Hs.182635	ESTs
	133192	AA393804	Hs.67052	vacuolar protein sorting 26 (yeast homol

133437	R57419	Hs.7370	phosphatidylinositol transfer protein, b
133449	AA094989	Hs.7381	voltage-dependent anion channel 3
133649	AA479139	Hs.75393	acid phosphatase 1, soluble
133814	M33882	Hs.76391	myxovirus (Influenza) resistance 1, homo
134378	AF006088	Hs.82425	actin related protein 2/3 complex, subun
134419	L08044	Hs.82961	trefoil factor 3 (intestinal)
134548	U41515	Hs.333495	Deleted in split-hand/split-foot 1 regio
134776	J05582	Hs.89603	mucin 1, transmembrane
135032	AA243497	Hs.173685	hypothetical protein FLJ12619

TABLE 45B

15 Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
127615	380951_1	AA626215 AA718919
100763	tigr_HT3800	X12432 Y08693
102223	221_265	AF013616 AA300945 X65907 AF062264 AF062250 Z47228 Z75389 Z75374 AF062152 AF062146 Z75398 X64153 AF062101 AF062218 S59161 Z75392 AF062196 AF062192 X65904 U24685 AF062181 Z47241 Z75376 AF062217 Z47234 X64152 AF062187 AF062173 AF062158 Z47229 M74018 M74021 X54441 M84512 L29115 M84508 Z75384 AJ244983 AJ245240 AJ245030 AJ245042 M26998 L03635 S64473 AJ244997 AJ245013 AJ279535 U89766 AF174049 AF174085 AF174086 U97246 AJ245011 AJ245017 AJ245028 AJ245041 AJ245051 AJ245065 AJ245236 U22391 Z49143 Z74665 AF087428 S66098 Z70650 AJ244929 AF006528 AF022004 AF021983 U00556 AJ245035 Z70617 Z70605 AJ245052 AJ245046 AF087424 AF174054 S67110 U21257 U21267 U21268 Z35492 U71103 AF021991 L23518 Z70644 AJ245036 Z49141 AF089001 Z74695 Z46304 AF021957 AF021990 AF022005 AF052527 AF021947 Z70604 Z70610 AF062104 Z49135 X64235 Z46341 Z46305 Z46307 Z49136 AJ244996 Z46342 AJ244931 AJ244935 AJ244937 AJ244938 L12192 AJ244939 AJ244940 AJ244941 AJ244991 AJ244990 AJ244988 AJ244973 X87440 AJ244985 AF174088 AJ279519 AJ279521 AJ279526 AJ245009 AJ279531 AJ245008 AJ244994 AJ244991 AJ244990 AJ244988 AJ244973 X87440 AJ245238 Z70625 Z70626 Z70641 Z70640 Z70643 AJ244975 Z70616 Z70637 AJ244982 AJ244967 AJ239377 AJ245057 AF021948 AF107239 AJ245040 L34163 AF062231 Z70627 AF062113 AF005527 AF174041 AJ279537 Z70642 U00497 Z70639 AJ245054 AJ244960 AJ279524 AJ244943 AJ249631 AF035041 AJ245039 AJ245050 AF107233 AJ239382 AJ244869 Z46278 Z46290 Z46274 Z46281 AJ239351 L25293 AJ244944 AJ244951 Z46280 Z46270 AJ245043 Z46276 AF107241 Z46271 Z46277 AJ245034 Z46273 AJ244992 Z46282 Z70638 Z46275 AJ222556 Z46329 Z46330 Z46269 AF087422 M74469 X64159 AF103243 X64156 AJ244942 Z46316 AJ222547 Z46322 Z46324 Z46326 Z46327 AJ222556 Z46315 Z46302 AJ222561 AJ222549 AJ222568 AJ222570 AJ222571 Z49139 AJ222578 AJ222562 AJ222577 Z46323 AJ222576 AJ222566 Z46317 AJ222557 AJ222564 AJ222559 AJ222573 AJ222575 Z46318 AJ222548 Z46319 AJ222552 AJ222550 AJ222567 AJ222558 AJ222563 Z46317 X87438 AJ222555 AJ240581 AF103161 AJ240580 AJ240594 Y17929 AJ240553 AJ240573 AJ240558 AJ240555 Y17927 Y17949 AJ240561 Y17948 Y17933 Y17947 Y17944 Y17928 Y17931 Y17934 AJ240595 Y17943 Y17932 Y17930 AJ240590 AJ240560 Y17945 AJ240556 S79918 AF103278 AW364256 AF103299 AF103122 X75022 AF004937 Z30557 Z30677 Z30573 Z30576 Z30561 Z30674 Z30562 Z30675 AW403129 AJ203192 AW404253 AW237246 AJ654630 H61354

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Table 46A lists about 714 genes upregulated in esophageal cancer relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

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Table 47A lists about 113 genes upregulated in esophageal tumors relative to normal esophagus. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

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TABLE 46A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigenes number
 Unigenes Title: Unigenes gene title
 R1: 90th percentile of esophageal tumor AIs divided by the 70th percentile of normal tissue AIs, where the 15th percentile of the normal tissue AIs was subtracted from both the numerator and denominator.

Pkey	ExAccn	UnigenelD	Unigenes Title	R1
413808	J00287		Homo sapiens mRNA for caldesmon, 3' UTR	31.57
411243	AB039886	Hs.69319	CA11	26.06
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	25.65
401781			Target Exon	23.23
424098	AF077374	Hs.139322	small proline-rich protein 3	21.35
425211	M18667	Hs.1867	progastricin (pepsinogen C)	20.37
417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	20.33
401780			NM_005557*Homo sapiens keratin 16 (foca	18.94
421948	L42583	Hs.334309	keratin 6A	18.13
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	18.01
429538	BE182592	Hs.11261	small proline-rich protein 2A	17.31
400666			NM_002425Homo sapiens matrix metallopro	17.28
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	16.96

	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	16.35
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	16.22
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	15.64
5	421582	AB910275		trefol factor 1 (breast cancer, estroge	14.86
	425679	X05997	Hs.159177	lipase, gastric	14.53
	421773	W69233	Hs.112457	ESTs	14.26
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	14.26
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	13.93
	444325	AW152618	Hs.16757	ESTs	13.24
10	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2052 (f	13.19
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	11.98
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.99
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	10.77
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	10.31
15	446292	AF081497	Hs.279682	Rh type C glycoprotein	9.69
	421978	AJ243662	Hs.110196	NICE-1 protein	9.68
	448811	AI590371	Hs.199460	ESTs	9.38
	453331	AI240665		ESTs	9.37
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	9.28
20	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	9.18
	406687	M31126		matrix metalloproteinase 11 (stromelysin	9.13
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	9.04
	450701	H39960	Hs.288467	hypothetical protein XP_098151	8.77
	418686	Z36830	Hs.87268	annexin A8	8.76
25	421110	AJ250717	Hs.1355	cathepsin E	8.42
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	8.42
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.38
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	8.18
	427666	AJ791495	Hs.180142	calmodulin-like skin protein (CLSP)	8.11
30	450375	AA009647		a disintegrin and metalloproteinase doma	8.03
	401785			NM_002275*-Homo sapiens keratin 15 (KRT1	7.97
	445891	AW391342	Hs.199460	DPCR1 protein	7.95
	437053	AU077018	Hs.3235	keratin 4	7.93
	423271	W47225	Hs.126256	interleukin 1, beta	7.80
35	409757	NM_001898	Hs.123114	cystatin SN	7.74
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	7.64
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	7.58
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	7.55
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	7.26
40	448045	AJ297436	Hs.20166	prostate stem cell antigen	7.14
	408243	Y00787	Hs.624	interleukin 8	7.13
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	7.08
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	7.04
	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	7.04
45	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.98
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	6.89
	414774	X02419	Hs.77274	plasminogen activator, urokinase	6.85
	439926	AW014875	Hs.137007	ESTs	6.84
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	6.82
50	429259	AA420450	Hs.292911	Plakophilin	6.77
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	6.71
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	6.67
	429228	AI553633	Hs.326447	ESTs	6.61
	426312	AF026939	Hs.181874	interferon-induced protein with tetrat	6.60
55	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	6.58
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli Ra	6.55
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	6.54
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	6.53
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.51
60	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	6.49
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	6.48
	428471	X57348	Hs.184510	stratiferin	6.46
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	6.45
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.44
65	401747			Homo sapiens keratin 17 (KRT17)	6.42
	421508	NM_004833	Hs.105115	absent in melanoma 2	6.42
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	6.42
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	6.41
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	6.38
70	422596	AF063611	Hs.118633	2'-5'-oligoadenylate synthetase-like	6.38
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	6.36
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	6.35
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	6.33
	425415	M13903	Hs.157091	involucrin	6.32
75	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.30
	415989	AJ267700		ESTs	6.23
	406673	M34996	Hs.198253	major histocompatibility complex, class	6.21
	449228	AJ403107	Hs.148590	protein related with psoriasis	6.21
	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	6.18
80	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	6.06
	418663	AK001100	Hs.41690	desmocollin 3	6.04
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	5.98
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	5.95

5	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	5.93
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	5.92
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	5.92
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum corn	5.84
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	5.76
10	400665			NM_002425:Homo sapiens matrix metallopro	5.75
	427747	AW411425	Hs.180655	serine/threonine kinase 12	5.72
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	5.72
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	5.71
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	5.70
15	439606	W79123	Hs.58561	G protein-coupled receptor 87	5.70
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	5.68
	433447	U29195	Hs.3281	neuronal pentraxin II	5.67
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	5.64
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	5.62
20	413219	AA878200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PL	5.60
	428450	NM_014791	Hs.184339	KIAA0175 gene product	5.53
	424408	A1754813	Hs.146428	collagen, type V, alpha 1	5.50
	416250	AA581386	Hs.73452	hypothetical protein MGC10791	5.48
	447164	AF026941	Hs.17518	Homo sapiens cig 5 mRNA, partial sequence	5.47
25	412326	R07565	Hs.73817	small inducible cytokine A3 (homologous	5.44
	439223	AW238299	Hs.250618	UL16 binding protein 2	5.44
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	5.42
	402994			NM_002463*:Homo sapiens myxovirus (influ	5.40
	447333	BE090580	Hs.70704	hypothetical protein dJ616B8.3	5.40
30	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	5.36
	454241	BE144666		gbr:CM2-HT0176-041099-017-c02 HT0176 Homo	5.33
	408716	A1567839	Hs.151714	Homo sapiens mRNA for KIAA1769 protein,	5.32
	449722	BE280074	Hs.23960	cyclin B1	5.31
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	5.30
35	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	5.29
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	5.29
	417720	AA205625	Hs.208067	ESTs	5.29
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	5.28
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	5.27
40	431620	AA126109	Hs.264981	Z'-5'-oligoadenylate synthetase 2 (69-71	5.26
	430280	AA361258	Hs.237868	interleukin 7 receptor	5.25
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	5.24
	402075			ENSP00000251056*:Plasma membrane calcium	5.24
	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin	5.22
45	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	5.22
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	5.21
	418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via death domai	5.20
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	5.20
	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide epider	5.19
50	406663	U24683	Hs.283441	immunoglobulin heavy constant mu	5.15
	409178	BE393948	Hs.50915	kallikrein 5	5.14
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	5.10
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	5.09
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	5.09
55	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.08
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet	5.07
	411274	NM_002776	Hs.69423	kallikrein 10	5.03
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	5.03
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	5.02
60	433800	A1034361	Hs.135150	lung type-I cell membrane-associated gly	5.02
	412755	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	5.02
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	5.00
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	5.00
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	4.97
65	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.96
	405770			NM_002352:Homo sapiens melanoma antigen,	4.94
	444783	AK001468	Hs.62180	antilin (Drosophila Scraps homolog), act	4.94
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.93
	426866	U02330	Hs.172816	neuregulin 1	4.92
70	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	4.92
	455601	A1368680	Hs.816	SRY (sex determining region Y)-box 2	4.91
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	4.90
	427786	BE407863	Hs.256871	ESTs	4.87
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kalini	4.86
75	444371	BE540274	Hs.239	forkhead box M1	4.86
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	4.85
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	4.84
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	4.83
	409402	AF208234	Hs.695	cystatin B (stefin B)	4.81
80	408202	AA227710	Hs.43658	DKFZP586L151 protein	4.79
	401994			Target Exon	4.77
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	4.74
	421574	AJ000152	Hs.105924	defensin, beta 2	4.69
	429299	A1620463	Hs.347408	hypothetical protein MGC13102	4.69
	422109	S73265	Hs.1473	gastrin-releasing peptide	4.68
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	4.68
	407944	R34008	Hs.239727	desmocollin 2	4.67

5	411296	BE207307	Hs.10114	growth suppressor 1	4.65
	433364	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	4.65
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothel	4.61
	421335	X99977	Hs.103505	ARS component 8	4.60
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.59
	453779	N35187	Hs.43388	28kD interferon responsive protein	4.59
	423575	C18863	Hs.163443	periostin (OSF-2os)	4.59
	417308	H60720	Hs.81892	KIAA0101 gene product	4.58
10	428651	AF196478	Hs.188401	annexin A10	4.58
	424354	NM_014314	Hs.145612	RNA helicase	4.58
	404996			Target Exon	4.56
	404240			NM_018950:Homo sapiens major histocompat	4.56
	453095	AW295660	Hs.252756	ESTs	4.55
15	410407	X66839	Hs.63287	carbonic anhydrase IX	4.55
	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	4.55
	450685	L15533	Hs.423	pancreatitis-associated protein	4.54
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolog	4.53
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.52
20	408380	AF123050	Hs.44532	diubiquitin	4.47
	443859	NM_013409	Hs.9914	folistatin	4.46
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	4.44
	412140	AA219691	Hs.73825	RAB6 interacting, kinesin-like (raklines	4.44
	421777	BE562088	Hs.108196	HSPC037 protein	4.44
25	408908	BE296227	Hs.250822	serine/threonine kinase 15	4.43
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	4.42
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	4.42
	400419	AF084545		Target	4.42
	452571	W31518	Hs.34665	ESTs	4.41
30	430044	AA464510	Hs.152812	ESTs	4.41
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	4.39
	448111	AA053486	Hs.20315	interferon-induced protein with tetratri	4.39
	443347	AI052543	Hs.133244	melanoma-derived leucine zipper, extra-n	4.39
	453884	AA355925	Hs.36232	KIAA0186 gene product	4.38
35	436481	AA378597	Hs.5199	HSPC150 protein similar to ubiquitin-con	4.37
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	4.37
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	4.37
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	4.36
	448357	N20169	Hs.108923	RAB38, member RAS oncogene family	4.36
40	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	4.34
	439999	AA115811	Hs.6838	ras homolog gene family, member E	4.34
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	4.34
	409703	NM_005187	Hs.56009	Z'-5'-oligoadenylate synthetase 3 (100 k	4.32
	402447			C1000201:gi204416 gb AAA02627.1 (L0519	4.31
45	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	4.28
	432731	R31178	Hs.287820	fibronectin 1	4.27
	422397	AJ223366	Hs.116051	Homo sapiens cDNA: FLJ22495 fis, clone H	4.27
	413670	AB000115	Hs.75470	hypothetical protein, expressed in ostao	4.25
	425580	L11144	Hs.1907	galanin	4.25
50	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	4.23
	409433	AA074382	Hs.135255	ESTs	4.23
	430630	AW269920	Hs.2621	cystatin A (stefin A)	4.22
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	4.21
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	4.20
55	432375	BE536069	Hs.2962	S100 calcium-binding protein P	4.20
	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	4.19
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	4.19
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	4.18
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	4.17
60	410286	AI739159	Hs.61898	DKFZP586N2124 protein	4.16
	448844	AI581519	Hs.177164	ESTs	4.16
	432680	T47364	Hs.278613	interferon, alpha-inducible protein 27	4.16
	417599	AA204688	Hs.62954	ESTs	4.16
	402992			Target Exon	4.15
65	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytolactin)	4.14
	422100	AI096988	Hs.111554	ADP-ribosylation factor-like 7	4.13
	409512	AW979187	Hs.293591	melanoma differentiation associated prot	4.12
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.11
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.10
70	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	4.10
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.10
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	4.09
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	4.08
	417933	X02308	Hs.82962	thymidylate synthetase	4.08
75	418689	AI360883	Hs.274448	hypothetical protein FLJ11029	4.06
	417678	X08560	Hs.82396	Z'-5'-oligoadenylate synthetase 1 (40-46	4.06
	451541	BE279383	Hs.28557	plakophilin 3	4.06
	433848	AF095719	Hs.93764	carboxypeptidase A4	4.06
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.04
80	429599	AA806106	Hs.123664	ESTs	4.03
	450823	T81223	Hs.22011	complement-c1q tumor necrosis factor-rel	4.02
	423787	AJ295745	Hs.236204	nuclear pore complex protein	4.00
	431250	BE264649	Hs.251377	taxol resistance associated gene 3	4.00
	416091	AF295370	Hs.283082	defensin, beta 3	3.97

	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	3.97
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.97
	402408			NM_030920*:Homo sapiens hypothetical pro	3.97
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	3.95
5	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	3.95
	452888	AW955454	Hs.30942	ephrin-B2	3.95
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.95
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.94
10	419693	AA133749	Hs.301350	FXVD domain-containing ion transport reg	3.94
	420596	NM_002692	Hs.99185	polymerase (DNA directed), epsilon 2	3.94
	422094	AF129535	Hs.272027	F-box only protein 5	3.93
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	3.93
	404286			C6001909:gi704441 dbj BAA18909.1 (D298	3.92
15	423961	D13666	Hs.136348	periostin (OSF-2os)	3.91
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	3.91
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	3.91
	435066	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin	3.91
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (I	3.91
20	421904	BE143533	Hs.109309	hypothetical protein FLJ20035	3.90
	441553	AA281219	Hs.121296	ESTs	3.90
	428093	AW594506	Hs.104830	ESTs	3.89
	441020	W79283	Hs.35962	ESTs	3.89
	447078	AW885727	Hs.9914	ESTs	3.89
25	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	3.87
	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	3.87
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	3.86
	426059	BE292842	Hs.166120	interferon regulatory factor 7	3.85
	419833	AA251131	Hs.220697	ESTs	3.85
30	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	3.83
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	3.83
	452203	X57522		transporter 1, ATP-binding cassette, sub	3.83
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	3.83
	414809	AI434699	Hs.77356	transferin receptor (p90, CD71)	3.82
35	442589	AF078037	Hs.324051	RelA-associated inhibitor	3.82
	405387			NM_022170*:Homo sapiens Williams-Beuren	3.82
	449539	W80363	Hs.58446	ESTs	3.81
	419079	AW014836	Hs.18844	ESTs	3.81
	410434	AF051152	Hs.63668	toll-like receptor 2	3.80
40	408660	AA525775		ESTs, Moderately similar to PC4259 feri	3.80
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	3.80
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.79
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.79
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp566i2022 (I	3.78
45	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.78
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.78
	414561	AI064813	Hs.195155	Homo sapiens amino acid transport system	3.77
	411789	AF245505	Hs.72157	Adican	3.77
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	3.76
50	449378	AW664026	Hs.59892	ESTs	3.76
	449961	AW265534	Hs.133100	ESTs	3.75
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	3.75
	407242	M18728		gb:Human nonspecific crossreacting antig	3.75
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	3.75
55	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	3.74
	422675	BE018517	Hs.119140	eukaryotic translation initiation factor	3.74
	422699	BE410590	Hs.119257	ems1 sequence (mammary tumor and squamou	3.74
	441954	AI744935	Hs.8047	Fancort anemia, complementation group G	3.73
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	3.72
60	422648	D86983	Hs.118893	Melanoma associated gene	3.71
	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfami	3.71
	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito	3.71
	428728	NM_016625	Hs.191381	hypothetical protein	3.71
	400245			Eos Control	3.70
65	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	3.70
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.70
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	3.69
	440659	AF134160	Hs.7327	claudin 1	3.67
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.67
70	413053	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.66
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	3.65
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	3.63
	428291	AA534009	Hs.183487	interferon stimulated gene (20kD)	3.63
	414883	AA926960		CDC28 protein kinase 1	3.63
75	428398	AI249368	Hs.98558	ESTs	3.63
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	3.63
	408482	NM_000676	Hs.45743	adenosine A2b receptor	3.63
	404287			C6001909:gi704441 dbj BAA18909.1 (D298	3.61
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	3.61
80	414110	BE251752		gb:501112444F1 NIH_MGC_16 Homo sapiens c	3.61
	427857	AL133017	Hs.2210	hypothetical protein FLJ22865	3.61
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	3.61
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	3.60
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	3.60

	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	3.60
	430994	AA490346	Hs.40530	Homo sapiens, clone MGC:17624, mRNA, com	3.60
	456534	X91195	Hs.100623	phosphatase C, beta 3, neighbor pseudo	3.59
5	437340	AL353935	Hs.135917	hypothetical protein DKFZp761D1823	3.59
	435793	AB037734	Hs.4993	KIAA1313 protein	3.59
	437016	AU076916	Hs.5398	guanine monophosphate synthetase	3.59
	420247	AA256930	Hs.44680	hypothetical protein FLJ20979	3.58
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	3.57
10	422282	AF019225	Hs.114309	apolipoprotein L	3.57
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	3.57
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.57
	408015	AW136771	Hs.244349	epidermal differentiation complex protei	3.56
	422856	BE545072	Hs.122579	ECT2 protein (Epithelial cell transform	3.56
15	449039	AI962602	Hs.74284	hypothetical protein MGC2714	3.56
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	3.55
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	3.55
	428977	AK001404	Hs.194698	cyclin B2	3.55
	402995			NM_002463*:Homo sapiens myxovirus (infl	3.55
20	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.54
	432917	NM_014125	Hs.241517	PRO0327 protein	3.54
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	3.53
	445411	AL137255	Hs.12646	hypothetical protein FLJ22693	3.52
	438113	AI467908	Hs.8882	ESTs	3.52
25	414420	AA043424	Hs.76095	immediate early response 3	3.51
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	3.50
	447208	BE315291	Hs.237971	hypothetical protein MGC5627	3.50
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	3.49
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	3.49
30	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	3.49
	429249	X81479	Hs.2375	egl-like module containing, mucin-like,	3.48
	413900	AW409747	Hs.75612	stress-induced-phosphoprotein 1 (Hsp70/H	3.48
	424242	AA337476	Hs.347408	hypothetical protein MGC13102	3.48
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.47
35	446480	NM_014578	Hs.15114	ras homolog gene family, member	3.46
	414825	X05370	Hs.77432	epidermal growth factor receptor (avian	3.46
	428865	BE544095	Hs.164960	BarH-like homeobox 1	3.46
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	3.46
	450506	NM_004460		fibroblast activation protein, alpha	3.46
40	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	3.45
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.45
	405545			Target Exon	3.45
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	3.44
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	3.44
45	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.44
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	3.44
	431228	AB006746	Hs.198282	phospholipid scramblase 1	3.44
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.43
	440502	AI824113	Hs.78281	regulator of G-protein signalling 12	3.43
50	448741	BE614567	Hs.19574	hypothetical protein MGC5469	3.43
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	3.43
	406646	M33600	Hs.308026	major histocompatibility complex, class	3.42
	413281	AA861271	Hs.222024	transcription factor BMAL2	3.42
	449101	AA205847	Hs.23016	G protein-coupled receptor	3.42
55	430890	X54232	Hs.2699	glypican 1	3.41
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.41
	412429	AV650262	Hs.75765	GRO2 oncogene	3.41
	443211	AI128388	Hs.143655	ESTs	3.41
	422209	AF005210	Hs.113222	chemokine (C-C motif) receptor 8	3.40
60	428303	AW974476	Hs.183601	regulator of G-protein signalling 16	3.39
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	3.39
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	3.39
	422101	AW404176	Hs.111611	ribosomal protein L27	3.39
	457670	AF119666	Hs.23449	insulin receptor tyrosine kinase substra	3.38
65	437033	AW248364	Hs.5409	RNA polymerase I subunit	3.37
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.37
	417059	AL037672	Hs.81071	extracellular matrix protein 1	3.37
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	3.36
	414812	X72755	Hs.77387	monokine induced by gamma interferon	3.36
70	436748	BE159107	Hs.159263	collagen, type VI, alpha 2	3.36
	401797			Target Exon	3.36
	428309	M97815	Hs.183650	cellular retinoic acid-binding protein 2	3.35
	421563	NM_006433	Hs.105806	granulysin	3.35
	402294			Target Exon	3.34
75	414024	AA134712	Hs.22410	gbzm79g08.r1 Stratagene neuroepithelium	3.34
	401961			NM_021626:Homo sapiens serine carboxypep	3.33
	418462	BE001596	Hs.85266	integrin, beta 4	3.33
	418857	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	3.33
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.33
80	412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.33
	404440			NM_021046:Homo sapiens melanoma antigen,	3.33
	432398	AA307808	Hs.2979	trefoil factor 2 (spasmolytic protein 1)	3.33
	421677	H64092	Hs.38282	ESTs	3.33
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	3.32

5	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	3.32
	417197	AW994561	Hs.151777	eukaryotic translation initiation factor	3.32
	429669	BE185499	Hs.2471	KIAA0020 gene product	3.32
	409636	AA305729	Hs.18272	amino acid transporter system A1	3.32
	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	3.32
10	405386			Target Exon	3.32
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	3.31
	448275	BE514434	Hs.20830	kinesin-like 2	3.31
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.31
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.31
15	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.31
	422575	AK000546	Hs.118552	hypothetical protein FLJ20539	3.31
	404171			NM_000636:Homo sapiens superoxide dismu	3.31
	418464	R87580	Hs.144531	gbym89h07.r1 Soares adult brain N2b4HB5	3.31
	425566	AW162943	Hs.250618	UL16 binding protein 2	3.31
20	410226	A1831958	Hs.61053	hypothetical protein	3.30
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.30
	443247	BE614387	Hs.333893	c-Myc target JPO1	3.30
	449717	AB040935	Hs.23954	cerebral cell adhesion molecule	3.30
	428336	AA503115	Hs.183752	microseminoprotein, beta-	3.29
25	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (3.29
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	3.28
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.28
	405778			NM_005361:Homo sapiens melanoma antigen,	3.28
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasm 3	3.27
30	421150	AJ913562	Hs.189902	ESTs	3.27
	406400			kalikrein 8 (neuropsin/kovasin) (KLK8)	3.27
	455813	BE141577		gb:QV2-HT0083-071299-018-a11 HT0083 Homo	3.27
	426064	BE387014	Hs.166145	Homer, neuronal immediate early gene, 3	3.27
	458814	A1498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	3.27
35	458791	BE615453	Hs.346509	dedicator of cyto-kinesis 1	3.27
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	3.26
	429002	AW248439	Hs.2340	junction plakoglobin	3.26
	450000	A1952787	Hs.10888	hypothetical protein FLJ21709	3.25
	407777	AA161071	Hs.71465	squalene epoxidase	3.25
40	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protei	3.25
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	3.24
	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, lol	3.24
	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	3.24
	447519	U46258	Hs.339665	ESTs	3.24
45	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	3.24
	448528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	3.24
	423198	M81933	Hs.1634	cell division cycle 25A	3.23
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	3.23
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.22
50	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	3.22
	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	3.22
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	3.22
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.22
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	3.21
55	409197	N54706	Hs.303025	chromosome 11 open reading frame 24	3.21
	412641	M16660	Hs.74335	heat shock 90kD protein 1, beta	3.21
	413436	AF238083	Hs.68061	sphingosine kinase 1	3.21
	408636	BE294925	Hs.46680	CGI-12 protein	3.21
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	3.21
60	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.21
	411573	AB029000	Hs.70823	KIAA1077 protein	3.20
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.19
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	3.19
	435014	BE560899	Hs.10026	mitochondrial ribosomal protein L17	3.18
65	401176			Target Exon	3.17
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	3.16
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.16
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	3.16
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	3.16
70	452012	AA307703	Hs.279766	kinesin family member 4A	3.16
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.15
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	3.15
	433020	A1375726	Hs.279918	hypothetical protein	3.14
	437915	A1637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	3.14
75	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	3.14
	420005	AW271106	Hs.133294	ESTs	3.14
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.13
	412270	AC005262	Hs.73797	guanine nucleotide binding protein (G pr	3.13
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	3.13
80	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	3.12
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.11
	431722	AF161528	Hs.268049	hypothetical protein	3.11
	427239	BE270447	Hs.174070	ubiquitin carrier protein	3.11
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	3.10
	439780	AL109688		gb:Homo sapiens mRNA full length insert	3.10
	422885	BE244068	Hs.121544	interleukin 12 receptor, beta 1	3.10
	418090	U57059	Hs.83429	tumor necrosis factor (ligand) superfam	3.10

	439755	AW748482	Hs.77873	B7 homolog 3	3.10
	404170			NM_000636: Homo sapiens superoxide dismu	3.09
	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	3.09
5	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	3.09
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	3.08
	421155	H87879	Hs.102267	lysyl oxidase	3.08
	441224	AU076964	Hs.7753	calumenin	3.08
	424326	NM_014479	Hs.145296	disintegrin protease	3.08
10	429413	NM_014058	Hs.201877	DESC1 protein	3.08
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	3.08
	446510	H58306	Hs.15165	retinoic acid induced 14	3.08
	442620	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668 protein,	3.07
	409637	AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	3.07
15	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	3.07
	448853	NM_012204	Hs.22302	general transcription factor III C, polyp	3.07
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.07
	408915	NM_016651	Hs.48950	heptacellular carcinoma novel gene-3 pro	3.06
	435505	AF200492	Hs.211238	Interleukin-1 homolog 1	3.06
20	412577	Z22968	Hs.74076	CD163 antigen	3.06
	410575	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	3.06
	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kin	3.05
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	3.05
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	3.04
25	451578	NM_016323	Hs.26663	cyclin-E binding protein 1	3.04
	444726	NM_006147	Hs.84981	interferon regulatory factor 6	3.04
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	3.04
	437741	BE561610	Hs.5809	putative transmembrane protein; homolog	3.04
	442643	U82756	Hs.3991	PRP4/STKWD splicing factor	3.04
30	429358	AB037825	Hs.200317	KIAA1404 protein	3.03
	410068	AI633888	Hs.58435	FYN-binding protein (FYB-120/130)	3.03
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotat	3.03
	409154	U72882	Hs.50842	interferon-induced protein 35	3.02
	442173	N76101	Hs.8127	KIAA0144 gene product	3.02
35	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	3.01
	450962	BE535647	Hs.25723	Sjogren's syndrome/scleroderma autoantig	3.01
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	3.01
	411387	AW842339	Hs.130815	hypothetical protein FLJ21870	3.01
40	438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	3.01
	459107	AA811881	Hs.28505	ubiquitin-conjugating enzyme E2H (homolo	3.00
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	3.00
	416110	Z42262	Hs.322844	hypothetical protein DKFZp564A176	3.00
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	3.00
	448569	BE382657	Hs.21486	signal transducer and activator of trans	3.00
45	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.00
	400200			NM_002788: Homo sapiens proteasome (pros	3.00
	403330			Target Exon	2.99
	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.99
	403416	AI744626		KIAA0564 protein	2.97
50	403438			NM_031419: Homo sapiens molecule possess	2.96
	447942	F12628	Hs.155470	hypothetical protein MGC16040	2.96
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.96
	414806	D14694	Hs.77329	phosphatidylserine synthase 1	2.94
	440086	NM_005402	Hs.288757	v-ral simian leukemia viral oncogene hom	2.94
55	429547	AW009166	Hs.99376	ESTs	2.93
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	2.90
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.89
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	2.89
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.86
60	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	2.86
	423425	AA375756	Hs.14449	KIAA1609 protein	2.86
	412851	AI826502	Hs.106149	ESTs	2.86
	400664			NM_002425: Homo sapiens matrix metallopro	2.86
	454140	AB040888	Hs.41793	hypothetical protein FLJ10474	2.85
65	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.85
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	2.84
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.83
	423767	H18283	Hs.132753	F-box only protein 2	2.82
	413476	U25849	Hs.75393	acid phosphatase 1, soluble	2.82
70	441801	AW242789	Hs.86386	ESTs	2.80
	441565	AW953575	Hs.303125	p53-induced protein PIGPC1	2.80
	416539	Y07909	Hs.79368	epithelial membrane protein 1	2.79
	428959	AF100779	Hs.194680	WNT1 Inducible signaling pathway protein	2.79
	422947	AA306782	Hs.122552	G-2 and S-phase expressed 1	2.75
75	417849	AW291587	Hs.82733	nidogen 2	2.74
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	2.73
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.72
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	2.71
	424874	AA347951	Hs.326413	Homo sapiens cDNA FLJ20812 fis, clone AD	2.71
80	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	2.71
	447854	AW138454	Hs.11594	ESTs	2.71
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.70
	412636	NM_004415		desmoplakin (DPI, DPL)	2.69
	420576	AA297634	Hs.54925	KIAA1858 protein	2.68

5	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	2.68
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.68
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.66
	428698	AA852773	Hs.334838	KIAA1866 protein	2.64
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	2.64
10	447347	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 pro	2.64
	429505	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.63
	406137			NM_000179*:Homo sapiens mulS (E. coli) h	2.63
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.62
	443054	AJ745185	Hs.8939	yes-associated protein 65 kDa	2.59
15	452620	AA436504	Hs.119286	ESTs	2.59
	420552	AK000492	Hs.98806	hypothetical protein	2.59
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.56
	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.56
	448454	NM_005879	Hs.21254	TRAF interacting protein	2.55
20	425776	U25128	Hs.159499	parathyroid hormone receptor 2	2.55
	436238	AK002163	Hs.301724	hypothetical protein FLJ11301	2.54
	440676	NM_004987	Hs.112378	LIM and senescent cell antigen-like doma	2.54
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.54
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.53
25	407804	AF228603	Hs.39957	pleckstrin 2 (mouse) homolog	2.51
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	2.49
	411908	L27943	Hs.72924	cytidine deaminase	2.48
	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	2.47
	430024	AI808780	Hs.227730	integrin, alpha 6	2.46
30	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	2.45
	425345	AU077297	Hs.155894	protein tyrosine phosphatase, non-recept	2.45
	423881	AK001720	Hs.134403	hypothetical protein FLJ10858	2.45
	407853	AA336797	Hs.40499	clcklopt (Xenopus laevis) homolog 1	2.45
	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	2.42
35	408296	AL117452	Hs.44155	DKFZP586G1517 protein	2.40
	413048	M93221	Hs.75182	mannose receptor, C type 1	2.39
	403851			C5002154*:gii7299015[gb]AAF54217.1[AE0	2.37
	433745	AF075320	Hs.28980	hypothetical protein FLJ14540	2.37
	423903	M57765	Hs.1721	interleukin 11	2.36
40	427700	AA262294	Hs.180383	dual specificity phosphatase 6	2.32
	419373	NM_003244	Hs.90077	TC-Interacting factor (TALE family homeo	2.31
	426827	AW067805	Hs.172665	methyltetrahydrofolate dehydrogenase	2.31
	440282	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	2.31
	406974	M57293		gb human parathyroid hormone-related pep	2.30
45	401924			ENSP00000246632*:CDNA FLJ20261 fis, clon	2.29
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	2.29
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	2.28
	436608	AA528980		down syndrome critical region protein DS	2.27
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	2.27
50	434398	AA121098	Hs.3838	serum-inducible kinase	2.26
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	2.25
	418030	BE207573	Hs.83321	neuromedin B	2.25
	404927			Target Exon	2.24
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	2.23
55	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	2.21
	411388	X72925	Hs.69752	desmocollin 1	2.18
	445757	AW449065	Hs.13264	KIAA0856 protein	2.17
	405069			NM_006212*:Homo sapiens 6-phosphofructo-	2.16
	414035	Y00630	Hs.75716	sarinate (or cysteine) proteinase inhibito	2.15
60	443168	AI038653	Hs.50500	ESTs	2.13
	444301	AK000136	Hs.10760	asporin (LRR class 1)	2.11
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	2.10
	426471	M22440	Hs.170009	transforming growth factor, alpha	2.08
	445019	AI205540	Hs.281295	ESTs	2.07
65	402021			NM_031891:Homo sapiens cadherin 20, type	2.05
	431866	NM_012098	Hs.8025	angiopoietin-like 2	2.04
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	2.03
	409571	AA504249	Hs.187585	ESTs	1.99
	450831	R37974	Hs.25255	ESTs	1.99
70	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.98
	445960	AI268399	Hs.140489	ESTs, Weakly similar to LIN1_HUMAN LINE-	1.97
	448356	AL120837	Hs.20993	high-glucose-regulated protein 8	1.91
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	1.90
	426850	BE247670	Hs.172766	MAP/microtubule affinity-regulating kina	1.90
75	427335	AA448542	Hs.251677	G antigen 7B	1.88
	450649	NM_001429	Hs.25272	E1A binding protein p300	1.88
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	1.88
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	1.86
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	1.85
80	433226	AW503733	Hs.9414	KIAA1488 protein	1.85
	413129	AF292100	Hs.104613	RP42 homolog	1.85
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	1.81
	446620	AA128808	Hs.179902	transporter-like protein	1.79
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	1.78
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	1.77
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	1.77
	423482	BE280172	Hs.129228	galactokinase 2	1.77

5	434370	AF130988	Hs.58346	ectodysplasin 1, anhidrotic receptor	1.76
	419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.75
	425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	1.74
	405102			C15001220:gi 4469558 gb AAD21311.1 (AF	1.74
	433201	AB040896	Hs.21104	KIAA1463 protein	1.73
	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	1.65
	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	1.62
	414961	U27266	Hs.927	myosin-binding protein H	1.61
10	428405	Y00762	Hs.2266	cholinergic receptor, nicotinic, alpha p	1.61
	422170	AI791949	Hs.112432	anti-Mullerian hormone	1.61
	431846	BE019924	Hs.271580	uroplakin 1B	1.58
	404468			C3000442:gi 11120696 ref NP_068518.1 c	1.57
	405779			NM_005367:Homo sapiens melanoma antigen,	1.55
15	441129	AA074904	Hs.296420	ESTs, Weakly similar to T18651 hypotheti	1.55
	427244	AA402400	Hs.178045	ESTs	1.52
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	1.52
	417777	AI823763	Hs.7055	ESTs, Weakly similar to I7885 serine/th	1.51
	418367	AA326035	Hs.59236	hypothetical protein DKFZp434L0718	1.51
20	440340	AW895503	Hs.125276	ESTs	1.48
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	1.47
	424750	D29956	Hs.152818	ubiquitin specific protease 8	1.46
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	1.44
	406374			C16001364:gi 11067373 ref NP_067689.1 C	1.43
25	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	1.40
	404405			Target Exon	1.39
	401258			NM_030932*:Homo sapiens diaphanous (Dros	1.38
	433323	AA805132	Hs.159142	ESTs	1.36
	427441	AA412605	Hs.343879	SPANX family, member C	1.33
30	444707	AI188613	Hs.41690	desmocollin 3	1.31
	409103	AF251237	Hs.112208	XAGE-1 protein	1.27
	451106	BE382701	Hs.25960	N-MYC oncogene	1.27
	434804	AA649530	Hs.348148	gbns44f05.s1 NCL CGAP_Alv1 Homo sapiens	1.23
	430686	NM_001942	Hs.2633	desmoglein 1	1.21
35	429325	AW088739	Hs.243770	ESTs	1.19
	406703	X13100	Hs.173084	myosin, heavy polypeptide 3, skeletal mu	1.03
	418827	BE327311	Hs.47166	HT021	1.01
	404104			C6001378:gi 1171748 sp P46530 NOTC_BRAR	1.00

TABLE 46B

40	Key:	Unique Eos probe/est identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
45	Pkey	CAT Number	Accession
	413808	2905_1	AI570199 AI888812 AW867550 AI921557 AW469096 AI925581 AI679986 AW473623 BE841640 BF061525 AI445703 AI925072 AW863188 AW863076 BE841731 AW863167 BE841390 BE841365 BF374078 BE841760 BE841694 BE841769 AA335110 BE841692 BF374073 AA335204 BF374079 BE841713 AA335167 BE841584 AW868103 BE841645 BE841765 AI076336 AW867433 BF373831 BE841758 AW868911 AW863155 AW868847 BE841651 AA335145 BE841670 BF374260 BF374088 BE841661 BE841728 B1335729 BE841739 BE841663 AW863104 AA335201 AA335141 BF906965 AW867493 BE841505 BF374250 BE841766 BF373837 AW863191 BE841705 AW863154 AW868673 AW867311 AA335896 BE841763 AW863407 BE937102 BF374252 BF374247 BF374255 BE841785 AW029590 AW131278 AI801021 AW058240 AW058400 AW029230 AW029432 AW130609 AW029128 AW130469 AI570155 AI620272 AW029259 AI801389 AI888662 AI926902 AI801799 AI610344 AI452852 AW131174 AI581069 AI225028 AI446689 AI923321 AI439430 AI801502 AI679707 AW028944 AI933684 AI801724 AI537779 AI354652 AI470250 AI536872 AI891151 AW868019 AW006034 AI702599 AA335192 AA335165 AA335189 AI933725 AW044393 AI888797 BE841677 BE841681 AA335141 AW008176 AA335223 AI888837 AW868622 AI803901 AW005718 AI538062 AI282258 AI580878 AI445803 AI445394 AI868168 AA335144 AI926349 AA335210 AA334919 AA335163 AA335216 AI678342 BF374135 AI932922 AA335214 AA335109 AI570325 AI452619 AI926109 AI453488 AI678606 AW869289 AW869211 BE841580 AI679368 AI888882 AI926170 BF508305 AW869315 AA334926 BE841712 AW026584 AA335200 BE841764 AV730339 AW474979 AI286344 AI446430 AI537612 AA335166 AW868051 AI679133 AI949520 BE841652 AI949532 BE937113 BE841789 BE841643 AW130556 BE841761 AW868716 AW868698 BE841669 BE937108 AA335158 AA335153 AA335159 AW867404 AW868692 BE841742 AW868711 AW867546 BE841699 AA335198 AA335146 AW868150 BE841660 T99129 BE841740 BE841714 AA335154 AW868815 BF373812 BE841657 BE841780 AI440394 AA335215 AA335202 AA335162 AA335160 AI801656 AI678499 BF374019 AW130236 AI826057 AI572459 AI932773 AA335197 AI611752 AA335224 AI452592 AA335147 AA335149 AA334928 AA335114 AA335111 AI567048 AW029395 AI570326 BF373838 BE841691 BE841776 AW863485 BF374093 AW130376 BE841732 AI446393 AI446781 AW867547 AW029012 AA335227 AW869307 AW869350 AW869709 AW869407 AW005017 AI679252 AI925523 AW151553 AW863109 AI445917 AI799620 AI921607 AW008153 AI520957 AI610620 AI679828 AI868151 AI537839 AI679547 T28354 AI282567 AA335207 R83655 BF906963 AW131160 AI925626 AW029396 AW028445 AW008410 AW152586 AW008476 AI801040 AI453669 AI621200 AA334925 BF374069 BF374075 N53208 BF374246 AW868723 BE937150 AA955002 AW863338 BE841767 X00474 NM_003225 X52003 M12075 B1765761 AW950155 AI571948 B1760569 AA308400 AA568312 B1761955 AA507595 AA614579 AA614409 BF747698 BM142326 AA307578 AI925552 AA578674 AA582084 AW009769 AA514776 AA588034 BG271505 AA582878 BM142503 AW050700 AI307407 AI202532 AA524242 AI909772 AI970839 BG236516 AW750216 AA587613 AI909749 AI909751 AI910083 AA614539 R55292 AA507418 BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF92089 R73999 T49904 R75732 B1057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993 H01642 BF510304 AA626915 AA746952 AI61014 AA099554 BG572534 AI803329 AI809932 AI808765 AA411449 AI378760 AA976929 AI378620 AA909684 R75632 AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF995484 AI240665 BF989591 B1056086 BG001590 BF107035 M31126 BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410 H59605 BE157601 AA113758 BC013389 BC017398 AI023543 AA191424 AI267700 AA469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236 AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 B1043873 AA019433 B1862068 BM468657 AU128438 BE384458 AL353967 B1857117 BF686525 B1465223 BM460132 AU129877 B122283 BG171592 B1043544 BG496295 BG750710 B1256542 BG108520 AU150719 AW510354 AU554256 AL353968 AA191092 BF132635 BE184942 BE184946 AW238414 BE144666
50			
55			
60			
65			
70	421582	13358_1	
75	450687	0_0	
	450375	16559_3	
	415989	10194_1	
	426991	29771_1	
	454241	685806_1	

452203	2630_1	BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL564623 AL560492 AL556882 AL541576 AL550654 B1823519 B1770023 AL554969 B1489906 A1304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 A1569694 AW073296 A1361433 AA564644 AA487429 BE858232 AA838610 A1539114 A1719375 A1829129 BG057675 A1423422 AU158860 BE300655 AW170777 AA588956 AL571889 AL556850 AL576404 AL582800 B1256544 BF342301 BG875994 AA054458 AA353161 A1940434 BE816522 AL577636 A1479650 AW150377 AL568505 AL576404 AL582800 B1256544 BF342301 BG875994 AA054458 AA353161 A1940434 BE816522 AL577636 A1479650 AW150377 AU154395 AW951271 A1032220 A1819778 A1346733 AW771150 AW512525 A1249904 AA279809 A1352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 B1819184 AV660190 AL556475 A1620020 AW089888 AW079179 Z21518 AA687601 F04651 A1783961 T57198 A1433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 A1266514 A1538823 A1475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 A1682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 W79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 B1560216 B1753586	
10	408660 400245	105529_1 12188_1	AW975281 AA664986 AA525775 AA056342 A1538978 X79449 BC017853 AL121035 BF196384 AW119044 A1028023 AW451110 A1971911 AW015069 A1079170 A1376367 A1264113 AA829646 AA737579 AA449679 AA740864 NM_001111 U18121 AL567297 BG773801 BF973874 AV687104 AA527579 AAB43525 BE706355 A1074589 A1523475 BE890249 AW408263 BE074258 AV729485 BF809610 BG058619 AA677244 BE179838 AA622264 A1460106 AA740411 A1499168 A1078223 A1682923 BE696559 AW375385 AA788739 BG984978 Z40874 T17054 F09669 AW844043 U10439 B1711870 AW245957 AU158567 AA679305 AA679316 W72510 A1346029 BG059762 AW251062 AA123273 A1925621 A1860230 A1340172 AW192891 A107980 A1094937 A1024215 A1200901 BE328452 AA644678 AA551209 BE351065 AA970761 N68609 AW002028 AA160826 A1422774 AW873114 AW073597 AW664483 A1218710 AW020550 AW190607 A1984545 A1871921 A1333970 A1452887 A1818335 AA398655 A1554424 A1274187 BE465703 AW512940 AW241366 A1923954 AA576649 AW168294 AA813181 AA912168 A1049738 AW514073 AA548255 A1569630 BE710031 AA244182 A1341697 AA563904 A1537990 AW517908 AW172943 Z39498 A1750294 AW150414 A1253293 BE825720 T31860 AW150775 D20310 A1150892 AU133933 BE781148 A1038957 BF910979 AA352297 BG988142 AW372175 BF229106 AW866705 BE093482 BG990396 A1499917 AA054452 H05484 A1285502 BM467331 AU140570 AL135417 BF947202 AW391926 BE813418 BF998473 T92021 B1021048 BM048783 AW501366 AW501342 AW501549 BE939021 BE707147 BE160974 BE305207 N49011 AA947119 AA678801 BE536876 AW897428 BG329648 BG818540 BE542344 B1919250 B1253018 AW130996 BE074249 BE695428 B1034862 BE083277 BF952166 AF274943 BG494894 A1719075 AA908783 A1935150 A122691 AA910644 AA583187 BM272167 A1828996 AA527373 AW972459 A1831360 AA772418 A1033892 AA100926 AU154749 A1459432 A1423513 A1094597 AA740817 A1991988 A1090262 A1312104 B1256707 AA459522 AA416871 A1075239 A1339996 AA701623 A1139549 A1338880 AA633648 A1989380 A1362835 AA399239 A1146955 BF514270 N92892 A1348243 A1278887 AA459292 A1494230 BF507531 A1492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 A149682 A1457100 AW589407 AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 A1537692 A1203723 A1857576 AA584410 AW371667 BM172363
25	414883	8371_2	BE253764 BE250764 BE255757 BE251752 BE251925 U09278 NM_004460 U76833 AF007822 AL550894 BG203919 AL575714 A1478772 AW022667 AW613820 A1435793 A1051768 AL200109 AA436611 BG208151 A1446661 BG215551 BM449645 AW630055 BG620125 AL550932 AW471133 AU136648 BE925603 BF828688 BE141577 BE141585 BE141587 AL109888 R23665 R26578
30	414110 450506	1634167_1 1529_1	BC005265 BG176720 AW006027 BM352064 AW026316 A1635822 A1880584 A1693769 A1092211 B1492387 A1400449 AW166297 BF939910 AA232282 AW021432 A1333893 AA494308 AA854899 A1436795 AW069256 AA862373 A1092748 AA993184 A1126077 A1081758 A1240686 A1261863 A1378423 AA465237 A1376086 AA035579 A1087306 AA448162 AA129977 A1090903 A1080686 A1288939 N33004 A1801240 AW021546 A1261863 A1378423 AA465237 A1376086 AA035579 A1087306 AA448162 AA129977 A1090903 A1080686 A1288939 N33004 A1801240 AW021546 A1370773 A1086064 AA669528 A1250053 A1870113 AA853181 AA858014 BG055562 BG939559 AW080765 AA032283 AW465787 H0506 D00762 NM_002788 AA641134 A1582295 A1417525 A1563975 A1093566 A1070743 A1290741 AW073417 BE875418 BM264076 BG876884 A1680535 AW854219 BE774635 AW854212 BG952443 AW854221 AW854208 BE156348 BE843056 AW858991 BE937569 BG878291 BG876450 AW819099 A1908570 AA449871 AU135228 BM478404 BF126296 AA375499 AA248473
35	455813 439780 400200	1515590_1 49082_1 3806_1	M77830 NM_004415 AF139065 BG681115 BG740377 B1712964 BG000656 AA128470 B1438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG880618 BG739778 B1765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 B1060445 B1060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 B1039774 BE713818 BE713548 AW170253 BE160433 B1039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 B1090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 B1036306 BG990973 B1040964 BF919911 AU140155 A1951766 A1434518 AW804674 BF752969 BE837009 BE925828 BF149265 AW959615 BE814264 B1039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA098981 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AA484723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE719915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE005561 BG959922 BF094833 BF094748 BF094583
40	412636	1438_1	AW377699 AW607238 BE082519 AW377700 BF349467 A1190590 A1554403 A1392926 AU158477 B1467252 AU147612 A1439101 AA451923 A1340326 A1590975 B1791553 A1700963 A1142882 A033975 AA946936 AA644381 BM314884 AA702424 A147612 AW190555 A1220573 A1304772 A1270345 A1627383 AA552300 A1911702 AW166807 A1346078 W95070 AA149191 AA026864 A1830049 AW780435 A1078449 A1819984 A1858282 B1468588 A1860584 A1025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 A1927207 A1205263 BF082491 AW021347 A1588096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 A1910434 BF082513 A1494069 A1270027 A1635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 B1762798 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 A1571075 BE067786 AV721320 A1022862 N29754 C03378 N84767 AA131077 H30146 BE714290 A1685869 A1568892 A1915596 A1055614 A1887258 A1538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 A1905927 BF992780 AW853812 BG954443 B1770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 B1089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 B1040941 AA337270 AW384371 AW847442 B1058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG943933 BE714441 AW996245 BE711801 A1284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 B1013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H09899 AW365145 W38382 A1498487 BC015981 A1301615 AA628980 A126603 BF184719
45			
50			
55			
60			
65			
70	436608	32229_2	

TABLE 46C

Pkey:	Unique number corresponding to an Eos probe set
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423

5	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
	400666	8118496	Plus	17982-18115,20297-20456
	401785	7249190	Minus	165776-165996,166189-166314,166408-16656
	401747	9789672	Minus	118596-118816,119119-119244,119609-11976
	400665	8118496	Plus	16879-17023
10	402994	2996643	Minus	4727-4969
	402075	8117407	Plus	121907-122035,122804-122921,124019-12416
	405770	2735037	Plus	61057-62075
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,4519
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
15	404240	5002624	Minus	116132-116407,116653-116922
	402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
	402992	7767907	Minus	42137-42515
	402408	9796239	Minus	110326-110491
	404286	2326514	Plus	51086-51301
20	405387	6587915	Minus	3769-3833,5708-5895
	404287	2326514	Plus	53134-53281
	402995	2996643	Minus	5962-6216
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	401797	6730720	Plus	6973-7118
25	402294	2282012	Minus	2575-3000
	401961	4581193	Minus	124054-124209
	404440	7528051	Plus	80430-81581
	405386	6579238	Minus	40959-41297
	404171	9930793	Plus	173667-173783,176876-177055
30	405778	7280331	Plus	18748-19757
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
	401176	9438469	Minus	20475-20734
	404170	9930793	Plus	168836-169248

TABLE 47A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Maximum of esophageal tumor Als divided by the 98th percentile of the normal esophagus Als

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
45	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	31.70
	411243	AB039886	Hs.69319	CA11	30.12
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	18.46
	444325	AW152618	Hs.16757	ESTs	18.22
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	17.52
50	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	16.28
	400666			NM_002425:Homo sapiens matrix metallopro	15.59
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	15.22
	425679	X05997	Hs.159177	lipase, gastric	14.60
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	13.14
55	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	12.60
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.00
	453331	AI240665		ESTs	11.20
	431620	AA126109	Hs.264981	Z'-5'-oligoadenylate synthetase 2 (69-71	10.77
	408380	AF123050	Hs.44532	diubiquitin	10.32
60	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.32
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	10.22
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	10.18
	408243	Y00787	Hs.624	interleukin 8	9.80
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	9.75
65	450375	AA009647		a disintegrin and metalloproteinase doma	9.12
	407366	AF026942	Hs.17518	gb:Homo sapiens clg33 mRNA, partial sequ	8.88
	433447	U29195	Hs.3281	neuronal pentadactin II	8.64
	421508	NM_004833	Hs.105115	absent in melanoma 2	8.46
	452862	AW378065	Hs.8687	ESTs	8.34
70	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	7.92
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fs, clone PL	7.86
	409757	NM_001898	Hs.123114	cystatin SN	7.62
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	7.60
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	7.58
75	452410	AL133619		Homo sapiens mRNA; cDNA DKFZp434E2321 (f	7.46
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	7.44
	406687	M31126		matrix metalloproteinase 11 (stromelysin	7.24
	430280	AA361258	Hs.237868	interleukin 7 receptor	7.18
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	7.13
80	429228	AI553633	Hs.326447	ESTs	7.04
	421110	AJ250717	Hs.1355	cathepsin E	6.98
	414004	AA737033	Hs.1755	ESTs, Moderately similar to 2115357A TYK	6.88
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	6.88
	406673	M34996	Hs.198253	major histocompatibility complex, class	6.72
	421582	AI910275		trefoil factor 1 (breast cancer, estroga	6.52

5	447164	AF026941	Hs.17518	Homo sapiens c1g5 mRNA, partial sequence	6.40
	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	6.32
	439926	AW014875	Hs.137007	ESTs	6.32
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	6.12
	411296	BE207307	Hs.10114	growth suppressor 1	6.03
	426312	AF026939	Hs.181874	interferon-induced protein with tetrat	5.86
	413441	AI929374	Hs.75367	Src-like-adaptor	5.88
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	5.81
	417715	AW969587	Hs.86366	ESTs	5.76
10	413808	J00287		Homo sapiens mRNA for caldesmon, 3' UTR	5.63
	400665			NM_002425:Homo sapiens matrix metallopro	5.60
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	5.53
	418299	AA279530	Hs.83968	Integrin, beta 2 (antigen CD18 (p95), ly	5.44
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.42
15	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	5.40
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	5.38
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	5.08
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	5.08
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	5.04
20	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	4.92
	436866	AI469355	Hs.127310	ESTs	4.80
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.60
	421362	AK000050	Hs.103853	hypothetical protein FLJ20043	4.53
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	4.48
25	404240			NM_018950:Homo sapiens major histocompat	4.36
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	4.34
	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	4.29
	425139	AW630488	Hs.25338	protease, serine, 23	4.24
	415989	AI257700		ESTs	4.20
30	408202	AA227710	Hs.43658	DKFZP586L151 protein	4.11
	450701	H39960	Hs.288467	hypothetical protein XP_098151	4.06
	423271	W47225	Hs.126256	Interleukin 1, beta	4.02
	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.96
	443907	AIJ076484	Hs.9963	TYRO protein tyrosine kinase binding pro	3.90
35	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.86
	444008	BE395085	Hs.10086	type I transmembrane protein Fn14	3.86
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	3.76
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	3.49
	408049	AW076098	Hs.345588	desmoplakin (DPI, DPII)	3.44
40	431629	AIJ077025	Hs.265827	interferon, alpha-inducible protein (clo	3.37
	435370	AI964074	Hs.225838	ESTs	3.29
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	3.19
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	3.18
	409154	U72882	Hs.50842	interferon-induced protein 35	3.13
45	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	3.12
	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.00
	406646	M33600	Hs.308026	major histocompatibility complex, class	2.76
	402992			Target Exon	2.57
50	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	2.54
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	2.52
	413945	NM_000591	Hs.75627	CD14 antigen	2.51
	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	2.50
	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito	2.48
	415149	X12451	Hs.78056	cathepsin L	2.47
55	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	2.46
	410422	AL042014	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	2.45
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	2.45
	409202	AA236881	Hs.51043	hexosaminidase B (beta polypeptide)	2.39
	422562	AI962080	Hs.118397	AE-binding protein 1	2.35
60	443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit,	2.28
	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subun	2.19
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet	2.19
	449717	AB040935	Hs.23954	cerebral cell adhesion molecule	2.03
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.03
65	428981	BE313077	Hs.93135	ESTs, Weakly similar to ALU2_HUMAN ALU S	1.83
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	1.79
	406778	H06273	Hs.101651	Homo sapiens mRNA; cDNA DKFZp434C107 (tr	1.70
	408716	AI567839	Hs.151714	Homo sapiens mRNA for KIAA1769 protein,	1.69
	412773	H15785	Hs.74573	similar to vaccinia virus HindIII K4L OR	1.66
70	414024	AA134712	Hs.22410	gb:zrn79g08.r1 Stratagene neuroepithelium	1.65
	426530	U24578	Hs.278625	complement component 4A	1.58
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.52

75

TABLE 47B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

80

Pkey	CAT Number	Accession
453331	16559_1	BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 BI057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW63674 AA190993

5	450375	16559_3	H01642 BF510304 AA626915 AA746952 AI161014 AA099554 BG572534 AI803329 AI809932 AI808765 AA411449 AI378760 AA976929 AI378620 AA909684 R75632 AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF995484 AI240665 BF989591 B1056088 BG001590 BF107035
	452410	59661_1	BG570706 BG572749 AW606284 H04021 AA151166 AW554405 AA131254 BG056461 W46291 H01532 HD4384 H03231 AA852876 H04410 HS9605 BE157601 AA113758
10	406687	0_0	AL133619 AI435410 AA622747 AW272464 AI215594 AI673758 AI476447 AI804128 AI581345 AI025826 AI300820 AW513621 AA256162 AI559724 AI493388 AA614641 AI125754 AI214351 AI567080 AI200813 AI476629 AI685732 AA602400 AA730140 AI565082 AI269603 AI807095 AA905453 AA505909 AI204595 AI582930 AI686077 AA757863 AA730154 AA664048 B1831663 AI734138 AI734130 AI732734 AW043563 AI741241 AI732741 BF111446 BE677727 AA437369 AA426284 AA433997 AA425820
	421582	13358_1	M31126
15	413808	2905_1	X00474 NM_003225 X52003 M12075 B1765761 AW950155 AI571948 B1760569 AA308400 AA568312 B1761955 AA507595 AA614579 AA614409 BF747698 BM142326 AA307578 AI925552 AA578674 AA582084 AW009769 AA514776 AA588034 BG271505 AA858276 BM142503 AW050700 AI307407 AI202532 AA524242 AI909772 AI970839 BG238516 AW750216 AA587613 AI909749 AI909751 AI910083 AA614539 R55292 AA507418 AI570199 AI888812 AW867550 AI921557 AW469096 AI925581 AI679986 AW473623 BE841640 BF061525 AI445703 AI925072 AW863188
			AW863076 BE841731 AW863167 BE841390 BE841365 BF374078 BE841760 BE841694 BE841769 AA335110 BE841692 BF374073 AA335204 BF374079 BE841713 AA335167 BE841584 AW868103 BE841645 BE841765 AI076336 AW867433 BF373831 BE841758 AW868911 AW863155 AW868847 BE841651 AA335145 BE841670 BF374260 BF374088 BE841661 BE841728 B1335729 BE841739 BE841663 AW863104 AA335201 AA335143 BF906965 AW867493 BE841505 BF374250 BE841766 BF373837 AW863191 BE841705 AW863154 AW868673 AW867311 AA335898 BE841753 AW863407 BE937102 BF374252 BF374247 BF374255 BE841785 AW029590 AW131278 AI801021 AW058240 AW058400 AW029230 AW029432 AW130609 AW029128 AW130469 AI570155 AI620272 AW029259 AI801389 AI888662 AI926902 AI801799 AI610344 AI452852 AW131174 AI581069 AI225028 AI466689 AI923321 AI439430 AI801502 AI679707 AW028944 AI933684 AI801724 AI537779 AI354652 AI470250 AI536872 AI891151 AW868019 AW006034 AI702599 AA335192 AA335165 AA335189 AI933725 AW044393 AI888797 BE841677 BE841681 AA335141 AW008176 AA335223 AI888837 AW868622 AI803901 AW005718 AI538062 AI282258 AI580678 AI445803 AI445394 AI868168
20			AA335144 AI926349 AA335210 AA335163 AA335216 AI678342 BF374135 AI932922 AA335214 AA335109 AI570325 AI452619 AI926109 AI453488 AI678606 AW869289 AW869211 BE841580 AI678368 AI888882 AI926170 BF508305 AW869315 AA334926 BE841712 AW026584 AA335200 BE841764 AV730339 AW474979 AI286344 AI446430 AI537612 AA335166 AW868051 AI679133 AI949520 BE841652 AI949532 BE937113 BE841789 BE841643 AW130556 BE841761 AW868716 AW868698 BE841669 BE937108 AA335158 AA335153 AA335159 AW867404 AW868692 BE841742 AW868711 AW867546 BE841699 AA335198 AA335146 AW868150 BE841660 T99129 BE841740 BE841714 AA335154 AW868815 BF373812 BE841657 BE841780 AI440394 AA335215 AA335202 AA335162 AA335160 AI801656 AI678499 BF374019 AW130236 AI826057 AI572459 AI932773 AA335197 AI611752 AA335224 AI452592 AA335147 AA335149 AA334928 AA335114 AA335111 AI567048
			AW029395 AI570326 BF373838 BE841691 BE841776 AW863485 BF374093 AW130376 BE841732 AI446393 AI446781 AW867547 AW029012 AA335227 AW869307 AW869350 AW868709 AW869407 AW005017 AI679252 AI925523 AW151553 AW863109 AI445917 AI799620 AI921607 AW008153 AI520957 AI810620 AI679828 AI868151 AI537839 AI679547 T28354 AI282567 AA335207 R83655 BF906963 AW131160 AI925626 AW029396 AW028445 AW008410 AW152586 AW008476 AI801040 AI453669 AI621200 AA334925 BF374069 BF374075 N53208 BF374246 AW868723 BE937150 AA955002 AW863338 BE841767
35	415989	10194_1	BCD13389 BCD17398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236

TABLE 47C

40	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.		
45	Strand:	Indicates DNA strand from which exons were predicted.		
	NL_position:	Indicates nucleotide positions of predicted exons.		
50	Pkey	Ref	Strand	NL_position
	400666	8118496	Plus	17982-18115,20297-20456
	400665	8118496	Plus	16879-17023
	404240	5002824	Minus	116132-116407,116653-116922
	402992	7767907	Minus	42137-42515

TABLE 48A:

55	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
60	UnigenelD:	Unigene number		
	Unigene Title:	Unigene gene title		
65	R1:	90th percentile of normal esophagus AIs divided by the 90th percentile of esophageal tumor AIs		
	Pkey	ExAccn	UnigenelD	Unigene Title
	407245	X90568	Hs.172004	titin
	426752	X69490	Hs.172004	titin
	425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com
70	407013	U35637		gb:Human nebulin mRNA, partial cds
	400440	X83957	Hs.83870	nebulin
	406704	M21685	Hs.929	myosin, heavy polypeptide 7, cardiac mus
	428087	AA100573	Hs.182421	troponin C2, fast
	417070	Z19077	Hs.172004	titin
	406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu
75	405001	U58196		interleukin enhancer binding factor 1
	418391	NM_003281	Hs.84673	troponin I, skeletal, slow
	418205	L21715	Hs.83760	troponin I, skeletal, fast
	422633	X56832	Hs.118804	enolase 3, (beta, muscle)
	400499			C10001858[6679124]ref[NP_032759.1] ne
	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myo
80	412519	AA196241	Hs.73980	troponin T1, skeletal, slow
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific
	413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)
	416373	AA195845	Hs.73680	ESTs, Weakly similar to S12658 cysteine-
	415672	N53097	Hs.193579	ESTs
	409096	AA194412	Hs.50550	sarcomeric muscle protein

	431360	NM_000427	Hs.251680	loricrin	9.42
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	9.20
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	9.15
5	422069	AJ010063	Hs.343503	titin-cap (telethonin)	8.96
	409028	AB014513	Hs.49998	Z-band alternatively spliced PDZ-motif	8.64
	437206	AW975934	Hs.283382	ESTs, Weakly similar to I38344 titin, ca	8.48
	421296	NM_002666	Hs.103253	perilipin	8.47
	412129	M21984	Hs.73454	troponin T3, skeletal, fast	8.39
10	434352	AF129505	Hs.86492	small muscle protein, X-linked	8.28
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	7.93
	408591	AF015224	Hs.46452	mammaglobin 1	7.88
	435124	AA725362	Hs.120456	ESTs	7.76
	430681	AW969675	Hs.291232	ESTs	7.70
	454229	AW957744	Hs.278469	lacrimal proline rich protein	7.68
15	424734	AI217685	Hs.96844	ESTs	7.59
	428221	U96781	Hs.183075	ATPase, Ca transporting, cardiac muscle,	7.57
	431204	F28841	Hs.250760	cytochrome c oxidase subunit VIa polypep	7.41
	443727	Z25389	Hs.18459	ESTs	7.21
	408753	AI337192	Hs.47438	SH3 domain binding glutamic acid-rich pr	7.04
20	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	6.98
	424485	AI685069	Hs.272556	peptidylarginine deiminase type I	6.93
	403805			Target Exon	6.87
	429997	NM_006789	Hs.227457	apolipoprotein B mRNA editing enzyme, ca	6.72
	418532	F00797	Hs.85844	neurotrophic tyrosine kinase, receptor,	6.70
25	419711	C02621	Hs.159282	ESTs	6.70
	422640	M37984	Hs.118845	troponin C, slow	6.68
	433839	F35430	Hs.146070	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.55
	405703	X13100	Hs.173084	myosin, heavy polypeptide 3, skeletal mu	6.34
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	6.27
30	446962	AJ351421	Hs.279709	muscle specific ring finger protein 1	6.20
	411102	AA401295	Hs.23926	triadin	6.17
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	6.15
	454059	NM_003154	Hs.37048	statherin	5.95
	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	5.85
35	434360	AW015415	Hs.127780	ESTs	5.57
	420813	X51501	Hs.99949	prolactin-induced protein	5.52
	417376	AA253314	Hs.154103	IIM protein (similar to rat protein kina	5.46
	424688	AA216287	Hs.1815	myosin, light polypeptide 3, alkali; ven	5.42
	446523	NM_003063	Hs.334629	sarcolipin	5.41
40	402270			Target Exon	5.25
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	5.24
	424982	U94777		phosphorylase, glycogen; muscle (McArdle	5.17
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	5.14
45	410621	AA194329	Hs.172004	titin	5.10
	429134	AA446953	Hs.99004	ESTs	5.06
	436519	AJ278124	Hs.238756	myozenin	5.04
	447023	AA356764	Hs.17109	integral membrane protein 2A	5.03
	427639	AW444530	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	5.02
	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	5.00
50	433635	AI074502	Hs.134292	hypothetical protein MGC12921	4.98
	429892	NM_003803	Hs.2504	myomesin 1 (skelemin) (185kD)	4.96
	411021	F00055	Hs.172004	titin	4.95
	416349	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	4.93
	424897	D63216	Hs.153684	frizzled-related protein	4.92
55	406741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	4.92
	428824	W23624	Hs.173059	ESTs	4.78
	418692	AK000268	Hs.87383	hypothetical protein	4.74
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	4.73
60	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.66
	424049	AB014524	Hs.138380	KIAA0624 protein	4.65
	439609	AW971945	Hs.293236	ESTs	4.65
	433122	AB019391	Hs.58049	ESTs	4.62
	415447	Z97171	Hs.78454	myocilin, trabecular meshwork inducible	4.59
65	415655	W05433		ESTs	4.59
	442376	W85588	Hs.129982	Homo sapiens cDNA FLJ12228 fis, clone MA	4.58
	452308	AI167560	Hs.61297	ESTs	4.57
	418072	F35210	Hs.86507	Human DNA sequence from clone RP3-353C17	4.56
	429413	NM_014058	Hs.201877	DESC1 protein	4.53
70	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.53
	438704	AI435060	Hs.32825	ESTs	4.50
	413391	AI223328	Hs.75335	glycine amidinotransferase (L-arginine:g	4.49
	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	4.48
	419050	NM_000036	Hs.89570	adenosine monophosphate deaminase 1 (iso	4.46
	422313	AF045941	Hs.115166	scellin	4.43
75	417045	F01180	Hs.332030	Homo sapiens ORF1	4.41
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	4.39
	435101	AI743156	Hs.131064	ESTs	4.37
	432408	N39127		ESTs, Weakly similar to A45010 X-linked	4.35
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	4.35
80	429930	AI580809	Hs.89569	ESTs	4.30
	429624	AA458648	Hs.99476	ESTs, Weakly similar to 1313184B alpha1	4.26
	429454	AL039940	Hs.202949	KIAA1102 protein	4.20
	411000	N40449	Hs.201619	ESTs, Weakly similar to S38383 SEB4B pro	4.11

5	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	3.99
	428560	AI243209	Hs.98669	ESTs, Weakly similar to B47411 ADPribosy	3.95
	438328	AI492261	Hs.32450	ESTs	3.84
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	3.84
	453876	AW021748	Hs.110406	ESTs, Weakly similar to I38022 hypotheti	3.83
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	3.82
	430171	AF086289	Hs.234766	skin-specific protein	3.80
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	3.75
10	446082	AI247139	Hs.156452	ESTs	3.74
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	3.70
	431205	AA194560	Hs.250763	tropomodulin 4 (muscle)	3.68
	443265	AI916207	Hs.9167	SH3 domain binding glutamic acid-rich pr	3.68
	424747	AA346241	Hs.231887	EST	3.67
	410223	S73775	Hs.60708	calsequestrin 1 (fast-twitch, skeletal m	3.63
15	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	3.62
	453817	AW755253	Hs.61920	ESTs	3.57
	418431	AW384459	Hs.172004	titin	3.52
	425971	AF135024	Hs.165296	kalikrein 13	3.49
	412452	AA215731	Hs.79265	suppression of tumorigenicity 5	3.48
20	421512	AB007923	Hs.265848	myomegalin	3.41
	413922	AI535895	Hs.221024	ESTs	3.37
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	3.36
	418067	AI127958	Hs.83393	cystatin E/M	3.32
25	428666	AL080190	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	3.29
	451681	Z28564	Hs.255950	ESTs, Weakly similar to AA64_HUMAN 64 KD	3.26
	420197	AW139647	Hs.88134	ESTs, Weakly similar to A57291 cytokine	3.23
	425869	AA524547	Hs.160318	FXD domain-containing ion transport reg	3.21
	404270			NM_006061:Homo sapiens specific granule	3.21
30	409169	F00991	Hs.50889	(clone PWHL.C2-24) myosin light chain 2	3.17
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	3.13
	452023	AB032999	Hs.27566	KIAA1173 protein	3.08
	417713	D42047	Hs.82432	KIAA0089 protein	2.99
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	2.97
35	450300	AL041440	Hs.58210	ESTs, Highly similar to ITH4_HUMAN INTER	2.97
	451814	AA847992	Hs.137003	ESTs	2.83
	452360	AI742082	Hs.98539	ESTs	2.67
	431938	AA938471	Hs.54431	specific granule protein (28 kDa); cyste	2.57
	408104	AW972927	Hs.293968	ESTs	2.57
40	444329	W73753	Hs.209637	hypothetical protein FLJ12921	2.54
	439652	W67826	Hs.55412	ESTs, Weakly similar to K1CJ_HUMAN KERAT	2.50
	432191	AA043193	Hs.273188	hypothetical protein, clone Telethon(lta	2.33
	425855	AF135025	Hs.159679	kalikrein 12	2.32
	430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	2.28
45	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.25
	411388	X72925	Hs.69752	desmocollin 1	2.25
	425721	AC002115	Hs.159309	uropod 1A	2.12
	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	2.10
	429441	AJ224172	Hs.204096	lipophilin B (utaroglobin family member)	2.02
50	417405	W28657	Hs.5307	ESTs	2.01
	434560	R13052	Hs.3964	Homo sapiens clone 24877 mRNA sequence	1.95
	417074	Z49878	Hs.81131	guanidinoacetate N-methyltransferase	1.79
	430513	AJ012008	Hs.241586	G6C protein	1.68
	454478	AW805749	Hs.318885	superoxide dismutase 2, mitochondrial	1.68
55	416559	AI039195	Hs.128060	ESTs	1.66
	447205	BE617015	Hs.11006	ESTs, Moderately similar to T17372 plasm	1.64
	415780	U75898	Hs.78846	heat shock 27kD protein 2	1.55
	409702	AI752244		eukaryotic translation elongation factor	1.50

60

TABLE 48B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

65

Pkey CAT Number Accession

70

407013 2073_7 U35637 AA192323 AA194508 BG011583 F25712 AL596820 BE185376
424982 25362_1 AK057547 BG181248 AA883756 F25670 AA778128 F27657 F18914 F25171 AA178844 F21556 F25872 F20457 F27617 F36059 F34817 F26967
F25922 F31278 F34666 F01176 F36333 F01226 F27406 F27130 F28742 F24126 F29891 AA195955 AA086351 W69291 F25880 F32791 F31311
F32380 F25216 F19679 F18656 F29700 F24954 F32741 F30404 F35470 F33989 F33141 F36382 F34118 F17714 AA176345 F24700 AA550940
F18617 F16859 F15633 F34575 F16528 F17281 AA086388 F30859 F21852 C02844 F29425 F25286 C03553 F35259 W80691 F16457 F24094
F16783 AA180319 F28443 F17763 F17448 F00542 AA197179 AA193012
415655 15499_1 AJ276240 N70563 F37502 F29200 F27903 F18577 F19683 F20867 Z28857 F30994 F31752 F17375 F15601 F17543 F17411
432408 2061_18 AV724258 AA247153 BF736219 BF513744 AW058048 AI082691 AA865520 N39127 AV724549 F20776 AA249747 AW970392 AA535433 F36984
F33894
409702 38388_1 AK056951 AK026458 BI439120 BM021106 F30243 BM055214 BM054962 BM069667 F37401 AA563621 AI752243 AI720773 AI933014 F18964
F35317 F35258 F27772 H39537 AW445222 F19408 H28557 F30608 F31797 F30950 BF837737 BF837688 AL551046 BI758668 BI765038 BI837440
BE392882 BI438801 AI093511 AI752244 AI784111 BG490221 BF338840 BF338974 BG896472 AL576843 AW966769 F25388 F37436 H28558
AI025548 AA782333 F30929 F36002 F21229 AI720539 AA719449 F21231 F18924 AA626886 F30774 F27704 F31411 F31127 F33381 F36153
F31793 F31138 F31966 F33901 AA298244 BI757347 AI810201 AI692843 F29441 H51409 F21804 AW973249 F18440 F15752 F32499 AA327152
AA534140 AI188088 F18893 F23362 AA010888 F18143 Z28500 H27651 AI720790 F22425 H13178 H28677 F21098 F37777 F21466 F16598
F23420 AL574723 R75610 F34035 F17845 F18560 F25902 R79117 F35534 F15713 AI612800 F16563 F15645 F33609 F29995 BG939623 F17385
F17384 F18660 F17922 F15523 AI093253 F18359 F31452 F00232 AI583430 BM021353 AA284108 H27650 H29935 BE708208 AA010737 H51451

80

Z19399 AI678418 AI952535 F17265 F17826 F37939 F35639 F17367 W75962 R70189 Z28755 R72106 AA335915 R75700 R79116 W72887
AI581552 R71403 F23388 C03913 BI756149 BI116109 BF790727 AL553994 R82966 W47487 AA456066 AW984608 BE708220 BG490537 W47419

5 TABLE 48C
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of
10 Strand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
405001	6015406	Minus	104646-104819
400499	9796071	Minus	148495-148806
15 403805	8140491	Minus	51483-51742,53429-53511
402270	3108020	Plus	117656-117822
404270	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965

20 Table 49A. 1562 genes upregulated in lung cancer relative to normal body tissues

25 Table 49A shows 1562 genes upregulated in lung cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains
30 indicative of have oncogenic function or of transducing intracellular signals, or of being modifiable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

35 Pkey: Unique Eos probeset Identifier number
ExAccn: Exemplar accession number, GenBank accession number
UniGeneID: UniGene number
Pred.Protdomains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other
UniGene Title: UniGene gene title
R1 90th percentile of lung tumor AIs divided by the 50th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from the
40 numerator and denominator.

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Protdomains; R1

421502; AF111856; Hs.105039; solute carrier family 34 (sodium phosphate), member 2; Ribosomal_L20,Na_Pi_cotrans;TM=Y; 24.06
439335; AA742697; Hs.62492; ESTs, Weakly similar to B39066 proline-rich protein 15 - rat [R.norvegicus]; none;SS=M; 21.70
406621; X57809; Hs.181125; Immunoglobulin lambda locus; ig.HSP70,Ppx-GppA;TM=M; 19.36
421341; AJ243212; Hs.279611; deleted in malignant brain tumors 1; zona_pellucida,CUB,SRCR;SS=M; 16.99
452304; AA025386; Hs.61311; ESTs, Weakly similar to S10590 cysteine proteinase [H.sapiens]; none;none; 16.67
429259; AA420450; Hs.292911; ESTs, Highly similar to S60712 band-6-protein [H.sapiens]; none;none; 16.50
454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member A1; aldedh; 16.24
50 408000; L11690; Hs.620; bulous pemphigoid antigen 1 (Z30/240kD); ehand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,Flid,bZIP,Tropomyosin,Myc-LZ,M,ldh_C,CH,AIP3;TM=M; 14.75
421798; N74880; Hs.29877; N-acylsphingosine amidohydrolase (acid ceramidase)-like; SAPA,Surfactant_B,none; 14.18
439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_HUMAN DEATH-ASSOCIATED PROTEIN 1 [H.sapiens]; none;none; 13.94
431846; BE019924; Hs.271580; uroplakin 18; transmembrane4;TM=Y;SS=M; 13.54
55 417079; U65590; Hs.81134; Interleukin 1 receptor antagonist; IL1;SS=M; 12.97
444381; BE387335; Hs.283713; ESTs, Weakly similar to S64054 hypothetical protein YGL050w - yeast (Saccharomyces cerevisiae) [S.cerevisiae]; Collagen;TM=M;SS=M; 12.92
408243; Y00787; Hs.624; Interleukin 8; HLH,PAS,IL8;TM=M; 12.76
448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec,MIP;TM=M;SS=M; 12.50
414809; A434699; Hs.77356; transferrin receptor (p90, CD71); PA;TM=Y; 12.12
60 436553; AW407157; Hs.181125; Immunoglobulin lambda locus; ig.HSP70,Ppx-GppA;TM=M; 12.00
418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino acid transporter, y system) member 11; none;none; 11.99
419693; AA133749; Hs.301350; FXD domain-containing ion transport regulator 3; ATP1G1_PLM_MAT8;TM=Y;SS=M; 11.88
417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA;SS=M; 11.38
414999; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin-like) receptor 1; lectin_c;TM=Y;SS=M; 11.21
65 428970; BE276891; Hs.194691; retinoic acid induced 3; 7tm_3;TM=Y;SS=M; 11.08
418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member B2; aldedh;TM=M;SS=M; 11.01
425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisomV,HATPase_c;SS=M; 10.69
418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4); ank; 10.65
439223; AW238299; Hs.250618; UL16 binding protein 2; ldl_recept_a,PKD,MHC_J;TM=M;SS=Y; 10.52
70 441835; AB036432; Hs.184; advanced glycosylation end product-specific receptor; homeobox,Acyltransferase,notch,EGF,ank,Acyltransferase; 10.47
451558; NM_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1), member 3; ABC_tran,SRP54;TM=Y;SS=M; 10.33
443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M; 10.21
452747; BE153855; Hs.61460; Ig superfamily receptor LNIF; Ig,Rhbd_glycop;TM=Y;SS=M; 10.14
417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor 2); PTN_MK;TM=M;SS=Y; 10.13
75 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR_LY6,toxin,Activin_recpt;TM=M;SS=Y; 10.12
454098; W27953; Hs.292911; ESTs, Highly similar to S60712 band-6-protein [H.sapiens]; none;none; 10.05
414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 9.98
430832; AI073913; Hs.100686; ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]; none;none; 9.79
422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; none,pkinase,fn3,jg; 9.60
80 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M; 9.54
439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,CoaE;TM=M; 9.52
430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 9.48

- 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive); Kunitz_BPT1,fn3,vwa, Collagen,beta-lactamase; TM=M;SS=M; 9.44
- 418882; NM_004996; Hs.89433; ATP-binding cassette, sub-family C (CFTR/MRP), member 1; ABC_membrane,ABC_tran; TM=Y;SS=M; 9.32
- 435472; AW972330; Hs.283022; triggering receptor expressed on myeloid cells 1; Ig; TM=M;SS=M; 9.26
- 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-macroglobulin receptor precursor [H.sapiens]; none,none; 9.18
- 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR/MRP), member 3; ABC_tran,ABC_membrane; TM=Y;SS=M; 9.06
- 441384; AA447849; Hs.288660; Homo sapiens cDNA: FLJ22182 lis, clone HRC00953; 7tm_3,none; 8.98
- 446292; AF081497; Hs.279582; Rh type C glycoprotein; Ammonium_transp,FecCD; TM=Y;SS=M; 8.74
- 436972; AA284679; Hs.25640; claudin 3; PMP22_Claudin; TM=Y;SS=M; 8.71
- 412187; AF146074; Hs.108660; ATP-binding cassette, sub-family C (CFTR/MRP), member 5; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU; TM=M;SS=M; 8.71
- 423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alpha 2/delta subunit 2; vwa,CACHE; TM=M; 8.66
- 439608; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1; TM=Y;SS=M; 8.63
- 438091; AW373062; ; nuclear receptor subfamily 1, group I, member 3; hormone_rec,zf-C4,none; 8.60
- 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK; TM=M; 8.57
- 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin; SS=M; 8.56
- 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase; SS=M; 8.52
- 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle, trypsin, plant_thionins; SS=M; 8.49
- 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin; TM=M; 8.42
- 413011; AW068115; Hs.821; biglycan; LRR,LRRNT; SS=M; 8.40
- 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT; TM=M;SS=Y; 8.39
- 411089; AA456454; ; cell division cycle 2-like 1 (PITSLRE proteins); none,none; 8.37
- 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (survivin); BIR; TM=M; 8.34
- 453922; AF053306; Hs.36708; budding uninhibited by benzimidazoles 1 (yeast homolog), beta; none; SS=M; 8.25
- 449018; A1949095; Hs.67776; ESTs, Weakly similar to T22341 hypothetical protein F47B8.5 - *Caenorhabditis elegans* [C.elegans]; none,none; 8.24
- 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase; TM=M; 8.22
- 416819; U77735; Hs.80205; pim-2 oncogene; pkinase; SS=M; 8.19
- 451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg; TM=M; 8.16
- 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; ABC_tran,M,SMC_N,SMC_C,DUF164,none; 8.16
- 429002; AW248439; Hs.2340; junction plakoglobin; Armadillo_seg; TM=M; 8.14
- 445033; AV652402; Hs.72901; mucin 13, epithelial transmembrane; ank; 8.14
- 421757; Z20897; Hs.296259; paraoxonase 3; Arylesterase; SS=Y; 8.10
- 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, receptor for (CD64); Ig; TM=Y;SS=M; 8.03
- 439285; AL133916; ; hypothetical protein FLJ20093; Ig,pkinase,LRR,LRRNT,LRRCT,none; 7.97
- 439738; BE246502; Hs.9598; sema domain, Immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B; Sema,PSI,Integrin_B; TM=Y; 7.86
- 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related kinase 2; pkinase; TM=M; 7.85
- 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4; TM=Y;SS=M; 7.85
- 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,Pi3_Pi4_kinase,FAT,FATC,BolA,RUN; TM=M; 7.84
- 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2); SH3,TPR; TM=M; 7.73
- 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, receptor for (CD16); Ig; TM=Y;SS=M; 7.72
- 430378; Z29572; Hs.2556; tumor necrosis factor receptor superfamily, member 17; IL2; SS=M; 7.71
- 451253; H48299; Hs.26126; claudin 10; PMP22_Claudin,Peptidase_M1,K_tetra; TM=Y;SS=M; 7.70
- 435575; AF213457; Hs.44234; triggering receptor expressed on myeloid cells 2; Ig; TM=Y;SS=M; 7.70
- 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase; TM=M; 7.70
- 426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54), human rhinovirus receptor; Ig,IgCAM_N; TM=M;SS=M; 7.67
- 422282; AF019225; Hs.114309; apolipoprotein L; MotA_ExtB; TM=Y;SS=M; 7.64
- 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence; SAM_PNT,none; 7.54
- 424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding protein; 7tm_1; TM=Y;SS=M; 7.52
- 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase); Y_phosphatase,DSPC; TM=M; 7.46
- 421071; A131238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen alpha 1(XI) chain precursor [H.sapiens]; none; TM=Y;SS=M; 7.40
- 421481; AW391972; Hs.104696; KIAA1324 protein; none; TM=M;SS=M; 7.39
- 438089; W05391; ; nuclear receptor subfamily 1, group 1, member 3; hormone_rec,zf-C4,none; 7.38
- 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino acid transporter, y system), member 5; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,Pi3_Pi4_kinase,FAT,FATC,BolA,RUN; TM=M; 7.36
- 448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A receptor, epsilon; Neur_chan_LBD,Neur_chan_memb; TM=Y;SS=M; 7.36
- 416178; A1808527; Hs.192822; serologically defined breast cancer antigen NY-BR-81; none; TM=M; 7.31
- 418506; AA084248; Hs.85339; G protein-coupled receptor 39; none,none; 7.25
- 441553; AA281219; Hs.121296; ESTs; none,FG-GAP,Integrin_A; 7.25
- 422311; AF073515; Hs.114948; cytokine receptor-like factor 1; fn3; TM=M; 7.21
- 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-type, Z polypeptide 1; fn3,Y_phosphatase,carb_anhydrase; TM=Y;SS=M; 7.20
- 438748; A1885815; Hs.184727; Human melanoma-associated antigen p97 (melanotransferrin) mRNA, 3' flank; transferrin,Guanylate_kin,PDZ,SH3; 7.20
- 412723; AA648459; Hs.335951; hypothetical protein AF301222; none; TM=M; 7.14
- 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 7.14
- 428582; BE336699; Hs.185055; BENE protein; none; TM=Y;SS=M; 7.12
- 418462; BE001596; Hs.85266; Integrin, beta 4; fn3,Integrin_B,Cbx-beta,EGF; TM=M;SS=M; 7.08
- 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5; TM=Y;SS=M; 7.02
- 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase; TM=M; 7.00
- 449230; BE613348; Hs.211579; melanoma cell adhesion molecule; Ig,Isochr,Ribosomal_L6,F-box; TM=Y;SS=M; 6.98
- 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47682 B-cell growth factor precursor [H.sapiens]; Furin-like,pkinase,Recep_L_domain,YLP,none; 6.97
- 421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN,HIN; TM=M; 6.96
- 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; ITAM; TM=Y;SS=M; 6.93
- 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to M; pkinase,ICE_p10,ICE_p20; TM=M;SS=M; 6.93
- 421532; A138207; Hs.146170; hypothetical protein FLJ22969; Armadillo_seg,HEAT; TM=M; 6.91
- 451035; AU076785; Hs.430; plastin 1 (I isoform); ethanol,CH,Adaptin_N; SS=M; 6.86
- 432407; AA221036; ; gbzr0312.r1 Stratagene NT2 neuronal precursor S37230 Homo sapiens cDNA clone 5' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN 1, mRNA sequence; DEAD,helicase_C,rm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,Pili,ebhydrolase,TGF-beta,DUF139,TPR,DSPC,isp_1,Ribosomal_S21,rvp; TM=M; 6.84
- 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank; TM=M; 6.77
- 448243; AW369771; Hs.52620; Integrin, beta 8; Integrin_B,none; 6.76
- 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6,ET,PLA2_inh; SS=M; 6.75
- 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase; TM=M;SS=M; 6.74
- 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glucose transporter), member 1; sugar_tr; TM=Y;SS=M; 6.73

- 430397; AI924533; Hs.105607; bicarbonate transporter related protein 1; HCO3_cotransp;TM=Y;; 6.71
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 6.71
 431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor); FG-GAP,Rhbd_glycop,integrin_A;TM=Y;SS=M; 6.70
 410434; AF051152; Hs.63668; toll-like receptor 2; LRR,LRRCT,TIR;TM=M;SS=M; 6.69
 424925; NM_002432; Hs.153837; myeloid cell nuclear differentiation antigen; PAAD_DAPIN,HIN; 6.69
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor); vwa,Integrin_A,FG-GAP;TM=Y;SS=M; 6.65
 428157; AJ738719; Hs.198427; hexokinase 2; hexokinase,hexokinase2,none; 6.64
 430770; AA765694; Hs.123296; ESTs; none,none; 6.63
 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G protein), alpha 15 (Gq class); G-alpha,arf;TM=M; 6.59
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2005735; IMPDH_C,IMPDH_N,CBS,Integrin_B,Ricin_B_lectin; 6.59
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPc;TM=M; 6.59
 413048; M93221; Hs.75182; mannose receptor, C type 1; fn2,lectin_c,Ricin_B_lectin,Xlink;TM=Y;SS=M; 6.58
 429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 6.58
 416110; Z42262; Hs.322844; hypothetical protein DKFP564A176; Sema,PSI,TIG,Integrin_B;TM=Y;SS=M; 6.58
 418883; BE387038; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos;TM=M;SS=M; 6.57
 426746; J03626; Hs.2057; uridine monophosphate synthetase 6 (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase); Priboyltran,OMPdecase;TM=M; 6.57
 402260; ; NM_001436; Homo sapiens fibrillarin (FBL), mRNA. transcript1 (F8A), mRNA; pkinase,Fibrillarin,none; 6.56
 456373; BE247706; Hs.89751; membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide); none;TM=Y; 6.53
 444006; BE395085; Hs.10086; type I transmembrane protein Fn14; ldl_recept_La,Pkd,MHC_1;TM=M;SS=Y; 6.53
 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; Inositol_P,ig;TM=M; 6.52
 435523; J03626; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; none;TM=Y;SS=M; 6.52
 432920; U37689; Hs.3128; polymerase (RNA) II (DNA directed) polypeptide H; none;TM=M; 6.48
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L ORF; PLDC;TM=M; 6.48
 409208; Y00093; Hs.51077; integrin, alpha X (antigen CD11C (p150), alpha polypeptide); vwa,FG-GAP,Integrin_A,vwa,Integrin_A,FG-GAP; 6.43
 424441; X14850; Hs.147097; H2A histone family, member X; histone,CBFD_NFYB_HMF; 6.43
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell receptor; lg;TM=Y;SS=M; 6.41
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PLACE2000103; HLH,death,TNFR_c6,Acyl-CoA_hydro; 6.41
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc_Y_phosphatase,Ribosomal_S3_N;TM=M; 6.39
 453914; NM_000507; Hs.574; fructose-1,6-bisphosphatase 1; FBPase;TM=M; 6.37
 424273; W40460; Hs.144442; phospholipase A2, group X; phosph;TM=M;SS=Y; 6.37
 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3;SS=M; 6.36
 432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 6.34
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese,none; 6.34
 451734; NM_006176; Hs.26944; neurogranin (protein kinase C substrate, RC3); IQ,7tm_1;TM=M; 6.34
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding protein; none;TM=M;SS=Y; 6.34
 401027; ; Target Exon; none,none; 6.26
 418299; AA279530; Hs.83968; Integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit); integrin_B,EGF,PSI;TM=Y;SS=M; 6.22
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD); SH2;SS=M; 6.21
 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone ADKAD2377; 7tm_3,none; 6.20
 408771; AW732577; Hs.47584; potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3; ehfand,ion_trans,K_tetra,none; 6.19
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudogene; LIM,PDZ,pkinase;SS=M; 6.18
 408482; NM_000676; Hs.45743; adenosine A2b receptor; 7tm_1;TM=Y;SS=M; 6.17
 426427; M88699; Hs.169840; TTK protein kinase; pkinase; 6.17
 445019; AJ205540; Hs.281295; ESTs; none,none; 6.16
 438552; AJ245820; Hs.6314; type I transmembrane receptor (seizure-related protein); none,none; 6.16
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal_L37ae,pkinase,POLO_box,IRNA-synt_1b,dynamin,dynamin_2,GED,bZIP,M; 6.14
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic polypeptide; PI3_P14_kinase,FAT,FATC;TM=M; 6.13
 417421; AL138201; Hs.82120; nuclear receptor subfamily 4, group A, member 2; hormone_rec,zf-C4;SS=M; 6.13
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm_2,HRM;TM=Y;SS=M; 6.12
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 6.12
 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase;TM=M; 6.12
 421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion_trans,K_tetra,asp; 6.11
 444143; AW747998; Hs.160999; ESTs, Moderately similar to A56194 thromboxane A2 receptor, endothelial [H.sapiens]; Bcl-2,none; 6.10
 423887; AL080207; Hs.134585; DKFZP434G232 protein; ABC_tran;TM=Y; 6.10
 409636; AA305729; Hs.18272; amino acid transporter system A1; Aa_trans;TM=Y; 6.09
 411020; NM_006770; Hs.67728; macrophage receptor with collagenous structure; SRCR,Collagen;TM=Y;SS=M; 6.09
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1;TM=Y;SS=M; 6.08
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD); PAF-AH_Ib,Lipase_GOSL;TM=M; 6.07
 421753; BE314828; Hs.107911; ATP-binding cassette, sub-family B (MDR/TAP), member 6; ABC_tran,ABC_membrane;TM=Y;SS=M; 6.07
 406908; Z25437; ; gb:H.sapiens protein-tyrosine kinase gene, complete CDS; none,none; 6.07
 425849; AJ000512; Hs.296323; serum/glucocorticoid regulated kinase; pkinase,pkinase_C;TM=M;SS=M; 6.06
 452363; AI582743; Hs.94953; Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279, mRNA, complete cds; C1q,Collagen;SS=M; 6.05
 414883; AA926960; ; CDC28 protein kinase 1; Cks; 6.05
 414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD,helicase_C,rrm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,Rlla,abhydrolase,TGF-beta,DUF139,TPR,DSPc,isp_1,Ribosomal_S21,rvp;TM=M; 6.03
 452888; AW955454; Hs.30942; ephrin-B2; Ephrin,fn2;TM=Y;SS=M; 6.03
 448782; AL050295; Hs.22039; KIAA0758 protein; 7tm_2,ig,GPS,SEA;TM=Y; 6.03
 449101; AA205847; Hs.23016; G protein-coupled receptor; 7tm_1;TM=Y;SS=M; 6.01
 445462; AA378776; Hs.288649; hypothetical protein MGC3077; none; 6.00
 424381; AA285249; Hs.146329; protein kinase Ck2; pkinase,FHA,Dna;TM=M; 6.00
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; pkinase;TM=M; 5.99
 439310; AF086120; Hs.102793; ESTs; casein_kappa,pkinase,lg,none; 5.97
 414972; BE263782; Hs.77695; KIAA0008 gene product; GKAP;TM=M; 5.97
 425976; C75094; Hs.334514; NG22 protein; voltage_CLC;TM=Y;SS=M; 5.94
 444946; AW139205; Hs.156457; hypothetical protein FLJ22408; abhydrolase,abhydrolase_2;TM=Y;SS=M; 5.93
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associated kinesin); kinesin;TM=M; 5.93
 421462; AF016495; Hs.104624; aquaporin 9; MIP;TM=Y;SS=M; 5.92
 426761; AI015709; Hs.172089; Homo sapiens mRNA; cDNA DKFZp586i2022 (from clone DKFZp586i2022); none;TM=Y;SS=M; 5.92
 407792; AI077715; Hs.39384; putative secreted ligand homologous to fix1; none;TM=M;SS=Y; 5.91
 428771; AB028992; Hs.193143; KIAA1069 protein; C2,PI-PLC_Y,PI-PLC_X;TM=M; 5.91
 438564; AA381553; Hs.198253; major histocompatibility complex, class II, DQ alpha 1; lg,MHC_II_alpha,none; 5.91

- 440006; AK000517; Hs.6844; hypothetical protein FLJ20510; AAA,NB-ARC,PAAD_DAPIN;NA;NA; 5.90
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49,EGF,Ig,Neuregulin;TM=M; 5.90
 408790; AW580227; Hs.47860; neurotrophic tyrosine kinase, receptor, type 2; Ig,pkinase,LRR,LRRNT,LRRCT;TM=Y;SS=M; 5.89
 413186; AU077141; Hs.75231; solute carrier family 16 (monocarboxylic acid transporters), member 1; sugar_tr;TM=Y;SS=M; 5.89
 430696; AA531276; Hs.59509; ESTs; pkinase,PP2C,none; 5.88
 422609; Z46023; Hs.118721; sialidase 1 (lysosomal sialidase); BNR,SH2,SH3,pkinase;TM=Y;SS=M; 5.88
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor type, C-associated protein; none;TM=M;SS=Y; 5.88
 429619; AL120751; Hs.211568; eukaryotic translation initiation factor 4 gamma, 1; none,none; 5.86
 437429; H79981; Hs.5613; Homo sapiens mRNA; cDNA DKFZp564E2222 (from clone DKFZp564E2222); SH2,SH3,BTB; 5.86
 436576; AI458213; Hs.77542; ESTs; 7tm_1,DnaJ; 5.85
 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic, calcium-dependent); C2,PLA2_B;TM=M; 5.85
 419981; AA897581; Hs.128773; ESTs; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 5.83
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfamily, member 6b, decoy; 60s_ribosomal,Ribosomal_L10,TNFR_c6,DEAD; 5.83
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; PSS;TM=Y;SS=M; 5.82
 451320; AW118072; diacylglycerol kinase, zeta (104kD); none;TM=M; 5.82
 400991; ; Target Exon; Armadillo_seg,lectin_c,none; 5.81
 456906; AF117648; Hs.156637; Cas-Br-M (murine) ectropic retroviral transforming sequence c; zf-C3HC4,Cbl_N,Cbl_N2,Cbl_N3;TM=M; 5.81
 434263; N34895; Hs.44648; ESTs; Ig,none; 5.81
 428293; BE250944; Hs.183556; solute carrier family 1 (neutral amino acid transporter), member 5; eIF6,SDF;TM=M; 5.78
 421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; p450;TM=Y;SS=M; 5.78
 449539; W80363; Hs.58446; ESTs; pkinase,Furin-like,Recep_L_domain,none; 5.77
 409012; AL117435; Hs.49725; DKFZP434I216 protein; PH,RhoGEF;TM=M;SS=M; 5.77
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (glycosylation-inhibiting factor); MIF,sugar_tr,none; 5.75
 409533; AW969543; Hs.21291; mitogen-activated protein kinase kinase kinase 13; Peptidase_C48,none; 5.73
 457001; J03258; Hs.2062; vitamin D (1,25-dihydroxyvitamin D3) receptor; hormone_rec,zf-C4,Metallothio_5;TM=M; 5.73
 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kinase); none,none; 5.72
 448569; BE382657; Hs.21486; signal transducer and activator of transcription 1, 91kD; SH2,STAT,STAT_bind,STAT_prot;TM=M; 5.72
 452295; BE379936; Hs.28866; programmed cell death 10; serpin,none; 5.72
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moiety X)-type motif 1; NUDIX;TM=M;SS=M; 5.72
 448733; NM_005629; Hs.187958; solute carrier family 6 (neurotransmitter transporter, creatine), member 8; SNF;TM=Y; 5.71
 417015; NM_03772; Hs.80876; flavin containing monooxygenase 3; FMO-like,pyr_redox;TM=Y;SS=M; 5.69
 453323; AF034102; Hs.32951; solute carrier family 29 (nucleoside transporters), member 2; Nucleoside_tran;TM=Y;SS=M; 5.69
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,Integrin_B;TM=Y;SS=M; 5.69
 412182; AA205588; Hs.155160; Splicing factor, arginine/serine-rich, 46kD; rm,hormone_rec,zf-C4,sugar_tr; 5.69
 418526; BE019020; Hs.85938; solute carrier family 16 (monocarboxylic acid transporters), member 3; none;TM=Y;SS=M; 5.66
 447250; AI878909; Hs.17883; protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; PP2C;TM=M; 5.65
 438113; AI467908; Hs.8882; ESTs; 7tm_1,none; 5.65
 421391; AW304350; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; Ig,none; 5.64
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypeptide E; Sm,pkinase; 5.64
 406137; ; NM_000179; Homo sapiens mutS (E. coli) homolog 6 (MSH6), mRNA. VERSION NM_000178.1 G; MutS_C,PWWP,MutS_N;TM=M; 5.63
 421917; AB028943; Hs.109445; KIAA1020 protein; BTB,zf-C2H2,PI3_P14_kinase,PI3Ka;TM=M; 5.62
 445873; AA250970; Hs.231946; poly(A)-binding protein, cytoplasmic 1-like; PABP,rm,pkinase,14-3-3; 5.62
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (GEF) 5; SH3,PH,RhoGEF;TM=M; 5.61
 446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G-protein coupled, 6; 7tm_1;TM=Y;SS=M; 5.59
 433662; W07162; Hs.150826; CATX-8 protein; ras,ABC_tran,ar;TM=M;SS=M; 5.59
 449029; N28989; Hs.22891; solute carrier family 7 (cationic amino acid transporter, y system), member 8; aa_permeases;TM=Y;SS=M; 5.58
 431236; AV656840; Hs.285115; Interleukin 13 receptor, alpha 1; tn3;TM=Y;SS=M; 5.57
 430508; AI015435; Hs.104637; ESTs; SDF;TM=Y;SS=M; 5.56
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mRNA, 3'UTR; 7tm_1;TM=Y;SS=M; 5.55
 421677; H64092; Hs.38282; ESTs; A1pp,Armadillo_seg,IBB; 5.54
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M; 5.54
 429563; BE619413; Hs.2437; eukaryotic translation initiation factor 2B, subunit 5 (epsilon, 82kD); hexapep,WZ,hormone2,DUF29;TM=M; 5.52
 412817; AL037159; Hs.74619; proteasome (prosome, macropain) 26S subunit, non-ATPase, 2; PC_rep;TM=M; 5.51
 452291; AFD15592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; pkinase;TM=M; 5.51
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (from clone DKFZp547C136); ABC_tran,GTP_EFTU,ABC_membrana,none; 5.50
 423778; Y09267; Hs.128221; flavin containing monooxygenase 2; FMO-like,pyr_redox;TM=Y;SS=M; 5.48
 422846; BE519394; Hs.1583; neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1); SH3,PX;TM=M; 5.48
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fs, clone HEMBB1001304; Nucleoside_tra2,none; 5.48
 426691; NM_006201; Hs.171834; PCTAIRE protein kinase 1; pkinase;TM=M; 5.48
 453905; NM_002314; Hs.36566; LIM domain kinase 1; pkinase,LIM,PDZ,zf-PARP;TM=M; 5.48
 412939; AW411491; Hs.75069; eukaryotic translation elongation factor 1 gamma; none,none; 5.44
 430488; BE062109; Hs.241551; chloride channel, calcium activated, family member 2; none;TM=Y;SS=M; 5.43
 430068; AI929659; Hs.237825; signal recognition particle 72kD; TPR,AIRC,SAICAR_synt; 5.40
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor type, C; kinesin,tn3,Y_phosphatase;TM=M; 5.40
 411825; AK000334; Hs.72289; hypothetical protein FLJ20327; SNF,Zip;TM=Y; 5.36
 400205; ; NM_006265; Homo sapiens RAD21 (S. pombe) homolog (RAD21), mRNA.(APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), mRNA; DUF173;SS=M; 5.35
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase;SS=M; 5.34
 407786; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 5.34
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase (NAD dependent), methenyltetrahydrofolate cyclohydrolase; myb_DNA-binding,THF_DHG_CYH,THF_DHG_CYH_C,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,M,xan_ur_permease,HCO3_cotransp;TM=M; 5.32
 400210; ; Eos Control; Adap_comp_sub,ClaL_adaptor_s;TM=M; 5.32
 414825; X06370; Hs.77432; epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog); Furin-like,pkinase,Recep_L_domain;TM=M;SS=M; 5.31
 414035; Y00630; Hs.75716; serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2; serpin;SS=M; 5.30
 416000; R82342; Hs.79856; ESTs; Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; none,sugar_tr; 5.30
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoeE; 5.29
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kinase; SH2,SH3,pkinase;TM=M; 5.29
 450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyrosine kinase substrate; none,none; 5.29
 456672; AK002016; Hs.114727; Homo sapiens, clone MGC:16327, mRNA, complete cds; none,PK,PK_C,myosin_head,RhoGAP; 5.28
 410088; AI633888; Hs.69435; FYN-binding protein (FYB-120/130); SH3;TM=M; 5.28
 456629; AW891965; Hs.279789; histone deacetylase 3; HSP90,HATPase_c,zf-C2H2,PHD,none; 5.27
 417218; AA005247; Hs.285754; met proto-oncogene (hepatocyte growth factor receptor); pkinase,Sema,PSI,TIG,Integrin_B;TM=Y;SS=M; 5.26
 444051; N48373; Hs.10247; activated leucocyte cell adhesion molecule; none,none; 5.26

- 404083; ; C6002159; gij628027[pilr]A53593 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor ty; none;SS=M; 5.26
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1; mito_carr;TM=M; 5.26
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase;TM=M; 5.26
 427732; NM_002980; Hs.2199; secretin receptor; 7tm_2,HRM;TM=M;SS=M; 5.25
 425921; NM_007231; Hs.162211; solute carrier family 6 (neurotransmitter transporter), member 14; SNF;TM=Y;SS=M; 5.25
 448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A, member 4A; none;TM=Y;SS=M; 5.24
 441607; NM_005010; Hs.7912; neuronal cell adhesion molecule; WD40,fn3,jg;TM=M; 5.23
 445620; AA128808; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 5.23
 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS,AIRS_C;TM=M; 5.23
 447131; NM_004585; Hs.17466; retinoic acid receptor responder (tazarotene induced) 3; none;TM=Y; 5.21
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrate 1; SH3,HS1_rep;TM=M; 5.20
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M; 5.19
 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX nuclease)-like 2 protein; Troponin,Exo_endo_phos,IQ;TM=M; 5.19
 446636; AC002563; Hs.15767; citron (rho-interacting, serine/threonine kinase 21); CNH,DAG_PE-bind,PH,Involucrin,M;TM=M; 5.19
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C;none; 5.19
 447081; Y13896; Hs.17287; potassium inwardly-rectifying channel, subfamily J, member 15; IRK;TM=Y; 5.19
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; Ribosomal_S14,ank,pkinase,death;none; 5.18
 442200; AW590572; Hs.235768; ESTs; none;none; 5.18
 445666; H95741; Hs.17914; membrane-spanning 4-domains, subfamily A, member 6A; none;TM=Y;SS=M; 5.18
 452690; AI536070; Hs.15085; ESTs; pou,homeobox,lig_chan,ANF_receptor; 5.18
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); Ion_trans,SPRY,RYDR,ITPR,RyR,MIR;TM=Y; 5.17
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y; 5.16
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase,PLAT;TM=M; 5.16
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta (Liddle syndrome); ASC;TM=Y;SS=M; 5.15
 429500; X78565; Hs.289114; hexabrachion (tenascin C, cytactin); EGF,fn3,fibrinogen,C,toxin_2,Keratin_B2;TM=M;SS=Y; 5.15
 411984; NM_005419; Hs.72988; signal transducer and activator of transcription 2, 113kD; SH2,STAT,STAT_bind,STAT_prot;TM=M; 5.15
 433470; AW960564; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 5.14
 452817; AA322859; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; pkinase,PBD;TM=M; 5.14
 453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz,Frizzled,7tm_2;TM=Y;SS=M; 5.14
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily, member 7; SRP14,TNFR_c6;SS=M; 5.14
 430563; AA481269; ; ATP-binding cassette, sub-family C (CFTR/MRP), member 5; ABC_tran,GTP_EFTU,ABC_membrane;none; 5.13
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar_tr;TM=Y; 5.12
 431183; NM_005855; Hs.250596; KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3; ER_lumen_recept;TM=M;SS=M; 5.12
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazarotene induced) 1; none;none; 5.11
 418613; AA744529; Hs.86557; mitogen-activated protein kinase kinase kinase kinase 1; pkinase,CNH;TM=M; 5.11
 409524; AW402151; Hs.54673; tumor necrosis factor (ligand) superfamily, member 13; TNF;TM=Y;SS=M; 5.11
 436856; AI469355; Hs.127310; ESTs; pkinase,rm;TM=M; 5.09
 411296; BE207307; Hs.10114; growth suppressor 1; 2OG-Fell_Oxy;TM=M;SS=M; 5.09
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; rm;TM=M; 5.09
 404440; ; NM_021048;Homo sapiens melanoma antigen, family A, 10 (MAGEA10), mRNA. VERSION NM_021049.1 GI; MAGE;TM=M; 5.08
 424977; AA349289; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; none;none; 5.08
 422100; AI096988; Hs.111554; ADP-ribosylation factor-like 7; arf,ras;TM=M; 5.07
 452222; AW806287; Hs.21432; SEX gene; Sema,TIG,PSI,GDI; 5.07
 430300; U60805; Hs.238648; oncostatin M receptor; fn3;TM=Y;SS=M; 5.07
 408369; R38438; Hs.182575; solute carrier family 15 (H?? transporter), member 2; PTR2;TM=Y; 5.07
 422112; BE540240; Hs.111783; Lsm1 protein; Sm,BAG;SS=M; 5.06
 449961; AW265634; Hs.133100; ESTs; pkinase,Furin-like,Recep_L_domain;none; 5.06
 430024; AI808780; Hs.227730; Integrin, alpha 6; Integrin_A,FG-GAP;TM=Y;SS=M; 5.06
 412641; M16660; Hs.74335; heat shock 90kD protein 1, beta; HSP90,HATPase_c;TM=M; 5.05
 437608; AA761605; Hs.292308; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; pkinase,RIO1;none; 5.05
 400296; AA305627; Hs.139336; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC_tran,ABC_membrane;TM=Y; 5.04
 446232; AI281848; Hs.194691; retinoic acid induced 3; 7tm_3;none; 5.04
 425262; D87119; Hs.155418; GS3955 protein; pkinase;SS=M; 5.04
 414703; BE243877; Hs.76941; ATPase, Na? transporting, beta 3 polypeptide; Na_K-ATPase;TM=Y;SS=M; 5.03
 434808; AF155108; Hs.256150; Homo sapiens, Similar to RIKEN cDNA 2810027O19 gene, clone MGC:14827, mRNA, complete cds; none;TM=M; 5.03
 425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member 21; death,TNFR_c6;TM=Y;SS=M; 5.03
 449437; AI702038; Hs.100057; Homo sapiens cDNA: FLJ22502 fis, clone KAT05581; none;none; 5.03
 448913; AA194422; Hs.22564; myosin VI; rm,zf-RanBP,pkinase,GST_C,Elis,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFIIS,AT_hook,SAM;TM=M; 5.02
 413441; AI929374; Hs.75367; Src-like-adaptor; SH2,SH3;TM=M; 5.02
 427618; NM_000760; Hs.2175; colony stimulating factor 3 receptor (granulocyte); fn3;TM=M;SS=M; 5.02
 417666; AI345001; Hs.82380; menage a trois 1 (CAK assembly factor); zf-C3HC4;TM=M; 5.02
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory subunit 1 (p35); CDK5_activator;none; 5.01
 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to ras-related protein RAB17; ras,arf,TK;SS=M; 5.01
 426285; U20620; Hs.343581; karyopherin alpha 1 (importin alpha 5); Armadillo_seq,IBB;TM=M; 5.01
 412133; AA209534; Hs.284243; tetraspan NET-6 protein; transmembrane4;TM=Y;SS=M; 5.01
 424517; AI539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643; SH2,STAT,STAT_bind,STAT_prot;none; 5.00
 425345; AU077297; Hs.155894; protein tyrosine phosphatase, non-receptor type 1; Y_phosphatase,DSPc;TM=M;SS=M; 5.00
 446946; AI878932; Hs.317; topoisomerase (DNA) I; Topoisomerase_I,TN,Topoisomerase_I,N,RnaAD,Hania_nucleocap;TM=M; 4.99
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/hsp90-organizing protein); TPR,PDZ,WW,Guanylate_kin;TM=M; 4.98
 412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor); 7tm_1;TM=Y;SS=M; 4.98
 400792; AA635062; ; Homo sapiens mRNA: cDNA DKFZp434O0515 (from clone DKFZp434O0515); zf-C3HC4,CARD,BIR;TM=M; 4.98
 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related oncogene homolog; SH2,SH3,pkinase;TM=M; 4.98
 427247; AW504221; Hs.174103; Integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide); vwa,Integrin_A,FG-GAP;TM=Y;SS=M; 4.98
 442080; AW444761; Hs.44565; ESTs; ank; 4.97
 454042; H22570; ; hypothetical protein FLJ20093; Ig,pkinase,LRR,LRRNT,LRRCT;none; 4.97
 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1;TM=Y;SS=M; 4.96
 416276; U41060; Hs.79136; LIV-1 protein, estrogen regulated; Peptidase_C4,Osteopontin,Zip;TM=Y;SS=M; 4.96
 408847; AW290997; Hs.30348; ESTs; pkinase,Ig;none; 4.96
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; Ig,pkinase;TM=Y;SS=M; 4.95
 450737; AW007152; Hs.203330; ESTs; trypsin_id_recept_a;none; 4.95
 443354; AW970672; Hs.9247; protein kinase, AMP-activated, alpha 1 catalytic subunit; pkinase,RIO1;TM=M; 4.94

- 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese, DSPc, Y_phosphatase; TM=M; 4.94
 424247; X14008; Hs.234734; lysosome (renal amyloidosis); lys, Ig, FAD, Synth, Jdh, C, kinase; SS=M; 4.94
 434206; AW136973; Hs.180479; ESTs, Weakly similar to S69890 mitogen inducible gene mig-2 [H.sapiens]; PH; TM=M; 4.93
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fusin); 7tm_1, 7tm_2; TM=Y; SS=M; 4.93
 408716; AJ567639; Hs.151714; Homo sapiens mRNA for KIAA1769 protein, partial cds; UvrD-helicase, RNB, Runt; TM=M; 4.93
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg, UQ_con, none; 4.92
 424241; AW995948; Hs.182339; Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence; Els, SAM_PNT; TM=M; 4.92
 414570; Y00285; Hs.76473; insulin-like growth factor 2 receptor, fn2, C1MR; TM=M; SS=M; 4.92
 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; Ig; TM=Y; SS=M; 4.92
 409512; AW979187; Hs.293591; melanoma differentiation associated protein-5; DEAD, helicase_C, CARD; TM=M; 4.91
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated alpha); Ig, JTAM, Zn_cus; TM=Y; SS=M; 4.91
 404289; ; NM_002944; Homo sapiens v-ros avian UR2 sarcoma virus oncogene homolog 1 (ROS1), mRNA; fn3, pkinase, DUF139; TM=Y; SS=M; 4.90
 428141; D50402; Hs.182611; solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1; Ntramp; TM=Y; 4.90
 407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none; TM=M; SS=Y; 4.89
 432179; X75208; Hs.2913; EphB3; EPH_lbd, fn3, pkinase, SAM; TM=Y; SS=M; 4.89
 401083; ; NM_016582; Homo sapiens peptide transporter 3 (LOC51296), mRNA. VERSION NM_016579.1 G; PTR2; TM=Y; SS=M; 4.89
 402211; AA811738; ; KIAA0430 gene product; ion_trans, K_tetra; TM=Y; 4.88
 421541; NM_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, polypeptide 4; pkinase, pkinase_C; TM=M; 4.87
 431810; X67155; Hs.270845; kinesin-like 5 (mitotic kinesin-like protein 1); kinesin; TM=M; 4.86
 425295; AA431366; Hs.37251; ESTs; pkinase, none; 4.86
 424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; DNA_ligase; 4.86
 419168; AJ338132; Hs.33718; Homo sapiens cDNA FLJ12641 fis, clone NT2RM4001953; none, none; 4.86
 442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequence; K_tetra, DUF51, none; 4.86
 425465; L18954; Hs.1904; protein kinase C, iota; pkinase, DAG, PE-bind, pkinase_C, OPR; TM=M; 4.86
 410293; AK000047; Hs.61960; hypothetical protein; K_tetra; TM=M; 4.86
 443623; AA345519; Hs.9641; complement component 1, q subcomponent, alpha polypeptide; C1q, Collagen; SS=M; 4.85
 445903; AJ347487; Hs.132781; class I cytokine receptor; fn3; TM=Y; 4.85
 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a ligand); 7tm_1; TM=Y; SS=M; 4.85
 428820; AA436187; Hs.172631; integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide); vwa, Integrin_A, FG-GAP; TM=Y; SS=M; 4.84
 445143; U29171; Hs.75852; casein kinase 1, delta; zf-C3HC4, Filamin, zf-B_box, NHL, pkinase, zf-MZ; TM=M; 4.82
 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG; TM=M; 4.81
 427857; AL133017; Hs.2210; hypothetical protein FLJ22865; myosin_head, IQ, zf-MYND; TM=M; SS=M; 4.81
 422293; X94453; Hs.114366; pyroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); aldedh, aaknase; TM=M; 4.81
 414280; BE410769; Hs.75873; zyxin; LIM, Ig, pkinase; TM=M; SS=M; 4.81
 424570; AA343306; Hs.133511; ESTs; SH3, ank, none; 4.80
 451144; AW956103; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme 1; HATPase_c, none; 4.80
 402705; AA214618; ; activator of S phase kinase; AhpC-TSA; TM=M; SS=M; 4.80
 410024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3; TM=M; 4.80
 419972; AL041465; Hs.182982; golgin-67; none, none; 4.80
 427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C, none; 4.80
 413476; U25849; Hs.75393; acid phosphatase 1, soluble; LMWPc; TM=M; SS=M; 4.80
 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, receptor for (CD32); Ig; TM=Y; 4.79
 402233; ; NM_030760; Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 8 (EDG8), mRNA; 7tm_1; TM=Y; SS=M; 4.79
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2; NusG; SS=M; 4.79
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinase; pkb; TM=M; 4.79
 405370; ; NM_005569; Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA; pkinase, LIM, PDZ; SS=M; 4.79
 416498; U3632; Hs.79351; potassium channel, subfamily K, member 1 (TWIK-1); ion_trans; TM=Y; SS=M; 4.78
 429921; AA526911; Hs.82772; collagen, type XI, alpha 1; Collagen, COL1T1, SPN, laminin_G, CorA; SS=M; 4.78
 424415; NM_001975; Hs.146580; enolase 2, (gamma, neuronal); enolase; TM=M; 4.78
 433133; AB027249; Hs.104741; PDZ-binding kinase; T-cell originated protein kinase; pkinase; TM=M; 4.78
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clone IFI-6-16); none; TM=M; SS=Y; 4.78
 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds; Ig, abhydrolase; 4.78
 450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2; TM=Y; SS=M; 4.78
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; pkinase; SS=M; 4.77
 409744; AW675258; Hs.56265; Homo sapiens mRNA; cDNA DKFZp586P2321 (from clone DKFZp586P2321); none; NA; NA; 4.77
 446196; AJ744888; Hs.149470; ESTs; zf-C3HC4, Sulfate_transp, STAS; 4.77
 429305; AF095727; Hs.287832; myelin protein zero-like 1; Ig, transmembrane4; TM=Y; SS=M; 4.77
 426812; AF105365; Hs.172613; solute carrier family 12 (potassium/chloride transporters), member 7; none; TM=Y; 4.77
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort 1, importin alpha 1); Armadillo_seg, IBB, DEAD, helicase_C, Sec63, DDT, PHD, bromodomain; TM=M; 4.77
 444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-STYX; DSPc; TM=M; 4.77
 452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fis, clone HEMBA1001702; GDI, 7tm_1, none; 4.76
 447207; AA442233; Hs.17731; hypothetical protein FLJ12892; none; TM=M; 4.76
 400846; ; ; sortilin-related receptor, L (DLR class) A repeats-containing (SORL1); EGF, fn3, Id1_recept, Id1_recept_b, granuln, BNR; TM=Y; SS=M; 4.76
 452355; N54926; Hs.29202; G protein-coupled receptor 34; 7tm_1, OATP_C; TM=Y; 4.75
 406809; AF000574; Hs.22405; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2; Ig, Germln_mov; TM=M; SS=M; 4.75
 427376; BE515037; Hs.177556; melanoma antigen, family D, 1; MAGE; TM=M; 4.75
 444042; NM_004915; Hs.10237; ATP-binding cassette, sub-family G (WHITE), member 1; ABC_tran, PRK, GBP; TM=Y; 4.74
 410406; AI969703; Hs.1466; glycerol kinase; FGGY, FGGY_C; TM=M; 4.73
 411653; AF070578; Hs.71168; Homo sapiens clone 24674 mRNA sequence; none; NA; NA; 4.73
 437667; BE616412; Hs.286218; junctional adhesion molecule 1; none, HLH; 4.73
 417781; BE279380; Hs.82563; KIAA0153 protein; TTL, Acyl_transf; 4.73
 453966; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin, Id1_recept, a, none; 4.73
 412228; AW503785; Hs.73792; complement component (3d/Epstein Barr virus) receptor 2; sushi; TM=Y; SS=M; 4.73
 418265; AW135405; Hs.37251; ESTs; pkinase, none; 4.73
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affinity glutamate transporter), member 3; SDF; TM=Y; SS=M; 4.73
 406906; Z25424; ; gb: H.sapiens protein-serine/threonine kinase gene, complete CDS; none, none; 4.73
 432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catalytic subunit; Metallophos; TM=M; 4.72
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese; SS=M; 4.72
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) expressed in; NDK, PH, Oxysterol_BP; SS=M; 4.71
 426136; AW957239; ; gb: EST369309 MAGE resequences, MAGD Homo sapiens cDNA, mRNA sequence; PP2C, none; 4.71
 446203; Z47553; Hs.14286; flavin containing monooxygenase 5; FMO-like, pyr_redox; TM=Y; SS=M; 4.71
 451295; AJ557212; Hs.17132; ESTs, Moderately similar to 154374 gene NF2 protein [H.sapiens]; pkinase, DAG, PE-bind, pkinase_C, OPR, none; 4.71

- 424099; AF071202; Hs.139336; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC_tran,ABC_membrane;TM=Y;; 4.70
- 424959; NM_005781; Hs.153937; activated p21cdc42Hs kinase; lkh,lkh_C,SH3,pkinase,UBA;TM=M;; 4.70
- 427206; NM_004586; Hs.173965; ribosomal protein S6 kinase; lkh,lkh_C,SH3,pkinase,UBA;TM=M;; 4.70
- 421662; NM_014141; Hs.106552; cell recognition molecule Caspr2; EGF,F5_F8_type_C,laminin_G,Sulfate_transp,STAS,7tm_3,xan_ur_permease;TM=Y;SS=M; 4.70
- 413431; AW246428; Hs.75355; ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13); UQ_con;TM=M;; 4.70
- 405484; ; C3002124*gi12737280[ref]XP_006682.2| keratin 18 [Homo sapiens]||6633; none;SS=M; 4.70
- 401345; M83738; ; protein tyrosine phosphatase, non-receptor type 9; none;TM=M; 4.70
- 416602; NM_006159; Hs.79389; nel (chicken)-like 2; EGF,ywc,TSPN;SS=Y; 4.69
- 412507; L36645; Hs.73964; EphA4; fn3,pkinase,SAM,EPH_lbd;TM=Y;SS=M; 4.69
- 437897; AA770581; Hs.146170; hypothetical protein FLJ22969; zF-DHHC;none; 4.69
- 432886; BE159028; Hs.279704; chromatin accessibility complex 1; none;TM=M; 4.69
- 400843; ; NM_003105*Homo sapiens sortilin-related receptor, L (DLR class) A repeats-containing (SORL1), mRNA; EGF,fn3,lol_recept_a,lol_recept_b,granulin,BNR;TM=Y;SS=M; 4.68
- 433409; AI278802; Hs.25661; ESTs; pkinase,pkinase; 4.68
- 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; none;TM=Y;SS=M; 4.68
- 430259; BE550182; Hs.127826; RafGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 4.68
- 425761; AW664214; Hs.196729; ESTs; SH3,Ribosomal_S3Ae; 4.68
- 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone COLO4544; pkinase,Furin-like,Recep_L_domain;none; 4.68
- 419493; AF001212; Hs.50744; proteasome (prosome, macropain) 26S subunit, non-ATPase, 11; CDKS_activator,PCI;none; 4.67
- 426986; NM_001761; Hs.1973; cyclin F; cyclin,F-box,cyclin_C;TM=M; 4.67
- 408056; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 4.67
- 453476; A1640500; Hs.24633; SAM domain, SH3 domain and nuclear localisation signals, 1; SH3,SAM;SS=M; 4.67
- 412926; A1879076; Hs.75061; macrophage myristoylated alanine-rich C kinase substrate; MARCKS;SS=M; 4.67
- 424635; AA420687; Hs.115455; Homo sapiens cDNA FLJ14259 fis, clone PLACE1001076; pkinase,Furin-like,Recep_L_domain;none; 4.66
- 446051; BE048061; Hs.37054; ephrin-A3; Ephrin_A_deamin,dsm,z-alpha; 4.66
- 436729; BE621807; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.66
- 408204; AA454501; Hs.43666; protein tyrosine phosphatase type IVA, member 3; Y_phosphatase;TM=M; 4.66
- 435542; AA687376; ; ESTs; SH3,jg,pkinase,PH,spectrin,RhoGEF;none; 4.66
- 429682; NM_006306; Hs.211602; SMC1 (structural maintenance of chromosomes 1, yeast)-like 1; ABC_tran,SMC_N,SMC_C,KID;TM=M; 4.66
- 417497; AW402482; Hs.82212; CD53 antigen; transmembrane4;TM=Y;SS=M; 4.66
- 418736; T18979; Hs.87908; Snf2-related CBP activator protein; helicase_CAT_hook,SNF2_N;TM=M; 4.65
- 415117; AF120499; Hs.78016; polynucleotide kinase 3'-phosphatase; Viral_helicase1;TM=M; 4.65
- 418629; BE247550; Hs.86859; growth factor receptor-bound protein 7; SH2,PH,RA;SS=M; 4.65
- 426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M; 4.64
- 429263; AA018004; Hs.198396; ATP-binding cassette, sub-family A (ABC1), member 4; ABC_tran,SRP54;TM=Y;SS=M; 4.64
- 431886; L77964; Hs.271980; mitogen-activated protein kinase 6; pkinase;TM=M; 4.63
- 435049; AL122067; Hs.4746; hypothetical protein FLJ21324; none;TM=M; 4.63
- 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1 (arthritis potentiating activity, collagenase inhibitor); TIMP,pkinase,DAG_PE-bind,RBD; 4.63
- 413436; AF238083; Hs.68061; sphingosine kinase 1; DAGK;TM=M; 4.63
- 421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; ehfand,lol_recept_a;SS=M; 4.62
- 442590; A1002686; Hs.130313; ESTs; none,Y_phosphatase,Band_41,connexin; 4.62
- 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium binding domain; ehfand;SS=M; 4.62
- 423740; U07701; Hs.293007; aminopeptidase puromycin sensitive; Peptidase_M1,Armadillo_seg; 4.61
- 429300; AB011108; Hs.198891; serine/threonine-protein kinase PRP4 homolog; pkinase;TM=M; 4.60
- 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; none;TM=M;SS=M; 4.60
- 412942; AL120344; Hs.75074; mitogen-activated protein kinase-activated protein kinase 2; pkinase;TM=M; 4.60
- 419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; DSPc; 4.59
- 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule 1); EGF,lactin_c,sushi;TM=M;SS=M; 4.59
- 411126; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 4.59
- 434683; AW381538; Hs.19807; hypothetical protein MGC12959; SH3,PH,WW,RhoGAP;SS=M; 4.58
- 447312; A1434345; Hs.36908; activating transcription factor 1; rm,zf-RanBP,pkinase,GST_C,Ets,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFIIS,AT_hook,SAM;TM=M; 4.58
- 435254; AW194689; Hs.30778; ESTs; pkinase,Bacterial_PQQ;none; 4.58
- 426925; NM_001196; Hs.315689; Homo sapiens cDNA: FLJ22373 fis, clone HRC06741; Esterase,enolase,Peptidase_S9;TM=M; 4.58
- 421685; AF189723; Hs.106778; ATPase, Ca transporting, type 2C, member 1; Ca2ion_ATPase_C,Ca2ion_ATPase_N,E1-E2_ATPase,Hydrolase,XPG_N;TM=Y; 4.58
- 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor type, U; fn3,jg,Y_phosphatase,MAM;TM=Y;SS=M; 4.58
- 427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Fizzled,calreticulin,7tm_2,rm,PAP_assoc;TM=Y;SS=M; 4.57
- 441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 fis, clone NT2RM4000200; none;none; 4.57
- 409581; U66243; Hs.55039; mitogen-activated protein kinase 12; pkinase;SS=M; 4.57
- 423184; NM_004428; Hs.1624; ephrin-A1; Ephrin;TM=M;SS=M; 4.56
- 443920; AL037764; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; none,FMO-like; 4.56
- 422627; BE336857; Hs.118787; transforming growth factor, beta-induced, 68kD; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 4.56
- 418869; AW516565; ; gb:qx01d05.x1 Scores_NHCCc_cervical_tumor Homo sapiens cDNA clone 3' similar to contains Alu repetitive element ;contains element MER11 repetitive element ; mRNA sequence; none,RasGAP,WW,IQ; 4.56
- 430016; NM_004736; Hs.227658; xenotropic and polytropic retrovirus receptor; SPX,EXS;TM=Y;; 4.56
- 437157; BE048860; Hs.120655; ESTs; IRK;none; 4.55
- 422769; AA938905; Hs.120017; olfactory receptor, family 7, subfamily E, member 38 pseudogene; none;none; 4.55
- 457918; AL359590; Hs.162604; hypothetical protein DKFZp762M186; PLD;TM=M; 4.55
- 434467; BE562368; Hs.231853; Homo sapiens cDNA FLJ13445 fis, clone PLACE1002962; 7tm_1;none; 4.55
- 421140; AA298741; Hs.102135; signal sequence receptor, delta (translocon-associated protein delta); none;TM=Y;SS=M; 4.55
- 406354; ; Target Exon; hexapep;TM=M; 4.55
- 443682; AA827165; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; Ig;none; 4.54
- 438939; H21012; Hs.287657; Homo sapiens cDNA: FLJ21291 fis, clone COLO1963; F5_F8_type_C,pkinase,Ets;none; 4.54
- 433435; BE545277; Hs.340959; Ts translation elongation factor, mitochondrial; EF_TS,UBA; 4.54
- 411165; NM_000169; Hs.69089; galactosidase, alpha; Melibiase;SS=M; 4.54
- 408956; AK001868; Hs.43344; hypothetical protein FLJ11008; ion_trans;TM=Y; 4.54
- 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related); SH3;TM=M; 4.53
- 410226; A1831958; Hs.161053; hypothetical protein; SH3,TPR;TM=M; 4.53
- 422753; A1928995; Hs.1575; small nuclear ribonucleoprotein D3 polypeptide (18kD); Sm;SS=M; 4.52
- 418355; L42563; Hs.1165; ATPase, H7 transporting, nongastric, alpha polypeptide; E1-E2_ATPase,Ca2ion_ATPase_C,Ca2ion_ATPase_N,Hydrolase;TM=Y;; 4.52
- 400261; ; Eos Control; ig,MHC_II_beta;TM=Y;SS=M; 4.52
- 444633; AF111713; Hs.286218; junctional adhesion molecule 1; Ig;TM=Y;SS=M; 4.52
- 422940; BE077458; ; gb:RC1-BT0606-090500-015-b04 BT0606 Homo sapiens cDNA, mRNA sequence; Sec7,PH,ANF_receptor,Ilg_chan,WD40,IRK; 4.52

- 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulated; none;none; 4.51
 412604; AW978324; Hs.1904; protein kinase C, ι ; pkinase,DAG_PE-bnd,ptkinase_C,OPR;TM=M; 4.51
 448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin;TM=M; 4.51
 457906; AW975933; Hs.153290; Homo sapiens cDNA FLJ14318 fis, clone PLACE3000402; none,ptkinase; 4.51
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none;TM=M; 4.51
 429690; AW956329; Hs.23721; ESTs; none,sugar_tr,Ribosomal_S25; 4.50
 424618; L29472; Hs.1802; major histocompatibility complex, class II, DO beta; Ig,MHC_II_beta;TM=Y;SS=M; 4.50
 444823; BE262989; Hs.12045; putative protein; Mra1,MBOAT;TM=M;SS=Y; 4.50
 405490; ; NM_031414; Homo sapiens serine/threonine kinase 31 (STK31), transcript variant 1, mRNA; pkinase,TUDOR;TM=M; 4.50
 424494; U78575; Hs.149255; phosphatidylinositol-4-phosphate 5-kinase, type I, alpha; PIP5K;SS=M; 4.50
 441031; A110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen_C,G-alpha,arf;TM=M;SS=M; 4.50
 443951; F13272; Hs.111334; ferritin, light polypeptide; PMP22,Claudin,none; 4.50
 410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-receptor type 6; SH2,Y_phosphatase,DSPC;TM=M; 4.50
 429556; AW139399; Hs.98988; ESTs; none;TM=M; 4.50
 458791; BE615453; Hs.346509; dedicator of cyto-kinesis 1; none;TM=Y; 4.49
 425209; AL049761; Hs.155140; casein kinase 2, alpha 1 polypeptide; pkinase,ABC1;TM=M; 4.49
 425695; NM_005401; Hs.159238; protein tyrosine phosphatase, non-receptor type 14; Y_phosphatase,Band_41,DSPC;TM=M; 4.49
 424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,DENN,uDENN;TM=M; 4.49
 412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanesa,DSPC;SS=M; 4.48
 400755; AA635062; ; Homo sapiens mRNA; cDNA DKFZp43400515 (from clone DKFZp43400515); zfc3HC4,CARD,BIR;TM=M; 4.48
 425566; AW162943; Hs.250618; UL16 binding protein 2; lcl_recept_a_PKD,MHC_1;TM=M;SS=Y; 4.48
 410151; X15723; Hs.59242; paired basic amino acid cleaving enzyme (furin, membrane associated receptor protein); Peptidase_S8,P;TM=Y;SS=M; 4.48
 423536; L22075; Hs.1666; guanine nucleotide binding protein (G protein), alpha 13; UCR_hinge,G-alpha,arf;TM=M; 4.48
 424711; NM_005795; Hs.152175; calcitonin receptor-like; 7tm_2,HRM;TM=Y;SS=M; 4.48
 427878; C05766; Hs.181022; CG1-07 protein; none,zf-C2H2; 4.48
 443991; NM_002250; Hs.10082; potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4; CaMBD,SK_channel,ion_trans;TM=Y;SS=M; 4.48
 422605; H16646; Hs.118666; hypothetical protein PP591; PAPS_reduct,MoCF_biosynth; 4.47
 410583; AW770280; Hs.36258; ESTs, Moderately similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]; SH3,PDZ,Guanylate_kin,none; 4.47
 434419; AL040606; Hs.296938; dual specificity phosphatase 7; DSPC;TM=M; 4.47
 410032; BE065985; ; gbr:RC3-BT0319-120200-014-a09 BT0319 Homo sapiens cDNA, mRNA sequence; abhydrolase_2,none; 4.46
 423078; M35198; Hs.123125; Integrin, beta 6; Integrin_B,EGF,pp-binding;TM=Y;SS=M; 4.46
 400263; ; Eos Control; GTP_EFTU,EFG_C,GTP_EFTU_D2,serpin;TM=M; 4.46
 441406; Z45957; Hs.7837; phosphoprotein regulated by mitogenic pathways; pkinase;TM=M; 4.45
 434551; BE387162; Hs.280858; ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 [H.sapiens]; none;TM=M; 4.45
 413227; M79082; ; ESTs; none,none; 4.45
 441321; H17182; Hs.7771; B-cell associated protein; Band_7;TM=M; 4.45
 457194; H20669; Hs.35406; ESTs, Highly similar to unnamed protein product [H.sapiens]; none,pkinase,PBD; 4.45
 414745; AA160511; Hs.5326; amino acid system N transporter 2; porcupine; none,none; 4.45
 404276; ; NM_002944; Homo sapiens v-ros avian UR2 sarcoma virus oncogene homolog 1 (ROS1), mRNA; fn3,pkinase,DUF139;TM=Y;SS=M; 4.45
 426966; AJ493134; ; sclerostin; DAN;TM=M;SS=M; 4.45
 408873; AL046017; Hs.182278; calmodulin 2 (phosphorylase kinase, delta); none,none; 4.44
 426486; BE178285; Hs.170056; Homo sapiens mRNA; cDNA DKFZp586B0220 (from clone DKFZp586B0220); pkinase,none; 4.44
 432798; AA565309; Hs.194015; ESTs; Integrin_B,Sema,PSI,TIG,none; 4.44
 439668; AJ091277; Hs.302634; frizzled (Drosophila) homolog 6; Frizzled,Fz,7tm_2,toxin_2;TM=Y;SS=M; 4.44
 417886; AA214584; ; ESTs; SPRY,7tm_3,ANF_receptor,none; 4.43
 452098; AJ858183; ; gb:W46a12.x1 NCL_CGAP_U11 Homo sapiens cDNA clone 3' similar to contains Alu repetitive element, mRNA sequence; SH3,none; 4.43
 426874; N67325; Hs.347487; ESTs; SH3,TonB_boxC,none; 4.43
 422714; AB018335; Hs.119387; KIAA0792 gene product; DUF221;TM=Y;SS=M; 4.42
 410741; Z11695; Hs.324473; mitogen-activated protein kinase 1; pkinase,none; 4.42
 432193; AA372264; Hs.273193; hypothetical protein FLJ10706; pkinase;TM=M; 4.41
 409506; NM_006163; Hs.64569; NCK adaptor protein 1; SH2,SH3;TM=M; 4.41
 429390; AB040942; Hs.201500; KIAA1509 protein; none;TM=M; 4.41
 421859; AA356620; Hs.108947; KIAA0050 gene product; ank,PH,ArfGAP;SS=M; 4.41
 451527; AF022813; Hs.26518; transmembrane 4 superfamily member 7; none,none; 4.41
 421748; NM_014718; Hs.107809; KIAA0726 gene product; cadherin;TM=Y; 4.40
 410416; BE410072; Hs.63304; protein phosphatase methyltransferase-1; none;TM=M; 4.40
 450457; AA367701; Hs.6639; KIAA1624 protein; none;TM=M;SS=M; 4.40
 433029; NM_014322; Hs.279926; opsin 3 (encephalopsin); 7tm_1,Monoxygenase;TM=Y;SS=M; 4.40
 408805; H69912; Hs.48269; vaccinia related kinase 1; pkinase;TM=M; 4.40
 421585; U95826; Hs.302043; chemokine (C-C motif) receptor-like 2; 7tm_1;TM=Y;SS=M; 4.40
 440014; AW960782; Hs.6856; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; SPRY,BAG,UPF0001; 4.40
 451154; AA015879; Hs.33536; ESTs; TIMP,none; 4.40
 433895; AJ287912; Hs.3628; mitogen-activated protein kinase kinase kinase kinase 4; pkinase,zf-C4,CNH,ERM;TM=M; 4.40
 422034; AC006488; Hs.333069; Ets2 repressor factor; Ets;TM=M; 4.39
 444009; AJ380792; Hs.135104; ESTs; TNFR_c6,TIL,none; 4.39
 420020; BE295868; Hs.94382; adenosine kinase; ptkB;SS=M; 4.39
 416207; NM_014745; Hs.79077; Homo sapiens, clone MGC:2908, mRNA, complete cds; none;TM=Y;SS=M; 4.39
 417655; AA780791; Hs.14014; hypothetical protein FLJ14813; pkinase,pkinase_C;TM=M; 4.39
 402915; ; ENSP0000020587; Bicarbonate transporter-related protein BTR1; HCO3_cotransp;TM=Y; 4.39
 453199; AJ336266; Hs.32353; mitogen-activated protein kinase kinase kinase 4; pkinase;TM=M; 4.38
 416033; NM_012201; Hs.78979; Golgi apparatus protein 1; cys_rich_FGFR;TM=Y;SS=M; 4.38
 453672; U73531; Hs.34526; G protein-coupled receptor; 7tm_1;TM=Y;SS=M; 4.38
 437852; BE001836; Hs.256897; ESTs, Weakly similar to dJ365O12.1 [H.sapiens]; GPS,7tm_2;TM=Y; 4.38
 420039; NM_004605; Hs.94581; sulfotransferase family, cytosolic, 2B, member 1; Sulfotransfer;SS=M; 4.38
 412834; R77123; Hs.78881; Homo sapiens cDNA: FLJ23006 fis, clone LNG00414; 7tm_1,none; 4.38
 452203; X57522; ; transporter 1, ATP-binding cassette, sub-family B (MDR/TAP); ABC_tran,ABC_membrane,SRP54,Thymidylate_kin;TM=Y;SS=M; 4.37
 425317; AW205118; Hs.210546; Interleukin 21 receptor; none;TM=Y;SS=M; 4.37
 432945; AL043883; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 4.37
 424028; AF055084; Hs.153692; Homo sapiens cDNA FLJ14354 fis, clone Y79AA1001384, highly similar to Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA; none,none; 4.37
 434071; AF116653; Hs.34192; Homo sapiens PRO0823 mRNA, complete cds; none;TM=M; 4.37
 412596; AA161219; Hs.799; diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor); EGF;TM=Y;SS=M; 4.36
 440270; NM_015986; Hs.7120; cytokine receptor-like molecule 8; fn3;SS=M; 4.36

- 432987; A1864771; Hs.27954; CD86 antigen (CD28 antigen ligand 2, B7-2 antigen); none; TM=Y; SS=M; 4.36
- 436943; AA773838; Hs.5353; caspase 10, apoptosis-related cysteine protease; ICE_p10, ICE_p20, DED; TM=M; 4.36
- 457897; A1356125; Hs.345168; ESTs, Weakly similar to HXA2_HUMAN HOMEBOX PROTEIN HOX-A2 [H.sapiens]; homeobox; NA; NA; 4.36
- 406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte growth factor receptor); Sema, pkinase, TIG, PSI, none; 4.36
- 413959; X14034; Hs.75648; phospholipase C, gamma 2 (phosphatidylinositol-specific); SH2, SH3, C2, PH, PI-PLC-Y, PI-PLC-X, PDGF; SS=M; 4.35
- 408101; AW968504; Hs.123073; CDC2-related protein kinase 7; none, none; 4.35
- 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dependent); Man-6-P_recep; TM=M; SS=M; 4.35
- 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-related subfamily, beta member 2; aldo_ket_red, none; 4.35
- 438937; AW952654; Hs.244624; ESTs; EPH_1bd, pkinase, fn3, SAM, none; 4.35
- 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 2489 expressed sequence; none, lectin_c; 4.35
- 436540; BE397032; Hs.14468; hypothetical protein MGC14226; rrm, 7tm_1, SNF; TM=M; 4.34
- 435267; N23797; Hs.110114; ESTs; none, Syja_N, Exo_endo_phos; 4.34
- 405616; ; Target Exon; none, SH3, BAR; 4.34
- 432141; BE410964; Hs.272736; nuclear receptor binding protein; pkinase; TM=M; 4.33
- 417927; R73095; Hs.24122; ESTs; none, pkinase; 4.33
- 429849; U33053; Hs.2499; protein kinase C-like 1; pkinase, pkinase_C, HR1; TM=M; 4.33
- 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2; TM=Y; 4.33
- 453863; X02544; Hs.572; orosomucoid 1; lipocalin, aldedh, ubiquitin, IRK; SS=M; 4.33
- 400847; ; NM_003105; Homo sapiens sortilin-related receptor, L (DLR class) A repeats-containing (SORL1), mRNA; EGF, fn3, ldl_recept_a, ldl_recept_b, granulin, BNR; TM=Y; SS=M; 4.33
- 414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT, FATC, PI3_P4_kinase; TM=M; 4.33
- 413858; NM_001610; Hs.75589; acid phosphatase 2, lysosomal; acid_phosphat; TM=Y; SS=M; 4.33
- 442539; AL119506; Hs.58220; Homo sapiens cDNA: FLJ23005 fis, clone LNC00396, highly similar to AF055023 Homo sapiens clone 24723 mRNA sequence; RasGAP, adenylate kinase; 4.33
- 419607; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; IMP4; TM=M; 4.32
- 436703; AW880614; Hs.146381; RNA binding motif protein, X chromosome; rrm, SH3, PH, CH, RhoGEF; 4.32
- 414899; AW975433; Hs.36288; ESTs; pkinase, SH2, SH3, none; 4.32
- 444895; A1674383; Hs.22891; solute carrier family 7 (cationic amino acid transporter, y system), member 8; ASC, death, TNFR_c6; 4.31
- 415135; AW673559; Hs.78040; KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1; ER_lumen_recept, none; 4.31
- 444070; NM_015367; Hs.10267; MIL1 protein; Bcl-2; TM=Y; 4.31
- 422611; AA158177; Hs.118722; fucosyltransferase 8 (alpha (1,6) fucosyltransferase); SH3, K-box; TM=M; SS=Y; 4.31
- 437162; AW005505; Hs.5464; thyroid hormone receptor coactivating protein; bromodomain; TM=M; 4.30
- 440983; M20681; Hs.7694; solute carrier family 2 (facilitated glucose transporter), member 3; sugar_tr; TM=Y; SS=M; 4.30
- 414080; AA135257; Hs.47783; B aggressive lymphoma gene; A1pp; TM=M; 4.30
- 415072; BE253687; Hs.77876; Homo sapiens, clone IMAGE:3461982, mRNA, partial cds; Metallophos, Armadillo_seg; TM=M; 4.30
- 442994; A1026718; Hs.16954; ESTs; ank, pkinase, death, Ribosomal_S14; 4.30
- 432328; A1572739; Hs.195471; 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3; PGAM, 6PF2K; TM=M; 4.29
- 439490; AW249197; Hs.100043; ESTs, Weakly similar to A46302 PTB-associated splicing factor, long form [H.sapiens]; none; TM=M; 4.29
- 422005; BE266556; Hs.110702; Homo sapiens mRNA; cDNA DKFZp761E1212 (from clone DKFZp761E1212); none, Na_H_Exchange; 4.29
- 415214; A1445236; Hs.125124; EphB2; fn3, pkinase, SAM, EPH_1bd; TM=Y; SS=M; 4.29
- 430316; NM_000875; Hs.239176; insulin-like growth factor 1 receptor; fn3, Furin-like, pkinase, Recep_L_domain; TM=M; SS=M; 4.29
- 429099; BE439952; Hs.196177; phosphorylase kinase, gamma 2 (testis); pkinase, Bac_DNA_binding; TM=M; 4.29
- 425843; BE313280; Hs.159627; death associated protein 3; myb_DNA-binding, PAH, BAH, bromodomain, PHD, SET; TM=M; 4.28
- 437603; AW979259; Hs.293673; ESTs; death, none; 4.28
- 439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triphosphate pyrophosphatase); Ham1p_like; TM=M; 4.28
- 424512; X53002; Hs.149846; Integrin, beta 5; Integrin_B, EGF; TM=Y; SS=M; 4.28
- 442980; AA857025; Hs.8878; kinesin-like 1; kinesin, Luteo_ORF3, DUF164; TM=M; 4.28
- 420166; AW732276; Hs.95583; transmembrane 4 superfamily member (tetraspan NET-7); transmembrane4; TM=Y; SS=M; 4.27
- 409582; R27430; Hs.271565; ESTs; none, Neur_chan_LBD, Neur_chan_memb; 4.27
- 439096; AA830185; ESTs; ras, none; 4.27
- 414561; A1064813; Hs.195155; Homo sapiens amino acid transport system N2 (SN2) mRNA, complete cds; Aa_trans; TM=Y; 4.27
- 411835; U29343; Hs.72550; hyaluronan-mediated motility receptor (RHAMM); bZIP; SS=M; 4.27
- 428781; AF164789; Hs.193384; putative 28 kDa protein; pkinase, DAG_PE_bind, pkinase_C, OPR; SS=M; 4.27
- 430603; A148164; Hs.247280; HBV associated factor; zf-C3HC4, zf-RanBP, pkinase; 4.27
- 415149; X12451; Hs.78056; cathepsin L; Peptidase_C1; SS=M; 4.26
- 444838; AV651680; Hs.208558; ESTs; integrin_A, FG-GAP, none; 4.26
- 402328; ; Target Exon; pkinase; TM=M; 4.26
- 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none, none; 4.26
- 420942; H03514; Hs.15589; ESTs; none, pkinase; 4.26
- 453902; BE502341; Hs.3402; ESTs; none, none; 4.26
- 425505; ALO36458; ; gb:DKFZp564D2062_r1 564 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564D2062 5', mRNA sequence; arf, G-alpha, none; 4.26
- 427344; NM_000969; Hs.2142; 5-hydroxytryptamine (serotonin) receptor 3A; Neur_chan_LBD, Neur_chan_memb; TM=Y; SS=M; 4.26
- 432269; NM_002447; Hs.2942; macrophage stimulating 1 receptor (c-met-related tyrosine kinase); pkinase, Sema, PSI, TIG, A4_EXTRA; TM=M; SS=M; 4.26
- 417007; AF224741; Hs.80768; chloride channel 7; CBS, voltage_CLC; TM=Y; 4.26
- 447960; AW954377; Hs.26412; ring finger protein 26; zf-C3HC4; TM=Y; SS=M; 4.26
- 442300; A1765908; Hs.129166; ESTs; none; SS=M; 4.25
- 421856; NM_016447; Hs.108931; MAGUK protein p57; Protein Associated with Lins 2; SH3, PDZ, Guanylate_kin, L27; TM=M; 4.25
- 452110; T47667; Hs.28005; Homo sapiens cDNA FLJ11309 fis, clone PLACE1010076; pkinase, Activin_recp, none; 4.25
- 422451; AA310753; Hs.42491; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; PDZ, SH2, STAT, STAT_bind, STAT_prot, none; 4.25
- 453955; AW579207; Hs.304666; ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; fn3, jg, MAM, none; 4.25
- 457670; AF119666; Hs.23449; insulin receptor tyrosine kinase substrate; SH3; TM=M; 4.25
- 419133; U46116; Hs.89627; protein tyrosine phosphatase, receptor type, G; fn3_Y, phosphatase, carb_anhydrase, DSPc; TM=Y; SS=M; 4.25
- 419660; BE280337; Hs.194693; solute carrier family 7 (cationic amino acid transporter, y system), member 7; aa_permeases; TM=Y; SS=M; 4.25
- 415198; AW009480; Hs.943; natural killer cell transcript 4; none; TM=M; 4.24
- 416440; A1823912; Hs.79335; Homo sapiens, Similar to SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1, clone MGC:15280, mRNA, complete cds; SWIB; TM=M; 4.24
- 419169; AW851980; Hs.262346; ESTs, Weakly similar to S72482 hypothetical protein [H.sapiens]; none, spectrin, SH3, PH, CH; 4.24
- 449444; AW818436; Hs.23590; solute carrier family 16 (monocarboxylic acid transporters), member 4; none; TM=Y; SS=M; 4.24
- 433848; AF095719; Hs.93764; carboxypeptidase A4; Zn_carb_Opept_Propep_M14; SS=M; 4.24
- 442213; N36110; Hs.305971; solute carrier family 2 (facilitated glucose transporter), member 10; sugar_tr; TM=Y; SS=M; 4.24
- 412681; AW983555; Hs.172004; tlin; fn3, jg, SGXSG, pkinase; TM=M; 4.24
- 424653; AW977534; Hs.151469; calcium/calmodulin-dependent serine protein kinase (MAGUK family); none, none; 4.24
- 421066; AU076725; Hs.101408; branched chain aminotransferase 2, mitochondrial; aminotran_4; 4.23

- 428338; AF147765; Hs.232093; ESTs; fn2, C1MR; TM=M; SS=M; 4.23
 443329; BE262943; Hs.9234; hypothetical protein MGC1936; none; TM=Y; SS=M; 4.23
 432314; AA533447; Hs.312989; ESTs; Xlnk; none; 4.23
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none; TM=M; 4.23
 454166; AW993356; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3; TM=M; SS=M; 4.23
 442596; AJ457102; Hs.347970; Human glucose transporter pseudogene; none; none; 4.23
 442549; AJ751601; Hs.8375; TNF receptor-associated factor 4; MATH,zf-TRAF,zf-C3HC4; SS=M; 4.22
 424154; AF026004; Hs.141660; chloride channel 2; voltage_CLC,CBS,EPO,TPO,PC_rep; 4.22
 433418; AJ830342; Hs.211272; ESTs; transmembrane4; none; 4.22
 421921; H83363; Hs.6820; translocase of inner mitochondrial membrane 10 (yeast) homolog; zf-Tim10,DDP,ethand,CH,spectrin,serpin; TM=M; 4.22
 445633; AJ453386; Hs.17287; ESTs; Weakly similar to S26689 hypothetical protein hc1 - mouse [M.musculus]; IRK; none; 4.22
 424812; AF059252; Hs.153299; DOM-3 (C. elegans) homolog 2; none; TM=M; 4.22
 410668; BE379794; Hs.65403; hypothetical protein; death,TNFR_c6; TM=Y; SS=M; 4.22
 416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic acid transporters), member 6; none; none; 4.22
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3; TM=M; 4.21
 447200; BE543146; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA100383; none; none; 4.21
 400208; ; Eos Control; FCH,RhoGAP,SH3; TM=M; 4.21
 405369; ; NM_005569; Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA.; pkinase,LIM,PDZ; SS=M; 4.21
 445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase_2; TM=M; 4.21
 441208; AJ339704; Hs.150401; ESTs; Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ion_trans,RYDR,ITPR,MIR; none; 4.21
 427217; AA399272; Hs.144341; ESTs; ANP,GHMP_kinases; none; 4.21
 400845; ; NM_003105; Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA.; EGF,fn3,kd1_recept_e,ld1_recept_b,granulin,BNR; TM=Y; SS=M; 4.21
 422667; H25642; ESTs; FMO-like,FMO-like; 4.21
 450056; BE047394; Hs.8208; ESTs; Weakly similar to S71512 hypothetical protein T2 - mouse [M.musculus]; ABC_tran,ABC_membrane,Ig,MHC,il_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 4.20
 448950; AF286687; Hs.9275; CGA-152 protein; E1-E2,ATPase,Hydrolase; TM=Y; 4.20
 408634; AW407254; Hs.182278; calmodulin 2 (phosphorylase kinase, delta); none; none; 4.20
 422335; AA375957; Hs.6682; solute carrier family 7, (cationic amino acid transporter, y system) member 11; none; none; 4.20
 426754; NM_014264; Hs.172052; serine/threonine kinase 18; pkinase; TM=M; 4.20
 435810; BC349853; Hs.2785; keratin 17; zf-Tim10,DDP,SH2,SH3,pkinase,PH,BTK,Ribosomal_L44; 4.20
 446143; BE245342; Hs.306079; sec61 homolog; NUDIX,secY,E1_dehydrog,transket_pyr; TM=Y; SS=M; 4.20
 426626; AI124572; Hs.323879; inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma; zf-C2H2; TM=M; 4.20
 403716; ; Target Exon; Adap_comp_sub,PDZ,DEP,DIX,Dshavelled,hexapep,W2,ABC_tran; 4.19
 415749; BE262529; Hs.78771; phosphoglycerate kinase 1; PGK; none; 4.19
 434599; AB002313; Hs.3989; plexin B2; PSI,Sema,TIG; NA; 4.19
 412600; L28824; Hs.74101; spleen tyrosine kinase; SH2,pkinase; 4.19
 416738; N29218; Hs.40290; ESTs; ABC_tran,ABC_membrane; none; 4.19
 410639; BE269047; Hs.65234; hypothetical protein FLJ20598; DEAD,helicase_C,PRKAIIP3; TM=M; 4.19
 431385; BE178538; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; none; none; 4.19
 407305; AA715284; ; gb:nc35f03.r1 NCI_CGAP_Br5 Homo sapiens cDNA clone similar to contains Alu repetitive element.; mRNA sequence; pkinase,integrin_B,Sema,PSI,TIG; none; 4.18
 452880; AA029332; Hs.87549; ESTs; none; Integrin_B; 4.18
 428245; AF151048; Hs.183180; anaphase promoting complex subunit 11 (yeast APC11 homolog); none; SS=M; 4.18
 421964; X73079; Hs.288579; polymeric immunoglobulin receptor; ig,Cobalamin_bld; TM=M; SS=M; 4.18
 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase; TM=M; 4.18
 421790; AW896201; Hs.22654; sodium channel, voltage-gated, type I, alpha polypeptide; ion_trans,IQ,PEP-utilizers_C; TM=Y; 4.18
 429668; AA626142; Hs.179991; ESTs; Weakly similar to S28942 protein kinase C [H.sapiens]; none; none; 4.18
 443068; AI188710; ESTs; Endonuclease,pkinase,Activin_rec; none; 4.18
 418827; BE327311; Hs.47166; HT021; none; TM=M; 4.18
 447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine protease; ICE_p10,ICE_p20,DED; TM=M; 4.18
 429109; AL008637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3,OPR,PX; TM=M; 4.18
 422083; NM_001141; Hs.111256; arachidonate 15-lipoxygenase, second type; none; none; 4.18
 438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ; SS=M; 4.18
 413407; AJ356293; Hs.75339; inositol polyphosphate phosphatase-like 1; SH2,SAM,Exo_endo_phos; SS=M; 4.18
 424954; NM_000546; Hs.1846; tumor protein p53 (Li-Fraumeni syndrome); P53,W40,IRK; TM=M; 4.17
 421836; AF109219; Hs.108787; phosphatidylinositol glycan, class N; none; none; 4.17
 431544; AK000770; Hs.299329; Homo sapiens cDNA FLJ20763 fis, clone COL09911; none; none; 4.17
 413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase 1; CBS,IMP,PDH_C,IMP,PDH_N,NPD; TM=M; 4.17
 452012; AA307703; Hs.279766; kinesin family member 4A; kinesin,DNA_topoisol_V,K-box; TM=M; 4.17
 425606; U52112; Hs.158331; renin-binding protein; none; 4.16
 416817; AA398045; Hs.104679; ESTs; Furin-like,pkinase,Recap_L_domain,fn3; none; 4.16
 402447; ; C1000201:gi2044416[gb]AA02627.1 [L05195] fructose transporter [Rattus norvegicus] gl[44]; none; TM=Y; SS=M; 4.16
 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 1177 expressed sequence; Euk_porin; TM=M; SS=M; 4.15
 426395; BE151985; Hs.5722; hypothetical protein FLJ23316; pkinase; none; 4.15
 404140; ; NM_006510; Homo sapiens ret finger protein (RFP), transcript variant alpha, mRNA.; zf-C3HC4,SPRY,zf-B_box; SS=M; 4.15
 432268; BE311856; Hs.274230; 3'-phosphoadenosine 5'-phosphosulfate synthase 2; APS_kinase,ATP-sulfurylase; TM=M; 4.15
 405516; ; ENSP00000200457; Thyroid receptor interacting protein 6 (TRIP6) (OPA-interacting protein 1) (Zydn related protein 1) (ZRP-1); LIM; TM=M; 4.15
 448390; AL035414; Hs.21068; hypothetical protein; FGGY_C; TM=M; 4.15
 435732; AF229178; Hs.123136; leucine rich repeat and death domain containing protein; none; none; 4.15
 414108; AJ267592; Hs.75761; SFRS protein kinase 1; enk,PH,Oxysterol_BP,pkinase; TM=M; 4.15
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A receptor, pi; Neur_chan_LBD,Neur_chan_memb; TM=Y; SS=M; 4.14
 424339; BE257148; Hs.145416; endoglycan; none; TM=Y; SS=M; 4.14
 427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog; Ig,pkinase; TM=Y; SS=M; 4.14
 440524; R71284; Hs.16798; ESTs; SH3,Ig,pkinase,PH,spectrin,RhoGEF; none; 4.14
 436115; AW512033; Hs.102004; ESTs; pkinase; none; 4.14
 447050; NM_016314; Hs.17200; STAM-like protein containing SH3 and ITAM domains 2; SH3,VHS,UIM; SS=M; 4.14
 418529; AW005695; Hs.250897; TRK-fused gene; Band_41,ERNA,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164; TM=M; 4.14
 420727; H75701; Hs.99886; complement component 4-binding protein, beta; sush; SS=M; 4.14
 433075; NM_002959; ; sortilin 1; Exo_endo_phos,Atrophin-1,BNR,Kelch; TM=M; 4.14
 422783; AA598956; Hs.120439; ethanolamine kinase; Choline_kinase; TM=Y; 4.14
 410726; AJ623859; Hs.15936; ESTs; pkinase,pro_isomerase; none; 4.14

- 417903; NM_002342; Hs.1116; lymphotoxin beta receptor (TNFR superfamily, member 3); TNFR_c5; TM=M; SS=M; 4.14
 426307; W27393; Hs.183648; protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1; SAM,SH3,HS1_rep; 4.14
 442434; AA959787; Hs.129583; ESTs; IRK; none; 4.13
 438361; AA805666; Hs.146217; Homo sapiens cDNA: FLJ23077 fis, clone LNG05840; kinase, pkinase_C; none; 4.13
 445580; AF167572; Hs.12912; skbl (S. pombe) homolog; none; SS=M; 4.13
 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; ehand,kazal,arf,ras,7tm_1; TM=M; 4.13
 400252; ; NM_004651; Homo sapiens ubiquitin specific protease 11 (USP11), mRNA, substrate 1 (PTPNS1), mRNA; UCH-1,UCH-2; TM=M; 4.13
 446641; AL049229; Hs.15787; Homo sapiens mRNA; cDNA DKFp5564O1016 (from clone DKFp5564O1016); none, pkinase, PBD; 4.13
 400209; ; NM_001666; Homo sapiens Rho GTPase activating protein 4 (ARHGAP4), mRNA, VERSION NM_006083.2 Gt; FCH, RhoGAP, SH3; TM=M; 4.13
 429012; AW629596; Hs.194726; BCL2-associated athanogene 4; Sm, BAG; SS=M; 4.13
 411826; AW947946; Hs.26706; CGI-121 protein; none, DSPc; 4.13
 423189; M59371; Hs.171596; EphA2; fn3, pkinase, SAM, EPH_1b; TM=Y; SS=M; 4.12
 413934; U03056; Hs.75619; hyaluronoglucosaminidase 1; integrin_B, Glyco_hydro_56; SS=M; 4.12
 414874; D26351; Hs.77515; inositol 1,4,5-trisphosphate receptor, type 3; lon_trans, MIR, RYDR, JTPR; TM=Y; 4.12
 432047; NM_016247; Hs.272380; interphotoreceptor matrix proteoglycan 200; EGF, SEA; TM=Y; SS=M; 4.12
 451820; AW058357; Hs.199248; ESTs; 7tm_1; TM=Y; SS=M; 4.12
 445515; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457003, mRNA; zf-C2H2, BTB, K_1etra, WD40, Syntaxin; 4.12
 424539; L02911; Hs.150402; Activin A receptor, type I (ACVR1) (ALK-2); pkinase, Activin_rec; TM=M; SS=M; 4.12
 405110; ; C7000199; gij12643960[sp]Q9Y6T7[KDGB_HUMAN DIACYLGLYCEROL KINASE, BETA (DIGLYCERIDE KINASE); none, none; 4.12
 441026; AW179058; Hs.99858; ribosomal protein L7a; pkinase, LRR, LRRCT, Ribosomal_L7a; none; 4.11
 443142; AI695513; Hs.108705; protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform; HEAT, Vitalogenin_N, HEAT_PBS; SS=M; 4.11
 450505; NM_004572; Hs.25051; plakophilin 2; Armadillo_seg; TM=M; 4.11
 459601; AL044470; Hs.270604; ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; none, SH3, PGAM, UBA; 4.10
 417300; AI765227; Hs.55610; solute carrier family 30 (zinc transporter), member 1; Cation_efflux; TM=Y; SS=M; 4.10
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFp5564N0763 (from clone DKFp5564N0763); none, spectrin, SH3, PH, CH; 4.10
 416239; AL038450; Hs.48946; ESTs; E1-E2_ATPase, Cation_ATPase_C, Cation_ATPase_N, Hydrolase; none; 4.10
 429311; AF080157; Hs.198998; conserved helix-loop-helix ubiquitous kinase; pkinase; none; 4.10
 412146; M92444; Hs.73722; APEX nuclease (multifunctional DNA repair enzyme); Exo_endo_phos, Atrophin-1, BNR, Kelch; TM=M; 4.10
 418420; AW604405; Hs.324874; hypothetical protein MGC3079; Phosphodiesterase; TM=Y; 4.10
 434396; AA632270; Hs.162851; Homo sapiens cDNA FLJ14317 fis, clone PLACE3000401; pkinase; none; 4.10
 454438; AA224053; Hs.172405; cell division cycle 27; SPRY, 7tm_3, ANF_receptor; 4.10
 439578; AW263124; Hs.315111; nuclear receptor co-repressor/HDAC3 complex subunit; WD40; TM=M; 4.10
 451995; AI827431; Hs.224645; ESTs, Weakly similar to IF16_HUMAN GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 [H.sapiens]; none, PAAD_DAPIN_HIN; 4.10
 420340; NM_000734; Hs.97087; CD32 antigen, zeta polypeptide (TT3 complex); ITAM; TM=M; SS=M; 4.10
 442942; AW167087; Hs.131562; ESTs; pkinase; none; 4.09
 428187; AI687303; Hs.285529; G protein-coupled receptor 49; 7tm_1, none; 4.09
 418838; AW385224; Hs.35198; ecdonucleotide pyrophosphatase/phosphodiesterase 5 (putative function); Phosphodiesterase; TM=Y; SS=M; 4.09
 416445; AL043004; Hs.79337; KIAA0135 protein; pkinase, PAS; TM=M; 4.08
 427001; NM_006482; Hs.173135; dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2; pkinase; TM=M; 4.08
 403608; ; C3001199; gij7494834[sp]T15308 hypothetical protein B0286.2 - Caenorhabditis elegans [4]; 7tm_1, 7tm_2, GPS, WIF; TM=Y; SS=M; 4.08
 427177; AB006537; Hs.173880; interleukin 1 receptor accessory protein; Ig_TIR; TM=Y; SS=M; 4.08
 401241; AB028989; ; mitogen-activated protein kinase 8 interacting protein 3; Cys_knot, TGF-beta, vwa, vwc, wtd, DUF139; SS=M; 4.07
 444805; AB007899; Hs.12017; homolog of yeast ubiquitin-protein ligase Rsp5; potential epithelial sodium channel regulator; WW, HECT, RNA_pol_A; none; 4.07
 448886; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M; 4.06
 426006; R49031; Hs.22627; ESTs; pkinase, TBC; 4.06
 434521; NM_002267; Hs.3886; karyopherin alpha 3 (importin alpha 4); Armadillo_seg, IBB; TM=M; 4.06
 408761; AA057264; Hs.238936; ESTs, Weakly similar to (define not available 749684) [C.elegans]; 7tm_1, none; 4.05
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN_HIN; SS=M; 4.05
 413109; AW389845; Hs.110855; ESTs; PHO4; none; 4.05
 426457; AW894667; Hs.169965; chimerin (chimaerin) 1; DAG_PE-bind, RhoGAP, SH2; TM=M; 4.05
 435730; AB020635; Hs.4984; KIAA0828 protein; AdoHcyase, TrkA-N, 2-Hacid_DH_C, TM=M; 4.04
 429747; M87507; Hs.2490; caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase); CARD, ICE_p10, ICE_p20; SS=M; 4.04
 444378; R41339; Hs.12569; ESTs; Ig_pkinase, LRR, LRRNT, LRRCT; none; 4.04
 449843; R85337; Hs.24030; solute carrier family 31 (copper transporters), member 2; none; TM=Y; SS=M; 4.04
 427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone LNG00414; 7tm_1, none; 4.04
 413095; AA494359; Hs.30715; potassium voltage-gated channel, Isk-related family, member 3; none, START; 4.04
 418540; AI821597; Hs.90877; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ank, CAP_GLY, 7tm_1; 4.03
 442007; AA301116; Hs.142838; nucleolar phosphoprotein Nopp34; rm, IRK; SS=M; 4.02
 448659; AF191838; Hs.21712; TANK-binding kinase 1; pkinase; TM=M; 4.02
 412935; BE267045; Hs.75064; tubulin-specific chaperone c; none; 4.02
 414844; AA296874; Hs.77494; deoxyguanosine kinase; dNK; 4.02
 445817; NM_003642; Hs.13340; histone acetyltransferase 1; none; TM=M; 4.02
 426728; NM_007118; Hs.171957; triple functional domain (PTPRF interacting); SH3, Ig_pkinase, PH, spectrin, RhoGEF; TM=M; 4.02
 402676; AI434780; Hs.4248; vav 2 oncogene; RhoGEF, PH, CH, SH2, SH3, DAG_PE-bind, none; 4.02
 405102; ; C15001220; gij4469558[gb]AAD21311.1 [AF126008] breast cancer nuclear receptor-binding aux; DAG_PE-bind, PH, RhoGEF, DC1; SS=M; 4.02
 439964; AI732902; Hs.124652; Homo sapiens cDNA FLJ12376 fis, clone MAMMA1002494; pkinase; none; 4.01
 429680; AL035754; Hs.2474; toll-like receptor 1; LRR, LRRCT, TIR; TM=M; SS=M; 4.01
 453891; AB037751; Hs.36353; Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1035904; none, none; 4.01
 426535; AU077012; Hs.288582; ESTs, Weakly similar to ubiquitously TPR motif, Y isoform [H.sapiens]; Kunitz_BPTI, Kunitz_BPTI, 7tm_2, HRM; 3.99
 424232; AB015982; Hs.143460; protein kinase C, nu; pkinase, DAG_PE-bind, PH; TM=M; 3.99
 408308; AL033377; Hs.44197; hypothetical protein DKFp5564O0462; none, none; 3.98
 449517; AW500106; Hs.23643; serine/threonine protein kinase MASK; pkinase; TM=M; 3.98
 404185; ; Target Exon; sugar_tr; TM=Y; SS=M; 3.98
 441226; BE563042; Hs.118820; Homo sapiens, Similar to RIKEN cDNA 0610012G03 gene, clone MGC:14132, mRNA, complete cds; none; TM=M; 3.98
 429638; AI916662; Hs.211577; kinesin 1 (kinesin receptor); bZIP, Tropomyosin, spectrin, LBP, BPI, CETP, B56; TM=Y; SS=M; 3.97
 417386; AL037228; Hs.82043; D123 gene product; NUDIX_secY, E1_dehydro, transket_pyr; TM=Y; SS=M; 3.97
 452721; AJ289529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate transporter), member 1; MORN, sugar_tr; TM=Y; SS=M; 3.96
 417183; J52089; Hs.172717; ESTs; pkinase, LRRCT, Ig, LRR, LRRNT; none; 3.95
 439176; AI446444; Hs.190394; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; none; TM=M; 3.94
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank, pkinase; TM=M; 3.94
 422610; AF153820; Hs.1547; potassium inwardly-rectifying channel, subfamily J, member 2; IRK; TM=Y; 3.94

- 450746; D82673; Hs.278589; general transcription factor II, ϵ ; none,SH3,PK; 3.94
 418516; NM_005218; Hs.85701; phosphoinositide-3-kinase, catalytic, alpha polypeptide; PI3_P14_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B;none; 3.94
 414217; AJ309298; Hs.278898; Homo sapiens cDNA: FLJ23165 fis, clone LNG0846; none,NA,NA; 3.93
 416537; T99086; Hs.144904; nuclear receptor co-repressor 1; myb_DNA-binding, RNA_pol_A; none; 3.93
 5 450747; AI064821; Hs.318535; ESTs, Highly similar to 1818357A EWS gene [H.sapiens]; mm,zf-RanBP,GAS2; 3.93
 444825; AW167613; ; mitogen-activated protein kinase kinase kinase 8; pkinase,TM=M; 3.93
 408354; AJ382803; Hs.159235; ESTs; none,none; 3.93
 453945; NM_005171; Hs.36908; activating transcription factor 1; mm,zf-RanBP,pkinase,GST_C,Ets,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFIIIS,AT_hook,SAM;TM=M; 3.93
 10 428532; AF157326; Hs.184786; TBP-interacting protein; Armadillo_seg,VHS,HEAT;TM=M; 3.92
 413957; AW204431; Hs.117853; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; Armadillo_seg,IBB,PHD,DOT;none; 3.91
 415905; AI751357; Hs.288741; Homo sapiens cDNA: FLJ22256 fis, clone HRC02860; Ephrin;none; 3.91
 450139; AK001838; Hs.296323; serum/glucocorticoid regulated kinase; none,none; 3.91
 440255; AI932285; Hs.160569; ESTs; none,pkinase; 3.90
 15 421077; AK000061; Hs.101590; hypothetical protein; ank,pkinase,death,SPRY,SAP,Ribosomal_L24a,SRP54,dDENN,DENN,uDENN;TM=M; 3.90
 433211; H11850; Hs.12808; MARK; pkinase,UBA,KA1,SS=M; 3.90
 433233; AB040927; Hs.301804; KIAA1494 protein; SH3,zf-C3HC4;TM=M; 3.90
 419609; NM_013272; Hs.270379; gb:HSU46415 Human pancreatic cancer cell line Patu 89881 Homo sapiens cDNA clone xs476, mRNA sequence; PWWP;none; 3.90
 20 433198; AA992841; Hs.27263; KIAA1458 protein; none,none; 3.89
 407721; Y12735; Hs.38018; dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3; pkinase;TM=M; 3.89
 427657; AV652249; Hs.180107; polymerase (DNA directed), beta; none;TM=M; 3.89
 453035; AV581943; Hs.334; Rho guanine nucleotide exchange factor (GEF) 5; none,none; 3.89
 446329; NM_013272; Hs.14805; solute carrier family 21 (organic anion transporter), member 11; kazal,OATP_N,OATP_C;TM=Y;SS=M; 3.89
 25 429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone;TM=M; 3.88
 432074; AA525248; Hs.149723; ESTs; Y_phosphatase;none; 3.88
 435143; R12375; Hs.194600; ESTs; SH3,Ig,pkinase,PH,spectrin,RhoGEF;none; 3.87
 423198; M81933; Hs.1634; cell division cycle 25A; Rhodanese;none; 3.87
 428474; AB023182; Hs.184523; KIAA0965 protein; pkinase;TM=M; 3.87
 30 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT2RP2002066, highly similar to Rattus norvegicus transmembrane receptor Unc5H2 mRNA; death,ZU5;SS=M; 3.86
 415457; AW081710; Hs.7369; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; MORN,sugar_tr;TM=Y;SS=M; 3.86
 447061; D86954; Hs.17211; dedicator of cyto-kinesis 2; SH3;TM=M; 3.86
 35 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; PAC,PAS;TM=M; 3.86
 451961; NM_003800; Hs.27345; RNA guanylyltransferase and 5'-phosphatase; mRNA_cap_enzyme,DSPc,DNA_ligase,mRNA_cap_C;TM=M; 3.86
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-receptor type 2; Y_phosphatase;TM=Y; 3.86
 446874; AW968304; Hs.56156; ESTs; none,RGS; 3.85
 418630; AI351311; Hs.251946; poly(A)-binding protein, cytoplasmic 1-like; pkinase;none; 3.85
 40 416140; AI918035; Hs.301198; roundabout (axon guidance receptor, Drosophila) homolog 1; none,none; 3.85
 425474; Z48054; Hs.158084; peroxisome receptor 1; TPR;TM=M; 3.85
 413073; AL038165; Hs.157187; translocase of outer mitochondrial membrane 20 (yeast) homolog; MAS20,zf-A20,VPS9;TM=M;SS=M; 3.85
 411770; NM_014278; Hs.71992; heat shock protein (hsp110 family); HSP70;TM=M; 3.84
 428782; X12830; Hs.193400; interleukin 6 receptor; fn3,Ig;TM=Y;SS=M; 3.84
 45 450684; AA82605; Hs.25333; interleukin 1 receptor, type II; Ig;TM=Y;SS=M; 3.84
 433376; A249361; Hs.74122; caspase 4, apoptosis-related cysteine protease; CARD,ICE_p10,ICE_p20;SS=M; 3.83
 440332; AI218517; Hs.188051; ESTs; fn3,pkinase,SAM,EPH_rbd;none; 3.83
 445803; AV655264; Hs.4283; ESTs; pkinase,RGS,PH,myosin_head,Myosin_tail; 3.83
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3,RhoGAP,FCH;TM=M; 3.83
 414991; C17898; gb:C17898 Human placenta cDNA (Tfujwara) Homo sapiens cDNA clone GEN-554E10 5', mRNA sequence; Zip;none; 3.83
 50 423067; AA321355; Hs.285401; colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage); fn3;TM=Y;SS=M; 3.82
 419088; AI538323; Hs.62620; integrin, beta 8; integrin_B;none; 3.82
 411704; AI499220; Hs.71573; hypothetical protein FLJ10074; pkinase;TM=M; 3.82
 459346; AW510557; Hs.258016; EST; none;TM=M; 3.82
 445330; RS2656; Hs.21691; ESTs; 7tm_1;none; 3.82
 55 451452; BE560055; Hs.26433; dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminophosphotransferase 1 (GlcNAc-1-P transferase); Glycos_transf_4;TM=Y;SS=M; 3.81
 405545; ; Target Exon; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 3.81
 448165; NM_005591; Hs.20555; meiotic recombination (S. cerevisiae) 11 homolog B; Metallophos,Ribosomal_L15e;SS=M; 3.81
 60 416305; AU076628; Hs.79187; coxsackie virus and adenovirus receptor; Ig;TM=Y;SS=M; 3.80
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate transporter), member 1; PHO4,UIM;TM=M; 3.80
 421684; BE281591; Hs.106768; hypothetical protein FLJ10511; Armadillo_seg;SS=M; 3.80
 438581; AW977768; Hs.292133; ESTs, Moderately similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; pkinase,RIO1;none; 3.79
 439199; R40373; Hs.26299; ESTs; ion_trans;none; 3.78
 450931; N25156; Hs.25648; tumor necrosis factor receptor superfamily, member 5; TNFR_c6;TM=Y;SS=M; 3.78
 65 417691; AU076610; Hs.82399; low density lipoprotein receptor defect C complementing; none;SS=M; 3.78
 430355; NM_006219; Hs.239818; phosphoinositide-3-kinase, catalytic, beta polypeptide; PI3_P14_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B;TM=M; 3.78
 448119; H38587; Hs.346509; dedicator of cyto-kinesis 1; none;TM=Y; 3.78
 442013; AA506476; Hs.10600; Human DNA sequence from clone RP11-353C18 on chromosome 20 Contains ESTs, STSs, GSSs and CpG islands. Contains the NIFS gene for cysteine desulfurase, two genes for novel proteins and the gene for the splicing factor CC1.3 with a second isoform (CC1.; none,none; 3.77
 70 425481; AW978162; Hs.18571; ESTs; none,Oxysterol_BP; 3.77
 411411; AA345241; Hs.55950; ESTs, Weakly similar to KIAA1330 protein [H.sapiens]; RNA_pol_A,Ig,MHCK_EF2_kinase;SS=M; 3.77
 426866; U02330; Hs.172816; neuregulin 1; Peptidase_M49,EGF,Ig,Neuregulin;TM=M; 3.77
 430395; D49742; Hs.241363; hyaluronan-binding protein 2; ank,death,ZU5,EGF,kringle,bypsin,Nebulin,UIM;SS=M; 3.77
 434398; AA121058; Hs.3838; serum-inducible kinase; pkinase,POLO_box;TM=M; 3.77
 75 415485; AW272990; Hs.18571; ESTs; none,Oxysterol_BP; 3.76
 453226; AA641926; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme 1; HATPase_c;none; 3.76
 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase,RIO1;TM=M; 3.76
 424842; AA034127; Hs.153487; signal transducing adaptor molecule (SH3 domain and ITAM motif) 1; SH3,VHS,UIM;TM=M; 3.75
 426500; NM_014638; Hs.170156; KIAA0450 gene product; C2,P1-PLC-Y;TM=M; 3.75
 80 419952; AK000967; Hs.93872; KIAA1682 protein; none;TM=M; 3.75
 425424; NM_004954; Hs.157199; ELK1 motif kinase; pkinase,UBA,KA1;TM=M; 3.75
 431696; AA259068; Hs.267819; protein phosphatase 1, regulatory (inhibitor) subunit 2; none;SS=M; 3.75

- 444184; T87841; Hs.282990; Human DNA sequence from clone RP1-28H20 on chromosome 20q13.1. Contains part of a gene for a novel protein similar to membrane transport proteins, the 5' end of a novel gene. ESTs, STSs, GSSs and three CpG islands; pkinase, RIO1, APH, KOW; TM=M; 3.75
- 405411; ; ENSP0000025213; SODIUM BICARBONATE COTRANSPORTER; none; TM=Y; SS=M; 3.75
- 405602; ; Target Exon; pkinase; SS=M; 3.75
- 429355; AW973253; Hs.292689; ESTs; pkinase, bZIP, Armadillo_seg, none; 3.75
- 430153; AW968128; Hs.336679; ESTs; pkinase, none; 3.74
- 414180; AJ863304; Hs.120905; Homo sapiens cDNA FLJ11448 fis, clone HEMBA1001391; P13_P14_kinase, P13Ka, P13K_C2, P13K_rbd, P13K_p85B, none; 3.74
- 432236; AA531132; ; gb:u47h06.s1 NCI_CGAP_P9 Homo sapiens cDNA clone, mRNA sequence; pkinase, none; 3.74
- 433390; AA586950; Hs.260180; Homo sapiens mRNA; cDNA DKFZp761G18121 (from clone DKFZp761G18121); complete cds; none, spectrin, SH3, PH, CH; 3.74
- 426485; NM_006207; Hs.170040; platelet-derived growth factor receptor-like; ig; SS=M; 3.74
- 408414; AI114688; Hs.17998; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; fn3, Ig; TM=Y; SS=M; 3.73
- 409793; AI825463; Hs.147996; protein kinase, X-linked; pkinase, pkinase_C; TM=M; 3.73
- 412456; T32689; Hs.7859; ESTs; BAG, none; 3.73
- 407894; AJ278313; Hs.41143; phosphoinositide-specific phospholipase C-beta 1; C2, PI-PLC-Y, PI-PLC-X; TM=M; 3.73
- 442229; AI885776; Hs.8164; Multibrey nanism; MATH, DENN, GRAM, zf-B_box, dDENN, uDENN; SS=M; 3.73
- 450151; AJ088196; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA sequence; ig, pkinase, none; 3.72
- 408331; NM_007240; Hs.44229; dual specificity phosphatase 12; DSPC; TM=M; 3.72
- 417821; BE245149; Hs.82643; protein tyrosine kinase 9; coflin, ADF; SS=M; 3.72
- 403391; ; C3001164; [gl]1730196[sp]P50573[3]GAR3_RAT GAMMA-AMINOBUTYRIC-ACID RECEPTOR RHO-3 SUBUNIT PRE; none; TM=Y; 3.72
- 417527; AA203524; ; gb:z56e10.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone 5', mRNA sequence; SH3; SS=M; 3.71
- 428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase); pkinase; TM=M; 3.71
- 428180; AI129767; Hs.182874; guanine nucleotide binding protein (G protein) alpha 12; G-alpha, arf; TM=M; 3.71
- 422127; AW504286; Hs.112049; SET binding factor 1; dDENN, DENN, GRAM, PH; SS=M; 3.70
- 430570; AI147881; Hs.292464; ESTs; 7tm_2, Fz, Fritzed, none; 3.70
- 452561; AI692181; Hs.49169; KIAA1634 protein; TPR, PDZ, WW, Guanylate_kin; TM=M; 3.69
- 432336; NM_002759; Hs.274382; protein kinase, interferon-inducible double stranded RNA dependent; dsrm, pkinase; TM=M; 3.69
- 419945; AW290975; Hs.118923; ESTs; SH3, PDZ, Guanylate_kin, transferrin; 3.69
- 426539; AB011155; Hs.170290; discs, large (Drosophila) homolog 5; SH3, PDZ, Guanylate_kin; TM=M; 3.68
- 436534; AA721628; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; Ig; TM=Y; SS=M; 3.68
- 407202; N58172; Hs.109370; ESTs; F5_F8_type_C, pkinase, Els, none; 3.67
- 420297; AI628272; Hs.88323; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; pkinase, TUDOR, none; 3.67
- 417863; AB000450; Hs.82771; vaccinia related kinase 2; pkinase; TM=M; 3.67
- 425304; AA463844; Hs.31339; fibroblast growth factor 11; FGF, Neur_chan_LBD, Neur_chan_memb, none; 3.67
- 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4; TM=Y; SS=M; 3.67
- 419511; AA429750; Hs.75113; general transcription factor IIIA; Glypican, none; 3.66
- 424315; AW614850; Hs.193384; putative 28 kDa protein; none, none; 3.66
- 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase; TM=M; 3.66
- 425838; NM_014071; Hs.159613; nuclear receptor coactivator RAP250; peroxisome proliferator-activated receptor interacting protein; thyroid hormone receptor binding protein; none; TM=M; 3.65
- 446983; AA157484; Hs.97199; complement component C1q receptor; EGF, lectin_c, Tissue_fac, Xlink, TIL; TM=Y; SS=M; 3.65
- 434350; AL042940; Hs.93872; KIAA1682 protein; none, none; 3.65
- 457317; AA683016; Hs.12210; hypothetical protein FLJ13732 similar to tensin; SH2; TM=M; 3.65
- 434416; AA805903; Hs.59498; cell division cycle 2-like 5 (cholinesterase-related cell division controller); pkinase, none; 3.65
- 410174; AA306007; Hs.59461; DKFZP434C245 protein; none, DSPC; 3.65
- 423598; BE247600; Hs.155538; ESTs; 7tm_1; TM=Y; SS=M; 3.65
- 440861; BE244115; Hs.7482; KIAA0682 gene product; rm, Guanylate_kin; TM=M; 3.64
- 454954; AW993013; Hs.49169; KIAA1634 protein; TPR, PDZ, WW, Guanylate_kin; TM=M; 3.64
- 430250; NM_016929; Hs.283021; chloride intracellular channel 5; none; TM=M; 3.64
- 450587; AI828854; Hs.258538; stratin, calmodulin-binding protein; pkinase, WD40; TM=Y; 3.64
- 424893; AW295112; Hs.153548; Homo sapiens cDNA FLJ13303 fis, clone OVARC1001372, highly similar to Homo sapiens liprin-alpha4 mRNA; SAM; SS=M; 3.64
- 425645; AA361027; ; gb:EST70242 T-cell lymphoma Homo sapiens cDNA 5' end, mRNA sequence; HMG_box, DNA_mis_repair, HATPase_c, none; 3.64
- 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF, laminin_Nterm, Integrin_B; SS=M; 3.63
- 451292; AB037716; Hs.26204; KIAA1295 protein; SH3; TM=M; 3.63
- 412314; AA825247; Hs.250899; heat shock factor binding protein 1; 7tm_1; TM=Y; SS=M; 3.63
- 418303; AA215701; Hs.186541; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; eIF5, eIF2B, VV2, pkinase, UBA, KA1; 3.63
- 452716; AI914925; Hs.222240; ESTs; SH2, STAT, STAT_bind, STAT_pro, none; 3.63
- 403869; ; NM_004520; Homo sapiens kinesin heavy chain member 2 (KIF2), mRNA member 3 (KCNQ3), mRNA; kinesin; TM=M; 3.63
- 450377; AB033091; Hs.74313; KIAA1265 protein; Zip; TM=M; SS=M; 3.63
- 417793; AW405434; Hs.82575; small nuclear ribonucleoprotein polypeptide B; rm; TM=M; 3.63
- 404942; U30825; ; splicing factor, arginine/serine-rich 9; CD36; TM=Y; SS=M; 3.63
- 429554; NM_012275; Hs.207224; Interleukin 1, delta; IL1; TM=M; 3.63
- 417871; AA521368; Hs.24252; ESTs; IBB, Armadillo_seg, none; 3.62
- 437672; AW748265; Hs.5741; flavohemoprotein b57; heme_1, NAD_binding, lipoygenase, FAD_binding_6; TM=M; 3.62
- 438698; AW297855; Hs.125815; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; lipoygenase, PLAT, none; 3.62
- 447217; BE465754; Hs.17778; neuropilin 2; CUB, MAM, F5_F8_type_C; TM=M; SS=M; 3.61
- 407961; AW672939; Hs.41694; origin recognition complex, subunit 2 (yeast homolog)-like; none, pkinase, pro_Isomerase; 3.61
- 428840; M15990; Hs.194148; v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1; SH2, SH3, pkinase; SS=M; 3.61
- 455608; BE011437; ; gb:CM4-BN0220-080500-170-f03 BN0220 Homo sapiens cDNA, mRNA sequence; none, CDK5_activator; 3.61
- 407748; AL079409; Hs.38176; KIAA0606 protein; SCN Circadian Oscillatory Protein (SCOOP); PP2C, LRR, PH; TM=M; 3.60
- 421474; U76362; Hs.104637; solute carrier family 1 (glutamate transporter), member 7; SDF; TM=Y; SS=M; 3.60
- 449987; AW079749; Hs.184719; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ABC_tran, ABC_membrane, ion_trans; 3.60
- 403142; ; NM_002706; Homo sapiens protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform (PPM1B), mRNA; PP2C; TM=M; 3.60
- 400844; ; NM_003105; Homo sapiens sortilin-related receptor, (LDLR class) A repeats-containing (SORL1), mRNA; EGF, fn3, jld_recept_a, jld_recept_b, granulin, BNR; TM=Y; SS=M; 3.59
- 450152; AI138635; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA sequence; ig, pkinase, none; 3.59
- 429782; NM_005754; Hs.220689; Ras-GTPase-activating protein SH3-domain-binding protein; rm, NTF2; TM=M; 3.59
- 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none; SS=M; 3.59
- 437400; AB011542; Hs.5599; EGF-like-domain, multiple 5; TNFR, c6, laminin_EGF; TM=Y; 3.58
- 426797; AW938258; Hs.342849; ADP-ribosylation factor-like 5; arf, Ca_channel_B, SH3; 3.58
- 431170; AW971246; Hs.291022; ESTs; LRR, CARD, none; 3.58
- 434542; AA769310; Hs.61260; hypothetical protein FLJ13164; PH, Oxysterol_BP; TM=M; SS=M; 3.58

- 420181; A1380089; Hs.158951; ESTs; none;lg, pkinase, LRR, LRRCT; 3.57
 450572; A1700863; Hs.202494; Homo sapiens cDNA FLJ13245 fis, clone OVARC1000681; Na_sulph_symp; none; 3.57
 433618; AA602539; Hs.345494; ESTs; G-alpha_A_deaminase; 3.57
 452695; AW780199; Hs.30327; mitogen-activated protein kinase-activated protein kinase 5; pkinase; none; 3.57
 418512; AW498974; ; diacylglycerol kinase, zeta (104kD); ras; none; 3.57
 451752; AB032997; Hs.26566; KIAA1171 protein; ATP-synt_C, TBC; TM=Y; SS=M; 3.57
 417129; A1381800; Hs.300684; calcitonin gene-related peptide-receptor component protein; none; none; 3.57
 449474; AA019344; Hs.2055; ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing); ThiF, UBACT, pkinase, UCH-2, UCH-1, mn, zf-C2H2, zf-RanBP, G-patch; 3.57
 412124; H43378; Hs.288550; Homo sapiens cDNA: FLJ23156 fis, clone LNG09609; none; none; 3.56
 435021; AA922192; Hs.54709; ESTs; EPH_bdb, pkinase, fn3, SAM; none; 3.56
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit, alpha type, 4; proteasome; TM=M; 3.56
 437387; A1198874; Hs.28847; AD026 protein; none; 7tm_1, WD40; 3.56
 422583; AA10508; Hs.27973; KIAA0874 protein; ank, G-alpha; TM=M; 3.56
 452102; U04343; Hs.27954; CD86 antigen (CD28 antigen ligand 2, B7-2 antigen); none; TM=Y; SS=M; 3.56
 420112; NM_005109; Hs.95220; oxidative-stress responsive 1; pkinase; TM=M; 3.55
 437639; AA827712; Hs.291880; ESTs; SH3; none; 3.55
 457500; NM_002759; Hs.274382; protein kinase, interferon-inducible double stranded RNA dependent; dsrm, pkinase; TM=M; 3.55
 415660; A1909007; Hs.78563; ubiquitin-conjugating enzyme E2G 1 (homologous to C. elegans UBC7); UQ_con; TM=M; 3.55
 423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase, PBD; TM=M; 3.55
 428727; AF078847; Hs.191356; general transcription factor IiH, polypeptide 2 (44kD subunit); PHO4, LIM; TM=M; 3.55
 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase, pkinase_C, HR1; TM=M; 3.55
 408683; R58665; Hs.46847; TRAF and TNF receptor-associated protein; Exo_endo_phos; TM=M; 3.55
 412350; A1659305; Hs.73826; protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte); Y_phosphatase, Band_41, PDZ; TM=M; 3.55
 446742; AA232119; Hs.16085; putative G-protein coupled receptor; none; TM=Y; SS=M; 3.55
 427283; AL119796; Hs.174185; ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin); Sulfatase, Somatomedin_B, Phosphodiesterase, Endonuclease; TM=M; SS=Y; 3.55
 414888; AL039185; Hs.77558; thyroid hormone receptor interactor 7; HMG14, 17; none; 3.55
 424848; A1263231; Hs.327090; EST; SH3, PDZ, Guanylate_kin; none; 3.54
 402704; ; C1001099; gijl6005896[ref]NP_009101.1 testis-specific protein kinase 2 [Homo sapiens] gij4; none; none; 3.54
 444099; D87432; Hs.10315; solute carrier family 7 (cationic amino acid transporter, y system), member 6; aa_permeases; TM=Y; SS=M; 3.54
 429687; A1675749; Hs.211608; nucleoporin 153kD; zf-RanBP, Integrin_B; TM=M; 3.53
 413879; AA132961; Hs.212533; Homo sapiens cDNA: FLJ22572 fis, clone HSI02313; none; none; 3.53
 431045; AW968560; Hs.301957; nudix (nucleoside diphosphate linked moiety X)-type motif 5; NUDIX, secY, E1_dehydrog, transket_pyr; TM=Y; SS=M; 3.53
 423855; AA331761; Hs.254859; ESTs; none; pkinase, UQ_con, vwa, FG-GAP, Integrin_A; 3.53
 440682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin, bZIP; TM=M; 3.52
 410686; A1733735; Hs.114905; IRE1, S. cerevisiae, homolog of; pkinase, Bacterial_PQ; TM=M; SS=M; 3.52
 449810; AB008681; Hs.23994; activin A receptor, type IIB; pkinase, Activin_rec; TM=Y; SS=M; 3.52
 418755; Y14443; Hs.88219; zinc finger protein 200; zf-C2H2, zf-BED; TM=M; 3.52
 448804; AW512213; Hs.342849; ADP-ribosylation factor-like 5; arf, Ca_channel_B, SH3; 3.52
 438507; AA809052; Hs.182018; ESTs; none; none; 3.52
 456559; A1336273; Hs.102548; glucocorticoid receptor DNA binding factor 1; none; PAS; 3.51
 410054; AL120050; Hs.58220; Homo sapiens cDNA: FLJ23005 fis, clone LNG00396, highly similar to AF055023 Homo sapiens clone 24723 mRNA sequence; RasGAP, adenylatekinase; 3.51
 422321; AA906427; Hs.181035; hypothetical protein MGC11296; none; TM=M; 3.51
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; SH2, PH; TM=M; 3.50
 407393; AB038237; ; gb: Homo sapiens mRNA for G protein-coupled receptor CSL2, complete cds.; 7tm_1; TM=Y; SS=M; 3.50
 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine protease; pkinase, ICE_p10, ICE_p20; TM=M; SS=M; 3.50
 420673; AB008112; Hs.99847; peroxisome biogenesis factor 1; AAA_APS_kinase; TM=M; SS=M; 3.49
 424663; NM_002351; Hs.151544; SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome); SH2; TM=M; 3.49
 429327; AA283981; Hs.199248; prostaglandin E receptor 4 (subtype EP4); 7tm_1; TM=Y; SS=M; 3.49
 400178; ; Eos Control; none, Somatomedin_B; 3.49
 439549; AW937885; Hs.137314; ESTs; SH2; none; 3.49
 436345; AA873008; Hs.121572; ESTs; CARD, BIR, zf-C3HC4, CARD, BIR, zf-C3HC4; 3.49
 427658; H61387; Hs.30868; nogo receptor; LRR, LRRNT, LRRCT; SS=M; 3.48
 402833; ; C1002508; gijl6691937[emb]CAB65797.1 (AL096770) bA150A6.2 (novel 7 transmembrane receptor; none; none; 3.48
 442363; A1337304; Hs.23120; PI3K; fn3, pkinase, PDZ, DUF139; TM=Y; SS=M; 3.48
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 non-catalytic subunit; none; TM=M; 3.47
 417971; Y08991; Hs.83050; phosphoinositide-3-kinase, regulatory subunit 4, p150; pkinase, WD40, HEAT; SS=M; 3.47
 432169; Y08971; Hs.2910; phosphoribosyl pyrophosphate synthetase 2; Pribosyltran; 3.47
 447425; A1963747; Hs.18573; acylphosphatase 1, erythrocyte (common) type; Acylphosphatase; SS=M; 3.47
 427231; AW851989; Hs.285814; sprouty (Drosophila) homolog 4; SH2, SH3; TM=M; SS=M; 3.46
 401851; ; NM_002401*Homo sapiens mitogen-activated protein kinase kinase 3 (MAP3K3), mRNA.; pkinase; SS=M; 3.46
 407877; AW016811; Hs.234478; Homo sapiens cDNA: FLJ22648 fis, clone HSI07329; pkinase, pkinase_C; none; 3.45
 432279; N95104; Hs.274260; ATP-binding cassette, sub-family C (CFTR/MRP), member 6; ABC_tran, ABC_membrane; none; 3.45
 437103; AW139408; Hs.152940; ESTs; Choline_kinase; none; 3.45
 420338; AA825595; Hs.88269; Homo sapiens, clone MGC:17339, mRNA, complete cds.; 7tm_1; TM=Y; SS=M; 3.44
 422209; AF005210; Hs.113222; chemokine (C-C motif) receptor 8; 7tm_1, 7tm_2; TM=Y; SS=M; 3.44
 410781; A1375672; Hs.165028; ESTs; pkinase, laminin_N, Nterm, laminin_EGF, cyclin, F-box, cyclin_C, serpin, ATP-synt_C; 3.44
 437286; AA350994; Hs.20281; KIAA1700; Rhodanese, DSPC; TM=M; 3.43
 419855; A1935182; Hs.144139; ESTs; zf-C3HC4, UBA, Cbl_N, Cbl_N2, Cbl_N3, zf-C3HC4, UBA, Cbl_N, Cbl_N2, Cbl_N3; 3.43
 433336; AF017986; Hs.31386; secreted frizzled-related protein 2; Fz_NTR; SS=M; 3.43
 428483; A1908539; Hs.184592; KIAA0344 gene product; none; none; 3.43
 445119; AF035121; Hs.12337; kinase insert domain receptor (a type III receptor tyrosine kinase); lg, pkinase; TM=Y; SS=M; 3.42
 454468; A1590319; Hs.19122; eukaryotic translation initiation factor 4E-like 3; none, Neur_chan_LBD, Neur_chan_membr, JF4E; 3.42
 410386; W26187; Hs.3327; Homo sapiens cDNA: FLJ22219 fis, clone HRC01637; pkinase, Guanylate_kin, PDZ, SH3, L27; none; 3.42
 422907; A1879263; Hs.77273; Human glucose transporter pseudogene; none; none; 3.42
 449816; A1701457; Hs.38694; ESTs; SET, BAH, PK, PK_C; 3.42
 440074; AA863045; Hs.10569; ESTs; Weakly similar to T00050 hypothetical protein KIAA0400 [H.sapiens]; SH3, ank, tubulin-binding, ArfGap, PH; TM=M; SS=M; 3.42
 425475; W56339; Hs.107057; ESTs; pkinase; none; 3.42
 401242; AB028989; ; mitogen-activated protein kinase 8 interacting protein 3; Cys_knot, TGF-beta, vwa, vwc, vwd, TIL, DUF139; SS=M; 3.41
 429276; AF056085; Hs.198612; G protein-coupled receptor 51; 7tm_3, ANF_receptor, bZIP; TM=Y; 3.41
 445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase, type I, 107kD; none; none; 3.41
 410908; AA121686; Hs.10592; ESTs; GTP_EFTU, GTP_EFTU_D3, GTP_EFTU_D2; none; 3.41

- 452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor type, E; Y_phosphatase:none; 3.40
 447898; AW969638; Hs.112318; 6.2 kd protein; none:none; 3.40
 450402; BE218027; Hs.89989; ESTs; SH3:none; 3.40
 441466; AW673081; Hs.54828; ESTs; pkinase,zf-C2H2,KRAB:none; 3.40
 408546; W49512; Hs.46348; bradykinin receptor B1; 7tm_1;TM=Y;SS=M; 3.40
 410927; T77635; ; gb:yc91h06.r1 Soares infant brain 1N1B Homo sapiens cDNA clone 5', mRNA sequence; none:none; 3.40
 409546; AW161391; Hs.709; deoxycytidine kinase; dNK;SS=M; 3.39
 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ12425 fis, clone COL04162; Sulfate_transp,STAS,HMG_box; 3.39
 449343; A1151418; ; protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha); none:none; 3.39
 450511; R07423; Hs.85092; thyroid hormone receptor interactor 11; Myosin_tail,EGF; 3.39
 414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain,PHD,PWWP,zf-MYND;TM=M; 3.38
 418428; Y12490; Hs.85092; thyroid hormone receptor interactor 11; bZIP,kinesin,GTP_cyclohydrol,M;TM=M; 3.37
 422369; AF005216; Hs.115541; Janus kinase 2 (a protein tyrosine kinase); SH2,pkinase;TM=M; 3.37
 456451; A1761180; Hs.94211; rcd1 (required for cell differentiation, S.pombe) homolog 1; none;TM=M; 3.37
 438543; AA810141; Hs.192182; ESTs; SH2,pkinase:none; 3.37
 401943; NM_012434; ; solute carrier family 17 (anion/sugar transporter), member 5; none;TM=M; 3.36
 415276; U88665; Hs.78353; SFRS protein kinase 2; pkinase;TM=M; 3.36
 447881; BE620886; Hs.75354; GCN1 (general control of amino-acid synthesis 1, yeast)-like 1; pkinase,pkinase; 3.35
 434533; AA639257; Hs.292549; ESTs; SH3,PDZ,Guanylate_kin:none; 3.35
 432639; AW973785; ; gb:EST385886 MAGE resequences, MAGM Homo sapiens cDNA, mRNA sequence; none,IRK; 3.35
 410678; BE540516; Hs.293732; hypothetical protein MGC3195; Armadillo_seg;TM=M;SS=Y; 3.35
 402807; ; ENSP00000235229:SEMB.; integrin_B,Sema,PSI;TM=Y; 3.35
 420189; AW296380; Hs.95821; osteoclast stimulating factor 1; SH3,ank; 3.34
 437389; AL359587; Hs.271586; hypothetical protein DKFZp762M115; secY,E1_dehydrog,transket_pyr:none; 3.34
 453423; NM_002647; Hs.32971; phosphoinositide-3-kinase, class 3; PI3_P14_kinase,PI3Ka,PI3K_C2;TM=M; 3.34
 414270; L20852; Hs.347527; solute carrier family 20 (phosphate transporter), member 2; Enterotoxin_A,PHO4;TM=Y;SS=M; 3.33
 417479; A1057052; ; ESTs; Weakly similar to Z195_HUMAN ZINC FINGER PROTEIN 195 [H.sapiens]; LRR,CARD:none; 3.33
 424946; M64572; Hs.153932; protein tyrosine phosphatase, non-receptor type 3; Band_41,PDZ,Y_phosphatase:none; 3.33
 452681; AF153330; Hs.30246; solute carrier family 19 (thiamine transporter), member 2; Folate_carrier;TM=Y;SS=M; 3.33
 426477; AA379464; ; gb:EST92386 Skin tumor I Homo sapiens cDNA 5' end, mRNA sequence; DUF6,MATH,BTB; 3.33
 438283; A1458931; Hs.37282; ESTs; none,transmembrane4; 3.33
 421327; AA837295; Hs.188802; ESTs; none,IMP4,Y_phosphatase; 3.33
 432481; AW451645; Hs.151504; Homo sapiens cDNA FLJ11973 fis, clone HEMBB1001221; laminin_G,Collagen,COLFI,CorA,TSPN:none; 3.33
 452682; AA456193; Hs.9071; progesterone membrane binding protein; homeobox:none; 3.32
 428997; AF065391; Hs.194718; zinc finger protein 265; zf-RanBP;TM=M; 3.32
 432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY_C;TM=M; 3.31
 443601; A1078554; Hs.15682; ESTs; ank,pkinase,death,Ribosomal_S14; 3.31
 430597; AF062006; Hs.285529; G protein-coupled receptor 49; 7tm_1,LRR,LRRNT;TM=Y;SS=M; 3.31
 419812; AF24745; Hs.8086; Rho guanine nucleotide exchange factor (GEF) 4; SH3,PH,RhoGEF;TM=M; 3.31
 400380; NM_018485; Hs.283078; G protein-coupled receptor C6L2; 7tm_1;TM=Y;SS=M; 3.31
 415993; A1438798; Hs.117078; Homo sapiens cDNA: FLJ23028 fis, clone LNG01852, highly similar to HSU08023 Human cellular proto-oncogene (c-met) mRNA; fin3,ig,pkinase;TM=Y;SS=M; 3.31
 441054; AA913591; Hs.126480; ESTs; none,7tm_1; 3.31
 418342; BE002723; ; leptin receptor; ICE_p20,DED,ICE_p10,ICE_p20,DED; 3.31
 446128; AW836779; Hs.113029; ribosomal protein S25; none,7tm_1; 3.31
 425086; AW957571; Hs.12319; Homo sapiens cDNA FLJ12774 fis, clone NT2RP2001663, moderately similar to ENOLASE (EC 4.2.1.11); none,Guanylate_kin,PDZ,SH3; 3.31
 425725; NM_012243; Hs.159322; solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3; DUF6;TM=Y;SS=M; 3.30
 422608; AF160644; Hs.118695; potassium voltage-gated channel, subfamily G, member 1; ion_trans,K_tetra;TM=Y; 3.30
 429061; Y14039; Hs.195175; CASP8 and FADD-like apoptosis regulator; ICE_p20,DED;TM=M; 3.30
 433656; AW974941; Hs.292385; ESTs; Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; pkinase,ABC1:none; 3.30
 413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent, catalytic) inhibitor alpha; PKI;SS=M; 3.30
 402603; ; ENSP00000251206:KIAA0778 PROTEIN (FRAGMENT); none;TM=Y; 3.30
 418801; AA228366; Hs.115122; ESTs; Integrin_AFG-GAP:none; 3.30
 40275; ; NM_006513:Homo sapiens seryl-tRNA synthetase (SARS), mRNA. (SAM68), mRNA; (RNA-synt_2b,Seryl_tRNA_N;TM=M; 3.29
 440286; U29589; Hs.7138; cholinergic receptor, muscarinic 3; 7tm_1;TM=Y; 3.29
 409101; NM_004297; Hs.50612; guanine nucleotide binding protein (G protein), alpha 14; G-alpha:none; 3.29
 432736; AA788898; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 3.29
 408738; NM_014785; Hs.47313; KIAA0258 gene product; none;TM=M; 3.29
 443195; BE148235; Hs.193063; Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002955; Aa_trans:none; 3.29
 405328; ; NM_005391:Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3), mRNA; HATPase_c;SS=M; 3.28
 418764; N30531; Hs.42215; protein phosphatase 1, regulatory subunit 6; none:none; 3.28
 408756; AA524743; Hs.44883; ESTs; Armadillo_seg,JBB,DEAD,helicase_C,Sec63,DDT,PHD,bromodomain;TM=M; 3.28
 415474; NM_014252; Hs.78457; solute carrier family 25 (mitochondrial carrier, ornithine transporter) member 15; mito_car;TM=M; 3.28
 417805; U38545; Hs.82587; phospholipase D1, phosphatidylcholine-specific; PH,PLDC,PX;TM=M; 3.28
 410254; BE004131; Hs.318510; Homo sapiens cDNA FLJ13682 fis, clone PLACE2000015, weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15; ehand:none; 3.28
 443968; AA287702; Hs.10031; KIAA0955 protein; CARD;TM=M;SS=M; 3.28
 438899; AF085833; Hs.135624; ESTs; none,PI3_P14_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B; 3.27
 415663; AW296841; Hs.313332; ESTs; UQ_con_Neur_chan_LBD,Neur_chan_memb; 3.27
 414087; W19712; ; gb:zb36d03.r1 Soares_papillary_thyroid_tumor_NbHPA Homo sapiens cDNA clone 5', mRNA sequence; pkinase:none; 3.27
 442833; AA328153; Hs.88201; ESTs; Weakly similar to A Chain A, Crystal Structure Of The Human Acyl Protein Thioesterase 1 At 1.5 A Resolution [H.sapiens]; abhydrolase_2;TM=M; 3.27
 444754; T83911; Hs.11881; transmembrane 4 superfamily member 4; none;TM=Y;SS=M; 3.26
 432579; AF043244; Hs.278439; nucleolar protein 3 (apoptosis repressor with CARD domain); CARD;TM=M; 3.26
 458943; AW249181; Hs.19954; ESTs; Weakly similar to T19873 hypothetical protein C41C4.2 - Caenorhabditis elegans [C.elegans]; none,pkinase,RGS; 3.26
 411974; AW880414; Hs.84264; acidic protein rich in leucines; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase,asp; 3.26
 437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbonate cotransporter, member 4; HCO3_cotransp;TM=Y; 3.25
 423387; AJ012074; ; vasoactive intestinal peptide receptor 1; 7tm_2,HRM,CSD;TM=Y;SS=M; 3.25
 442643; U82756; Hs.3991; PRP4/STK/WD splicing factor; WD40;SS=M; 3.25
 417525; R93355; Hs.192991; ESTs; Weakly similar to ALUB_HUMAN !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]; SH3,ig,pkinase,PH,spectrin,RhoGEF;SS=M; 3.25
 412283; BE069084; ; gb:QV3-BT0379-140100-058-g12 BT0379 Homo sapiens cDNA, mRNA sequence; ion_trans,RYOR,TIPR,MIR:none; 3.25
 411213; AA676939; Hs.69285; neuropilin 1; MAM,F5_F8_type_C,CUB,CUB,MAM,F5_F8_type_C; 3.25
 400352; AF227133; ; taste receptor, type 2, member 7; none;TM=Y;SS=M; 3.25

- 402974; ; ; Target Exon; Y_phosphatase, GnRH, hormone5, hormone4; 3.25
 407644; D16815; Hs.37288; nuclear receptor subfamily 1, group D, member 2; hormone_rec, zf-C4; TM=M; SS=M; 3.25
 421654; AW163267; Hs.106469; suppressor of var1 (S.cerevisiae) 3-like 1; helicase_C; SS=M; 3.25
 438022; AW517524; Hs.135201; NOD2 protein; LRR, CARD, GTP_CDC, Viral_helicase1; TM=M; 3.24
 449964; AW001741; Hs.24243; hypothetical protein FLJ10706; pkinase; TM=M; 3.24
 428816; AA004986; Hs.193852; ATP-binding cassette, sub-family C (CFTR/MRP), member 2; EGF, sushi, trypsin, CUB, ABC_tran, ABC_membrane; SS=M; 3.24
 427319; AW631495; Hs.27135; B-cell receptor-associated protein BAP29; filament; TM=Y; SS=M; 3.24
 421970; AF227156; Hs.110103; RNA polymerase I transcription factor RRN3;
 aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, P13, P14_kinase, FAT, FATC, BclA, RUN; TM=M; 3.24
 411887; AW182924; Hs.128790; ESTs; pkinase; TM=M; 3.24
 430180; AA331406; Hs.75456; A kinase (PRKA) anchor protein 10; RGS; SS=M; 3.24
 410267; AW978005; Hs.12600; N-ethylmaleimide-sensitive factor attachment protein, beta; none, NTF2; 3.23
 410240; AL157424; Hs.61289; synaptotagmin 2; Exo_endo_phos, Syja_N, rm, Gram-v, porins; TM=M; 3.23
 434510; AF143885; Hs.18190; EST; SH3, FCH, none; 3.22
 422592; BE081857; Hs.94211; rcd1 (required for cell differentiation, S.pombe) homolog 1; none, PI-PLC-X, PH, PI-PLC-Y, C2; 3.22
 439803; AA001021; Hs.6685; thyroid hormone receptor interactor 8; none, none; 3.22
 448520; AB002367; Hs.21355; doublecortin and CaM kinase-like 1; pkinase, DCX; TM=M; 3.22
 409245; AA361037; Hs.288036; tRNA Isopentenylpyrophosphate transferase; Armadillo_seg; TM=M; 3.22
 458946; AA009716; Hs.42311; ESTs; none, DSPc, Y_phosphatase; 3.22
 409048; H59990; Hs.37699; ESTs; Armadillo_seg, IBB, none; 3.22
 420357; U94333; Hs.97199; complement component C1q receptor; EGF, lectin_c, Tissue_fac, Xlink, TIL; TM=Y; SS=M; 3.22
 426230; AA367019; Hs.241395; protease, serine, 1 (trypsin 1); trypsin, toxin_4; SS=M; 3.21
 411352; NM_002890; Hs.758; RAS p21 protein activator (GTPase activating protein) 1; SH2, SH3, C2, PH, RasGAP; TM=M; SS=M; 3.21
 438333; R39382; Hs.25283; cyclin-dependent kinase 8; pkinase, none; 3.20
 414202; BE275653; Hs.270379; transmembrane 6 superfamily member 1; 7tm_5, none; 3.20
 429651; D79248; Hs.279870; ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]; MglE, none; 3.20
 400987; ; ; C11000939; gijl11464993; ref[NP_065260.1] gene for odorant receptor MOR83 [Mus musculus] gijl; none; TM=Y; SS=M; 3.20
 413760; Z25101; Hs.25127; Homo sapiens mRNA for KIAA1725 protein, partial cds; none, ank, ArfGAP; 3.20
 408468; A1909712; Hs.93837; phosphatidylinositol transfer protein, membrane-associated; PX, PH, PLDc, PH, PLDc, PX; 3.20
 409463; A1458165; Hs.17296; hypothetical protein MGC2376; K_tetra; TM=M; 3.20
 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; none; TM=M; 3.19
 423798; AF047033; Hs.132904; solute carrier family 4, sodium bicarbonate cotransporter, member 7; HCO3_cotransp; TM=Y; SS=M; 3.19
 407753; AL045916; Hs.293419; ESTs; Ephrin, none; 3.19
 419355; AA428520; Hs.90061; progesterone binding protein; heme_1; TM=Y; SS=M; 3.19
 454128; AL031259; Hs.41639; programmed cell death 2; zf-MYND; TM=M; 3.19
 421202; AF193339; Hs.102506; eukaryotic translation initiation factor 2-alpha kinase 3; pkinase; TM=Y; SS=M; 3.19
 446360; N42553; Hs.267914; homolog of mouse transient receptor potential-phospholipase C-interacting kinase ChAK; hypothetical protein FLJ20117;
 ion_trans, MHCK_EF2_kinase; TM=M; 3.18
 458882; R34993; Hs.226668; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; CRAL_TRIO, PKI; 3.18
 424124; AA335609; Hs.7589; ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]; pkinase, TBC; 3.18
 444745; AF117754; Hs.11861; thyroid hormone receptor-associated protein, 240 kDa subunit; none; TM=M; 3.18
 426399; AA652588; Hs.301348; Homo sapiens cDNA FLJ13271 fis, clone OVARC1001000; SH3, HS1_rep, none; 3.18
 425836; AW955696; Hs.90960; ESTs; Cbl_N, Cbl_N2, Cbl_N3, UBA, zf-C3HC4, none; 3.18
 403335; ; ; NM_021815; Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA; SSF; TM=Y; SS=M; 3.17
 428788; AF082283; Hs.193516; B-cell CLL/lymphoma 10; CARD; TM=M; 3.17
 429558; A1391454; Hs.207251; nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein; none; SS=M; 3.17
 440248; AA876138; Hs.153136; ESTs; SH2, none; 3.17
 423706; U95218; Hs.131924; G protein-coupled receptor 65; 7tm_1; TM=Y; SS=M; 3.17
 429752; H52348; Hs.36836; ESTs; pkinase, pkinase; 3.17
 446163; AA026880; Hs.25252; Homo sapiens cDNA FLJ13603 fis, clone PLACE1010270; none; NA; NA; 3.17
 456773; A1038192; Hs.129764; EGF-like repeats and discoidin-like domains 3; rm, SH3, myosin_head, IQ, MyTH4, EGF, F5_F8_type_C, Band_41; TM=M; 3.17
 434392; AW983709; Hs.250824; Homo sapiens cDNA: FLJ23435 fis, clone HRC12631; pkinase, none; 3.16
 435972; W95088; Hs.114198; ESTs; pkinase, OPR, none; 3.16
 441401; A1824338; Hs.126891; ESTs; Tissue_fac; TM=M; SS=M; 3.16
 410497; AL157648; Hs.157078; Homo sapiens cDNA FLJ12793 fis, clone NT2RP2002033; none, none; 3.16
 401113; H25505; ; solute carrier family 22 (organic cation transporter), member 1-like; none; SS=M; 3.16
 424833; NM_003894; Hs.153405; period (Drosophila) homolog 2; PAS; SS=M; 3.15
 453880; A1803166; Hs.28462; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; HSP70, none; 3.15
 435391; AA704588; Hs.58934; ESTs; PIP5K, none; 3.15
 428065; A1634046; Hs.157313; ESTs; ICE_p20, DED, ICE_p10, ICE_p20, DED; 3.15
 452688; AA721140; Hs.49930; ESTs, Weakly similar to putative p150 [H.sapiens]; SH3, none; 3.15
 426839; M74782; Hs.172689; Interleukin 3 receptor, alpha (low affinity); none; TM=M; SS=M; 3.15
 421247; BE391727; Hs.102910; general transcription factor IIH, polypeptide 4 (52kD subunit); none; TM=M; 3.14
 440249; A1246590; Hs.249175; ESTs; TatD_DNase, pkinase, death, none; 3.14
 409618; AK001015; Hs.55220; BCL2-associated athanogene 2; BAG; TM=M; 3.13
 446135; AW130288; Hs.170318; hypothetical protein FLJ10147; hormone_rec, zf-C4; SS=M; 3.13
 400440; X83957; Hs.83870; nebulin; SH3, Nebulin; 3.12
 409099; AK000725; Hs.50579; hypothetical protein FLJ20718; Armadillo_seg; TM=M; 3.12
 434237; AF119908; Hs.235516; hypothetical protein PRO2955; none; SS=M; 3.12
 428179; A1127772; Hs.279696; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; pkinase, PX, pkinase_C; SS=M; 3.12
 422824; NM_012108; Hs.121128; BCR downstream signaling 1; SH2, PH; TM=M; 3.11
 409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B14E12, mRNA sequence; 7tm_1, zf-C3HC4, fn3, SPRY, KRAB, zf-C2H2, rve, zf-B_box; TM=Y; SS=M; 3.11
 435411; AW444619; Hs.138211; ESTs; none, pkinase; 3.11
 424852; A1222779; Hs.144848; ESTs; adenylatekinase, SH2, pkinase, none; 3.11
 441970; AW959918; Hs.155160; ESTs; rm, zf-C2H2; 3.11
 453370; A1470523; Hs.139336; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC_tran, ABC_membrane; TM=Y; 3.11
 413285; BE078405; ; gb:CV2-BT0617-080300-071-g03 BT0617 Homo sapiens cDNA, mRNA sequence; GCV_T; SS=M; 3.10
 429458; BE161832; Hs.292689; ESTs; pkinase, bZIP, Armadillo_seg, none; 3.10
 401185; ; ; NM_021625; Homo sapiens vanilloid receptor-related osmotically activated channel; OTRPC4 protein (OTRPC4), mRNA; ank, ion_trans; TM=Y; 3.10
 404537; Z25884; ; chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant); none; TM=Y; 3.10
 417089; H52280; Hs.18612; Homo sapiens cDNA: FLJ21909 fis, clone HEP03834; voltage_CLC, CBS, none; 3.09
 450792; AA400323; Hs.183041; ESTs; none, ABC_tran; 3.09

- 420361; N92054; Hs.194718; zinc finger protein 265; zf-RanBP, 7tm_1; 3.09
 444040; AF204231; Hs.182982; golgin-57; SH3, C2, PH, RhoGEF, ehfand; TM=M; 3.09
 416990; AF124145; Hs.80731; autocrine motility factor receptor; zf-C3HC4, CUE; TM=Y; 3.09
 442215; AI703172; Hs.129005; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; none, none; 3.09
 424187; AA336561; Hs.17287; ESTs, Weakly similar to S26689 hypothetical protein hc1 - mouse [M.musculus]; IRK, none; 3.09
 426623; AA382826; Hs.132793; ESTs; none, TM=M; 3.08
 419577; L36531; Hs.91296; Integrin, alpha 8; integrin_A, FG-GAP; TM=Y; 3.08
 426618; AL036456; Hs.171374; smg GDS-ASSOCIATED PROTEIN; Armadillo_seg; TM=M; 3.08
 445133; AW157646; Hs.153506; ESTs; ehfand, spectrin, GAS2, SH3, Plectin, RA, Xylose_isom, FliD, bZIP, Tropomyosin, Myo-LZ, M, Idh_C, CH, AIP3; TM=M; 3.08
 423581; AB023215; Hs.131525; Homo sapiens mRNA; cDNA DKFZp434E199 (from clone DKFZp434E199); partial cds; TTL; TM=M; 3.08
 428730; AA625947; Hs.25750; ESTs; HECT, none; 3.08
 427976; AW977808; Hs.80545; mitogen-activated protein kinase 8 interacting protein 2; Ribosomal_L37e, pkinase; 3.08
 412448; L12964; Hs.73895; tumor necrosis factor receptor superfamily, member 9; TNFR_c6; TM=Y; SS=M; 3.08
 416814; AW192307; Hs.80042; dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylglucosyltransferase; Alg6, Alg8, 7tm_1; TM=Y; SS=M; 3.08
 427395; AW298741; Hs.97861; ESTs, Moderately similar to I38022 hypothetical protein [H.sapiens]; none, aldedh, aakine; 3.08
 436267; AW450938; Hs.180115; ESTs; none, PFK; 3.07
 422309; U79745; Hs.114924; solute carrier family 16 (monocarboxylic acid transporters), member 6; sugar_tr; TM=Y; SS=M; 3.07
 439238; N47305; Hs.48668; ESTs; 7tm_1; TM=Y; SS=M; 3.07
 458760; AI496311; Hs.111334; ferritin, light polypeptide; cystatin, ferritin, histone, HCO3_cotransp, SH3, RhoGAP, xan_ur_permease, FCH; SS=M; 3.07
 424236; AW058114; Hs.7837; phosphoprotein regulated by mitogenic pathways; pkinase; TM=M; 3.06
 427286; AW732802; Hs.2132; epidermal growth factor receptor pathway substrate 8; SH3, TonB_boxC; TM=M; 3.06
 423878; AI907090; Hs.52891; hypothetical protein PRO1853; cystatin, ferritin, histone, HCO3_cotransp, SH3, RhoGAP, xan_ur_permease, FCH; SS=M; 3.06
 419270; NM_005232; Hs.89839; EphA1; fn3, pkinase, SAM, EPH_Lbd; TM=M; SS=M; 3.06
 450407; NM_000810; Hs.24969; gamma-aminobutyric acid (GABA) A receptor, alpha 5; Neur_chan_LBD, Neur_chan_memb; TM=Y; 3.06
 456249; AI206144; Hs.82508; HRIHFB2206 protein; none; SS=M; 3.06
 441560; F13386; Hs.7888; Homo sapiens clone 23736 mRNA sequence; pkinase, Recep_L_domain, Furin-like, YLP; none; 3.05
 446488; AB037782; Hs.15119; KIAA1361 protein; pkinase; SS=M; 3.05
 447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-inducing factor); pyr_redox; TM=M; 3.05
 425390; AI092634; Hs.156114; protein tyrosine phosphatase, non-receptor type substrate 1; ig; TM=Y; SS=M; 3.04
 409705; M37762; Hs.56023; brain-derived neurotrophic factor; NGF; SS=M; 3.04
 413952; AA331563; Hs.24678; sphingosine-1-phosphatase; PAP2; TM=Y; 3.04
 426578; R23027; gb:yh27e07.r1 Soares placenta Nb2HP Homo sapiens cDNA clone 5, mRNA sequence; pkinase, none; 3.04
 438005; BE151746; gb:PM1-HT0305-061299-003-a06 HT0305 Homo sapiens cDNA, mRNA sequence; pkinase, UBA_KA1, none; 3.04
 438316; AA789249; Hs.80042; gb:aj27g08.s1 Soares testis_NHT Homo sapiens cDNA clone 1391582 3', mRNA sequence; none, none; 3.04
 452850; H23230; Hs.22481; ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]; CBS, voltage_CLC; none; 3.03
 405266; ; Target Exon; arf, G-alpha; SS=M; 3.03
 402815; ; C1003844*gi1691255[ref]NP_036483.1 olfactory receptor, family 10, subfamily J, member 1; none; TM=Y; SS=M; 3.03
 422803; WF28669; Hs.139041; ESTs; transmembrane4, none; 3.02
 439325; AF086139; Hs.150423; cyclin-dependent kinase 9 (CDC2-related kinase); pkinase, Mur_ligase, Mur_ligase_C; 3.02
 416389; AA180072; Hs.149846; Integrin, beta 5; Integrin_B, none; 3.02
 418836; AI655499; Hs.161712; ESTs; pkinase, Activin_rec, PDZ, ZU5, death; 3.02
 438996; AW748336; Hs.110613; KIAA0421 protein; none; TM=M; 3.02
 422678; D28481; Hs.1570; histamine receptor H1; 7tm_1; TM=Y; SS=M; 3.02
 450267; AW505638; Hs.243620; ESTs; pkinase, none; 3.01
 400566; ; Target Exon; none; TM=Y; 3.01
 407816; AW500857; Hs.40137; anaphase-promoting complex 1; meiotic checkpoint regulator; PI-PLC-X, C2, SH2, PH, SH3, PI-PLC-Y, PAN; none; 3.01
 429573; AA884407; Hs.211595; protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase); Y_phosphatase, Band_41, PDZ; SS=M; 3.00
 417067; AJ001417; Hs.81086; solute carrier family 22 (extraneuronal monoamine transporter), member 3; sugar_tr; TM=Y; SS=M; 3.00
 403212; ; NM_019595; Homo sapiens intersectin 2 (ITSN2), mRNA. (CHRNA9), mRNA; SH3, ehfand, C2, PH, RhoGEF; TM=M; 3.00
 410141; R07775; Hs.287657; Homo sapiens cDNA: FLJ121291 fis, clone COL01963; F5_F8_type_C, pkinase, Eis; none; 3.00
 421059; AI654133; Hs.30212; thyroid receptor interacting protein 15; none, none; 3.00
 452335; AW188944; Hs.61272; ESTs; none, IRK; 2.99
 437644; AA748575; Hs.136748; lectin-like NK cell receptor; lectin_c; TM=Y; SS=M; 2.99
 435876; AW612588; Hs.160271; G protein-coupled receptor 48; 7tm_1, LRR, LRRNT; TM=Y; SS=M; 2.99
 429177; AA447527; Hs.207429; ESTs; 7tm_1, none; 2.99
 449289; BE466057; Hs.225660; ESTs; 3Beta_HSD, pkinase; 2.99
 454701; AW854930; gb:PM0-CT0263-201099-003-106 CT0263 Homo sapiens cDNA, mRNA sequence; SH2, STAT, STAT_bind, STAT_prot, none; 2.99
 409995; AW960597; Hs.129206; ESTs; pkinase, none; 2.98
 446860; AV660685; Hs.282953; ESTs; none, PP2C; 2.98
 438684; AA830105; Hs.194976; SH2 domain-containing phosphatase anchor protein 1; ig; TM=Y; SS=M; 2.98
 434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase; TM=M; 2.98
 403290; ; C10001011*gi14758212[ref]NP_004411.1 dual specificity phosphatase 8 [Homo sapiens] gi1601; none; TM=M; 2.97
 433556; W56321; Hs.111460; calcium/calmodulin-dependent protein kinase (CaM kinase) II delta; pkinase, none; 2.97
 421990; T31811; Hs.110480; DC12 protein; GKAP, DUF159; TM=M; 2.97
 428315; AA688152; Hs.98505; ESTs; pkinase, none; 2.97
 411140; AW819463; gb:RCS-ST0293-061299-031-C07 ST0293 Homo sapiens cDNA, mRNA sequence; Choline_kinase, Cam_acyltransf, Sulfatase, Cam_acyltransf; 2.97
 453998; H47802; Hs.7557; FK506-binding protein 5; none, none; 2.97
 401342; ; Target Exon; none, none; 2.97
 453020; AL162039; Hs.31422; Homo sapiens mRNA; cDNA DKFZp434M229 (from clone DKFZp434M229); dNK; none; 2.96
 410976; R36207; Hs.25092; hypothetical protein MGC10744; none; TM=M; SS=M; 2.96
 431074; BE072772; Hs.153279; ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]; none, serpin; 2.96
 443829; AI087954; Hs.23348; S-phase kinase-associated protein 2 (p45); F-box, none; 2.96
 400356; AF227137; ; taste receptor, type 2, member 13; none; TM=Y; SS=M; 2.95
 422559; AW247696; Hs.155839; hypothetical protein MGC12934; adh_zinc, PGK, Serratidhyde_dh; SS=M; 2.95
 423482; BE280172; Hs.129228; galactokinase 2; GHMP_kinases; TM=M; 2.95
 438330; AW450572; Hs.257316; ESTs; pkinase, zf-C4, ERM, CNH; none; 2.95
 414581; AA256213; Hs.72010; ESTs; none, Cam_acyltransf, Choline_kinase, SCO1-SenC, Glycos_transf_3, Glycos_trans_3N; 2.95
 453058; AW612293; Hs.288684; Homo sapiens cDNA FLJ11750 fis, clone HEMBA1005568; SH2, SH3, C2, PH, RasGAP; none; 2.95
 430556; AW997807; Hs.13797; ESTs; HECT, none; 2.94
 400471; ; Target Exon; none; TM=M; 2.94
 419459; AW291128; Hs.278422; DKFZP586G1122 protein; Metallophos, 7tm_1; 2.94
 407013; U35637; gb:Human nebulin mRNA, partial cds; SH3, Nebulin; 2.94
 421476; AW953805; Hs.21887; ESTs; Ptw, PAZ, Ptw; 2.94

- 426806; T19228; Hs.172572; hypothetical protein FLJ20093; *ank, kinase, UPF0073*; SS=M; 2.94
 405588; ; NM_000299; Homo sapiens plakophilin 1 (ectodermal dysplasia/skin fragility syndrome) (PKP1), mRNA; Armadillo_seg; TM=M; 2.94
 443614; AV655386; Hs.7645; fibrinogen, B beta polypeptide; none, none; 2.94
 416737; AF154335; Hs.79691; LIM domain protein; LIM, PDZ; TM=M; 2.93
 428522; R10184; Hs.191987; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; none, ArfGap, PH, TNFR_c6; 2.93
 447818; W79940; Hs.21906; Homo sapiens clone 24670 mRNA sequence; none, kinase; 2.93
 432925; AA878324; ; ESTs; none, none; 2.93
 443670; AW178935; Hs.238707; ESTs; RmaAD, DENN, dDENN, uDENN; TM=M; 2.93
 447555; AJ31662; Hs.160963; Homo sapiens, clone MGC:12318, mRNA, complete cds; none, TM=M; 2.93
 435092; AL137310; Hs.4749; Homo sapiens mRNA; cDNA DKFZp761E13121 (from clone DKFZp761E13121); partial cds; none, TM=M; 2.93
 417670; R07785; ; gb:Y15c06.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone 5' similar to contains Alu repetitive element; contains MSR1 repetitive element; mRNA sequence; YYPX, ABC, membrane, ABC, tran; 2.93
 424148; BE242274; Hs.1741; Integrin, beta 7; Integrin_B, EGF, metallo, PSI; TM=Y; SS=M; 2.92
 439090; H65724; Hs.347158; gb:Y76a11.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone 5', mRNA sequence; kinase, none; 2.92
 408048; NM_007203; Hs.42322; A kinase (PRKA) anchor protein 2; Paralemmin; TM=M; 2.92
 428796; AU076734; Hs.193665; solute carrier family 28 (sodium-coupled nucleoside transporter), member 2; Nucleoside_tra2, BPD, transp_2; TM=Y; 2.92
 415272; AA164215; Hs.203186; ESTs; none, Exo_endo, phos, BNR, Atrophin-1, B56, pkinase, Jg, TPR; 2.92
 424775; AB014540; Hs.153026; SWAP-70 protein; ehand, PH, Neuregulin; TM=M; 2.92
 439569; AW602166; Hs.222399; CEGP1 protein; EGF, TNFR_c6, granulin, CUB, Keralin_B2, TIL; TM=M; SS=M; 2.92
 441680; AW444598; Hs.7940; RAP1, GTP-GDP dissociation stimulator 1; Armadillo_seg; TM=M; 2.91
 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodiesterase 1; Somatomedin_B, Endonuclease, Phosphodiester; TM=Y; SS=M; 2.91
 400398; AF137396; Hs.283879; ubiquitin 3; 7tm_1, Abi; TM=Y; SS=M; 2.91
 435592; AJ830490; Hs.1466; glycerol kinase; FGGY, FGGY_C; TM=M; 2.90
 400539; ; Target Exon; none, TM=M; 2.90
 403743; ; c1002604.g1|B33668|ref|NP_058989.1| kinase interacting with leukemia-associated gene (st; none, TM=M; 2.90
 418913; BE046745; Hs.91579; Homo sapiens clone 23783 mRNA sequence; Y_phosphatase, IMP4, none; 2.90
 428169; AJ928984; Hs.182793; golgi phosphoprotein 2; photoRC, UPF0118; TM=Y; 2.90
 403912; ; C5000394.g1|12737280|ref|XP_006682.2| keratin 18 [Homo sapiens]||6633; none, TM=M; 2.89
 431868; BE246400; Hs.285176; acetyl-Coenzyme A transporter; none, TM=Y; 2.89
 421558; AB011125; Hs.105749; KIAA0553 protein; none, TM=M; 2.89
 444100; AA383343; Hs.22116; CDC14 (cell division cycle 14, S. cerevisiae) homolog B; Y_phosphatase, DSPC; TM=M; 2.89
 447437; U07225; Hs.339; purinergic receptor P2Y, G-protein coupled, 2; 7tm_1, SH2; TM=Y; SS=M; 2.89
 431512; BE270734; Hs.2795; lactate dehydrogenase A; Idh, Idh_C, SH3, pkinase, UBA; TM=M; 2.89
 446601; AJ312783; Hs.155772; Homo sapiens thymic stromal co-transporter mRNA, complete cds; sugar_tr; TM=Y; 2.89
 420747; BE294407; Hs.99910; phosphofructokinase, platelet; PFK; TM=M; 2.88
 49459; BE546846; Hs.195048; ESTs; *ank, ras, PH, ArfGap, HCO3_cotransp*; 2.88
 405099; ; Target Exon; C2, PI-PLC-Y, PI-PLC-X; TM=M; 2.88
 445890; AF055019; Hs.21906; Homo sapiens clone 24670 mRNA sequence; kinase, pkinase; 2.88
 401445; ; NM_021161; Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA; ion_trans; TM=Y; SS=M; 2.87
 405480; ; Target Exon; none, none; 2.87
 400189; ; Eos Control; LRR, PPTA; TM=M; 2.87
 450125; AA005418; Hs.158186; ESTs; CIDE-N, 7tm_1, none; 2.87
 432056; AB040973; Hs.272385; G protein-coupled receptor 72; 7tm_1; TM=Y; SS=M; 2.86
 423619; T48691; Hs.249159; adrenergic, alpha-2A-, receptor; 7tm_1, 7tm_2; TM=Y; SS=M; 2.86
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleoside transporters), member 1; xan_ur, permease, RA; 2.86
 420035; F26725; Hs.187908; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; HATPase_c, MOZ, SAS, zf-C2H2; 2.86
 425480; AB023198; Hs.158135; KIAA0981 protein; PIP5K; SS=M; 2.86
 446700; AW206257; Hs.156326; Human DNA sequence from clone RP11-145L22 on chromosome 6p21.32-22.2. Contains the gene for myelin/oligodendrocyte glycoprotein MOG, (part of) the gene for a novel KRAB box containing C2H2 type zinc finger protein, ESTs, STSs, GSSs and a putative CpG; none, TM=M; 2.86
 444595; AL121094; Hs.83572; hypothetical protein MGC14433; Y_phosphatase, SH2, Y_phosphatase, SH2; 2.85
 411331; AW837178; ; gb:QV1-LT0037-070300-100-d11 LT0037 Homo sapiens cDNA, mRNA sequence; SH2, none; 2.85
 410763; AF279145; Hs.8966; hypothetical protein FLJ21776; none, none; 2.85
 440617; AA894880; Hs.181181; ESTs; none, none; 2.85
 454071; AJ041793; Hs.42502; ESTs; 7tm_1, none; 2.85
 411040; AF007393; Hs.177574; protein-kinase, Interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor); HLH; TM=M; 2.85
 402183; ; NM_004491; Homo sapiens glucocorticoid receptor DNA binding factor 1 (GRF1), mRNA; none, SS=M; 2.85
 428753; AW939252; Hs.192927; hypothetical protein FLJ20251; none, TM=M; 2.84
 417070; Z19077; Hs.172004; *tin; fn3, Jg, SGXXSG, pkinase*; TM=M; 2.84
 458456; AJ122709; Hs.153609; ESTs; bZIP, Armadillo_seg, rrm, NTF2, none; 2.84
 421226; AL096748; Hs.102708; DKFZP434A043 protein; Armadillo_seg, Integrin_B, PSI, TIG; TM=M; SS=M; 2.84
 436733; BE327477; Hs.166941; ESTs; 7tm_3, oxidored_q5_N, Presenilin, PWI; 2.84
 427161; AJ024595; Hs.97508; a disintegrin and metalloproteinase domain 6; Ig; TM=Y; SS=M; 2.84
 419462; AF071076; Hs.112255; nucleoporin 98kD; DEAD, helicase_C, Nucleoporin_FG, homeobox; SS=M; 2.83
 413658; AA055369; Hs.75456; A kinase (PRKA) anchor protein 10; none, none; 2.83
 400749; ; NM_003105; Homo sapiens sortilin-related receptor, L (DLR class) A repeats-containing (SORL1), mRNA; EGF, fn3, Idl_recept_a, Idl_recept_b, granulin, BNR; TM=Y; SS=M; 2.83
 447388; AW630534; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; TB2_DP1_HVA22; TM=Y; SS=M; 2.83
 413243; AA769266; Hs.193657; ESTs; pkinase, zf-C4, ERM, CNH, none; 2.83
 423690; AA329648; Hs.23804; ESTs, Weakly similar to PN0099 son3 protein [H.sapiens]; ion_trans, IQ, none; 2.82
 447993; AW139525; Hs.170362; ESTs; none, none; 2.82
 423061; AJ290473; Hs.44807; ESTs; Integrin_B, Sema, PSI, TIG, none; 2.82
 440619; AW408586; Hs.91052; ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; abhydrolase_2, none; 2.82
 423497; U92642; Hs.129701; G protein-coupled receptor 45; 7tm_1; TM=Y; SS=M; 2.81
 446126; AW085909; Hs.10177; pleckstrin homology domain interacting protein; none, none; 2.81
 452488; N74921; Hs.184389; ESTs; none, TM=M; 2.80
 449515; AJ653378; Hs.302012; ESTs; ion_trans; TM=Y; SS=M; 2.79
 443881; R64512; Hs.237146; hypothetical protein FLJ12752; none, none; 2.79
 449536; AJ656608; Hs.281328; ESTs, Weakly similar to T00378 KIAA0841 protein [H.sapiens]; pkinase, hormone3; TM=Y; SS=M; 2.78
 424348; AB020523; Hs.266258; endonuclease G-like 1; Endonuclease; TM=M; SS=M; 2.78
 418844; M62982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase, PLAT; TM=M; 2.78
 442233; AW967149; Hs.28439; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; MIF, sugar_tr, none; 2.78

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- 450010; AW293801; Hs.255052; ESTs; ARID,7tm_1; 2.78
 452813; U54727; Hs.191445; ESTs; pkinase,Activin_recpt,none; 2.78
 418177; N44967; ; ESTs; pkinase,none; 2.78
 408014; AA723782; Hs.41749; protein kinase, cGMP-dependent, type II; cNMP_binding,pkinase;SS=M; 2.77
 448362; AA641767; Hs.21015; hypothetical protein DKFZp564L0864 similar to HIAT1; sugar_tr,TM=Y;SS=M; 2.77
 423994; X01057; Hs.1724; interleukin 2 receptor, alpha; sushi;TM=Y;SS=M; 2.77
 427342; AL110150; Hs.176580; Homo sapiens mRNA; cDNA DKFZp586D0724 (from clone DKFZp586D0724); none;NA;NA; 2.76
 447574; AF162666; Hs.18895; tousel-like kinase 1; pkinase;TM=M; 2.76
 442681; AI809182; Hs.130907; ESTs; transketolase,E1_dehydrog,transket_pyr,transketolase_C,pkinase; 2.75
 433637; AW024214; Hs.102307; ESTs; Na_sulph_symp,aa_permeases;TM=Y;SS=M; 2.75
 458997; AW937420; Hs.69662; ESTs; SH3,RhoGAP,FCH;TM=M; 2.75
 432284; AA532807; Hs.105822; ESTs; pkinase,none; 2.74
 406139; ; Target Exon; Ig,Tub;TM=Y;SS=M; 2.74
 439518; W76326; ; gb:zd60d04.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone 5' similar to contains Alu repetitive element; mRNA sequence; Armadillo_seg,none; 2.74
 428536; AI141339; Hs.2288; visinin-like 1; ehfand;SS=M; 2.73
 400211; ; NM_003899; Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. VERSION NM_003897.1 GI; SH3,PH,RhoGEF,Terpene_synth;TM=M; 2.73
 402129; ; Target Exon; SH2,Peptidase_C9;TM=M; 2.73
 424238; AA337401; Hs.137635; ESTs; none;TM=M;SS=M; 2.73
 433834; AA620742; Hs.130786; ESTs; SPX,EXS;TM=Y; 2.73
 409339; AB020686; Hs.54037; ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function); Sulfatase,Phosphodiester;TM=M;SS=M; 2.73
 408163; AW779842; Hs.258217; ESTs; 7tm_1,zf-B_box,zf-C3HC4,7tm_1,zf-B_box,zf-C3HC4; 2.73
 422358; AL133030; Hs.115429; Homo sapiens mRNA for KIAA1666 protein, partial cds; SH3;TM=M; 2.73
 426409; AA594207; ; gb:nn29e01.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone 3', mRNA sequence; pkinase,Fibrillarin,none; 2.72
 400645; ; Target Exon; lig_chan,SBP_bac_3,ANF_receptor,none; 2.72
 443661; AA336609; Hs.10862; Homo sapiens cDNA: FLJ123313 fis, clone HEP11919; adenylatekinase,none; 2.71
 442572; AJ001922; Hs.135121; hypothetical protein FLJ22415; none,HSP70; 2.71
 409317; U20165; Hs.53250; bone morphogenetic protein receptor, type II (BMPR2); pkinase,Activin_recpt;TM=M;SS=M; 2.71
 403201; ; Target Exon; none; 2.71
 459357; AW848421; ; gb:IL3-CT0214-150200-075-B11 CT0214 Homo sapiens cDNA, mRNA sequence; ABC_tran,ABC_membrane,ion_trans; 2.70
 439935; S75105; Hs.8358; glutamate receptor, ionotropic, kainate 2; ANF_receptor,lig_chan,none; 2.70
 414924; C06267; Hs.44247; ESTs; none,none; 2.69
 421008; BE259378; Hs.103147; hypothetical protein FLJ21347; DUF255; 2.69
 449951; AA004982; Hs.120904; ESTs; DED,Calsequestrin; 2.69
 411226; AW833022; ; gb:RC3-TT0005-191099-012-d04 TT0005 Homo sapiens cDNA, mRNA sequence; pkinase,none; 2.68
 417625; U59305; Hs.44708; Ser-Thr protein kinase related to the myotonic dystrophy protein kinase; pkinase,bZIP,G-gamma,K-box,pkinase_C;SS=M; 2.68
 408051; AI623351; Hs.172148; ESTs; PH,RhoGAP,none; 2.68
 412521; AW753481; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M; 2.68
 413922; AI535895; Hs.221024; ESTs; ion_trans,RYDR,JTPR,MIR,UDPGT; 2.68
 432188; AI362952; Hs.2928; solute carrier family 7 (cationic amino acid transporter, y system), member 1; aa_permeases;TM=Y;SS=M; 2.67
 415516; F11411; ; gb:HSC2WF081 normalized infant brain cDNA Homo sapiens cDNA clone c-2wf08, mRNA sequence; ion_trans,none; 2.67
 419749; X73608; Hs.93029; sparco/osteonectin, cwcv and kazal-like domains proteoglycan (testican); kazal,thyroglobulin_1;SS=M; 2.66
 416095; AW014327; Hs.221951; ESTs; Weakly similar to I38022 hypothetical protein [H.sapiens]; Ig,zf-C3HC4,Cbl_N,Cbl_N2,Cbl_N3,none; 2.66
 403609; ; C3001199;gi7494834|pir|T15308 hypothetical protein B0286.2 - Caenorhabditis elegans|41; 7tm_1,7tm_2,GPS,WIF;TM=Y;SS=M; 2.66
 458213; AL047521; Hs.12210; hypothetical protein FLJ13732 similar to tensin; pkinase,none; 2.66
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.66
 435410; AL135067; Hs.117182; ESTs; none,pkinase,RBD,DAG_PE-bind; 2.66
 437838; AI307229; Hs.184304; ESTs; CARD,ICE_p20,ICE_p10,HIT,voltage_CLC,CBS,HCCA_isomerase; 2.66
 430293; AI416988; Hs.238272; Inositol 1,4,5-trisphosphate receptor, type 2; ion_trans,RYDR,JTPR,MIR,none; 2.65
 433090; AJ720050; ; immortalization-upregulated protein; none;SS=M; 2.65
 432103; T15803; Hs.272458; protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha); Metallophos;TM=M; 2.65
 435852; H72303; Hs.36011; ESTs; pkinase,none; 2.64
 433327; AI674779; Hs.126744; ESTs; none,7tm_1; 2.64
 438459; T49300; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; none,FMO-like; 2.64
 432251; AW972983; Hs.232165; polycythemia rubra vera 1; cell surface receptor; none;TM=M;SS=M; 2.63
 446963; AI862668; Hs.176333; ESTs; OMPdecase,Phosphotyran,pkinase,RhoGEF,PH; 2.63
 444821; AA035564; Hs.12040; STE20-like kinase; pkinase;TM=M; 2.63
 436206; AK001451; ; CD2-associated protein; none,none; 2.63
 434370; AF130988; Hs.58346; ectodysplasin 1, anhidrotic receptor; death,Kunitz_BPTI;TM=Y;SS=M; 2.63
 439039; AI656707; Hs.48713; ESTs; pkinase,none; 2.63
 449658; AA002008; Hs.188633; ESTs; PIP5K,none; 2.63
 429341; X73874; Hs.2393; phosphorylase kinase, alpha 1 (muscle); none;TM=M; 2.62
 445174; AV652850; Hs.172004; titin; fn3,Ig,SGXXSG,none; 2.62
 424950; AA602917; Hs.156974; ESTs; none,CDP-OH_P_transf; 2.62
 438141; AW946881; ; gb:RC2-ET0022-080500-012-d02 ET0022 Homo sapiens cDNA, mRNA sequence; SH2,STAT,STAT_bind,STAT_prot,none; 2.61
 434938; AW500718; Hs.8115; Homo sapiens, clone MGC:16169, mRNA, complete cds; pkinase,TBC,Rhodanese;TM=M; 2.61
 409264; NM_014937; Hs.52463; KIAA0966 protein; Syja_N;TM=M; 2.60
 458438; AI141520; Hs.151464; ESTs; Weakly similar to ALUC_HUMAN |||| ALU CLASS C WARNING ENTRY ||| [H.sapiens]; pkinase,none; 2.60
 400719; ; NM_004055; Homo sapiens calpain 5 (CAPN5), mRNA. VERSION NM_004335.2 GI; C2,Peptidase_C2,Calpain_III;TM=M; 2.60
 427318; AF186081; Hs.175783; zinc transporter; Zip;TM=Y;SS=M; 2.59
 426086; T94907; Hs.188572; ESTs; PH,Ets,CH,spectrin,Ca_channel_B,none; 2.59
 430105; X70297; Hs.2540; cholinergic receptor, nicotinic, alpha polypeptide 7; Neur_chan_LBD,Neur_chan_memb,pkinase;TM=Y;SS=M; 2.58
 411495; AP000693; Hs.70359; KIAA0136 protein; HATPase_c,bZIP;TM=M; 2.58
 438167; R28363; Hs.24286; ESTs; none;TM=Y;SS=M; 2.58
 418749; N75147; Hs.22488; ESTs; none,zf-C2H2,KRAB,pkinase; 2.58
 454289; AL137554; Hs.49927; protein kinase NYD-SP15; dCMP_cyt_deam;TM=M; 2.58
 443605; H06865; Hs.134131; ESTs; ehfand,ion_trans,none; 2.57
 429429; AA829725; Hs.334437; hypothetical protein MGC4248; none,transmembrane4; 2.57
 403088; ; NM_003319; Homo sapiens titin (TTN), mRNA. mRNA; fn3,Ig,SGXXSG;TM=M; 2.57
 409190; AU076536; Hs.50984; sarcoma amplified sequence; transmembrane4;TM=Y;SS=M; 2.57
 426696; AW363332; Hs.171844; Homo sapiens cDNA: FLJ22296 fis, clone HRC04468; Ig;TM=Y;SS=M; 2.56
 403328; ; Target Exon; Glyco_hydro_35;TM=M; 2.56

- 426167; AF039023; Hs.167496; RAN binding protein 6; Armadillo_seg.HEAT_PBS;; 2.56
- 428695; A1355647; Hs.189999; purinergic receptor (family A group 5); 7tm_1; TM=Y; SS=M; 2.54
- 419285; D31887; Hs.89868; KIAA0062 protein; Zip; TM=Y; SS=M; 2.54
- 415740; N80486; Hs.39911; Homo sapiens mRNA for FLJ00089 protein, partial cds; CBM_21; TM=M; 2.53
- 403305; NM_006825; transmembrane protein (63kD), endoplasmic reticulum/Golgi intermediate compartment; pkinase; TM=Y; SS=M; 2.53
- 443804; AL135352; Hs.255883; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; Peptidase_M18; Peptidase_M18_Y_phosphatase; 2.53
- 450425; H06607; Hs.6099; ESTs; E1-E2_ATPase, Cation_ATPase, C.Cation_ATPase_N_Hydrolase, none; 2.51
- 401702; ; NM_001171; Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 6 (ABCC6), mRNA; ABC_tran, ABC_membrane; TM=Y; SS=M; 2.50
- 439453; W63034; ; gb:zd46f01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone 5', mRNA sequence; fn3_Y_phosphatase, none; 2.50
- 425975; AB011082; Hs.165559; organic cationic transporter-like 4; sugar_tr; TM=Y; 2.50
- 443259; AW090601; Hs.69171; protein kinase C-like 2; pkinase, pkinase_C, HR1, none; 2.50
- 400777; ; NM_007325; Homo sapiens glutamate receptor, ionotropic, AMPA 3 (GRIA3), transcript variant flip, mRNA; lig_chan, SBP_bac_3, ANF_receptor; TM=M; SS=Y; 2.49
- 426044; AA502490; Hs.170280; ESTs; none, none; 2.48
- 454564; AW807573; ; gb:MR1-ST0088-021299-004-g01 ST0088 Homo sapiens cDNA, mRNA sequence; pkinase, none; 2.48
- 415938; BE383507; Hs.78921; A kinase (PKA) anchor protein 1; KH-domain, TUDOR; TM=M; SS=M; 2.47
- 426481; AW963941; ; gb:EST376014 MAGE resequences, MAGH Homo sapiens cDNA, mRNA sequence; Y_phosphatase, Band_41, DSPc, none; 2.46
- 426005; AA377499; ; gb:EST90341 Synovial sarcoma Homo sapiens cDNA 5' end, mRNA sequence; tubulin, FKBP, COX6B, 7tm_1, tubulin_C, SS=M; 2.46
- 424879; AA348013; Hs.273385; ESTs; arl-G-alpha, none; 2.46
- 415156; X84908; Hs.78060; phosphorylase kinase, beta; none; TM=M; 2.46
- 416508; R39769; ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; SH3, PDZ, Guanylate_kin, ZU5, none; 2.46
- 408087; AW150645; ; gb:xg54f07.s1 NCL_CGAP_U4 Homo sapiens cDNA clone 3', mRNA sequence; XYPPX, ABC_membrane, ABC_tran; 2.46
- 433434; AA588429; ; gb:nc02b03.s1 NCL_CGAP_Py22 Homo sapiens cDNA clone 3', mRNA sequence; pkinase, DNA_mis_repair, HATPase_c; 2.45
- 446768; AV660305; Hs.110286; ESTs; ICE_p20, DED, ICE_p10, ICE_p20, DED; 2.45
- 437158; AW090198; ; KIAA1150 protein; none; NA; NA; 2.45
- 430177; AW969233; Hs.302746; MSTP028 protein; K_tetra, none; 2.45
- 422270; AF114494; Hs.114062; protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a; none; TM=Y; 2.45
- 430680; AW138724; Hs.168974; ESTs, Highly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; Y_phosphatase, Adaplin_N_Y_phosphatase; 2.44
- 446589; AW248031; Hs.155839; hypothetical protein MGC12934; adh_zinc, PGK, Semaikhyde_dh; SS=M; 2.44
- 411902; AW875344; ; gb:RC1-PT0009-220300-013-06 PT0009 Homo sapiens cDNA, mRNA sequence; none, pkinase, ank; 2.43
- 430057; AW450303; Hs.2534; bone morphogenetic protein receptor, type IA (BMPRI1A) (ALK-3); Activin_rec, pkinase; TM=Y; SS=M; 2.43
- 446338; AL289121; Hs.206978; ESTs; none, SH3; 2.42
- 426221; AB007881; Hs.110613; KIAA0421 protein; none, Ribosomal_S8; 2.42
- 446796; AL652497; Hs.110103; RNA polymerase I transcription factor RRN3; none, none; 2.41
- 428360; H10291; Hs.30974; ESTs; pkinase, PBD, none; 2.40
- 428379; X06026; Hs.2259; CD3G antigen, gamma polypeptide (TIT3 complex); ITAM; TM=Y; SS=M; 2.40
- 432488; AA551010; Hs.216840; ESTs; Na_sulph_sym, none; 2.40
- 407235; D20569; Hs.169407; SAC2 (suppressor of actin mutations 2, yeast, homolog)-like; none, Ribosomal_S13, Galactosyl_T, Zip, adh_short, zf-C3HC4; 2.40
- 448595; AB014544; Hs.21572; KIAA0644 gene product; LRR, LRRCT; TM=Y; SS=M; 2.40
- 428283; AL430996; Hs.323079; Homo sapiens mRNA; cDNA DKFZp564P116 (from clone DKFZp564P116); Y_phosphatase, fn3, lg, none; 2.39
- 432460; H12912; Hs.274691; adenylate kinase 3; adenylate kinase, none; 2.38
- 429549; AL333013; Hs.250505; retinoic acid receptor, alpha; none, zf-C3HC4, BRCT, lig_chan; 2.38
- 429303; AW137635; Hs.44238; ESTs, Weakly similar to S65557 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; Phosphodiast, Somatomedin_B, Endonuclease, none; 2.36
- 417473; M55268; Hs.82201; casein kinase 2, alpha prime polypeptide; pkinase, ABC1; TM=M; 2.35
- 453186; AK001708; Hs.32271; hypothetical protein FLJ10846; TK, DUF300; TM=Y; SS=M; 2.33
- 447276; AL049795; Hs.17987; hypothetical protein MGC1203; none; TM=M; 2.33
- 445310; AL242490; Hs.153250; Homo sapiens cDNA FLJ14318 fis, clone PLACE3000402; none, pkinase; 2.31
- 432942; AF083955; Hs.279852; G protein-coupled receptor; 7tm_1, globin; TM=Y; SS=M; 2.30
- 434693; AW976001; Hs.337603; ESTs; none, none; 2.26
- 452034; F12234; Hs.75893; ankyrin 3, node of Ranvier (ankyrin G); ZU5, death, none; 2.25
- 423732; AF058056; Hs.132183; solute carrier family 16 (monocarboxylic acid transporters), member 7; sugar_tr; TM=Y; SS=M; 2.25
- 404958; ; C1003210; glj6912582[ref]NP_036524.1| peflin [Homo sapiens] glj6009487[kb]BAAB4922.1| (AB; none, PI3_P14_kinase, PI3K_C2, PI3K_rbd, PX, PI3Ka_C2; 2.24
- 452183; NM_006594; Hs.28298; adaptor-related protein complex 4, beta 1 subunit; Adaplin_N_Y_phosphatase; 2.23
- 420529; D25259; Hs.319844; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; pkinase, DAG_PE-bind, RBD, ras, DC1, GFP; TM=M; 2.21
- 408808; BE074219; Hs.17230; hypothetical protein FLJ22087; Armadillo_seg; TM=M; SS=M; 2.21
- 451932; AA360954; Hs.27268; Homo sapiens cDNA: FLJ21933 fis, clone HEP04337; SH3, PH, RhogEF; TM=M; 2.21
- 432008; AW295791; Hs.193170; hypothetical protein FLJ21687; LIM, Synaptophysin, lon_trans, KOW; 2.20
- 455840; BE145897; ; gb:MR0-HT0208-221299-204-b07 HT0208 Homo sapiens cDNA, mRNA sequence; PI3_P14_kinase, PI3Ka, PI3_P14_kinase, PI3Ka; 2.19
- 429236; NM_002849; Hs.198288; protein tyrosine phosphatase, receptor type, R; Y_phosphatase; TM=Y; SS=M; 2.19
- 430975; AA490055; ; gb:ab05b09.s1 Strata gene fetal retina 937202 Homo sapiens cDNA clone 3', mRNA sequence; adenylate kinase, Thymidylate_kin; TM=M; 2.17
- 407174; T79938; Hs.77062; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5; lg, none; 2.16
- 450921; AA098790; Hs.146245; ESTs, Moderately similar to T17242 hypothetical protein DKFZp586B1417.1 [H.sapiens]; none; NA; NA; 2.15
- 427209; H06509; Hs.92423; KIAA1566 protein; pkinase; TM=M; 2.14
- 401917; AL050149; ; RAN binding protein 3; Orexin, SH2, STAT, STAT_bind, STAT_pro, lon_trans, PAC, PAS, none; 2.12
- 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; adenylate kinase, none; 2.07
- 439520; W76548; Hs.336821; ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; lon_trans, none; 2.06
- 410439; R35943; Hs.63758; transferrin receptor 2; PA; TM=Y; 2.05
- 448599; AL564769; Hs.173070; EST, Weakly similar to ZN42_HUMAN ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1) [H.sapiens]; none, zf-C2H2; 2.04
- 449543; AF070632; Hs.23729; Homo sapiens clone 24405 mRNA sequence; K_tetra, lon_trans, none; 2.04
- 453498; AA442103; Hs.33084; solute carrier family 2 (facilitated glucose/fructose transporter), member 5; sugar_tr; TM=Y; SS=M; 2.02
- 443952; AL149106; Hs.143530; ESTs; pkinase, none; 2.02
- 437589; AA761322; Hs.269662; ESTs; SH2, SH3, C2, PH, RasGAP, none; 2.02
- 422637; AA399024; Hs.118836; myoglobin; globin; TM=M; 2.01
- 450253; AL133047; Hs.24715; Homo sapiens mRNA; cDNA DKFZp434D0215 (from clone DKFZp434D0215); partial cds; SH3; TM=M; 1.97
- 401894; ; C17000146; glj2143629[pri]A57156 Ca2+calmodulin-dependent protein kinase (EC 2.7.1.123) 1; pkinase; 1.96
- 453464; AB884911; Hs.32989; receptor (calcitonin) activity modifying protein 1; none; TM=Y; 1.95
- 417733; AL048678; Hs.82503; H.sapiens mRNA for 3'UTR of unknown protein; none; NA; NA; 1.94
- 411450; HA9619; Hs.127301; ESTs; pkinase, none; 1.82
- 406303; ; C16000922; glj7499103[pri]T20903 hypothetical protein F14F4.3b - Caenorhabditis elegans gl; ABC_tran, GTP_EFTU, PRK, ABC_membrane; TM=Y; 1.80
- 425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor type, M; fn3, lg, Y_phosphatase, MAM; TM=Y; SS=M; 1.74

425280; U31519; Hs.1872; phosphoenolpyruvate carboxykinase 1 (soluble); PEPCK;TM=M; 1.65
 425958; AW163271; Hs.301839; Intracellular antigen detected by monoclonal antibody Ki-1; Intracellular hyaluronan-binding protein; Y_phosphatase,DSpc;TM=M; 1.63
 432563; NM_013261; Hs.198468; peroxisome proliferative activated receptor, gamma, coactivator 1; rrm;TM=M; 1.51

5 TABLE 49B

Key: Unique Eos probates identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

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Pkey	CAT Number	Accession
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF165189 BE058931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AV676125 AI185720 AW510698 AA987230 BE467708 AW888628 AW898544 AI146584 AW043642 AI288245 AI186932 AI635262 AI39455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955833 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955833 D54678 D53933 R67100 BG925552 BF999056 R63430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581
411089	5597_6	BI009308 BI009893 BF922023 BF922909 BF922913 BF922096 BF957733 BE701791 AA456454 AA579876 BF933710 AA091294 BI007291 AW905577 AW975593 AA713730 AW836781 AA665384 AA551106 BF594606 AI082382 AI955808 AI679895 AI679386 BF435555 AA586369 AA551351 AA595822 AA565188 BF808855 AA584921 N86077 AA601031 AA633188 AA514764 AA454562 AA551297 AA936109 BI009389 AW897806 BE815442 BF739374 BI009310 BF925422 BF933709 BF922034 BF925465 BI009580 AF086101 AL133916 AW955684 AW950828 AI346341 AI867454 BM263376 BF432231 AI421279 AI655270 AW014882 BF439949 AA775552 N62351 AA626243 N59253 AI341407 AA456968 AA457077 AI358918 AA364013 N79113 N54784 BE175639 N76721 AV727392 Z45529 Z44343 F05908 F05403 F05398
438089	22448_4	BM475565 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW516902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG999664 H91240 R60548 N41701
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25	439096 425505 400208	1241997_1 1228213_1 16640_1	AW978432 AA830185 N67023 R80000 AL036458 AA358806 AW962990 X78817 NM_001666 D50921 AW002308 AW575456 BF507511 AW467767 A1910663 BF905778 BG251264 AL562106 A1890538 AW769258 A1590391 A1913055 AW083235 A1078474 A1925022 AW504628 AW129725 BE466589 AW002786 AW591760 A1968816 AW006268 AW593787 BG236814 AW769893 AW407608 AW075982 A1248207 A1762509 A1812070 A1249937 AW083561 AW080697 BF663046 BG745612 BG979546 AW793245 B1014177 AL519126 BE575314 AW806520 B1870778 BF879549 BE714919 BF847786 BG684161 AV695278 BG491029 BE793244 BE830893 BE798121 R09703 B1013066 A1758223 AW469334 BF940841 AW080348 A1270383 A1055892 BE464168 BF431797 BE350144 BF448739 A1693409 BF432999 D62848 AA398070 A1383375 AW611490 AA715338 AA715284 AA715344 AV752763 A1032142 N30308 N22181 H95390 AW675632 X98248 NM_002959 AU127082 AU143346 BE327147 A1168442 AA426361 BF056336 AA418378 A1470560 A1365213 B1032745 B1032986 AA969895 AA233278 AW291971 AA418326 A1198417 A1337018 B1032747 AA888000 AU099083 AU129681 AL038681 AA418275 BF887436 BF767448 AA232975 B1094055 B1859449 AL079651 BF877391 AW902319 BF878798 BG281450 AA418268 BG770672 BE890328 B1520437 BE387505 AW375004 B1020046 B1033747 BF800905 BF869732 N99710 BF905459 BE715637 BE746496 BF918537 BF751392 BF751390 BF369123 BG949840 AA984366 H85743 AW593418 A1990196 T92267 AA018359 H38111 BM050097 BF692315 AW805907 A1547305 AA631091 BF845219 BG949806 T92310 BE277220 U44839 NM_004651 BC000350 B1458316 AU117940 BG759024 BG749694 BE799505 BG831537 A1816335 AA325352 AL547005 AW157038 A1859331 A1816186 AU150786 AL043549 AW152880 AU159233 A143169 T03478 BE727648 AA764725 BE206603 A1369814 A1984369 AW157545 BE221486 H99016 AU159025 A1074496 A1494516 BE245950 AA704385 AA280862 A1479595 A1369776 BE671398 T05538 AA682249 B1677303 BE645335 A1359434 H92868 D52599 D53609 D54715 T06015 BE222174 A1954706 D53218 D53787 R69889 W86896 A1497670 R70771 BF309414 BE620147 BG910597 AW964968 BE836120 AL579715 H58512 D55956 B1044097 AL555239 BF220278 AA081991 A1819544 AW001573 AW131600 A1858764 D52367 W22034 BG818979 BG024561 BE702779 B1458863 B1910399 BG707755 BF348284 H10055 B1083615 BE620574 H41088 B119517 W23267 W21941 AA328817 X78817 NM_001666 D50921 AW002308 AW575456 BF507511 AW467767 A1910663 BF905778 BG251264 AL562106 A1890538 AW769258 A1590391 A1913055 AW083235 A1078474 A1925022 AW504628 AW129725 BE466589 AW002786 AW591760 A1968816 AW006268 AW593787 BG236814 AW769893 AW407608 AW075982 A1248207 A1762509 A1812070 A1249937 AW083561 AW080697 BF663046 BG745612 BG979546 AW793245 B1014177 AL519126 BE575314 AW806520 B1870778 BF879549 BE714919 BF847786 BG684161 AV695278 BG491029 BE793244 BE830893 BE798121 R09703 B1013066 AV659361 BE075267 BF743302 AL549208 A1950002 A1224961 A471552 A1356537 AA768943 AA677028 A1358509 A1147596 A1208057 A1042009 AA156840 AA156603 AA151281 AA151341 N73171 AL540476 A1950893 BG960775 AL573355 D78831 C17898 D78863 AW747857 B1062758 AW629481 AA837630 AA557850 AA531132 AW973986 AW747856 AA203524 W88451 BE539344 AA361027 BF328781 BE011405 BE011437 BE011402 BE011395 BE011428 BE011421 BE011407 BMD46773 AA224297 T33786 T08951 T09274 T08952 T30936 AA350905 NM_018485 AB038237 U69668 AA448366 X63105 BC016514 BE694436 A1555840 AW235355 BG427984 AA612862 AA448223 BM145813 BM194565 A1870824 BE973573 BM148408 AA448232 AA454176 AA740959 AA884391 AA808545 AW070759 BM144223 N75518 BE542983 BE241942 A124022 AA761687 BF908518 BF907890 R11490 AL536642 BF109180 AA953881 A1783716 BE822908 A1621005 AW148784 A1690114 AW275000 A1765790 BF222859 AW167268 A1990460 AW300443 AA779660 A1620568 BF115024 BE504703 AW628332 A1922851 BE006636 AU158376 A1168279 AA809916 A1469757 AA830828 AA830388 N64324 A1049683 AA970275 BF477364 BG261301 AA326388 AU150565 AU158374 AA687967 N58510 A1650450 AL549572 BF349280 BF349269 BM463016 AW836798 AL120598 AW836891 AW385525 BE175733 BE175727 BE175723 BF092430 B1061782 AU135358 BE175731 BE175754 BE175756 BE841747 BF798384 AU128251 BF095246 BG223262 AW047833 A1356643 AW366516 AW391532 BE934857 BF925057 AW438446 R86246 AW179270 BE087782 B1832144 AW956025 AW956024 BE550261 BF747649 BF802668 AA369961 AV747207 AW973072 BE467756 N51927 AA531539 AW241296 A1797097 B1492823 AW021886 F10837 BE715542 BE715487 AW087443 AA533638 R51354 AW131541 R51852 N53741 R39257 T77635 BF955795 BF331656 F13236 AW810749 AK055378 BE896053 AV722833 B1032095 BF952019 BG547204 A1151418 W03542 W60401 A1346936 AA862855 W60310 N72501 BF963436 C04881 H00600 AA001203 A1863984 A1932612 A1499771 A1187944 AA501896 AA714924 H00689 AA918680 AA573996 AA521308 AW182868 BF996707 AA908959 A1628880 AW173363 AW665845 AA130178 A1818267 A1653663 A1828924 AA746655 A1951984 A1635625 A1093113 A1377976 A1624029 A1418242 R76291 W92652 A1207798 AV708224 AA742467 AA641806 W61229 AA130170 AA160170 H85007 W72474 W61163 H97873 AL047509 R76567 AA812071 H81599 AA021275 H85004 H85894 BG537537 BF830518 W76228 W46673 Z43839 R78710 C01747 H00789 B1036345 W92828 BE150445 AW3080821 AW173095 H85630 H81598 H86032 R84855 R13223 AA774992 AW973785 H60163 AA557608 A1057052 A1241633 T89416 AA379611 AA379464 AA379463 BG025680 AW890852 BE002723 BE763824
587			

400275	18707_1	NM_006513 BC009390 X91257 BC000716 BM450041 BI771139 AV710955 AU120415 AU141179 AU121081 BE409287 AU141397 AU122238 BI256788 BE386217 AU143368 AU133780 AU139704 BG531086 BE268235 BE545230 AU143414 AV761720 AU129842 AU143343 BE270064 BG473378 BE298813 BI772360 BE617354 AU140124 BE277005 BG746716 BE814960 AW161287 AV762084 BG898985 AW674875 AA313975 AV749916 AA374328 BM011248 AU098465 AW238888 BG940091 BG284599 AW410037 AA378483 DA9914 AL573323 AL545819 AL572282 AL572871 AL568117 AL571945 AL547790 AL581217 AL514659 AL573926 AL540816 AW410038 BI262249 BG284713 AI659394 AI093582 AW965848 AA652206 AI686014 AA654357 AU146982 AW273447 AW157715 AW574750 BG683509 AW887824 AI818522 AA703770 BE542873 AA515504 AU154982 AA831254 AA828521 AI088602 AA854654 AA190869 BF062816 AA464944 BG261335 AI003584 BG402820 AA932098 W68695 AW182900 W37334 AI073864 C17924 C18528 AI299318 BF154399 BG319570 BF764242 BF764209 AI520320 T06029 BF447193 F29285 AL548949 BI333775 BE743602 BE618230 BE268139 BF036434 BE562718 BG774381 AA659833 AA297649 AA010945 BG105512 BE269205 T32623 BG015679 AL518518 AL517118 AL538396 AI049861 AL581976 AV752041 W26586 BE181609 AI963016 BG057603 AI720256 AA844560 AA055570 BE619606 C17428 AI042174 N33945 N69743 BF795208 AW057940 BI091359 AW975179 AA909938 H28712 W55445 AL515439 W37117 H66514 T85737 W37369 W19712 BE247277
5		L13288 AA928785 AI608912 AW872978 AA566555 AI022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805 R46356 AA418798 BM129553 BM129126 BM129292 BM128865 AI808418 AI689932 AI806573 BF431808 AW872985 AW166269 H73241 T16182 AI264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 AI797007 BE045543 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902 BI763932 BI910138 AW936035 AW935951 AW935789 AW935881 AW936018 AW935892 BE069084 BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031001 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445 BE078405 BE078404 BE168534
10		AV742719 R23027 R63874 AA381749 BG542693 D63271 T94955 AA774994 BF697879 BG984482 AW854930 AW854941 AW814115 AW814431 AW814190 BF325887 BF325890 BF985536 AW819463 AW819514 AW819617 AW819618 AW819609 U35637 AA192323 AA194508 BG011583 F25712 AI596820 BE185376 AA878324 AI619686 AI014377 T85948 R07785 T86972
15	414087 1632650_1 423387 2612_2	Y08200 NM_004581 BC003093 BE733834 BI753321 BG773890 BF091906 BI917541 AI023762 AA587230 BF435086 AI264262 AI687392 AI810536 AW589886 AI244419 AA749261 AA535435 AW205689 AI765770 AI765431 C02465 AW305347 AI818456 AA322111 AW381845 AW381829 AV749407 AA811636 AU159893 AA603065 AA652542 AI468878 R49616 AW381863 BE389867 BE182387 BF087771 AA527551 AA134051 AA831504 AA134052 AI871759 AW089048 BI913532 AA367709 BG288155 BF093014 AW837178 T77002 F13038
20	412263 1163164_1 409745 MH1944_5	AK056654 AJ420421 AI127111 AA705921 AA749298 AA776967 AI343768 AW070583 AA766587 AA804876 AA460658 AA394137 W72279 AW071467 AI343843 AA333817 AW763379 AA861873 AA715043 AW512448 AI452856 AI819873 T17354 AW779778 BF477620 AI783605 AI624523 AA261906 AA514931 BI964124 AW576481 AI864544 AA490883 AA850972 BI963076 AI632879 AA291985 AA255873 BI966876 BI963833 Z38970 BI495302 BI495301 AI784395 AI185472 AA652150 AA652026 D20449 BI088167 BI260636 BE869946 AI935271 BI792882 AI762915 AI809275 AI813351 BF447139 AI052089 AI057127 AA398950 AA291984 AA292934 AA262543 BF760287 R64455 R72980 H90786 BE698016 AW959314 BI031449 AL574617 AA776284 AA393770 BM455617 BI602104 BI793150 N36710 H59529 BI005937 BI000748 BF085914 BF085907 BF835429 BF835210 BF085926 AA226136 BF836829 BF836606 BM007373 AI369807 BF085930 W25119 B252884 BI001270 BE549079 BF238403 R56934
25	413285 12794_9 426578 358276_1 438005 694209_2 454701 352355_1 411140 1071177_1 407013 2073_7 432925 225876_1 417670 2139687_1 400189 2140_1	AF086341 W76326 W72300 NM_003899 D63476 BM456434 AA778936 AA452871 AI052466 AW014138 AA448725 BE673088 AW028198 BI856378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 AI032663 AA704686 AA652189 AA179463 AL535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE246232 D17055 AW013876 AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 AL044534 AA258853 BI037915 AA448037 BM461769 BI825965 BE763352 AW167531 Z45588 AV721881 AA527273 AI573219 AA457036 AW439651 AW264418 AA577618 AI802954 AA902292 AA468752 AI380374 AA722690 AI867708 AA916982 AI291576 AW190427 BI338089 AI653744 AI306665 AW513541 AW440077 AI370014 AA904269 AW188378 AI671644 AW193386 AI261832 AA775336 BF436811 AI582703 AI278635 BE440186 AA817898 AA648948 BI491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 AI369564 AW503675 AA777194 BE501048 BF222087 AA042973 AI868087 AA911480 Z41274 AI919082 T16746 AAA47634 AI282422 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916696 AW444935 M78398 AW581147 AW608258 AA651910 AA132152 AW806285 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW984920 AA325930 BI833627 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG888685 AA456880 BG001842 BF809452 AW882083 BF944342 T49551 W69981 BF764519 T15869 AA132030
30		AW954027 AA377709 AW848421 T71427 T62567 AW833022 AW833054 H20760 R15237 Z43915 BF372479 F11411 AB038318 BC008888 BE905346 BE301941 AA705936 AW014954 BE387842 AI720050 BE395327 BG951204 AK001451 AU151098 AW515640 AW439618 BI671555 AW504953 AA565885 AI829434 AW590882 AI889234 AW117522 AA847824 AI636224 AA883540 AA169387 AW771571 AI130803 BF438773 AA088710 AI972691 AI972638 AI762358 AI473907 AI925905 AA502277 BG943806 BG218468 AA194853 AU128875 AA306025 BG986896
35	411331 1076355_1 418177 6503_2	AA778849 AW946871 AW946782 AW946955 AF086283 W69200 W69304 AW807573 AW807572 AW963941 AA379825 AW963944 AA379564 NM_054014 X52220 BC005147 BI551326 AI393601 AW592611 AA608921 AA731698 W96331 AW590007 AI076813 AI022644 AA158365 AI699321 AI148747 AW296894 H85337 AA017692 AA354519 AA018512 D20081 R02704 AA825671 AA017651 AI135600 R02585 AA018849 BG749616 BF689840 R85326 AA677955 AA702354 AI076645 AI057359 H53178 WB6484 H53074 BG988909 AW962456 AA367328 AA377499 R39769 T53143 H60012
40		AW150845 AW811024 AW811148 AW811068 BF812525 AW504832 AI972567 AA588429 AI299694 AL050058 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021968 BF083327 BF593552 AA630766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602 AA962057 AW516069 AI582546 BF221924 BF222543 AI801808 AW468599 AW000736 AI866625 AW235356 BM021837 AA911956 AI680606 W86516 T03370 AW611634 HA1653 AI68349 H19588 AW090198 AW043993 R39847
45	439518 23842_1 400211 3532_1	AW875344 AW875287 AW875285 AW875286 BF381295 AW875402 AW875400 BE145816 BE145897 BF349721 BE145885 AK057266 BI767614 BI828586 AW069362 BI829572 AI826091 BI819382 AL040402
50		
55		
60	426409 320121_1 459357 1086411_1 411226 1073516_1 415518 1875286_1 433090 7504_2 436206 31207_1	
65	438141 1173217_1 439463 23351_1 454564 1061820_1 426481 1229053_1 426005 MH790_19	
70		
75	416508 1974161_1 408087 633688_1 433434 194862_1 437158 59575_1	
80	411902 1141058_1 455840 1518844_1 430975 56593_2	

TABLE 49C

5	Pkey:	Unique number corresponding to an Eos probaset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
10	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
	401027	7230983	Minus	70407-70554,71060-71160
	400991	8096825	Plus	159197-159320
	406137	9166422	Minus	30487-31058
15	404083	9944029	Minus	16650-17082
	404440	7528051	Plus	80430-81581
	400792	7382433	Plus	134339-134593
	404289	2769644	Plus	15049-15286,30267-30457
20	401083	3242744	Plus	33192-33360
	402211	7689783	Minus	67414-68229
	402705	8782736	Plus	89961-90114,90773-90895,91131-91261
	402233	7690102	Plus	90281-91477
25	405370	2078469	Minus	38980-39111
	400846	9188605	Plus	39310-39474
	405484	5922025	Plus	199214-199579,199672-199920,200262-20049
	401345	9926424	Plus	148042-148392
30	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,
	406384	9256114	Minus	50715-50833
	405490	7705240	Plus	20683-20850
	400755	8119083	Minus	120084-120889
35	404276	9885189	Plus	127624-127856
	402915	7406502	Minus	140-276
	405616	5649378	Minus	2782-3308
	400847	9188605	Plus	44643-44835
40	402328	4464283	Minus	13758-13922,14558-14752
	405369	2078469	Minus	34183-34357,35686-35751
	400845	9188605	Plus	34428-34612
	403716	7239689	Plus	86899-87122
45	402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
	404140	9843520	Plus	37761-38147
	405516	9454624	Plus	112707-112876,113676-113854
	405110	8096888	Minus	118940-119100
50	403608	8308266	Minus	121321-121476
	401241	4827300	Minus	30503-30844,31056-31248
	405102	8076881	Minus	120922-121296
	404185	4572584	Minus	129171-129327
55	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	405411	3451356	Minus	17503-17778,18021-18290
	405602	4753260	Plus	44647-44778
	403391	9438337	Plus	42410-42544,83317-83540,86840-86922,8797
60	403869	7280046	Minus	34379-34583
	404942	7382153	Plus	92085-92252
	403142	9444521	Plus	89286-90131
	400844	9188605	Plus	24746-24872,25035-25204
65	402704	8782736	Plus	37368-37493
	402833	8918545	Plus	26987-27778
	401851	7770425	Minus	148443-146664,147794-147971,148351-14848
	401242	4827300	Minus	32616-32863
70	401943	4914397	Plus	65925-66371
	402807	6456148	Minus	101542-101660,103476-103656
	402603	9909396	Minus	141663-141852
	405328	3253114	Plus	21399-21583
75	402974	9663349	Plus	124035-124321
	400987	8086488	Minus	22052-22185
	403335	8568884	Plus	112307-112524,114074-114703
	401113	9968541	Minus	19419-19969
80	401185	9625304	Minus	177393-177691
	404537	8247909	Minus	188775-189573
	405266	4156171	Minus	63337-63552
	402615	9926801	Plus	131390-132157
85	400566	9884730	Plus	64486-64714
	403212	7630897	Minus	156037-156210
	403290	8083176	Plus	19288-20076
	401342	9908882	Plus	3095-3242
90	400471	9931670	Minus	105629-105760
	405588	5002511	Plus	46180-46366
	400539	7574902	Plus	8559-8721
	403743	7652003	Minus	136463-136646
95	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
	405099	8074292	Minus	114365-114514,128635-128831
	401445	8218584	Minus	93700-93886
	405480	2766593	Plus	33325-33659
100	402183	7658390	Minus	100618-104298
	400749	7331445	Minus	9162-9293
	406139	9166758	Minus	72397-72602

5	402129	7704953	Minus	166156-166365
	400645	8117693	Minus	58471-58716
	403201	9958297	Minus	109782-109934
	403609	8308266	Minus	125974-126320
	400719	8118911	Minus	44579-44656,45294-45487,46449-46641
	403088	8954241	Plus	169894-170193,170504-170806
	403328	8469086	Minus	120428-120703
	403305	8099945	Plus	114632-114805
10	401702	1871197	Minus	68182-68325
	400777	8131663	Plus	70745-71121
	404956	7387343	Plus	55883-56203
	401917	9502466	Plus	25054-25229
	401984	4454511	Plus	103825-104024
15	406303	8575868	Plus	173622-173786

20 Table 50A lists about 414 genes up-regulated in non-seminomatous mixed germ cell testicular cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" non-seminomatous mixed germ cell testicular cancer to "average" normal adult tissues was greater than or equal to 2. The "average" non-seminomatous mixed germ cell testicular cancer level was set to the 85th percentile amongst non-seminomatous mixed germ cell testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

25 Table 51A lists about 518 genes up-regulated in seminomatous testicular cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" seminomatous testicular cancer to "average" normal adult tissues was greater than or equal to 2. The "average" seminomatous testicular cancer level was set to the 85th percentile amongst seminomatous testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

30 Table 52A lists about 673 genes up-regulated in testicular cancer (non-seminomatous and seminomatous) compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" testicular cancer to "average" normal testicular adult tissues was greater than or equal to 6. The "average" testicular cancer level was set to the 75th percentile amongst testicular cancers. The "average" normal adult testicular tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

35 Table 53A lists about 735 genes up-regulated in testicular cancer (non-seminomatous and seminomatous) compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" testicular cancer to "average" normal adult tissues was greater than or equal to 3. The "average" testicular cancer level was set to the 95th percentile amongst testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

40 Table 54A lists about 476 testis-specific genes downregulated in testicular cancer (non-seminomatous and seminomatous). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio (R1) of normal testis to normal adult tissues was greater than or equal to 3. R1 was calculated as the mean number of interquartile range values over the median normal adult body tissue expression among normal testicular samples. The ratio (R2) of "average" normal testis to "average" testicular cancer among these genes was greater than or equal to 2. The "average" normal testis level was set to the 50th percentile amongst normal testis. The "average" normal testicular cancer level was set to the 95th percentile amongst testicular cancer samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

45 Table 55A lists about 586 genes up-regulated in non-seminomatous mixed germ cell testicular cancer compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" non-seminomatous mixed germ cell testicular cancer to "average" normal adult testicular tissues was greater than or equal to 4. The "average" non-seminomatous mixed germ cell testicular cancer level was set to the 95th percentile amongst non-seminomatous mixed germ cell testicular cancers. The "average" normal adult testicular tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal testicular tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

50 Table 56A lists about 812 genes up-regulated in seminomatous testicular cancer compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" seminomatous testicular cancer to "average" normal adult testicular tissues was greater than or equal to 4. The "average" seminomatous testicular cancer level was set to the 50th percentile amongst seminomatous testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal testicular tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

55
60
65 TABLE 50A:
Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of non-seminomatous mixed germ cell testicular cancer compared to normal adult tissues

70	Pkey	ExAccn	UniGene	Unigene Title	R1
	432686	AW204069		ESTs, Weakly similar to unnamed protein	74.60
	432730	AJ066520	Hs.131358	ESTs	50.55
	450581	AF081513	Hs.25195	TGF-beta 4	47.85
75	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	44.05
	423458	AI204212		ESTs	35.60
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	30.60
	448981	AI968719	Hs.195387	ESTs	26.40
	407710	AW022727	Hs.23616	ESTs	24.00
80	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	19.35
	451105	BE382701	Hs.25960	N-MYC oncogene	18.85
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [Hsapi	18.40
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fs, clone HE	18.25

	424578	AK001973	Hs.150890	hypothetical protein	17.86
	418756	AA252254	Hs.226949	ESTs	17.20
	404996			Target Exon	16.15
	447534	AW953935	Hs.288655	ESTs	15.80
5	456847	AI360456	Hs.37776	ESTs	15.00
	446979	AI654443	Hs.197683	ESTs	14.80
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	14.75
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	14.70
	449322	AI638616	Hs.196566	ESTs	14.35
10	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	14.20
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	12.95
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	12.70
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	12.55
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	12.43
15	406547			Target Exon	12.35
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	12.10
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	11.65
	408908	BE296227	Hs.250822	serine/threonine kinase 15	11.55
20	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	11.05
	430676	AF084866		gb:Homo sapiens envelope protein RUC-3 (10.08
	426866	U02330	Hs.172816	neuregulin 1	10.05
	446791	AI632278	Hs.195922	ESTs	10.05
	433159	AB035898	Hs.150587	kinesin-like protein 2	9.85
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	8.95
25	427521	AW973352		ESTs	8.92
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	8.90
	427486	AA974433		fibroblast growth factor 4 (heparin secr	8.52
	425266	J00077	Hs.155421	alpha-fetoprotein	8.50
30	408465	AW196940	Hs.253277	ESTs	8.47
	444971	AI651116	Hs.148659	ESTs	8.35
	413318	AI076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	8.35
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	8.00
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.95
35	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	7.75
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	7.65
	407340	AA810168	Hs.284289	vitellogenesis-associated protein VIT-1	7.50
	453884	AA355925	Hs.36232	KIAA0186 gene product	7.36
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	7.25
40	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.22
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [Hs	7.13
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	7.13
	435918	AF263538	Hs.86232	growth differentiation factor 3	7.08
	412537	AL031778		nuclear transcription factor Y, alpha	7.05
45	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	6.88
	428916	AF003001	Hs.194562	telomeric repeat binding factor (NIMA-in	6.88
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.75
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	6.75
	437052	AA861697	Hs.120591	ESTs	6.75
50	425427	AI652662	Hs.157205	branched chain aminotransferase 1, cytos	6.72
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	6.71
	457465	AW301344	Hs.122908	DNA replication factor	6.62
	442832	AW206560	Hs.253569	ESTs	6.54
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	6.30
55	453913	AW004683	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	6.30
	448588	AI970276	Hs.156905	KIAA1676	6.12
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	6.09
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	5.95
	412642	BE244598	Hs.809	hepatocyte growth factor (hepatopoietin A;	5.85
60	443068	AI188710		ESTs	5.85
	438450	AI050868	Hs.65853	nodal, mouse, homolog	5.81
	441287	AW293132	Hs.131373	ESTs	5.80
	425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	5.76
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	5.75
65	436902	AW247145	Hs.192729	ESTs	5.70
	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	5.60
	440304	BE159984	Hs.125395	ESTs	5.60
	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	5.56
	436812	AW298067		gb:U1-H-BWD-ajp-g-09-0-ULs1 NCL_CGAP_Su	5.55
70	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	5.51
	431354	BE046956	Hs.251873	DNA (cytosine-5)-methyltransferase 3 be	5.51
	430044	AA464510	Hs.152812	ESTs	5.47
	437036	AI571514	Hs.133022	ESTs	5.45
	435663	AI023707	Hs.134273	ESTs	5.40
75	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	5.40
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.21
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	5.15
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	5.15
	430272	X04898	Hs.237658	apolipoprotein A-II	5.12
80	427951	AW293165	Hs.143134	ESTs	5.05
	424315	AW614850	Hs.193384	putative 26 kDa protein	5.05
	409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN !!!	5.00
	418477	AW022983		gb:U146h12.y1 Morton Fetal Cochlea Homo	5.00
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	4.95

5	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.94
	443537	D13305	Hs.203	cholecystokinin B receptor	4.92
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	4.90
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	4.85
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	4.80
10	449592	AI655494	Hs.195718	ESTs	4.75
	407300	AA102616	Hs.120769	gbzn43e07.s1 Stratagene HeLa cell s3 93	4.73
	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	4.68
	446700	AW206257	Hs.155326	Human DNA sequence from clone RP11-145L2	4.61
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.60
15	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.50
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.50
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-I	4.48
	402145			Target Exon	4.48
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	4.47
20	453289	AI188161	Hs.144627	ESTs	4.45
	430252	AI638774	Hs.105328	testes development-related NYD-SP20	4.40
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	4.32
	426427	M86699	Hs.169840	TTK protein kinase	4.30
	420047	AJ478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	4.20
25	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	4.18
	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (4.15
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.10
	438188	AA779975	Hs.128859	ESTs	4.10
	435514	AW592804		ESTs	4.10
30	442333	AI650877	Hs.129302	ESTs	4.06
	413627	BE182082	Hs.246973	Intron of Bicaudal D homolog 1	4.00
	445140	AI650599	Hs.197913	ESTs, Weakly similar to SCP3 MOUSE SYNAP	4.00
	448038	AW015073	Hs.232026	ESTs, Weakly similar to ROS2_HUMAN S2 KD	4.00
	458814	AJ498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	3.95
35	419423	D26488	Hs.90315	KIAA0007 protein	3.85
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	3.95
	441553	AA281219	Hs.121296	ESTs	3.95
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	3.91
	409757	NM_001898	Hs.123114	cystatin SN	3.89
40	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.88
	450351	BE547267	Hs.59791	hypothetical protein MGC13183	3.85
	403780			C4001759:gl 133250 sp P19474 ROS2_HUMAN	3.84
	421917	AB028943	Hs.109445	KIAA1020 protein	3.84
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	3.84
45	429120	AK001673	Hs.196530	hypothetical protein FLJ10811	3.82
	410193	AJ132592	Hs.59757	zinc finger protein 281	3.80
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	3.80
	415829	AW450198	Hs.163742	ESTs	3.78
	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT	3.77
50	439780	AL109888		gb:Homo sapiens mRNA full length insert	3.70
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.68
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.68
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	3.65
	420900	AL045633	Hs.44269	ESTs	3.65
55	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.65
	426496	D31765	Hs.170114	KIAA0061 protein	3.60
	452461	N78223	Hs.108106	transcription factor	3.60
	418379	AA218940	Hs.137516	fidgulin-like 1	3.50
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	3.48
60	428301	AW628666	Hs.98440	ESTs, Weakly similar to 138022 hypotheti	3.45
	419384	AA490866	Hs.39429	ESTs	3.44
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	3.43
	446293	AJ420213	Hs.149722	LIM domain transcription factor LIM-1 (h	3.41
	422094	AF129535	Hs.272027	F-box only protein 5	3.40
65	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.40
	423198	M81933	Hs.1634	cell division cycle 25A	3.39
	424153	AA451737	Hs.141496	MAGE-like 2	3.38
	417705	AW134952	Hs.175220	hypothetical protein FLJ14541	3.37
	443715	AI583187	Hs.9700	cyclin E1	3.34
70	420281	AI623693	Hs.323494	Predicted cation efflux pump	3.34
	449571	AW016812	Hs.200266	ESTs	3.34
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.31
	452807	AA028933	Hs.162434	ESTs	3.31
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	3.30
75	421650	AA781795	Hs.122587	ESTs	3.30
	418355	L42563	Hs.1165	ATPase, H7 transporting, nongastric, atp	3.28
	438494	AA908678	Hs.130183	ESTs	3.23
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.22
	433764	AW753676	Hs.39982	zinc finger protein RINZF (NM_023928)	3.20
80	427642	R40761	Hs.9834	ESTs	3.20
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	3.18
	403432			NM_001622:Homo sapiens alpha-2-HS-glycop	3.18
	442618	R56222	Hs.26514	ESTs	3.17
	415799	AA653718	Hs.225841	DKFZP434D193 protein	3.17
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	3.15
	450431	AW136797	Hs.266041	ESTs	3.13
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.12

	430835	AI240006	Hs.192326	ESTs	3.12
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.10
	417791	AW965339	Hs.111471	ESTs	3.10
5	434609	R76593		gb:yi60c11.1 Soares placenta Nb2HP Homo	3.05
	430253	AK001514	Hs.236844	hypothetical protein FLJ10552	3.04
	411975	AI916058	Hs.144583	ESTs	3.01
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	3.00
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	2.99
10	440207	AI371978	Hs.128326	ESTs	2.98
	435726	BE535787	Hs.113170	ESTs	2.97
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.97
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	2.95
	435373	AW665538	Hs.117689	ESTs	2.93
	452571	W31518	Hs.34665	ESTs	2.93
15	454679	AW813110		gb:CM4-ST0189-051099-021-05 ST0189 Homo	2.91
	414972	BE263782	Hs.77695	KIAA0008 gene product	2.90
	437496	AA452378	Hs.146668	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	2.90
	420092	AA814043	Hs.88045	ESTs	2.89
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	2.89
20	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	2.87
	422746	NM_004484	Hs.119651	glypican 3	2.87
	446258	AI283476	Hs.263478	ESTs	2.86
	444371	BE540274	Hs.239	forkhead box M1	2.86
	409517	X90780		troponin I, cardiac	2.85
25	414034	U89277	Hs.305985	early development regulator 1 (homolog o	2.84
	443169	AI038687	Hs.133338	ESTs	2.84
	447519	U46258	Hs.339665	ESTs	2.84
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.84
	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.83
30	416201	AA467752	Hs.195161	ESTs	2.83
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	2.82
	457191	AI376228		Friend leukemia virus integration 1	2.82
	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	2.81
	413646	BE155042		gb:PMO-HT0349-101299-002-E04 HT0349 Homo	2.80
35	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	2.75
	427719	AI393122	Hs.134726	ESTs	2.75
	451684	AF216751	Hs.26813	CDA14	2.75
	414590	NM_000506	Hs.76530	coagulation factor II (thrombin)	2.74
	442032	AW016786		ESTs	2.73
40	437123	AL049285	Hs.302053	Homo sapiens mRNA; cDNA DKFZp564M193 (fr	2.72
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	2.72
	442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	2.71
	438180	AA808189	Hs.272151	ESTs	2.70
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.69
45	423765	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.69
	420949	AA934093	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	2.68
	413813	M96955	Hs.75561	teratocarcinoma-derived growth factor 1	2.67
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	2.67
	445413	AA151342	Hs.12677	CGI-147 protein	2.66
50	448769	N66037	Hs.38173	ESTs	2.66
	411022	AW936378		gb:QV4-DT0021-301299-071-05 DT0021 Homo	2.65
	423600	AI633559	Hs.310359	ESTs	2.65
	447175	AI365208	Hs.293606	ESTs	2.65
55	414151	AW976468	Hs.257245	ESTs	2.65
	448877	AI583696	Hs.253313	ESTs	2.62
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	2.61
	440591	AA431599	Hs.132799	hypothetical protein FLJ23451	2.61
	449665	AI655391	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.61
60	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	2.60
	429228	AI553633		ESTs	2.60
	410929	H47233	Hs.30643	ESTs	2.59
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.58
	446142	AI754693	Hs.145968	ESTs	2.56
65	445093	AI207197		ESTs	2.56
	413686	AI469213	Hs.71404	ESTs	2.55
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	2.55
	420218	AW958037		ribosomal protein L4	2.55
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_U14 Homo sapiens	2.55
70	414312	AA155694	Hs.191060	ESTs	2.55
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide syntha	2.55
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	2.52
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	2.51
	435096	AA664977		gb:nu73b07.s1 NCI_CGAP_Alv1 Homo sapiens	2.50
	422468	AA355210		gb:EST63589 Jurkat T-cells V Homo sapien	2.50
75	449576	AW014631	Hs.225068	ESTs	2.50
	415684	D69356		sorbitol dehydrogenase	2.50
	452226	AA024898	Hs.157103	ESTs	2.50
	421451	AA291377	Hs.50831	ESTs	2.50
80	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.49
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.49
	453941	U39817	Hs.36820	Bloom syndrome	2.49
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.49
	449655	AI021987	Hs.59970	ESTs	2.49

	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	2.49
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	2.48
	414618	A1204600	Hs.96978	hypothetical protein MGC10764	2.48
5	445363	NM_005993	Hs.12570	tubulin-specific chaperone d	2.47
	452404	AW450675	Hs.212709	ESTs	2.46
	444823	BE262989	Hs.12045	putative protein	2.46
	427675	AW138190	Hs.180248	zinc finger protein 124 (H2F-16)	2.45
	444159	AF116846	Hs.10431	dead ringer (Drosophila)-like 2 (bright	2.45
10	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	2.45
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.45
	433183	AF231338	Hs.222024	transcription factor BMAL2	2.45
	447350	A1375572		v-erb-a avian erythroblastic leukemia vi	2.45
	428728	NM_016625	Hs.191381	hypothetical protein	2.43
15	407325	AA291180	Hs.328476	ESTs, Weakly similar to alternatively sp	2.43
	410276	A1554545		angiotensin-2	2.42
	444670	H58373	Hs.332938	hypothetical protein MGC5370	2.42
	419029	AA233397	Hs.326290	hypothetical protein FLJ12581	2.42
	437908	AJ082424		ESTs	2.41
20	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.41
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	2.40
	425212	AW962253	Hs.171618	ESTs	2.39
	423787	AJ295745	Hs.236204	nuclear pore complex protein	2.38
	425601	AW629485	Hs.140720	GSK-3 binding protein FRAT2	2.38
25	449676	AW380579	Hs.209657	ESTs	2.38
	429467	NM_004477	Hs.203772	FSHD region gene 1	2.37
	453227	AW135862	Hs.243991	ESTs	2.37
	417833	AW003251	Hs.86264	hypothetical protein FLJ14549	2.36
	451999	AW176401	Hs.27424	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.36
30	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.35
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	2.35
	410060	NM_001448	Hs.58367	glypican 4	2.35
	449138	AW294215	Hs.195631	ESTs	2.35
35	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.35
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	2.35
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	2.34
	410275	U85858	Hs.61796	transcription factor AP-2 gamma (activat	2.34
	407818	AL021938	Hs.40154	jumonji (mouse) homolog	2.34
	417777	AJ823763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	2.33
40	401704			NM_021195*Homo sapiens claudin 6 (CLDN6	2.33
	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	2.32
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.32
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	2.31
	429271	AF039850	Hs.198515	dead ringer (Drosophila)-like 1	2.30
45	432865	AJ753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	2.30
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.30
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	2.30
	448755	AW503807	Hs.21907	histone acetyltransferase	2.30
	403433			NM_001622*Homo sapiens alpha-2-HS-glycop	2.29
50	441031	AJ110684	Hs.7645	fibrinogen, B beta polypeptide	2.29
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.28
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	2.27
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.26
	401220			branched chain aminotransferase 1, cytos	2.26
55	453985	N44545	Hs.251865	ESTs	2.25
	414890	BE281095	Hs.77573	uridine phosphorylase	2.25
	409014	H83115	Hs.49760	origin recognition complex, subunit 6 (y	2.25
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	2.25
	424765	AA428211		hypothetical protein FLJ14033 similar to	2.25
60	419278	AU076799	Hs.1247	apolipoprotein A-IV	2.24
	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	2.24
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	2.23
	417273	AK002209	Hs.81831	Homo sapiens cDNA FLJ11347 fis, clone PL	2.23
	449722	BE280074	Hs.23960	cyclin B1	2.22
	443184	A1638728	Hs.131973	ESTs	2.22
65	416391	A1878927	Hs.79284	mesoderm specific transcript (mouse) hom	2.21
	440983	M20681	Hs.7594	solute carrier family 2 (facilitated glu	2.21
	435045	BE297155	Hs.143698	ESTs	2.21
	414883	AA926960		CDC28 protein kinase 1	2.21
70	446323	A1288274	Hs.345792	ESTs	2.20
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.20
	448757	A1365784	Hs.48820	TATA box binding protein (TBP)-associate	2.20
	450254	NM_004885	Hs.99231	neuropeptide G protein-coupled receptor;	2.20
	418973	AA233056	Hs.191518	ESTs	2.20
75	413582	AW295647	Hs.71331	hypothetical protein MGC5350	2.20
	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	2.20
	443748	AW206447		gb:UL-H-B11-afg-g-02-Q-ULs1 NCL_CGAP_Su	2.20
	415989	A1267700		ESTs	2.20
	400195			NM_007057*Homo sapiens ZW10 interactor	2.20
80	428878	AA436884	Hs.48926	ESTs	2.20
	431805	NM_014053	Hs.270594	FLVCR protein	2.19
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	2.19
	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	2.18
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.18

5	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	2.18
	413992	W26276	Hs.104557	RNA, U2 small nuclear	2.18
	412722	AJ343300	Hs.15091	ESTs	2.18
	409089	NM_014781	Hs.50421	KIAA0203 gene product	2.17
	430809	AJ791150	Hs.262009	ESTs, Moderately similar to I38022 hypot	2.17
	406542			C19000726*:g 12585552 sp Q9Y2Q1 Z257_HU	2.17
	420509	MB3554	Hs.1314	tumor necrosis factor receptor superfam	2.17
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypoteti	2.17
10	425580	L11144	Hs.1907	galanin	2.16
	439398	AA284267	Hs.221504	ESTs	2.16
	452833	BE559681	Hs.30736	KIAA0124 protein	2.15
	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	2.15
	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibitor	2.15
15	449410	AA001356	Hs.18159	ESTs	2.15
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypoteti	2.15
	427953	AA417944	Hs.44331	ESTs	2.15
	422281	M36803	Hs.346935	hemopexin	2.15
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	2.14
20	444960	AJ611317	Hs.341531	ESTs	2.14
	415890	H08225	Hs.268712	ESTs	2.14
	402099			ENSP00000217725*:Laminin alpha-1 chain p	2.14
	427779	AA906997	Hs.180780	TERA protein	2.14
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien	2.14
25	422170	AJ791949	Hs.112432	anti-Mullerian hormone	2.14
	414161	AA136106	Hs.184852	KIAA1553 protein	2.14
	437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	2.13
	449810	AB008681	Hs.23994	activin A receptor, type IIB	2.11
	450663	H43540	Hs.25292	ribonuclease H1, large subunit	2.11
30	419525	T79257	Hs.1259	asialoglycoprotein receptor 2	2.11
	424727	AW590378	Hs.152519	hypothetical protein FLJ20674	2.10
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.10
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	2.10
	430821	AA487264	Hs.154974	Homo sapiens mRNA; cDNA DKFZp687N064 (tr	2.09
35	418552	AF198254	Hs.86088	IGF-II mRNA-binding protein 1	2.09
	408291	AB023191	Hs.44131	KIAA0974 protein	2.09
	425474	Z48054	Hs.158084	peroxisome receptor 1	2.09
	453028	AB006532	Hs.31442	RecQ protein-like 4	2.09
40	447831	AJ433293	Hs.164115	ESTs	2.08
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.08
	429166	AB033096	Hs.197668	KIAA1270 protein	2.08
	432446	AA542845	Hs.294088	GAI protein	2.08
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.07
	431093	AB031038	Hs.301704	eomesodermin (Xenopus laevis) homolog	2.07
45	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	2.07
	449569	AI656634	Hs.195389	ESTs	2.07
	429999	AJ761902	Hs.99597	ESTs	2.06
	420552	AK000492	Hs.98806	hypothetical protein	2.06
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	2.05
50	406137			NM_000179*:Homo sapiens mitS (E. coli) h	2.05
	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.05
	450375	AA009647		a disintegrin and metalloproteinase doma	2.05
	409066	AA062980	Hs.66960	ESTs	2.05
	425700	AF076292	Hs.159251	forkhead box H1	2.05
55	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	2.05
	409093	BE243834	Hs.50441	CGI-04 protein	2.05
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.04
	408446	AW450669	Hs.45068	hypothetical protein DKFZp434I143	2.04
	417115	AW952792	Hs.334612	small nuclear ribonucleoprotein polypept	2.04
60	429840	AA459699	Hs.99496	ESTs	2.03
	409717	AW452871	Hs.56043	CGI-115 protein	2.02
	418113	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	2.02
	448275	BE514434	Hs.20830	kinesin-like 2	2.02
	432731	R31178	Hs.287820	fibronectin 1	2.02
65	405157			NM_003213*:Homo sapiens TEA domain fami	2.02
	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	2.01
	423739	AA398155	Hs.97600	ESTs	2.01
	421310	AW630087	Hs.103315	trinucleotide repeat containing 1	2.00
	457107	AA418246	Hs.185796	ESTs, Weakly similar to Z184_HUMAN ZINC	2.00
70	437257	AJ283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	2.00
	407259	LQ2256		gb:Human Fab fragment binding syncytial	2.00

TABLE 508:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
80	432666	144_7
	423458	30480_1
		AA558585 AA565499 AJ360576 AW204069 AAS91648 AA854939
		BC018070 BG702493 AJ204212 AA460929 AA993606 BF926635 AA226938 BG190705 BG188496 AW291865 BG183340 BG195301 BG214539
		BG215094 BG198867 BG196332 BG208220 BG212418

430676	60836_2	BG433950 BE061583 T05808 BE144813 AW812038 BE144812 AW812040 AW812041 AU124350 BE061602 BE061604 BF922595 BE061603		
427521	513212_1	AJ352469 BE061601 BI062752 AW818206 BF887722		
427486	684159_1	AW973352 BF222929 AW016853 BF059130 AJ651829 BE551767 AA558414 AI339359 BF059601 AJ961162 AI341422 AI206248 AI206165		
412537	14066_1	AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892		
		BF510715 BE673055 BE464111 AW590620 AI637939 AA404324 AW236441 AI650952 BF056796 AA974433		
		AK025201 AA425472 AI694282 BG057305 AA907787 AI286170 AI684577 AJ420494 AI809865 BF058095 AI478773 AI160445 AL044114		
		AW665529 AI129239 AW297152 AI268215 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AV759188 BI259364		
		BF445142 BG232065 AI141758 AI631202 AI167566 AI208445 AA889823 BF982682 N90322 BI090882 BF208005 AW953918 AL044113 AI016793		
		AA382556 AW235763 AA927051 AI862075 BE886691 BE619282		
		AV752763 AI032142 N30308 N22181 H95390 AW675632		
		AW978773 AW298067 AA810101 AW194180 AA731645 AI690673		
		BC022538 AI990847 BF478249 BG217996 BG212702 BG182057 AW589883 BF000085 AA993969 BG479023 BG220014 BG679466 BE907092		
		AI623855 AA223956 AA223917 AW022983 AW090580 AW573219 BF514491 BF445397 AA884705 AI910424		
		AA218925 AW952081 AA354237		
		AW954733 AA315006 AW856665		
		AA683356 AW592804 AI150287		
		AL109688 R23665 R26578		
		AF147390 R76593 R76594		
		AW813110 BF771370 BF771371 AW813113 AW003381		
		AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422		
		AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298		
		AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175		
		BF854337		
		NM_000363 X54163 M64247 AI265781 AI760600 AI367238 BE140258 AW207185 AI657074 C03333 AI193911 C05024 C03193 AI950215 C05070		
		C05613 W17389 C05351 AA311399 C04180 C04896 C05502 C05482 C04456 C04543 C04558 C04551 C03114 C03103 AI369979 AI652255		
		T12391 T12073 W19390 C02994 C02730 C04434 W07136 R57607 C03339		
		M31126		
		AI216469 AI354789 AA446136 H24336 AA446443 AI376228 R48940		
		AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523		
		BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866		
		AW840671		
		BE155042 BE155040 BE154987 BE155012		
		BF223060 BF222818 AI950472 AW016786 AI207136 AI969730 BF222890 AI633857 AI968711 AA974235 AI352637		
		AW936378 AW936544 AW813513		
		BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620		
		AW969605 AI553633		
		AI207197 BF773544 AW196462		
		AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756		
		AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727		
		H30075 AA684977 AW975278		
		AW962701 AA310998 AW962699		
		BF666746 D59356 BG678312 N56640 AA166861		
		AI375572 AI480404 BF430912 T06882		
		AA083514 AI554545 AW169852 AI363822 AI633826 AI656026 AI765624 AA147545 AA147552		
		AI740586 AA771806 BE500996 AW204531 AI082424 AI033879 BF093176 AA771764 D38676		
		T65754 AA229658 AA229857		
		AK021881 AU145974 AU145787 C16964 AA428211 AU119698 AA993264 BF999192 AW903017 AA346559 AU119446 AW581679 AA991677		
		AW898165 AW386878 AW890957 Z18340		
		AF274943 BG494894 AI719075 AA908783 AI935150 AA22691 AA910644 AA583187 BM272167 AI828996 AA527373 AW972459 AI831360		
		AA772418 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740617 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871		
		AI075239 AI339996 AA701623 AI139549 AI336880 AA533648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278887		
		AA459292 AI494230 BF507631 AI492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 N49682 AI457100 AW589407		
		AW300758 BE220715 BE220698 BE569091 BM009547 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363		
		BM467830 AI084433 AW206447 AI400976 AI248530 R16553		
		BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909960 BF095153		
		BG285837 AI720344 BF541715 AA355086 AA172236		
		BM477554 BM423967 BC020979 AF067656 NM_007057 BI869291 BG468263 BG760599 BI261788 AA855060 BE257094 BF212452 BE888249		
		BI259219 AW409765 BE089556 AL564377 BI258884 AW440401 AL578460 AL578434 AL556136 BG036804 AL531381 AW371767 BG610641		
		BF102552 BE294929 BF792282 BG121657 BG502285 BG777493 AL564510 AW770358 AA573448 AA564001 AA969560 AW078946 AW750065		
		AL573860 AA143778 H99221 AA969210 AW103401 AW750073		
		BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410		
		H59605 BE157601 AA113758		
65	TABLE 50C			
	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
70	NL_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	NL_position
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
	406547	7711513	Minus	172780-174358
75	402145	8018280	Plus	113086-114800
	403780	8076989	Plus	93160-93409
	403432	9719611	Minus	68204-68392
	401704	3097841	Plus	24712-25374
	403433	9719611	Minus	72225-72437
80	401220	9929324	Minus	48079-48279
	406542	7711499	Plus	117335-118473
	402099	8117697	Plus	121553-121742,123265-123423
	406137	9166422	Minus	30487-31058

405157 9966228 Plus 156363-156502,157573-157746

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TABLE 51A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of seminomatous testicular cancer compared to normal adult tissues

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	Pkey	ExAccn	UnigenelD	Unigene Title	R1
15	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	55.62
	432666	AW204069		ESTs, Weakly similar to unnamed protein	49.00
	432730	AI066520	Hs.131358	ESTs	37.64
	426534	U58096	Hs.2051	testis specific protein, Y-linked	37.60
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila))-like	32.70
20	420367	AA259090	Hs.257028	ESTs	29.98
	420347	AL033539	Hs.97124	Human DNA sequence from clone RP1-309H15	26.50
	437052	AA861697	Hs.120591	ESTs	26.42
	407710	AW022727	Hs.23616	ESTs	23.85
	420528	AF130728	Hs.98586	doublesex and mab-3 related transcriptio	23.12
25	424578	AK001973	Hs.150890	hypothetical protein	22.27
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	22.06
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	20.46
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	18.44
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	15.92
30	430252	AI638774	Hs.105328	testes development-related NYD-SP20	15.44
	423458	AI204212		ESTs	15.28
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	15.26
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	14.84
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	12.98
35	426427	M86699	Hs.169840	TTK protein kinase	12.44
	420401	AK001907	Hs.97464	hypothetical protein	12.40
	406937	U14622		gb:Human transketolase-like protein gene	11.60
	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	11.55
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	11.52
40	418477	AW022983		gb:d46h12.y1 Morton Fetal Cochlea Homo	10.94
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	10.78
	436812	AW298067		gb:U1-H-BW0-ajp-g-09-0-ULs1 NCL_CGAP_Su	10.54
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	10.40
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	10.32
45	421241	X91817	Hs.102866	transketolase-like 1	10.14
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	10.02
	418134	AA397769	Hs.86617	ESTs	9.76
	433159	AB035898	Hs.150587	kinesin-like protein 2	9.56
	433975	AA971953	Hs.122055	ESTs	9.36
50	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	9.30
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	9.22
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	9.16
	436899	AA764852		ESTs	8.76
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	8.76
55	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	8.64
	408908	BE296227	Hs.250822	serine/threonine kinase 15	8.50
	413627	BE182082	Hs.246973	intron of Bicaudal D homolog 1	8.42
	425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	8.30
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	8.14
60	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	8.14
	406547			Target Exon	8.02
	424153	AA451737	Hs.141496	MAGE-like 2	7.90
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	7.64
	437421	AA917062		ESTs	7.53
65	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.50
	419423	D26488	Hs.90315	KIAA0007 protein	7.38
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	7.38
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	7.32
	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (7.29
70	436608	AA628980	Hs.192371	down syndrome critical region protein DS	7.25
	435206	AI432364	Hs.160594	ESTs	7.20
	414972	BE263782	Hs.77695	KIAA0008 gene product	7.12
	407340	AA810168	Hs.284289	vitiligo-associated protein VIT-1	7.10
	426518	Z43039	Hs.170198	KIAA0009 gene product	7.10
75	436513	AJ278110	Hs.125507	DEAD-box protein	7.04
	427521	AW973352		ESTs	6.96
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	6.92
	422232	D43945	Hs.113274	transcription factor EC	6.90
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	6.83
80	431041	AA490967	Hs.197955	KIAA0704 protein	6.76
	427335	AA448542	Hs.251677	G antigen 7B	6.58
	422797	AB033064	Hs.236463	KIAA1238 protein	6.55
	418379	AA218940	Hs.137516	fidgetin-like 1	6.46

5	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	6.45
	433764	AW753676	Hs.39982	zinc finger protein RINZF (NM_023929)	6.44
	422665	AJ011812	Hs.119018	transcription factor NRF	6.38
	433701	AW445023	Hs.15155	ESTs	6.34
	436909	AA907120		ESTs	6.28
10	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	6.27
	429228	AJ553633		ESTs	6.26
	419384	AA490866	Hs.39429	ESTs	6.23
	435514	AW592804		ESTs	6.08
	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	5.90
15	430835	AJ240006	Hs.192326	ESTs	5.89
	438188	AA779975	Hs.128859	ESTs	5.88
	429120	AK001673	Hs.196530	hypothetical protein FLJ10811	5.80
	408758	NM_003686	Hs.47504	exonuclease 1	5.78
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	5.70
20	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	5.67
	428153	AW513143	Hs.98367	SRY (sex determining region Y)-box 17 (S	5.64
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	5.58
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	5.58
	419556	U29615	Hs.91093	chitinase 1 (chitinotriosidase)	5.55
25	438494	AA908678	Hs.130183	ESTs	5.52
	421974	AA301270		gb:EST14192 Testis tumor Homo sapiens cD	5.52
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	5.48
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	5.45
	413623	AA825721	Hs.246973	intron of Bicaudal D homolog 1	5.36
30	402145			Target Exon	5.30
	414136	AA812434		SMC2 (structural maintenance of chromoso	5.28
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	5.22
	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	5.16
	408460	AA054726	Hs.285574	ESTs	5.14
35	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	5.12
	420900	AL045633	Hs.44269	ESTs	5.08
	426496	D31765	Hs.170114	KIAA0061 protein	5.01
	407122	H20276	Hs.31742	ESTs	5.00
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	4.95
40	402199			Target Exon	4.90
	409103	AF251237	Hs.112208	XAGE-1 protein	4.90
	416859	H43437	Hs.80305	hypothetical protein MGC14258	4.84
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	4.82
	410929	H47233	Hs.30643	ESTs	4.73
45	417886	AA214584		ESTs	4.73
	426223	AW977812	Hs.130391	ESTs	4.72
	409421	AA199883	Hs.67624	ESTs	4.72
	428249	AA130914	Hs.183291	zinc finger protein 268	4.71
	429999	AI761902	Hs.99597	ESTs	4.68
50	431721	AB032996	Hs.268044	KIAA1170 protein	4.68
	408321	AW405882	Hs.44205	corlstatin	4.67
	419197	N48921	Hs.27441	KIAA1615 protein	4.66
	428329	AA426091	Hs.98453	ESTs, Moderately similar to R27328 2 [H.	4.64
	418235	BE072634		gb:PM4-BT0548-171299-001-h08 BT0548 Homo	4.64
55	427119	AW880562	Hs.272525	ESTs	4.64
	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.64
	414034	U89277	Hs.305985	early development regulator 1 (homolog o	4.64
	409066	AA062980	Hs.66960	ESTs	4.62
	416201	AA467752	Hs.195161	ESTs	4.53
60	433330	AW207084	Hs.132816	hypothetical protein MGC14801	4.52
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	4.50
	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	4.46
	415799	AA653718	Hs.225841	DKFZP434D193 protein	4.46
	412530	AA766268	Hs.268273	hypothetical protein FLJ13346	4.34
65	418221	Z45514	Hs.83775	DiGeorge syndrome gene D	4.32
	418971	AA360392	Hs.87113	ESTs	4.30
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (4.29
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	4.21
	415717	AA167270	Hs.130435	ESTs	4.18
70	423198	M81933	Hs.1634	cell division cycle 25A	4.12
	433849	BE465884	Hs.280728	ESTs	4.12
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	4.11
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	4.07
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	4.07
75	414725	AA769791		ring finger protein 21, interferon-respo	4.05
	408291	AB023191	Hs.44131	KIAA0974 protein	4.05
	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	4.04
	416773	AK000340	Hs.79828	hypothetical protein FLJ20333	4.04
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	4.03
80	421917	AB028943	Hs.109445	KIAA1020 protein	4.02
	430647	AC003682	Hs.127988	ESTs, Weakly similar to Z211_HUMAN ZINC	4.02
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	4.01
	436360	AI962796	Hs.156100	ESTs	4.00
	438624	AA889055	Hs.123468	ESTs	3.99
	434609	R76593		gb:yf60c11.1 Soares placenta Nb2HP Homo	3.92
	411945	AL033527	Hs.92137	L-myc-2 protein(MYCL2)	3.90
	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Homo	3.90

	413833	Z15005	Hs.75573	centromere protein E (312kD)	3.90
	421010	AW974553	Hs.267124	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.88
	438456	AA913381	Hs.20594	ESTs	3.88
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.87
5	412537	AL031778		nuclear transcription factor Y, alpha	3.86
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.85
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	3.83
	422094	AF129535	Hs.272027	F-box only protein 5	3.82
10	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.80
	416350	AF188625	Hs.189507	phospholipase A2, group IID	3.78
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	3.76
	401435			C14000397*:gij749898[pir]T33295 hypoth	3.76
	424557	AA343057	Hs.164588	ESTs, Moderately similar to neuronal thr	3.74
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	3.70
15	409089	NM_014781	Hs.50421	KIAA0203 gene product	3.70
	426067	AW664691	Hs.97053	ESTs	3.67
	415684	D59356		sorbitol dehydrogenase	3.66
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	3.62
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	3.62
20	427761	AA412205	Hs.140996	ESTs	3.61
	433641	AF080229		gb:Human endogenous retrovirus K clone 1	3.60
	418216	AA662240	Hs.283099	AF15q14 protein	3.59
	438180	AA808189	Hs.272151	ESTs	3.58
	424281	AA766243		gb:aa13b11.s1 NC1_CGAP_GCB1 Homo sapiens	3.56
25	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	3.55
	428878	AA435884	Hs.48926	ESTs	3.54
	438885	AI886558	Hs.184987	ESTs	3.53
	416445	AL043004	Hs.79337	KIAA0135 protein	3.52
	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	3.51
30	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	3.49
	427298	AA400495		ESTs	3.48
	420218	AW958037		ribosomal protein L4	3.40
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	3.40
	410420	AA224053	Hs.172405	cell division cycle 27	3.40
35	432809	AA565509	Hs.131703	ESTs	3.36
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	3.34
	421373	AA808229	Hs.46677	ESTs	3.34
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	3.31
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	3.30
40	431077	AI669133	Hs.115660	hypothetical protein FLJ12810	3.30
	418049	AA211467		Homo sapiens, Similar to nuclear localiz	3.26
	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypothi	3.22
	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	3.21
	434288	AW189075	Hs.116266	fibronin3	3.20
45	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	3.19
	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	3.17
	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	3.17
	420161	AI683069	Hs.120817	ESTs	3.17
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	3.16
50	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.14
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosi	3.14
	423419	R55336	Hs.23539	ESTs	3.13
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.12
	408092	NM_007057	Hs.42650	ZW10 interactor	3.12
55	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	3.12
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	3.12
	415912	H08859	Hs.208469	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.12
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.11
	420552	AK000492	Hs.98806	hypothetical protein	3.11
60	402408			NM_030920*-Homo sapiens hypothetical pro	3.10
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.10
	415829	AW450198	Hs.163742	ESTs	3.09
	423739	AA398155	Hs.97600	ESTs	3.07
	418459	R85436	Hs.268814	ESTs	3.07
65	421972	M18185	Hs.1454	gastric inhibitory polypeptide	3.07
	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	3.06
	429830	AI537278	Hs.225841	DKFZP434D193 protein	3.06
	420624	AB010575	Hs.98547	amiloride-sensitive cation channel 3, te	3.06
	433023	AW864793		thrombospondin 1	3.04
70	421633	AF121860	Hs.106260	sorting nexin 10	3.04
	420507	AF093408	Hs.98397	A kinase (PRKA) anchor protein 3	3.04
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	3.03
	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	3.03
	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (3.03
75	425312	AA354940	Hs.145958	ESTs	3.02
	425474	Z48054	Hs.158084	peroxisome receptor 1	3.01
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	3.01
	432446	AA542845	Hs.294088	GAJ protein	3.01
	424513	BE385864	Hs.149894	mitochondrial translational initiation f	3.00
80	436902	AW247145	Hs.192729	ESTs	3.00
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	3.00
	430056	X97548	Hs.228059	KRAB-associated protein 1	2.98
	427617	D42063	Hs.199179	RAN binding protein 2	2.98

	406367		NM_022357: Homo sapiens putative metalloprotease	2.97
	418866	T65754	gb:yc11c07.s1 Stratagene lung (937210) H	2.97
	435918	AF263538	Hs.86232 growth differentiation factor 3	2.97
	436511	AA721252	Hs.291502 ESTs	2.96
5	402680		Target Exon	2.96
	414161	AA136106	Hs.184852 KIAA1553 protein	2.95
	427239	BE270447	ubiquitin carrier protein	2.95
	433683	AI817723	Hs.22678 hypothetical protein FLJ21832	2.94
10	417576	AA339449	Hs.82285 phosphoribosylglycinamide formyltransferase	2.94
	402299		Target Exon	2.92
	420697	AA827705	Hs.26605 ESTs	2.90
	427719	AJ393122	Hs.134726 ESTs	2.90
	419131	AA406293	Hs.109526 ESTs	2.89
	410048	W76467	Hs.343874 proline oxidase homolog	2.89
15	427314	AB033024	Hs.175475 KIAA1198 protein	2.89
	424315	AW614850	Hs.193384 putative 28 kDa protein	2.88
	430335	D80007	Hs.239499 KIAA0185 protein	2.87
	410361	BE391804	Hs.62661 guanylate binding protein 1, interferon-inducible	2.87
	413686	AA469213	Hs.71404 ESTs	2.87
20	429183	AB014604	Hs.197955 KIAA0704 protein	2.86
	430292	AK000634	Hs.238270 hypothetical protein FLJ20527	2.86
	422726	U11690	Hs.1572 facio-genital dysplasia (Aarskog-Scott syndrome)	2.86
	437834	AA769294	gb:nz36g03.s1 NCL CGAP_GCB1 Homo sapiens	2.86
25	435159	AA668879	Hs.116649 ESTs	2.84
	428361	NM_015905	Hs.183858 transcriptional intermediary factor 1	2.84
	430388	AA356923	Hs.240770 nuclear cap binding protein subunit 2, 2	2.84
	434070	AF116652	Hs.270087 hypothetical protein PRO0813	2.83
	429323	NM_001649	Hs.2391 apical protein, Xenopus laevis-like	2.83
30	433247	AB040948	Hs.142856 KIAA1515 protein	2.82
	415884	H22966	Hs.13471 ESTs	2.82
	427668	AA298760	Hs.180191 hypothetical protein FLJ14904	2.82
	437162	AW005505	Hs.5464 thyroid hormone receptor coactivating protein	2.81
	401091		decay accelerating factor for complement	2.81
35	425601	AW629485	Hs.140720 GSK-3 binding protein FRAT2	2.79
	428597	AK000147	Hs.295909 hypothetical protein FLJ10700	2.79
	417705	AW134952	Hs.175220 hypothetical protein FLJ14541	2.79
	438243	AI581311	ESTs	2.78
40	418203	X54942	Hs.83758 CDC28 protein kinase 2	2.78
	410704	BE076754	gb:CM1-BT0601-180200-121-b10 BT0601 Homo	2.77
	429063	AW363845	Hs.322903 ESTs, Weakly similar to A46010 X-linked	2.76
	427147	AA398587	Hs.97414 ESTs	2.76
	430552	AA176374	Hs.243886 nuclear autoantigenic sperm protein (his)	2.76
	437660	W31708	Hs.55304 ESTs	2.74
45	425237	U07695	Hs.155227 EphB4	2.72
	419335	AW960146	Hs.284137 hypothetical protein FLJ12888	2.72
	426386	AA748850	Hs.125830 bladder cancer overexpressed protein	2.70
	423123	NM_012247	Hs.124027 SELENOPHOSPHATE SYNTHETASE ; Human selen	2.70
	430958	AW972830	gb:EST384925 MAGE resequences, MAGL Homo	2.70
50	420596	NM_002692	Hs.99185 polymerase (DNA directed), epsilon 2	2.68
	419741	NM_007019	Hs.93002 ubiquitin carrier protein E2-C	2.68
	401464		histone deacetylase 5	2.68
	411856	H67899	Hs.4190 Homo sapiens cDNA: FLJ23269 fis, clone C	2.68
	411365	M76477	Hs.289082 GM2 ganglioside activator protein	2.68
55	419029	AA233397	Hs.326290 hypothetical protein FLJ12581	2.67
	421654	AW163267	Hs.105469 suppressor of var1 (S.cerevisiae) 3-like	2.66
	421535	AB002359	Hs.105478 phosphoribosylformylglycinamide synthetase	2.66
	423453	AW450737	Hs.128791 CGI-09 protein	2.66
	412673	AL042957	Hs.31845 ESTs	2.65
60	410006	AW732308	Hs.57783 eukaryotic translation initiation factor	2.65
	434159	AW135214	Hs.191828 ESTs	2.65
	427260	AA663848	gb:aa70b06.s1 Stratagene schizo brain S1	2.64
	439053	BE244588	Hs.6456 chaperonin containing TCP1, subunit 2 (b)	2.64
	414706	AW340125	Hs.76989 KIAA0097 gene product	2.64
65	433979	AA620999	gb:ag03a08.s1 Soares_testis_NHT Homo sap	2.64
	403969		ENSP00000034663: Zinc finger protein 131	2.64
	420582	BE047878	Hs.99093 Homo sapiens chromosome 19, cosmid R2837	2.64
	418355	L42563	Hs.1165 ATPase, H7 transporting, nongastric, alp	2.63
	411127	AA668995	Hs.218329 hypothetical protein	2.62
70	437205	AL110232	Hs.279243 Homo sapiens mRNA; cDNA DKFZp564D2071 (f	2.62
	412123	BE251328	Hs.73291 hypothetical protein FLJ10881	2.61
	436481	AA379597	Hs.5199 HSPC150 protein similar to ubiquitin-con	2.60
	408446	AW450669	Hs.45068 hypothetical protein DKFZp434I143	2.59
	437033	AW248364	Hs.5409 RNA polymerase I subunit	2.58
75	418592	X99226	Hs.284153 Fanconi anemia, complementation group A	2.58
	415585	R59946	Hs.184852 KIAA1553 protein	2.57
	424800	AL035588	Hs.153203 MyoD family inhibitor	2.57
	426470	AA528794	Hs.128844 ESTs	2.57
	426919	AL041228	ELAV (embryonic lethal, abnormal vision, X-linked)	2.56
80	421209	AJ010230	Hs.102576 ret finger protein-like 1 antisense	2.56
	437496	AA452378	Hs.146668 Homo sapiens mRNA; cDNA DKFZp547J125 (fr	2.56
	401837		NM_025109: Homo sapiens hypothetical prot	2.56
	428743	AL080060	Hs.301549 Homo sapiens mRNA; cDNA DKFZp564H172 (fr	2.56
	422809	AK001379	Hs.121028 hypothetical protein FLJ10549	2.55

	418648	AW979223	Hs.292478	ESTs	2.55
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.54
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	2.54
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	2.54
5	428728	NM_016625	Hs.191381	hypothetical protein	2.53
	423755	AB037735	Hs.132560	hypothetical protein FLJ10312	2.52
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	2.52
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.52
	422406	AF025441	Hs.116206	Opa-interacting protein 5	2.52
10	433228	F28212	Hs.14953	KIAA1491 protein	2.51
	411943	BE502436	Hs.7962	ESTs, Weakly similar to S44608 C02F5.6 p	2.51
	426181	AA371422	Hs.334371	hypothetical protein MGC13095	2.50
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	2.50
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	2.48
15	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	2.48
	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	2.47
	435726	BE535787	Hs.113170	ESTs	2.47
	404068			Target Exon	2.46
	403137			NM_005381*:Homo sapiens nucleolin (NCL),	2.46
20	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	2.46
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.46
	429652	AA766810	Hs.259290	ESTs	2.45
	416204	AW972270	Hs.195161	ESTs	2.45
	414713	BE465243	Hs.12664	ESTs	2.44
25	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.44
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	2.44
	435244	N77221	Hs.187824	ESTs	2.44
	402679			NM_000478:Homo sapiens alkaline phosphat	2.43
30	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	2.42
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	2.41
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisocu	2.41
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.41
	423232	BE244625	Hs.125742	leucine-rich neuronal protein	2.40
	427578	AI591305	Hs.169084	ESTs, Highly similar to TUL3_HUMAN TUBBY	2.40
35	409934	R91601	Hs.190466	hypothetical protein FLJ22584	2.39
	423787	AJ295745	Hs.236204	nuclear pore complex protein	2.39
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	2.39
	438869	AF075009		gb:Homo sapiens full length insert cDNA	2.38
40	434981	AW182577	Hs.293077	ESTs	2.38
	417911	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (2.37
	409210	AA251812	Hs.51120	cathelicidin antimicrobial peptide	2.37
	424425	AB031480	Hs.146824	SPR1 protein	2.37
	411885	AA452636	Hs.131057	ESTs, Moderately similar to CRGD_HUMAN G	2.37
45	421567	AJ272137	Hs.198265	matrix metalloproteinase 25	2.37
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.37
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	2.36
	431197	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k	2.36
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	2.36
50	410668	AA199907	Hs.67397	homeo box A1	2.36
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	2.36
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	2.36
	412389	AW947655		gb:RCO-MT0003-140300-031-b07 MT0003 Homo	2.35
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.35
55	403780			C4001759:gi133250 sp P19474 RO52_HUMAN	2.34
	437681	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	2.34
	400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	2.34
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sans	2.34
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.34
60	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	2.33
	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	2.33
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.32
	418821	AA436002	Hs.183161	ESTs	2.32
	437437	AA226889		hypothetical protein DKFZp762L0311	2.31
65	413437	BE313164	Hs.75361	gene from NF2/meningioma region of 22q12	2.31
	425848	BE242709	Hs.159637	valyl-tRNA synthetase 2	2.30
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	2.30
	430183	BE010039		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	2.30
	409342	AU077058	Hs.54089	BRCA1 associated RING domain 1	2.29
	430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	2.29
70	427726	AJ359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	2.29
	417115	AW952792	Hs.334612	small nuclear ribonucleoprotein polypept	2.28
	412721	AW183165	Hs.95600	ESTs	2.28
	404071			C12000514*:gi17302471 gb AAF57556.1 (AE	2.27
75	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.26
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.26
	424935	AI655010	Hs.120363	hypothetical protein MGC15634	2.26
	415791	H09366	Hs.78853	uracil-DNA glycosylase	2.26
	431667	AA812573	Hs.246787	ESTs	2.25
	424169	AA336399	Hs.153797	ESTs	2.25
80	436540	BE397032	Hs.14468	hypothetical protein MGC14225	2.25
	418113	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	2.24
	403242			Target Exon	2.24
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	2.24

5	421002	AF116030	Hs.100932	transcription factor 17	2.24
	438833	BE612940	Hs.88252	ESTs	2.24
	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	2.23
	433844	AA610175	Hs.179647	Homo sapiens cDNA FLJ12195 fis, clone MA	2.23
	427528	AJ077143	Hs.179565	minichromosome maintenance deficient (S.	2.23
10	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	2.23
	421016	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	2.23
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.23
	418826	AK000375	Hs.88820	HDCMC28P protein	2.23
	428612	AA770001		ESTs	2.22
15	433220	AJ076192	Hs.131933	ESTs	2.22
	422225	BE245652	Hs.118281	zinc finger protein 266	2.22
	437549	AA759149	Hs.128757	gb:rah70e03.s1 Soares_testis_NHT Homo sap	2.22
	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.22
	408665	T88845	Hs.112200	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.22
20	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	2.21
	420062	AW411096	Hs.94785	TGF(beta)-induced transcription factor 2	2.21
	432820	AI554057	Hs.152477	ESTs	2.21
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	2.21
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.20
25	407275	AJ364186		gb:qxw34h07.x1 NCL_CGAP_U14 Homo sapiens	2.20
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	2.20
	423675	AI905059	Hs.131342	small inducible cytokine subfamily A (Cy	2.20
	433698	H24201	Hs.247423	adducin 2 (beta)	2.19
	409101	NM_004297	Hs.50612	guanine nucleotide binding protein (G pr	2.19
30	435541	AA687361	Hs.221318	ESTs	2.19
	412019	AA485890	Hs.69330	Homo sapiens cDNA FLJ13835 fis, clone TH	2.19
	418753	BE217818	Hs.87016	hypothetical protein FLJ22938	2.19
	435461	AJ075846	Hs.133996	ESTs	2.19
	402260			NM_001436:Homo sapiens fibrillarin (FBL	2.18
35	421098	AI697901	Hs.192425	ESTs	2.18
	400587			C10000649:gij7296574[gb]AAF51857.1] (AE	2.18
	407832	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	2.18
	427159	U80735	Hs.173854	PAX transcription activation domain inte	2.17
	405770			NM_002362:Homo sapiens melanoma antigen,	2.17
40	412722	AJ343300	Hs.15091	ESTs	2.16
	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	2.16
	438192	AI859065	Hs.293807	Homo sapiens AFG3L1 isoform 1 mRNA, part	2.16
	417420	T85150	Hs.268814	ESTs	2.16
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	2.16
45	412851	AI826502	Hs.97269	ESTs	2.16
	414702	L22005	Hs.76932	cell division cycle 34	2.16
	409670	AI368109		KIAA1856 protein	2.16
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	2.15
	417863	AB000450	Hs.82771	vaccinia related kinase 2	2.15
50	434750	BE019254	Hs.4112	t-complex 1	2.15
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	2.15
	418574	N28754		M-phase phosphoprotein 9	2.15
	409019	AW385412		myosin regulatory light chain 2, smooth	2.15
	416608	R11499	Hs.189716	ESTs	2.14
55	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse l	2.14
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	2.13
	422805	AA436989	Hs.121017	H2A histone family, member A	2.13
	410284	U50939	Hs.61828	amyloid beta precursor protein-binding p	2.13
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	2.12
60	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	2.12
	433252	AB040957	Hs.151343	KIAA1524 protein	2.12
	416819	U77735	Hs.80205	plm-2 oncogene	2.12
	437218	AL117497	Hs.58185	ESTs, Weakly similar to T42727 prolifera	2.12
	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	2.12
65	433947	AA927996	Hs.112876	ESTs, Weakly similar to AF129535 1 F-box	2.11
	424727	AW590378	Hs.152519	hypothetical protein FLJ20674	2.11
	435703	AW630133	Hs.83313	GK003 protein	2.11
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.11
	422192	AA305159	Hs.113019	fts485	2.11
70	407961	AW672939	Hs.41694	origin recognition complex, subunit 2 (y	2.10
	410193	AJ132592	Hs.59757	zinc finger protein 281	2.10
	414151	AW976468	Hs.257245	ESTs	2.10
	434789	AW292515	Hs.194317	ESTs, Weakly similar to T08680 hypotheti	2.10
	424196	AL133660	Hs.142926	Homo sapiens beta cysteine string protei	2.10
75	408831	AF090114	Hs.48433	endocrine regulator	2.09
	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	2.09
	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	2.09
	409637	AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	2.09
	403532			NM_024638:Homo sapiens hypothetical prot	2.09
80	432141	BE410964	Hs.272736	nuclear receptor binding protein	2.08
	409014	H83115	Hs.49760	origin recognition complex, subunit 6 (y	2.08
	410575	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	2.08
	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	2.08
	418755	Y14443	Hs.88219	zinc finger protein 200	2.08
	406137			NM_000179:Homo sapiens mutS (E. coli) h	2.07
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	2.07
	421413	AI826128	Hs.55209	ESTs, Weakly similar to A49364 59 protei	2.07

5	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	2.07
	417230	U40988	Hs.81728	unc119 (C.elegans) homolog	2.07
	425966	NM_001761	Hs.1973	cyclin F	2.07
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	2.06
	407162	N63855	Hs.142634	zinc finger protein	2.06
10	422382	D79988	Hs.115778	KIAA0166 gene product	2.05
	402677			NM_000478:Homo sapiens alkaline phosphat	2.05
	433017	Y15067	Hs.279914	zinc finger protein 232	2.05
	424577	U09414		zinc finger protein 137 (clone pHZ-30)	2.05
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.05
15	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.05
	402678			Target Exon	2.05
	408146	R45621	Hs.81057	hypothetical protein MGC2718	2.05
	420027	AF009746	Hs.94395	ATP-binding cassette, sub-family D (ALD)	2.04
	427447	T65414	Hs.6647	Homo sapiens cDNA FLJ13088 fis, clone NT	2.04
20	433219	AB040916	Hs.24106	KIAA1483 protein	2.04
	431126	AF085243	Hs.283619	zinc finger protein 236	2.04
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	2.04
	419669	AJ007041	Hs.92236	KIAA0304 gene product	2.04
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.03
25	426242	AL096727	Hs.168249	Homo sapiens mRNA; cDNA DKFZp434B104 (fr	2.02
	432185	AA221032	Hs.272838	hypothetical protein FLJ10494	2.02
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	2.02
	408636	BE294925	Hs.46680	CGI-12 protein	2.02
	420005	AW271106	Hs.133294	ESTs	2.02
30	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.02
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	2.02
	425358	AL079658	Hs.338207	FK506 binding protein 12-rapamycin assoc	2.01
	409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	2.01
	438450	AJ050896	Hs.65853	nodal, mouse, homolog	2.00
35	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	2.00
	424934	U75370	Hs.153880	polymerase (RNA) mitochondrial (DNA dire	2.00
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	2.00
	414251	AL042306	Hs.97689	VASA protein	2.00

TABLE 51B

Key: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Key	CAT Number	Accession
40	432666	144_7
	423458	30480_1
	418477	4172_1
	436812	659779_1
	436899	1000797_1
50	437421	978554_1
	430676	60836_2
	427521	513212_1
	436909	596835_1
	429228	215430_1
55	435514	132288_1
	422689	874209_1
	421974	864120_1
	414136	30243_1
	417886	1031334_1
60	418235	886897_1
	414725	19377_1
	434609	14739_1
	408055	101881_1
	412537	14066_1
65	415684	18695_18
	433641	35983_1
	424281	892055_1
	436291	BE568452
	414251	AL042306
70	436812	659779_1
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	430676	60836_2
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	422689	874209_1
	421974	864120_1
80	414136	30243_1
	417886	1031334_1
	418235	886897_1
	414725	19377_1
	434609	14739_1

5	427298	115241_1	AA933717 BF061897 AW628327 AA641788 AA400495
	420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA458950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756
	418049	12052_4	AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
	433023	3970_8	AJ314647 NM_052888 BI494693 AA835065 AI634477 AI336678 AI807696 BF477887 AI701147 Z39187 R38979 F02234 AA984711 BI222234
	418866	245947_1	AV731417 R42406 HD4996 T98498 R12489 R12577 R42405
10	427239	20459_2	BE999967 BF438599 AW864793 AI802899 BE815132 AW468888 AI672189 AI052004 BF112024 AA772335 AW275054 AA573845 AI144148
			AI968683 AA846876 AA927355 H80424 AW973295 R88209 F29868 BE928871
			T65754 AA229658 AA229657
			AL532350 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881
			AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478
15			AI251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839
			AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420
			AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260
			AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427
			BF187773 BF18645 AW074868 BE857822
20	437834	294580_1	BG110129 AW749287 BE535498 AW749299 AW749293 AW749302 AW749298 AW749291 AW749294 AW749289 AW749288 AW749296
			AA769294 AW749297 AW749295 AW749292 BE002573
	438243	2532601_1	AI581311 AA781682 AA781678
	410704	1054673_1	AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
			BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877458 AW877537 BE076866
25	430968	1237115_1	AW840571
	427260	11272_50	AW972830 AA489820 AA527647 AA570362
	433979	2076469_1	AA401424 AA400100 AA663848
	426919	347372_1	NS0454 AA620999 T16375
			BI917595 AI203314 AL041228 AV727959 D61361 D82004 BI753157 AA961066 AI990307 BF439651 AI453076 AI376075 AI014836 AI018308
30	438869	52134_1	AW183530 AA393346 AA935601 AA628633 AI150282 AI028574 AI217182 AA431478 AW087473 AW900295 H50055 AL041229 BI917726
	412389	1174403_1	AF075009 R63109 R63068
	400205	2538_1	AW947655 AW984020
			NM_006265 D38551 X98294 BM477931 BM461566 AU123557 AU133303 AU134649 AW500421 BM172439 AW500587 AW503665 AW504355
			AW503640 BM152454 AW505260 AI815984 AW504075 AW500716 AL597310 BC001229 BM474371 AA984202 AU135205 BE090841 AW163750
35			BF747730 BF898637 AI206506 AV660870 AV692110 AW388830 AV656831 NB4710 AW993470 BF086802 BF758454 BG960772 BF757769
			BI870853 BE018627 C75436 AW148744 BF757753 BG622067 BE909924 AA708208 BG530266 BF968015 AW992930 BF888862 BG536628
			AA143164 AW748953 BG498922 BF885190 BF889005 BF754781 BF800003 BM476529 AI527668 AW028126 AL046011 BF590668 AI017447
			AA579936 AI367597 AA699622 BE280597 AI24620 AI082548 AW274985 AA677870 AI056767 BE551689 AA287642 H94499 AI752427 AI652365
			AW002374 AW062651 AA360834 N68822 AU135442 AU125960 Z78334 BE545813 AI092115 BF312771 BF242859 BG533616 BG533761
40			BG164745 BG492433 BM473183 AA172043 AA172069 AU157092 AU151353 AU155318 BE302211 AI375022 AA085641 AU157923 H88858
			AA132730 AA115113 AA909781 AI475256 AA424206 AW572383 AW084296 AI184820 AI469178 AA782432 H92184 AA340562 BF195818
			AA852821 AW576342 AA827107 AA173317 AW190014 AI918514 AA729372 AA729718 AI055958 AA331424 BE328601 AA515690 BI018896
			AW628277 AA748368 AA626222 BG492636 AW380620 BF800058 AW370956 AA290909 R25857 BG952995 BF801437 AA172077 AU155890
			AU149783 AI720904 AA902936 AA865727 AI470830 AV740677 AA142982 AA482485 AU145485 AW576399 AU156042 R63448 BF246427
45	425331	1227464_1	BE928472 D25910 BF758439 BF968785 BE565238 AA355981 AI905607 BG291148 BG533096 BG532888 BF030886 BG613756 BE928471
	437437	6087_1	BG574501 AA187596 AA361196 T95557 BG531446 BG527242 BG527513 BG611106 AA085995 BF847252 BG024608 BE540261 BG531236
			AL579993 BG108733 BG483503 BG571032 BG492505
			AA427363 AW962128 AA355353
			BC009352 BC014630 AU131857 AL527140 AU131768 BI769362 BI753220 AU129886 AU128771 AA314135 AU126819 AI333799 AA479336
50			AA258503 AL597351 AL359619 BG697218 BI254283 AI743846 AA236444 AA397533 AA247450 AI051464 AI224533 AU153442 AU151001
			AU152621 AU151829 AU153069 AW269958 AU154195 AI862754 AI589780 AW273839 AI338155 AI126632 BE046048 AA976930 AI289304
			AI625961 AI222288 AI280054 AA973329 AI524262 AI242371 AA296517 AI567865 AI590681 AJ346616 AW247913 AI422051 AI475352 AI689531
			AW469308 AW198034 AA936939 AU151059 AU148134 AA486419 AU151953 AI830968 BI493265 BI493264 AU149861 BE268763 AV763495
			AW962827 BM480300 AA226869 AL529368 BM451957 AU132714 BI871319 AA380739 BI911351 BF795906 BE548653 AW579751
55	430183	17316_1	AK055746 AA039909 BE183282 W60721 AA464867 AA398986 T67280 BF995651 AI675065 BG001051 BF764727 BF766707 BF764717 BF764852
	430504	5477_6	BF173139 BE010038
			BE219720 BF475241 AI571723 BE219848 BI789268 AI224899 AA724864 AW771467 AA480255 AW845616 AI440295 H52800 BE218790 AI681575
	428612	1383189_1	AW300064 AW262133 H21568 AI363015 AI884914 H86948
	409670	8882_8	AA770001 AA431112 AA432126
60			AI625045 AW504152 AI469086 AA905873 AW504662 AW136114 AI927270 BE041754 AI648386 AA662655 AA400052 AI143501 AI744934
	418574	12009_2	AI400147 AI381657 AA676551 AA974367 AW117437 AI570383 AI242456 AI274581 AA678138 R49939 AI393928 AA345854 AW605850 AI869780
	409019	32320_4	AW391171 R77044
			AW955043 AI990326 AA776406 AI016250 AW451882 AA843678 BF916900 AW945895 AI979339 N23129 W70051 AA322672 N23137
			BM480413 N28908 H39792 BE240826 BE882093 BE240827 AW868637 BF739795 AA700834 AA769597 AA489668 AW968806 AW085196
65			AI093280 AI218457 AA063138 AI632958 AW515005 AI570530 Z41724 AA748789 AI696584 AA062544 AA773643 AA490285
	430935	15297_3	BC017923 AA789302 AW466994 BF513878 AI819642 AI184913 AW469044 AI205072 AW072916 AI280239 AI473611 AW841126 D60937
			AA489195 N59350 AA693435 BG531204 AA484243 AW514092
	424677	2518_37	U09414 NM_003438 AA503545 AI022449 AA043458 AA768074 AA765442 AA805052 AI028211 AW609708

TABLE 51C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

75	Pkey	Ref	Strand	NL_position
	406547	7711513	Minus	172780-174358
	402145	8018280	Plus	113086-114600
	402199	8576116	Minus	84187-84744
	401435	8217934	Minus	54508-55233
80	402408	9796239	Minus	110326-110491
	406367	9256126	Minus	58313-58489
	402680	8113438	Plus	137634-137768,139702-139893,140475-14059
	402299	6693370	Plus	23367-25175
	401091	9958240	Plus	94760-94898

5	401464	6682291	Minus	170688-170834
	403969	8569909	Plus	31237-31375,32405-32506
	401837	7630990	Minus	120893-121095,121660-121729
	404068	3168621	Minus	18123-18766
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,9394
	402679	8113438	Plus	132079-132216
	403780	8076989	Plus	93160-93409
	404071	7210053	Minus	167354-167859,168810-168920,169000-16910
10	403242	7637817	Minus	11297-12511
	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
	400587	9887626	Plus	25435-25588,25668-25747
	405770	2735037	Plus	61057-62075
	403532	8076842	Minus	81750-81901
	406137	9166422	Minus	30487-31058
15	402677	8113438	Plus	22135-22309,23063-23238
	402678	8113438	Plus	37395-37514,37866-37981

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TABLE 52A:

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

25

R1: Ratio of testicular cancer (non-seminomatous and Seminomatous) compared to normal adult testicular tissues

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
30	414438	AI879277	Hs.76136	thioredoxin	51.77
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	49.93
	416680	AW245540	Hs.79516	brain abundant, membrane attached signal	49.20
	412948	BE243313	Hs.334851	LIM and SH3 protein 1	44.46
	438091	AW373062		nuclear receptor subfamily 1, group I, m	40.70
35	406658	AI920965	Hs.77961	major histocompatibility complex, class	39.64
	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	38.70
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	38.25
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	37.50
	430542	AI557486	Hs.119122	ribosomal protein L13a	37.22
40	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	35.98
	432730	AI066520	Hs.131358	ESTs	35.25
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	31.69
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	31.33
	417088	M54915	Hs.81170	pim-1 oncogene	31.20
45	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	29.93
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	29.35
	426295	AW367283		zinc finger protein 6 (CMPX1)	29.32
	406856	AW515336	Hs.29797	ribosomal protein L10	28.93
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	27.99
50	440207	AI371978	Hs.128326	ESTs	27.75
	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	26.95
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	26.90
	420367	AA259090	Hs.257028	ESTs	26.50
	429878	AA249027		ribosomal protein S6	26.43
55	440440	Z28925	Hs.7188	sama domain, immunoglobulin domain (Ig),	26.36
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	26.23
	412636	NM_004415		desmoplakin (DPI, DPL)	26.15
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	25.25
60	446899	NM_005397	Hs.16426	podocalyxin-like	25.25
	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	25.15
	406656	M16714	Hs.89643	major histocompatibility complex, class	25.13
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	24.78
	423961	D13666	Hs.136348	periostin(OSF-2os)	24.48
	425543	R23313	Hs.334895	ribosomal protein L10a	24.38
65	420676	AI434780	Hs.4248	vav 2 oncogene	24.18
	406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	23.96
	440869	NM_014297	Hs.7486	protein expressed in thyroid	23.80
	447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	23.56
	414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	23.22
70	446627	AI973016	Hs.15725	hypothetical protein SBB148	22.93
	449571	AW016812	Hs.200266	ESTs	22.83
	413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	22.81
	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	22.68
75	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	22.45
	422714	AB018335	Hs.119387	KIAA0792 gene product	22.45
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	22.30
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	21.69
	406648	AA563730	Hs.277477	major histocompatibility complex, class	21.58
	448588	AI970276	Hs.156905	KIAA1676	21.23
80	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	21.19
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	20.70
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	20.60
	407882	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	20.57

5	420754	W79431	Hs.346911	ribosomal protein L22	20.40
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	20.15
	424800	AL035588	Hs.153203	MyoD family inhibitor	20.10
	412915	AW087727	Hs.74823	NM_004541: Homo sapiens NADH dehydrogenas	20.01
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	19.89
10	410143	AA188169		KIAA1191 protein	19.41
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	19.08
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	19.03
	425535	AB007937	Hs.158287	KIAA0468 gene product	18.78
	411573	AB029000	Hs.70823	KIAA1077 protein	18.63
15	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	18.53
	408669	AA93591	Hs.78146	platelet/endothelial cell adhesion molec	18.52
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	18.50
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020.1 E2IG5	18.50
	429183	AB014604	Hs.197955	KIAA0704 protein	18.48
20	450000	AJ952797	Hs.10888	hypothetical protein FLJ21709	18.44
	450377	AB033091		KIAA1265 protein	18.40
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	18.15
	440528	BE313555	Hs.7252	KIAA1224 protein	18.05
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	17.98
25	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	17.80
	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	17.75
	428782	X12830	Hs.193400	interleukin 6 receptor	17.48
	415221	W07418	Hs.78225	annexin A1	17.47
	429614	AJ371172	Hs.211539	hypothetical protein MGC4248	17.40
30	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	17.30
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	17.14
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	17.13
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	17.10
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	17.03
35	425996	W67330		hypothetical protein AL110115	16.98
	402474			NM_004079: Homo sapiens cathepsin S (CTSS	16.98
	450937	R49131	Hs.26267	ATP-dependant Interferon response protei	16.98
	427521	AW973352		ESTs	16.93
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	16.93
40	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	16.53
	449338	H73444	Hs.394	adrenomedullin	16.36
	429469	M64580	Hs.27	glycine dehydrogenase (decarboxylating;	16.23
	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	16.21
	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	16.15
45	427691	AW194426	Hs.20726	ESTs	16.13
	406786	AW161678	Hs.111334	ferritin, light polypeptide	16.11
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	16.10
	451106	BE382701	Hs.25960	N-MYC oncogene	16.09
	408380	AF123050	Hs.44532	diubiquitin	16.00
50	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	15.93
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	15.70
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	15.69
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	15.64
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	15.55
55	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	15.55
	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	15.53
	410185	BE294068	Hs.737	immediate early protein	15.49
	422105	AI929700	Hs.111680	endosulfine alpha	15.23
	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	15.23
60	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	15.05
	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	15.02
	426552	BE297660	Hs.170328	moesin	14.96
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	14.88
	436860	H12751	Hs.5327	PRO1914 protein	14.85
65	418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	14.84
	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	14.78
	412623	R28898	Hs.74170	metallothionein 1E (functional)	14.70
	408989	AW361666	Hs.49500	KIAA0746 protein	14.53
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	14.48
70	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	14.31
	410325	AB023154	Hs.62264	KIAA0937 protein	14.23
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	14.20
	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase II	14.19
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	14.18
75	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	14.13
	447211	AL161961	Hs.17767	KIAA1554 protein	14.08
	417426	NM_002291	Hs.82124	laminin, beta 1	14.08
	414420	AA043424	Hs.76095	immediate early response 3	14.04
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	14.02
80	454413	AI653672	Hs.40092	PNAS-123	13.93
	452651	AI218918	Hs.30209	KIAA0854 protein	13.86
	450581	AF081513	Hs.25195	TGF-beta 4	13.85
	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	13.78
	407112	AA070801	Hs.51515	ESTs, Weakly similar to ALU7_HUMAN ALU S	13.63
	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	13.59
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila))-like	13.57
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	13.53

	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	13.43
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	13.41
	447534	AW953935	Hs.288655	ESTs	13.33
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	13.31
5	428065	AI634046	Hs.157313	ESTs	13.30
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	13.28
	436398	H87136	Hs.5174	ribosomal protein S17	13.18
	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	12.93
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	12.90
10	445817	NM_003642	Hs.13340	histone acetyltransferase 1	12.90
	408437	AW957744	Hs.278469	lacrimal proline rich protein	12.90
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	12.89
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	12.83
	406743	AA911568	Hs.279860	tumor protein, translationally-controlled	12.79
15	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	12.78
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	12.75
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	12.73
	430630	AW269920	Hs.2621	cystatin A (stefin A)	12.68
	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	12.65
20	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	12.50
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regl	12.48
	437374	AL359571	Hs.44054	ninein (GSK3B interacting protein)	12.43
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	12.43
	409963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	12.41
25	412247	AF022375	Hs.73793	vascular endothelial growth factor	12.41
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	12.40
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	12.38
	432409	AA806538	Hs.130732	KIAA1575 protein	12.33
	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	12.33
30	419384	AA490866	Hs.39429	ESTs	12.32
	410275	U86558	Hs.61796	transcription factor AP-2 gamma (activat	12.32
	432805	X94630	Hs.3107	CD97 antigen	12.25
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	12.13
35	450719	AI096837	Hs.21349	ESTs, Weakly similar to RB88_HUMAN RAS-R	12.12
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	12.03
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	12.01
	402145			Target Exon	12.00
	407179	AA206465		thymosin, beta 4, X chromosome	11.95
40	433208	AW002834	Hs.24095	ESTs	11.90
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	11.83
	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	11.75
	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	11.75
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	11.68
45	427761	AA412205	Hs.140996	ESTs	11.58
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	11.50
	436075	BE090176	Hs.179902	transporter-like protein	11.35
	440774	AI420611	Hs.153934	ESTs	11.25
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	11.08
50	419223	X60111	Hs.1244	CD9 antigen (p24)	11.08
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	10.98
	444656	AI277924	Hs.145199	ESTs	10.96
	420943	AI718702	Hs.279930	major histocompatibility complex, class	10.92
	450294	H42587	Hs.238730	hypothetical protein MGC10823	10.83
55	413686	AI489213	Hs.71404	ESTs	10.78
	406701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	10.75
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	10.75
	407252	AA659037	Hs.163780	ESTs	10.70
	445929	AI089660	Hs.323401	dpy-30-like protein	10.69
60	451864	N20370	Hs.69547	ESTs	10.64
	429307	AU076592	Hs.198951	Jun B proto-oncogene	10.63
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	10.63
	447519	U46258	Hs.339665	ESTs	10.59
	417365	D50683	Hs.82028	transforming growth factor, beta recepto	10.55
65	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	10.54
	408776	T16206	Hs.237164	ESTs, Highly similar to LDH_HUMAN L-LAC	10.50
	437103	AW139408	Hs.152940	ESTs	10.50
	449961	AW265634	Hs.133100	ESTs	10.49
	441244	BE612935	Hs.184052	PP1201 protein	10.48
70	450139	AK001838		serum/glucocorticoid regulated kinase	10.48
	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	10.47
	449944	AF290512	Hs.58215	Homo sapiens, Similar to rheokin, clone	10.43
	446682	AW205832	Hs.211198	ESTs	10.43
	413886	AW958264	Hs.103832	similar to yeast Upt3, variant B	10.40
75	430068	AA464954		gb:zx80f10.s1 Soares ovary tumor NbHOT H	10.40
	424950	AA602917	Hs.156974	ESTs	10.33
	434442	AA737415		ESTs	10.33
	438089	W05391		nuclear receptor subfamily 1, group I, m	10.30
	432559	AW452948	Hs.257631	ESTs	10.30
80	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	10.28
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	10.27
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	10.27
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	10.27
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	10.23

	445245	AB032973	Hs.12461	LCHN protein	10.18
	445488	AB037782	Hs.15119	KIAA1361 protein	10.15
	410611	AW954134	Hs.20924	KIAA1628 protein	10.15
5	425875	ALU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	10.14
	416926	H03109	Hs.263395	HT018 protein	10.07
	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	10.05
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	10.04
	411975	AI916058	Hs.144583	ESTs	10.03
10	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	10.00
	408784	AW971350	Hs.63386	ESTs	9.95
	444795	AI193356	Hs.160316	ESTs	9.93
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	9.90
	400440	X83957	Hs.83870	nebulin	9.90
15	414829	AA321568	Hs.77436	pleckstrin	9.88
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	9.88
	426827	AW067805	Hs.172665	methyltetrahydrofolate dehydrogenase	9.85
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	9.83
	446795	AI797713	Hs.156471	ESTs	9.78
20	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	9.67
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	9.65
	419904	AA974411	Hs.18672	ESTs	9.63
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	9.63
	414405	AI362533		KIAA0306 protein	9.58
25	418840	AI821614	Hs.185831	ESTs	9.53
	453716	AA037675	Hs.152675	ESTs	9.50
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	9.50
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	9.45
	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	9.45
30	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	9.43
	434423	NM_005769	Hs.3844	LIM domain only 4	9.43
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	9.43
	416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	9.42
	410397	AF217517	Hs.63042	DKFZp564J157 protein	9.37
35	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	9.37
	434524	AA635931	Hs.249716	ESTs	9.36
	422960	AW890487		cadherin 13, H-cadherin (heart)	9.35
	414774	X02419	Hs.77274	plasminogen activator, urokinase	9.32
40	411960	R77776	Hs.18103	ESTs	9.30
	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	9.28
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	9.28
	441455	AI271671	Hs.7854	zinc/ferron regulated transporter-like	9.27
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	9.27
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypotheti	9.25
45	427968	AI857607	Hs.181301	cathepsin S	9.23
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	9.23
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	9.23
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	9.18
	417315	AI080042	Hs.180450	ribosomal protein S24	9.18
50	421098	AI697901	Hs.192425	ESTs	9.18
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	9.17
	433166	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	9.17
	425246	AI085561	Hs.155321	serum response factor (c-fos serum respo	9.15
55	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	9.14
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	9.13
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	9.12
	426689	BE245550	Hs.171825	basic helix-loop-helix domain containing	9.10
	420099	D80011	Hs.95140	KIAA0189 gene product	9.08
60	424768	AA353895	Hs.152983	HUS1 (S. pombe) checkpoint homolog	9.08
	441436	AW137772	Hs.185980	ESTs	9.08
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	9.08
	437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	9.07
	430556	AW967807	Hs.13797	ESTs	9.06
65	450147	AW373713	Hs.146324	CGI-145 protein	9.05
	442806	AW294522	Hs.149991	ESTs	9.05
	431187	AW971146	Hs.293187	ESTs	9.03
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	9.03
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	9.02
70	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	9.00
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	8.99
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	8.98
	432314	AA533447	Hs.312989	ESTs	8.95
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	8.94
75	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	8.93
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxicin)	8.90
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	8.90
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	8.89
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	8.88
	417228	AL134324	Hs.7312	ESTs	8.88
80	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	8.88
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	8.85
	438980	AW502384		gb:UH-HF-BR0p-aka-f-12-0-ULr1 NIH_MGC_5	8.85
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	8.85
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	8.85

	430592	AJ224864	Hs.9688	leukocyte membrane antigen(IRC1)	8.83
	445612	N94126	Hs.12959	hypothetical protein	8.80
	427254	AL121523	Hs.97774	ESTs	8.80
5	428970	BE276891	Hs.194691	retinoic acid induced 3	8.79
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subunit	8.75
	430162	AW450843	Hs.346348	ESTs	8.73
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	8.73
	446659	AI335361	Hs.226376	ESTs	8.73
10	447198	D61523	Hs.283435	ESTs	8.70
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-decay accelerating factor for complement	8.68
	401091			ESTs	8.68
	442832	AW206560	Hs.253569	ESTs	8.63
	442495	AI184717		ESTs	8.63
15	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	8.61
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	8.59
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	8.55
	425580	L11144	Hs.1907	galanin	8.55
	449656	AA002008	Hs.188633	ESTs	8.54
20	412093	BE242691	Hs.14947	ESTs	8.54
	407833	AW955632	Hs.66666	ESTs, Weakly similar to S19560 proline-r	8.53
	411979	X85134	Hs.72984	retinoblastoma-binding protein 5	8.51
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	8.45
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	8.45
25	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	8.45
	425284	AF155568		NS1-associated protein 1	8.43
	441623	AA315805		desmoglein 2	8.42
	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	8.40
	441021	AW578716	Hs.7644	H1 histone family, member 2	8.40
30	446630	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr	8.35
	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	8.33
	433655	AL036559	Hs.3463	ribosomal protein S23	8.32
	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	8.31
	446975	BE246446	Hs.16695	ubiquitin-activating enzyme E1-like	8.30
35	436797	AA731491	Hs.334477	hypothetical protein MGC14879	8.30
	414662	AL036058	Hs.76807	major histocompatibility complex, class	8.29
	414601	AV660804	Hs.301417	AHNAK nucleoprotein (desmoyokin)	8.28
	406699	L06505	Hs.182979	ribosomal protein L12	8.28
	443884	N20617	Hs.194397	leptin receptor	8.26
40	442821	BE391929	Hs.8752	transmembrane protein 4	8.24
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	8.23
	435968	AW161481	Hs.111577	integral membrane protein 3	8.23
	440327	R12581	Hs.191146	ESTs	8.22
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	8.16
45	435684	NM_001290	Hs.4980	LIM domain binding 2	8.15
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	8.14
	427523	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3	8.13
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown (Hs	8.10
	448094	H24387	Hs.32061	ESTs, Weakly similar to I38022 hypotheti	8.09
50	421395	D90084	Hs.1023	pyruvate dehydrogenase (lipoamide) alpha	8.08
	431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	8.07
	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	8.03
	423523	AW299828	Hs.193580	ESTs	8.03
	426759	AI590401	Hs.21213	ESTs	8.03
55	426780	BE242284	Hs.172199	adenylate cyclase 7	8.03
	426215	AW963419	Hs.155223	stannocalcin 2	8.00
	435748	AA699756	Hs.117335	ESTs	8.00
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	8.00
	447500	AI381900	Hs.159212	ESTs	8.00
60	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	8.00
	428728	NM_016625	Hs.191381	hypothetical protein	7.99
	434511	R28982	Hs.18106	ESTs	7.98
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	7.95
	424875	AI187945	Hs.199310	ESTs	7.95
65	419378	R24922	Hs.90078	nucleotide-sugar transporter similar to	7.93
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	7.91
	425277	NM_001241	Hs.155478	cyclin T2	7.90
	451831	NM_001674	Hs.460	activating transcription factor 3	7.90
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	7.90
70	407013	U35637	Hs.83870	gb:Human nebulin mRNA, partial cds	7.90
	429999	AI761902	Hs.99597	ESTs	7.89
	445493	AI915771		metallothionein 1E (functional)	7.88
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	7.88
	422392	NM_005908	Hs.115945	mannosidase, beta A, lysosomal	7.87
75	453485	BE620712	Hs.33026	hypothetical protein PP2447	7.85
	434159	AW135214	Hs.191828	ESTs	7.83
	432666	AW204089		ESTs, Weakly similar to unnamed protein	7.83
	430915	AA488953		gb:aa55e05.r1 NCL_CGAP_GCB1 Homo sapiens	7.80
	425913	AA365799		SEC22, vesicle trafficking protein (S. c	7.80
80	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	7.79
	438763	AI583207	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	7.78
	435905	AW997484	Hs.5003	KIAA0456 protein	7.78
	406663	U24583		immunoglobulin heavy constant mu	7.78
	427395	AW298741	Hs.97861	ESTs, Moderately similar to I38022 hypot	7.78

	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	7.75
	438962	BE046594		gbchn41c11.x1 NCL_CGAP_RDF2 Homo sapiens	7.75
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	7.73
5	422900	AA641201	Hs.222051	ESTs	7.73
	432598	AJ341227	Hs.157106	ESTs	7.72
	449322	AJ638616	Hs.196566	ESTs	7.71
	416987	D86957	Hs.80712	KIAA0202 protein	7.67
	410800	BE280421	Hs.94499	ESTs	7.67
10	416801	X98834	Hs.79971	sal (Drosophila)-like 2	7.67
	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	7.65
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	7.65
	401466			vesicle-associated membrane protein 4	7.65
	406870	AA075144		gb:zm66f06.s1 Stralagene ovarian cancer	7.64
15	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	7.63
	457250	AA811987	Hs.125779	ESTs	7.63
	412949	AJ471639	Hs.71913	ESTs	7.63
	406819	AA908472		gb:og82a10.s1 NCL_CGAP_Ov8 Homo sapiens	7.62
	441612	AJ802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	7.62
20	414799	AJ752416	Hs.77326	insulin-like growth factor binding prote	7.61
	435937	AA830893	Hs.119769	ESTs	7.60
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	7.60
	407719	AW963866	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,	7.60
	417336	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mltogen	7.56
25	418134	AA397769	Hs.86617	ESTs	7.55
	451812	X81889	Hs.152151	plekophlin 4	7.55
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	7.54
	429083	Y09397	Hs.227817	BCL2-related protein A1	7.54
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	7.52
30	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	7.52
	407784	AW139585	Hs.12708	ESTs	7.52
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	7.50
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	7.50
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	7.48
35	446013	AI360167	Hs.152774	ESTs	7.48
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	7.48
	415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.45
	417450	AA314435	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	7.45
	431773	BE409442	Hs.268557	pleckstrin homology-like domain, family	7.44
40	447082	T85314	Hs.54629	thioredoxin-like	7.43
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	7.43
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	7.43
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	7.43
	442233	AW967149	Hs.28439	ESTs, Weakly similar to I38022 hypothe	7.43
45	436394	AA531187	Hs.126705	ESTs	7.39
	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	7.39
	446258	AI283476	Hs.263478	ESTs	7.38
	410570	AI133096	Hs.64593	ATP synthase, H transporting, mitochondr	7.37
	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	7.36
50	435541	AA687361	Hs.221318	ESTs	7.35
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	7.35
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	7.35
	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	7.35
	418336	BE179882		glutathione peroxidase 3 (plasma)	7.35
55	448877	AI583696	Hs.253313	ESTs	7.35
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	7.35
	444838	AV651680	Hs.208558	ESTs	7.33
	422693	BE300073	Hs.279860	tumor protein, translationally-controlled	7.31
	424577	U09414		zinc finger protein 137 (clone pHZ-30)	7.30
60	441878	AI801869	Hs.127982	ESTs	7.29
	406542			C19000728~g 12585552 sp Q9Y2Q1 Z257_HU	7.28
	408418	AW963897	Hs.44743	KIAA1435 protein	7.28
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	7.26
	442492	AA528489	Hs.234518	ribosomal protein L23	7.25
65	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	7.25
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	7.25
	426501	AW043782	Hs.293616	ESTs	7.25
	411251	R19774	Hs.22835	HHGP protein	7.25
	444670	H58373	Hs.332938	hypothetical protein MGCS370	7.25
	418117	AI922013	Hs.83496	linker for activation of T cells	7.24
70	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	7.24
	434817	AA082118	Hs.102737	golliath protein	7.23
	419970	AW612022		ESTs	7.23
	432290	AK001099	Hs.274273	Homo sapiens cDNA FLJ10237 fis, clone HE	7.23
75	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	7.23
	433891	AA613792		gb:nc97h03.s1 NCL_CGAP_Pr2 Homo sapiens	7.21
	454038	X06374	Hs.37040	platelet-derived growth factor alpha pol	7.21
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	7.20
	443247	BE614387	Hs.333893	c-Myc target JPO1	7.20
	441224	AJ076964	Hs.7753	calumenin	7.18
80	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	7.18
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	7.15
	447341	AF106941	Hs.18142	arrestin, beta 2	7.15
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	7.14

5	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	7.14
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	7.13
	421633	AF121860	Hs.105260	sorting nexin 10	7.10
	410668	BE379794	Hs.159651	hypothetical protein	7.09
	435812	AA700439	Hs.188490	ESTs	7.08
10	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	7.08
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	7.08
	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	7.06
	408605	AF025374	Hs.46465	T-cell, Immune regulator 1	7.06
	416401	N80139	Hs.268916	ESTs	7.05
15	415799	AA653718	Hs.225841	DKFZP434D193 protein	7.05
	415995	NM_004573		phospholipase C, beta 2	7.05
	414812	X72755	Hs.77367	monokine induced by gamma interferon	7.05
	417535	AA203569	Hs.191482	ESTs	7.04
	449567	AI990790	Hs.188614	ESTs	7.03
20	429355	AW973253	Hs.292689	ESTs	7.03
	442460	NM_014135	Hs.8345	PRO0641 protein	7.03
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	7.03
	430280	AA361258	Hs.237868	interleukin 7 receptor	7.03
	426124	AI268389	Hs.250597	phosphatidylinositol glycan, class F	7.02
25	442685	AB033017	Hs.8594	KIAA1191 protein	7.01
	433735	AA608955	Hs.109653	ESTs	7.00
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	6.98
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	6.96
	416655	AW968613	Hs.79428	BCL2adenovirus E1B 19kD-interacting pro	6.95
30	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	6.95
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	6.93
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	6.93
	451653	W18193		ESTs, Moderately similar to HERC2 [H.sap	6.93
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothe	6.93
35	451838	AW005866	Hs.193969	ESTs	6.91
	436812	AW298067		gb:UH-BW0-ajp-g-09-0-ULs1 NCI_CGAP_Su	6.90
	443749	R38828	Hs.143463	ESTs	6.90
	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	6.90
	427919	AA173942	Hs.326416	Homo sapiens mRNA: cDNA DKFZp564H1916 (f	6.90
40	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	6.90
	435655	AW105663	Hs.6947	HSPC069 protein	6.90
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	6.85
	418259	AA215404		ESTs	6.85
	407244	M10014		fibrinogen, gamma polypeptide	6.85
45	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	6.83
	441321	H17182	Hs.7771	B-cell associated protein	6.80
	433162	AI025842		ESTs	6.80
	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	6.80
	434372	AA631373		gb:np86c01.s1 NCI_CGAP_Tty1 Homo sapiens	6.80
50	456629	AW891965		histone deacetylase 3	6.78
	430283	BE391688		RAB7, member RAS oncogene family	6.77
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	6.76
	406858	AI865720	Hs.29797	ribosomal protein L10	6.75
	429582	AI569068	Hs.22247	ESTs	6.75
55	401113			solute carrier family 22 (organic cation	6.75
	449576	AW014631	Hs.225068	ESTs	6.75
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	6.72
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	6.72
	430451	AA836472	Hs.297939	cathepsin B	6.72
60	410503	AW975746	Hs.188662	KIAA1702 protein	6.70
	415682	AI347128	Hs.191870	ESTs	6.70
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Clona savigny]	6.70
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	6.70
	457073	AA233210	Hs.179943	ribosomal protein L11	6.69
65	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	6.68
	436137	AI056769	Hs.133512	ESTs	6.68
	425787	AA363867	Hs.155029	ESTs	6.67
	437802	AI475995	Hs.122910	ESTs	6.65
	432636	AA340864	Hs.278562	claudin 7	6.65
70	407340	AA810168	Hs.284289	vitiligo-associated protein VIT-1	6.65
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	6.65
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	6.63
	441355	AI822034	Hs.137097	ESTs	6.63
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	6.63
75	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	6.63
	447232	AW499834	Hs.327	Interleukin 10 receptor, alpha	6.62
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	6.60
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	6.60
	449057	AB037784	Hs.22941	KIAA1363 protein	6.60
80	446979	AI654443	Hs.197683	ESTs	6.60
	452382	N38902	Hs.211539	hypothetical protein MGC4248	6.60
	424868	AI568170	Hs.96886	ESTs	6.59
	409485	S80990	Hs.252136	ficollin (collagen/fibrinogen domain-cont	6.58
	451603	BE379499	Hs.173705	Homo sapiens cDNA: FLJ22050 fis, clone H	6.58
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	6.58
	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	6.57
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	6.56

	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	6.56
	444207	AI565004		cathepsin D (lysosomal aspartyl protease	6.55
	418459	R85436	Hs.268814	ESTs	6.55
5	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	6.55
	406745	AW511970	Hs.279860	tumor protein, translationally-controlled	6.55
	446173	BE565849	Hs.14158	copine III	6.53
	436566	BE545586	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	6.53
	423825	NM_004402	Hs.133089	DNA fragmentation factor, 40 kD, beta po	6.53
	443441	AW291196	Hs.92195	ESTs	6.51
10	428403	AI393048	Hs.326159	leucine rich repeat (in FLJ) interactin	6.50
	431971	BE274907	Hs.77385	myosin, light polypeptide 6, alkali, smo	6.50
	450219	AI826999	Hs.224624	ESTs	6.50
	408896	AI610447	Hs.48778	niban protein	6.50
	442618	R56222	Hs.26514	ESTs	6.49
15	422773	AB028962	Hs.301552	KIAA1039 protein	6.48
	413663	BE247585	Hs.75462	BTG family, member 2	6.48
	418905	BE539674		actinin, alpha 4	6.48
	405086			NM_006662: Homo sapiens Snf2-related CBP	6.45
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	6.45
20	407284	AI539227	Hs.214039	hypothetical protein FLJ23556	6.45
	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	6.45
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	6.43
	426496	D31765	Hs.170114	KIAA0061 protein	6.43
	422303	AW410382	Hs.27556	hypothetical protein FLJ22405	6.42
25	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown (Hs	6.41
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	6.40
	435918	AF263538	Hs.86232	growth differentiation factor 3	6.38
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	6.38
	412220	BE350058	Hs.36787	chromodomain helicase DNA binding protei	6.38
30	436716	AI433540		gb:U69g05.x1 NCI_CGAP_XG11 Homo sapien	6.38
	413703	BE158360		gb:PM1-HT0383-131299-001-h08 HT0383 Homo	6.38
	413326	H88621	Hs.19762	ESTs, Weakly similar to KIAA1140 protein	6.38
	441970	AW959918	Hs.73737	ESTs	6.38
	430835	AI240006	Hs.192326	ESTs	6.38
35	414890	BE281095	Hs.77573	uridine phosphorylase	6.37
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.37
	414768	AW376989	Hs.259855	elongation factor-2 kinase	6.36
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	6.36
	407198	H91679		gb:yy04e07.s1 Soares fetal liver spleen	6.35
40	432586	AA568548		ESTs	6.35
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	6.35
	420012	AW957965	Hs.99014	Homo sapiens, clone IMAGE:3632168, mRNA	6.35
	432879	AW815932	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.35
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.35
45	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	6.35
	437296	AA350994	Hs.20281	KIAA1700	6.35
	427747	AW411425	Hs.180655	serine/threonine kinase 12	6.33
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 14	6.33
	410387	AI277367	Hs.47094	ESTs	6.33
50	413677	AW503116	Hs.301819	zinc finger protein 146	6.31
	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	6.31
	443634	H73972	Hs.134460	ESTs	6.30
	409453	AI885516	Hs.95612	ESTs	6.29
55	443035	Z45822	Hs.8906	Homo sapiens clone 24889 mRNA sequence	6.29
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	6.29
	410532	T53088	Hs.155376	hemoglobin, beta	6.28
	428453	AB011110	Hs.184367	GTPase activating protein-like	6.27
	410597	W16518	Hs.278518	amyloid beta (A4) precursor-like protein	6.26
	458965	AA010319	Hs.60389	ESTs	6.25
60	419926	AW900992	Hs.93796	DKFZP586D2223 protein	6.25
	426797	AW936258	Hs.342849	ADP-ribosylation factor-like 5	6.25
	412528	AI123478	Hs.32112	ESTs	6.25
	410079	U94362	Hs.58589	glycogenin 2	6.25
	427477	AW973119	Hs.178391	ribosomal protein L44	6.24
65	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	6.24
	435961	BE293127	Hs.283722	GTT1 protein	6.23
	424090	X99699	Hs.139262	XIAP associated factor-1	6.23
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	6.23
70	451061	AW281487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	6.23
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	6.23
	440129	AA865818		ESTs, Weakly similar to S71885 Ste20-lik	6.22
	428773	BE256238	Hs.193163	bridging integrator 1	6.20
	436372	AW972301	Hs.310286	ESTs	6.19
75	440719	AA150869	Hs.26267	ATP-dependent Interferon response protai	6.18
	406685	M18728		gb:Human nonspecific crossreacting entig	6.18
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	6.17
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	6.16
	458659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	6.15
	406806	AW088535		ribosomal protein, large, P0	6.15
80	420151	AA255931	Hs.186704	ESTs	6.14
	413441	AI929374	Hs.75367	Src-like-adaptor	6.13
	449317	AW293413	Hs.132906	19A24 protein	6.13
	421568	W85858	Hs.99804	ESTs	6.13

5	435919	AI052189	Hs.114104	ESTs	6.13
	417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	6.13
	448946	AI652855	Hs.23363	hypothetical protein FLJ10983	6.13
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.11
	406857	AA613726	Hs.29797	ribosomal protein L10	6.11
	417944	AJ077196	Hs.82985	collagen, type V, alpha 2	6.10
	425095	AW014160	Hs.182585	KIAA1276 protein	6.10
	435756	AJ418466	Hs.33665	ESTs	6.10
10	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	6.10
	413813	M96956	Hs.75551	teratocarcinoma-derived growth factor 1	6.10
	451052	AA281504	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	6.08
	450511	R07423	Hs.85092	thyroid hormone receptor interactor 11	6.08
	447832	AI433357		ESTs	6.08
15	434421	AI915927	Hs.34771	ESTs	6.08
	437438	AL359620	Hs.14217	hypothetical protein DKFZp762P2111	6.08
	449525	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	6.07
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	6.06
	433339	AF019226	Hs.8036	glioblastoma overexpressed	6.06
20	435511	AA683336	Hs.189046	ESTs	6.06
	423458	AI204212		ESTs	6.06
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prole	6.06
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	6.06
	444621	AA298065	Hs.11465	glutathione-S-transferase like; glutathi	6.05
25	455263	AW961702		Homo sapiens cDNA FLJ14028 fis, clone HE	6.05
	432925	AA878324	Hs.264750	ESTs	6.05
	457752	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	6.04
	449810	AB008681	Hs.23994	activin A receptor, type IIB	6.04
	406797	AI432224		ribosomal protein L6	6.03
30	450157	AW961576	Hs.60178	ESTs	6.03
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.03
	407635	AW370213	Hs.295232	ESTs, Moderately similar to A46010 X-lin	6.03
	453331	AI240665		ESTs	6.02
	430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	6.01
35	444708	AW971049	Hs.11774	protein (peptidyl-prolyl cis/trans isome	6.00
	409945	AW015935	Hs.122642	ESTs	6.00
	419641	BE170548	Hs.118190	Homo sapiens cDNA: FLJ21081 fis, clone C	6.00
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	6.00
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	6.00

TABLE 52B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

45	Pkey	CAT Number	Accession
50	438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE457708 AW898528 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI078007 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095508 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA63522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581 BE880923 BG390191 AW470082 AW014585 AI423255 BI714731 BG054894 AW780248 N31683 AW664132 AW467353 AI983152 AA617918 BF447795 AI088357 AA807328 AA576970 AI741153 AI755003 AI474016 AI422030 AI348114 AW997085 BM271753 AI363147 BM311311 AI146640 AI246771 AW512619 AI359020 BG054897 AI292234 AI215830 AI283838 C06205 AW503423 AW272680 N33205 AW873021 AA070724 AI753886 AW192487 AI087151 AA658909 AI346368 AI335677 AA825442 AW440066 AW131357 AW513210 AI082314 AI085455 BE551404 AA780704 AW008596 AI796964 AA917471 AI400531 AA688626 N72207 AI306482 AW440562 AI084687 AA347280 AA063536 BF477389 AI241662 AA931543 AA484310 AA812486 AI032216 AA665779 AI916338 AI350590 BF198106 AI433377 AI300638 AI672626 AI282741 AI351487 AW105544 AA973627 AW517914 AA715424 AA508454 BF334080 AI274618 AW367201 AW572619 AW469088 AA382095 AI368364 AI146934 AI357180 AI361181 BI911347 BI871044 AA136325 BF084010 BF084007 AA335788 AI920878 AA805614 BE932941 AI678261 C75308 AI148479 BE178174 W88513 BM013627 BE738425 BE738323 BM126944 AW629678 AW265195 AI916735 AI394255 AI573090 AI354442 AW612857 AI339558 AI919424 AI377532 AI354441 AI308821 AA772275 AW055215 AI589705 AI336532 AA806547 AV682125 H33575 AW071172 AW769904 AI863985 AW265018 AW195655 D79662 BE042393 N75017 AW014741 C75509 BE748621 H92431 AW079261 AW901780 AA329482 AW960115 BI260621 AI767525 R31663 BI918664 AW963195 C06195 AI678018 M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350963 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 BE710353 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AI127260 AW364859 BF993352 CG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW365566 BI090368 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 CG990973 BI040954 BF919911 AI140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AI140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE002030 AW365153 BE184941 BF749421 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE819390 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG865845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW793304 AL603116 BE149760 BE705957 BE705966 BE705968 AW848723
55			
60	426295	510_1	
65			
70	429978	35194_2	
75	412636	1438_1	
80			

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AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211
 AW597139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE719915 AW799309 BF872345 BF088676 BE705939 AW752599
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 A1439101 AA451923 A1340326 A1590975 B1791553 A1700963 A1142882 A1039975 AA946936 AA644381 BM314884 AA702424 A1471612
 AW190555 A1220573 A1304772 A1270345 A1627383 AA552300 A1911702 AW166807 A1346078 W95070 AA149191 AA026864 A1830049 AW780435
 A1078449 A1819984 A1858282 A1648588 A1860584 A1025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 A1927207
 A1205263 BF082491 AW021347 A1568096 BE939862 AA088866 D12052 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181
 H44405 A1910434 BF082513 A1494069 A1270027 A1635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654
 AV745530 B1762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 A1571075 BE067786 AW721320
 A1022862 N29754 C03378 N84767 AA131077 H30146 BE714290 A1686869 A1568892 A1915596 AW105614 A1887258 A138577 BE926474
 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763
 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 A1905927 BF92780 AW853812 BG954443 B1770853 BG679406
 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 B1089483 BE006273 BE872225 AW391912 BE925515 BG677012
 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 B1040941 AA337270 AW84371 AW847442
 B1058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 A1284090
 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 B1013292 BE001925 AW365156 AW365154 AW606653
 BF763109 BE931637 BE187181 BE713879 BF354008 BF678728 H90899 AW365145 W38382 A198487
 AK056685 BG399272 A1187835 BF821903 AV660550 AV660556 AV660502 BG664397 BE739584 BF446961 A1653056 AW973709 A1653173
 BG054997 A1266043 B1054879 A1566750 A1492830 AW021142 A1472184 AW170056 A1082443 A1167921 DE9940 B1492088 H74180 AW130886
 A1348677 A1278577 AA761517 A1698203 AA115535 A1264790 AW205074 AA860452 AA554902 A1000715 D62102 BE544768 A1376090 D59939
 AW242249 AA525421 R34211 R34328 BF248064 BF241437 BF572759 BF218832
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 AA720684 AA862331 AA605146 BM313650 A1089749 A1359738 N69107 AW995424 A1086917 A1083995 AW340217 N93662 A1829449 A1089839
 A1608761 A1342365 A1199076 AA908944 A1248943 A1160053 A1191245 A1218477 A1077943 AA864930 A1310394 AA872478 A1279782 W61343
 AA565955 W46596 AA126874 AA223241 AA491574 R84813 AA491520 BG055114 A1636689 BE464590 AW664539 H67097 A1534332 C21397
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50	430504	5477_6	
55			TABLE 52C Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Strand: Indicates DNA strand from which exons were predicted. NL_position: Indicates nucleotide positions of predicted exons.
60			TABLE 52C Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Strand: Indicates DNA strand from which exons were predicted. NL_position: Indicates nucleotide positions of predicted exons.
65			TABLE 52C Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Strand: Indicates DNA strand from which exons were predicted. NL_position: Indicates nucleotide positions of predicted exons.
70			TABLE 52C Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Strand: Indicates DNA strand from which exons were predicted. NL_position: Indicates nucleotide positions of predicted exons.
75			TABLE 52C Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Strand: Indicates DNA strand from which exons were predicted. NL_position: Indicates nucleotide positions of predicted exons.
80			TABLE 52C Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Strand: Indicates DNA strand from which exons were predicted. NL_position: Indicates nucleotide positions of predicted exons.

	426534	U58096	Hs.2051	testis specific protein, Y-linked	44.05
	423458	AI204212		ESTs	36.60
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	34.65
	420367	AA259090	Hs.257028	ESTs	32.60
5	451106	BE382701	Hs.25960	N-MYC oncogene	30.10
	437052	AA861697	Hs.120591	ESTs	29.35
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	29.05
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	28.45
	420347	AL033539	Hs.97124	Human DNA sequence from clone RP1-309H15	28.25
10	407710	AW022727	Hs.23616	ESTs	26.86
	448981	AI968719	Hs.195387	ESTs	26.40
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	25.55
	420528	AF130728	Hs.98586	doublesex and mab-3 related transcriptio	25.10
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	23.70
15	430252	AI638774	Hs.105328	testes development-related NYD-SP20	21.95
	454077	AC005962	Hs.37062	Insulin-like 3 (Leydig cell)	21.73
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	20.15
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	19.65
	424578	AK001973	Hs.150890	hypothetical protein	19.16
20	427335	AA448542	Hs.251677	G antigen 7B	19.05
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	18.95
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	18.86
	449322	AI638616	Hs.196566	ESTs	18.30
	430691	C14187	Hs.157208	aristless-related homeobox protein ARX	18.00
25	430676	AF084866		gb:Homo sapiens envelope protein RJC-3 (17.96
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [H.s	17.41
	418756	AA252254	Hs.226949	ESTs	17.20
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	16.20
	447534	AW953935	Hs.288655	ESTs	16.04
30	407122	H20276	Hs.31742	ESTs	15.95
	446979	AI654443	Hs.197683	ESTs	15.90
	406547			Target Exon	15.70
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	15.65
	456847	AI360456	Hs.37776	ESTs	15.50
35	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	15.00
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	14.95
	408908	BE296227	Hs.250822	serine/threonine kinase 15	14.65
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (Interstitial	14.20
	422828	AL133396		prion protein 2 (dublet)	14.08
40	433330	AW207084	Hs.132816	hypothetical protein MGC14801	14.05
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	14.05
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	13.90
	418134	AA397769	Hs.86617	ESTs	13.85
	454438	AA224053	Hs.172405	cell division cycle 27	13.70
45	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	13.40
	426427	M86699	Hs.169840	TTK protein kinase	13.35
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	13.20
	419384	AA490866	Hs.39429	ESTs	13.10
	418477	AW022983		gb:cd46h12.y1 Morton Fetal Cochlea Homo	12.85
50	453822	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	12.80
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	12.78
	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	12.72
	443068	AI188710		ESTs	12.65
55	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	12.60
	420401	AK001907	Hs.97464	hypothetical protein	12.50
	410361	BE391804	Hs.62661	guanylate binding protein 1, Interferon-	12.45
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	12.25
	406937	U14622		gb:Human transketolase-like protein gene	12.10
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	11.86
60	404996			Target Exon	11.85
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	11.60
	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-fin	11.55
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	11.50
	421241	X91817	Hs.102866	transketolase-like 1	11.45
65	414972	BE263782	Hs.77695	KIAA0008 gene product	11.37
	426866	U02330	Hs.172816	neuregulin 1	11.35
	433159	AB035898	Hs.150587	kinesin-like protein 2	11.24
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	11.12
	440207	AI371978	Hs.128326	ESTs	11.10
70	407276	AI951118	Hs.326736	Homo sapiens breast cancer antigen NY-BR	11.05
	450142	AW207469	Hs.24485	chondroitin sulfate proteoglycan 6 (bama	10.95
	449576	AW014631	Hs.225068	ESTs	10.95
	414251	AL042306	Hs.97689	VASA protein	10.90
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	10.85
75	436812	AW298067		gb:U1-H-BWO-ajp-g-09-0-UI.s1 NCL_CGAP_Su	10.81
	427521	AW973352		ESTs	10.80
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	10.62
	442832	AW206560	Hs.253569	ESTs	10.60
	436899	AA764852		ESTs	10.55
80	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	10.45
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	10.15
	435206	AI432364	Hs.160594	ESTs	10.10
	433975	AA971953	Hs.122055	ESTs	10.10

	446791	AI632278	Hs.195922	ESTs	10.05
	422232	D43945	Hs.113274	transcription factor EC	10.00
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	9.71
5	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	9.50
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	9.44
	438188	AA779975	Hs.128859	ESTs	9.30
	418973	AA233056	Hs.191518	ESTs	9.25
	413627	BE182082	Hs.246973	intron of Bicucalinal D homolog 1	9.25
10	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	9.15
	436608	AA828980	Hs.192371	down syndrome critical region protein DS	9.11
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	9.08
	426518	Z43039	Hs.170198	KIAA0009 gene product	9.05
	440968	N36327		gb:yx82b06.r1 Soares melanocyte 2NbHM Ho	9.05
15	440952	AI291804	Hs.118101	ESTs	9.05
	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	9.05
	442618	R56222	Hs.26514	ESTs	8.96
	419423	D26488	Hs.90315	KIAA0007 protein	8.95
	428153	AW513143	Hs.98367	SRY (sex determining region Y)-box 17 (S	8.80
20	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	8.76
	444971	AI651116	Hs.148659	ESTs	8.75
	436513	AJ278110	Hs.125507	DEAD-box protein	8.60
	427486	AA974433		fibroblast growth factor 4 (heparin secr	8.59
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	8.58
25	428847	AJ954833	Hs.98881	ESTs	8.57
	408465	AW196940	Hs.253277	ESTs	8.54
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	8.53
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	8.50
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.50
30	450480	X82125	Hs.25040	zinc finger protein 239	8.50
	425266	J00077	Hs.155421	alpha-fetoprotein	8.50
	453884	AA355925	Hs.36232	KIAA0186 gene product	8.42
	413318	AU076607	Hs.75285	Inter-alpha (globulin) inhibitor, H2 pol	8.35
	430835	AI240006	Hs.192326	ESTs	8.33
35	416859	H43437	Hs.80305	hypothetical protein MGC14258	8.30
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	8.26
	407340	AA810168	Hs.284289	vitiligo-associated protein VIT-1	8.25
	449260	AA741180	Hs.29879	ESTs	8.25
40	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	8.18
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	8.17
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	8.14
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	8.14
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	8.03
	425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	7.98
45	410420	AA224053	Hs.172405	cell division cycle 27	7.90
	453878	AW964440	Hs.19025	DC32	7.75
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	7.68
	453913	AW004683	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	7.65
50	421974	AA301270		gb:EST14192 Testis tumor Homo sapiens cD	7.65
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	7.65
	451950	AW292317	Hs.213307	ESTs	7.60
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	7.59
	435514	AW592804		ESTs	7.55
55	431041	AA490967	Hs.197955	KIAA0704 protein	7.55
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.51
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	7.38
	409421	AA199883	Hs.67624	ESTs	7.35
	449433	AI672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bindl	7.35
60	458570	AW971698	Hs.12627	TJ8 protein	7.30
	441287	AW293132	Hs.131373	ESTs	7.30
	434609	R76593		gb:yt60c11.r1 Soares placenta Nb2HP Homo	7.25
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.25
	441425	AA933590	Hs.28937	homeobox protein from AL590526	7.25
	446293	AI420213	Hs.149722	LIM domain transcription factor LIM-1 (h	7.21
65	414136	AA812434		SMC2 (structural maintenance of chromoso	7.20
	409089	NM_014781	Hs.50421	KIAA0203 gene product	7.19
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	7.18
	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	7.15
	452226	AA024898	Hs.157103	ESTs	7.15
70	435918	AF263538	Hs.86232	growth differentiation factor 3	7.14
	418661	NM_001949	Hs.1189	E2F transcription factor 3	7.10
	436360	AI962796	Hs.156100	ESTs	7.10
	442950	AI500417	Hs.46764	ESTs	7.00
75	415684	D59356		sorbitol dehydrogenase	7.00
	448336	R53848	Hs.44976	ESTs	7.00
	453163	AW086185	Hs.223856	ESTs	7.00
	444434	NM_004849	Hs.11171	APG5 (autophagy 5, S. cerevisiae)-like	6.95
	422665	AJ011812	Hs.119018	transcription factor NRF	6.95
80	437421	AA917062		ESTs	6.95
	428916	AF003001	Hs.194562	telomeric repeat binding factor (NIMA-in	6.94
	408045	AW138959	Hs.245123	ESTs	6.90
	448588	AI970276	Hs.156906	KIAA1676	6.89
	433764	AW753676	Hs.39982	zinc finger protein RINZF (NM_023929)	6.85
	439780	AL109688		gb:Homo sapiens mRNA full length insert	6.85

	449911	AI262106	Hs.12653	ESTs	6.85
	417791	AW965339	Hs.111471	ESTs	6.80
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.75
	453160	AI263307		H2B histone family, member L	6.75
5	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	6.75
	425427	AI652662	Hs.157205	branched chain aminotransferase 1, cytos	6.73
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	6.70
	418379	AA218940	Hs.137516	fidgulin-like 1	6.70
	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	6.70
10	414618	AI204600	Hs.96978	hypothetical protein MGC10764	6.69
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	6.66
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	6.65
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	6.65
	433247	AB040948	Hs.142856	KIAA1515 protein	6.65
15	430647	AC003682	Hs.127988	ESTs, Weakly similar to Z211_HUMAN ZINC	6.65
	417886	AA214584		ESTs	6.64
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	6.62
	412537	AL031778		nuclear transcription factor Y, alpha	6.61
	426614	AA411925	Hs.301960	ESTs	6.57
20	457465	AW301344	Hs.122908	DNA replication factor	6.52
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	6.50
	440801	AA906366		ESTs	6.50
	453116	AI276680	Hs.146086	ESTs	6.50
	436909	AA907120		ESTs	6.50
25	402199			Target Exon	6.50
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	6.46
	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	6.41
	438494	AA908678	Hs.130183	ESTs	6.41
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	6.40
30	408758	NM_003686	Hs.47504	exonuclease 1	6.40
	442671	AI005668	Hs.130673	EST	6.40
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	6.38
	413833	Z15005	Hs.75573	centromere protein E (312kD)	6.35
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	6.33
35	441878	AI801869	Hs.127982	ESTs	6.31
	429120	AK001673	Hs.196530	hypothetical protein FLJ10811	6.31
	418221	Z45514	Hs.83775	DiGeorge syndrome gene D	6.30
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	6.30
	421650	AA781795	Hs.122587	ESTs	6.30
40	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	6.28
	408291	AB023191	Hs.44131	KIAA0974 protein	6.26
	438180	AA808189	Hs.272151	ESTs	6.25
	412026	AA383618	Hs.73073	testis-specific ankyrin motif containing	6.25
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	6.20
45	423642	AW452650	Hs.157148	hypothetical protein MGC13204	6.20
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (6.18
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	6.12
	426223	AW977812	Hs.130391	ESTs	6.10
	445038	AI635444	Hs.143917	dJ467N11.1 protein	6.10
50	419197	N48921	Hs.27441	KIAA1615 protein	6.09
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	6.05
	436902	AW247145	Hs.192729	ESTs	6.05
	429228	AI553633		ESTs	5.99
	457065	AI476318	Hs.192480	ESTs	5.90
55	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	5.90
	449132	BE045641	Hs.197573	ESTs	5.90
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	5.89
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	5.85
	457289	AW573204	Hs.137078	ESTs	5.85
60	433849	BE465884	Hs.280728	ESTs	5.85
	412642	BE244598	Hs.809	hepatocyte growth factor (hepatopoietin A;	5.85
	438450	AI050866	Hs.65853	nodal, mouse, homolog	5.81
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	5.80
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	5.77
65	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	5.77
	408460	AA054726	Hs.285574	ESTs	5.75
	442461	AW062564	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	5.75
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	5.75
	428249	AA130914	Hs.183291	zinc finger protein 268	5.74
70	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (5.72
	402145			Target Exon	5.71
	447178	AW594641	Hs.192417	ESTs	5.70
	458814	AA98957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	5.65
	442980	AA857025	Hs.8878	kinesin-like 1	5.65
75	419131	AA406293	Hs.109526	ESTs	5.60
	450254	NM_004885	Hs.99231	neuropeptide G protein-coupled receptor;	5.60
	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	5.60
	440304	BE159984	Hs.125395	ESTs	5.60
	440553	AA889416	Hs.344043	Homo sapiens cDNA FLJ14459 fis, clone HE	5.58
80	442333	AI650877	Hs.129302	ESTs	5.58
	453941	U39817	Hs.36820	Bloom syndrome	5.57
	415799	AA653718	Hs.225841	DKFZP434D193 protein	5.57
	413623	AA825721	Hs.246973	Intron of Bicaudal D homolog 1	5.55

	427147	AA398587	Hs.97414	ESTs	5.55
	451050	AW937420		ESTs	5.55
	450113	AI683098	Hs.200866	ESTs, Moderately similar to ALU7_HUMAN A	5.54
5	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	5.54
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisou	5.53
	431354	BE046956	Hs.251673	DNA (cytosine-5)-methyltransferase 3 be	5.51
	449592	AI655494	Hs.195718	ESTs	5.50
	445517	AF208855	Hs.12830	hypothetical protein	5.50
10	416658	U03272	Hs.79432	fibrillin 2 (congenital contractual ara	5.48
	430044	AA464510	Hs.152812	ESTs	5.47
	437036	AI571514	Hs.133022	ESTs	5.47
	423006	U29700	Hs.123014	anti-Mullerian hormone receptor, type II	5.46
	409103	AF251237	Hs.112208	XAGE-1 protein	5.45
15	420900	ALD45633	Hs.44269	ESTs	5.45
	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	5.45
	440738	AI004650	Hs.225674	WD repeat domain 9	5.45
	412723	AA648459	Hs.335951	hypothetical protein AF301222	5.45
	441122	H56777	Hs.121084	eppin-3	5.42
20	414151	AW976468	Hs.257245	ESTs	5.40
	435663	AI023707	Hs.134273	ESTs	5.40
	448986	H42169	Hs.347310	hypothetical protein FLJ14627	5.39
	433701	AW445023	Hs.15155	ESTs	5.39
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	5.35
25	440842	AA907288	Hs.130173	ESTs	5.35
	432407	AA221036	Hs.13273	gb:zr0312.r1 Stratagene NT2 neuronal pr	5.34
	401837			NM_025109:Homo sapiens hypothetical prot	5.32
	423739	AA398155	Hs.97600	ESTs	5.31
	424315	AW614850	Hs.193384	putative 28 kDa protein	5.31
30	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	5.30
	415717	AA167270	Hs.130435	ESTs	5.30
	428329	AA426091	Hs.98453	ESTs, Moderately similar to R27328 2 [H.	5.26
	427119	AW880562	Hs.272525	ESTs	5.25
	432117	AL036195	Hs.2909	protamine 1	5.24
35	446837	AW273055	Hs.156598	ESTs	5.23
	442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	5.21
	422797	AB033064	Hs.236463	KIAA1238 protein	5.19
	446258	AI283476	Hs.263478	ESTs	5.18
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	5.17
40	445413	AA151342	Hs.12677	CGI-147 protein	5.17
	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	5.16
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.15
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	5.15
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	5.15
45	448038	AW015073	Hs.232026	ESTs, Weakly similar to RO52_HUMAN 52 KD	5.15
	430272	X04898	Hs.237658	apolipoprotein A-II	5.14
	422094	AF129535	Hs.272027	F-box only protein 5	5.13
	420424	AB033036	Hs.97594	KIAA1210 protein	5.13
	447924	AI817226	Hs.313413	ESTs, Weakly similar to T23110 hypothet	5.10
50	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	5.10
	453448	AL036710	Hs.209527	ESTs	5.10
	436378	AW970529	Hs.86434	hypothetical protein FLJ21816	5.06
	418235	BE072634		gb:PM4-BT0548-171299-001-h08 BT0548 Homo	5.05
55	427961	AW293165	Hs.143134	ESTs	5.05
	441553	AA281219	Hs.121296	ESTs	5.05
	429999	AI761902	Hs.99597	ESTs	5.04
	426496	D31765	Hs.170114	KIAA0061 protein	5.02
	410929	H47233	Hs.30643	ESTs	5.01
60	448757	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	5.01
	457107	AA418246	Hs.185796	ESTs, Weakly similar to Z184_HUMAN ZINC	5.00
	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	5.00
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	5.00
	407568	AA740964	Hs.62699	ESTs	5.00
	409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN IIII	5.00
65	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	5.00
	416350	AF188625	Hs.189507	phospholipase A2, group IID	4.99
	452197	AW023595	Hs.232048	ESTs	4.98
	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	4.97
70	403780			C4001759:gl[133250]sp[P19474]RO52_HUMAN	4.97
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	4.95
	418894	W73921	Hs.50743	ESTs	4.95
	426623	AA382826	Hs.132793	ESTs	4.95
	443537	D13305	Hs.203	cholecystokinin B receptor	4.94
	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.94
75	453716	AA037675	Hs.152675	ESTs	4.90
	402299			Target Exon	4.90
	411945	AL033527	Hs.92137	L-myc-2 protein (MYCL2)	4.89
	414034	U89277	Hs.305985	early development regulator 1 (homolog o	4.87
80	409066	AA062980	Hs.66950	ESTs	4.85
	437496	AA452378	Hs.146668	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	4.85
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	4.85
	450375	AA009647		a disintegrin and metalloproteinase doma	4.85
	416201	AA467752	Hs.195161	ESTs	4.85
	420348	AL137385	Hs.97140	Homo sapiens mRNA; cDNA DKFZp434M1126 (f	4.84

	423198	M81933	Hs.1634	cell division cycle 25A	4.82
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.81
	418971	AA360392	Hs.87113	ESTs	4.80
5	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	4.80
	409517	X90780		troponin I, cardiac	4.80
	424322	AL157491	Hs.145211	Homo sapiens mRNA; cDNA DKFZp434K1111 (f	4.80
	443169	AI038687	Hs.133338	ESTs	4.80
	438624	AA899055	Hs.123468	ESTs	4.79
	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	4.76
10	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.76
	443715	AI583187	Hs.9700	cyclin E1	4.76
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	4.75
	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens	4.71
	444431	AW513324	Hs.42280	Homo sapiens, clone MGC:9010, mRNA, comp	4.71
15	440591	AA431599	Hs.132799	hypothetical protein FLJ23451	4.71
	424281	AA766243		gb:aa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	4.70
	447175	AI365208	Hs.293606	ESTs	4.70
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.69
20	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	4.68
	416445	AL043004	Hs.79337	KIAA0135 protein	4.66
	429652	AA766810	Hs.259290	ESTs	4.65
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	4.65
	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dy	4.64
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.62
25	427298	AA400495		ESTs	4.62
	412863	AA121673	Hs.59757	zinc finger protein 281	4.61
	446700	AW206257	Hs.156326	Human DNA sequence from clone RP11-145L2	4.60
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	4.60
30	446751	AA766998	Hs.79126	Human DNA sequence from clone RP11-16L21	4.60
	432656	NM_000246	Hs.3076	MHC class II transactivator	4.60
	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	4.60
	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	4.59
	421830	AA789269	Hs.122509	ESTs, Weakly similar to dJ1018D12.3 [H.s	4.58
35	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-II	4.58
	450719	AI096837	Hs.21349	ESTs, Weakly similar to RB88_HUMAN RAS-R	4.58
	431721	AB032996	Hs.268044	KIAA1170 protein	4.55
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	4.55
	453529	AA036729	Hs.335639	ESTs	4.55
40	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.55
	444386	BE065183		gb:RC1-BT0314-020200-012-c04 BT0314 Homo	4.55
	428976	AL037824	Hs.194695	ras homolog gene family, member 1	4.55
	449510	AI653154	Hs.328147	ESTs	4.55
	414725	AA769791		ring finger protein 21, interferon-respo	4.54
45	424153	AA451737	Hs.141496	MAGE-like 2	4.53
	414466	AA349211	Hs.76205	cytochrome P450, subfamily XIA (choleste	4.52
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.50
	458443	AV647010	Hs.27	glycine dehydrogenase (decarboxylating;	4.48
	453289	AI188161	Hs.144627	ESTs	4.48
50	433641	AF080229		gb:Human endogenous retrovirus K clone 1	4.45
	440196	N72847	Hs.125221	ESTs	4.45
	452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	4.45
	428855	AI435901	Hs.89563	nuclear cap binding protein subunit 1, 8	4.45
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	4.45
55	442240	AI791883	Hs.292719	ESTs	4.45
	421917	AB028943	Hs.109445	KIAA1020 protein	4.45
	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypothi	4.44
	449676	AW380579	Hs.209657	ESTs	4.43
	433183	AF231338	Hs.222024	transcription factor BMAL2	4.40
60	439314	AA382413	Hs.178144	ESTs	4.40
	425312	AA354940	Hs.145958	ESTs	4.39
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	4.39
	430444	AW296421	Hs.121035	ESTs	4.35
	416773	AK000340	Hs.79828	hypothetical protein FLJ20333	4.35
65	421010	AW974553	Hs.267124	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.34
	418216	AA662240	Hs.283099	AF15q14 protein	4.32
	450351	BE547267	Hs.59791	hypothetical protein MGC13183	4.32
	454073	AW206286	Hs.116727	ESTs	4.30
	417006	AW673608	Hs.80758	aspartyl-tRNA synthetase	4.30
70	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.28
	448877	AI583696	Hs.253313	ESTs	4.27
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	4.25
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	4.25
	430292	AK000634	Hs.238270	hypothetical protein FLJ20627	4.25
75	427778	AA412323	Hs.105323	ESTs	4.25
	418768	T39310		gb:ya04a09.r2 Stratogene lung (937210) H	4.25
	409268	AA625304		ESTs	4.25
	442010	AI032680	Hs.132213	ESTs	4.24
	452807	AA028933	Hs.162434	ESTs	4.23
80	401435			C14000397:g[7499899]p[ir]T33295 hypoth	4.23
	447519	U46258	Hs.339655	ESTs	4.21
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	4.21
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	4.20
	453909	AW004045	Hs.203365	ESTs	4.20

	431126	AF085243	Hs.283619	zinc finger protein 236	4.20
	429628	H09604	Hs.13268	ESTs	4.20
	415989	AI267700		ESTs	4.20
	421373	AA808229	Hs.46677	ESTs	4.20
5	433979	AA620999		gb:ag03a08.s1 Soares_testis_NHT Homo sap	4.20
	408321	AW405882	Hs.44205	cootistatin	4.19
	410193	AJ132592	Hs.59757	zinc finger protein 281	4.17
	430335	D80007	Hs.239499	KIAA0185 protein	4.17
10	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	4.16
	438885	AI886558	Hs.184987	ESTs	4.15
	451578	NM_016323	Hs.26663	cyclin-E binding protein 1	4.15
	432446	AA542845	Hs.294088	GAJ protein	4.13
	445076	AI206888	Hs.154131	ESTs	4.11
	420218	AW958037		ribosomal protein L4	4.10
15	453628	AW243307	Hs.83937	hypothetical protein	4.10
	418459	R85436	Hs.268814	ESTs	4.10
	418866	T65754		gb:yc11c07.s1 Stragene lung (937210) H	4.08
	440404	AI015881	Hs.324527	mitochondrial ribosomal protein S5	4.06
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	4.06
20	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	4.05
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	4.05
	449687	W68520		intermediate filament protein syncoilin	4.05
	452109	AI525873	Hs.61164	hypothetical protein FLJ14909	4.05
	401464			histone deacetylase 5	4.05
25	444670	H58373	Hs.332938	hypothetical protein MGC5370	4.05
	415884	H22966	Hs.13471	ESTs	4.05
	442068	BE502147	Hs.128418	ESTs	4.04
	402098			ENSP00000217725*:Laminin alpha-1 chain p	4.02
	404287			FGENESH predicted novel CUB-domain conta	4.01
30	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	4.01
	449704	AK000733	Hs.23900	GTPase activating protein	4.00
	445685	AW779829		gb:hn88a05.x1 NCL_CGAP_Kid11 Homo sapien	4.00
	444379	N99035	Hs.30352	ESTs	4.00
	435373	AW665538	Hs.117689	ESTs	4.00
35	424557	AA343057	Hs.164588	ESTs, Moderately similar to neuronal thr	4.00
	413646	BE155042		gb:PMO-HT0349-101299-002-E04 HT0349 Homo	4.00
	418648	AW979223	Hs.292478	ESTs	4.00
	446074	AA079799	Hs.343103	hypothetical protein FLJ11896	4.00
	447353	AI375701	Hs.25884	ESTs	4.00
40	410100	AA081636	Hs.271916	ESTs, Weakly similar to S41044 chromosom	4.00
	428856	AA436735	Hs.183171	hypothetical protein FLJ22002	4.00
	445140	AI650699	Hs.197913	ESTs, Weakly similar to SCP3 MOUSE SYNAP	4.00
	406367			NM_022357:Homo sapiens putative metallo	3.99
	437834	AA769294		gb:zn36g03.s1 NCL_CGAP_GCB1 Homo sapiens	3.99
45	453985	N44545	Hs.251865	ESTs	3.98
	408446	AW450669	Hs.45068	hypothetical protein DKFZp434l143	3.97
	408562	AI436323	Hs.31141	roundabout (axon guidance receptor, Dros	3.97
	414713	BE465243	Hs.12664	ESTs	3.96
50	426067	AW664691	Hs.97053	ESTs	3.96
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	3.96
	454679	AW813110		gb:CMA-ST0189-051099-021-05 ST0189 Homo	3.95
	451865	H43737	Hs.33186	ESTs, Weakly similar to unknown protein	3.95
	403137			NM_005381*:Homo sapiens nucleolin (NCL),	3.95
	445730	AI624342	Hs.179082	ESTs	3.95
55	451993	AA765776	Hs.122983	ESTs	3.95
	428819	AL135623	Hs.193914	KIAA0575 gene product	3.92
	433583	AI817723	Hs.22678	hypothetical protein FLJ21832	3.91
	420812	AA715303	Hs.107369	ESTs	3.90
	423806	AA331247	Hs.86617	ESTs	3.90
60	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	3.90
	449211	AI922972	Hs.196073	ESTs	3.90
	409757	NM_001898	Hs.123114	cystatin SN	3.90
	436027	AI854053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	3.89
	432512	NM_003284	Hs.3017	transition protein 1 (during histone t	3.89
65	440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	3.88
	449099	AI629041	Hs.46908	ESTs	3.88
	408092	NM_007057	Hs.42650	ZW10 Interactor	3.85
	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	3.85
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.84
70	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	3.83
	433023	AW864793		thrombospondin 1	3.82
	452571	W31518	Hs.34665	ESTs	3.81
	421413	AI826128	Hs.55209	ESTs, Weakly similar to A49364 59 protol	3.80
	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT	3.80
75	420697	AA827705	Hs.26605	ESTs	3.80
	407275	AI364186		gb:xqw34h07.x1 NCL_CGAP_Uit4 Homo sapiens	3.80
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	3.80
	411855	H57895	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	3.80
	449529	AI990559	Hs.232033	ESTs	3.80
80	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	3.78
	444656	AI277924	Hs.145199	ESTs	3.77
	448674	W31176	Hs.154140	ovary-specific acidic protein	3.77
	415829	AW450198	Hs.163742	ESTs	3.76

5	436188	AK001049	Hs.48712	hypothetical protein FLJ120736	3.75
	402178			C19001998:gil5453813[ref][NP_008926.2] b	3.75
	418179	X51630	Hs.1145	Wilms tumor 1	3.75
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.75
	429063	AW363845	Hs.322903	ESTs, Weakly similar to A46010 X-linked	3.75
10	437440	AA846804		ESTs	3.75
	427366	AA885108	Hs.223806	TATA box binding protein (TBP)-associate	3.74
	438456	AA913381	Hs.20594	ESTs	3.73
	418821	AA436002	Hs.183161	ESTs	3.73
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	3.73
15	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.71
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	3.70
	409928	AL137163	Hs.57549	hypothetical protein dJ47384	3.70
	414206	AW276887	Hs.46609	ESTs	3.70
	427761	AA412205	Hs.140996	ESTs	3.69
20	428728	NM_016625	Hs.191381	hypothetical protein	3.68
	452631	AJ188658	Hs.87496	ESTs	3.68
	427719	AJ393122	Hs.134726	ESTs	3.68
	431869	AA521135	Hs.190176	ESTs	3.67
	429830	AJ537278	Hs.225841	DKFZP434D193 protein	3.67
25	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.66
	421972	M18185	Hs.1454	gastric inhibitory polypeptide	3.66
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.65
	456030	AA136106	Hs.184852	KIAA1553 protein	3.65
	402408			NM_030920:Homo sapiens hypothetical pro	3.65
30	452387	AI680772	Hs.308094	trinucleotide repeat containing 12	3.65
	416608	R11499	Hs.189716	ESTs	3.65
	417553	L09190		trichohyalin	3.65
	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Homo	3.65
	431077	AJ669133	Hs.115660	hypothetical protein FLJ12810	3.64
35	452461	N78223	Hs.108106	transcription factor	3.60
	437660	W31708	Hs.55304	ESTs	3.60
	420552	AK000492	Hs.98806	hypothetical protein	3.60
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	3.59
	420161	AI683069	Hs.120817	ESTs	3.59
40	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	3.59
	448571	AW016812	Hs.200266	ESTs	3.56
	424727	AW590378	Hs.152519	hypothetical protein FLJ120674	3.55
	441820	AA969119	Hs.143502	ESTs, Weakly similar to envelope protein	3.55
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	3.55
45	427532	AA442152	Hs.104744	hypothetical protein DKFZP434J0617	3.55
	437700	AA766080	Hs.301209	myeloid/lymphoid or mixed-lineage leukem	3.55
	438176	AW138970	Hs.122113	ESTs	3.55
	453062	AW207538	Hs.61603	KIAA1677	3.55
	447054	AB002350	Hs.17262	KIAA0352 gene product	3.55
50	430056	X97548	Hs.228059	KRAB-associated protein 1	3.54
	418049	AA211467		Homo sapiens, Similar to nuclear localiz	3.54
	434288	AW189075	Hs.116265	fibrillin3	3.54
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	3.52
	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	3.52
55	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	3.52
	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	3.51
	430958	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	3.50
	449467	AW205006	Hs.197042	ESTs	3.50
	405935			Target Exon	3.50
60	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	3.50
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	3.49
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (raklines	3.49
	429183	AB014604	Hs.197955	KIAA0704 protein	3.49
	428878	AA436884	Hs.48926	ESTs	3.49
65	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.48
	435068	H16262	Hs.31415	ESTs	3.48
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	3.48
	451065	AW295132	Hs.222231	ESTs, Weakly similar to granule cell mar	3.48
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.48
70	406542			C19000728:gil12585552[sp]Q9Y2Q1[Z257_HU	3.47
	422406	AF025441	Hs.116206	Opa-interacting protein 5	3.46
	402099			ENSP00000217725-Laminin alpha-1 chain p	3.45
	418826	AK000375	Hs.88820	HDCMC28P protein	3.45
	424513	BE385864	Hs.149894	mitochondrial translational initiation f	3.45
75	427617	D42063	Hs.199179	RAN binding protein 2	3.45
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.45
	400268			NM_003292:Homo sapiens translocated prom	3.45
	443596	AW026048	Hs.134124	ESTs	3.45
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	3.45
80	416031	T30290	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	3.45
	435244	N77221	Hs.187824	ESTs	3.45
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	3.45
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	3.45
	420686	AI350339	Hs.40782	ESTs	3.44
	429467	NM_004477	Hs.203772	FSHD region gene 1	3.43
	448769	N66037	Hs.36173	ESTs	3.43
	423453	AW450737	Hs.128791	CGI-09 protein	3.41

	417705	AW134952	Hs.175220	hypothetical protein FLJ14541	3.41
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	3.41
	404068			Target Exon	3.40
	401644			Target Exon	3.40
5	422364	AF067800	Hs.115515	C-type (calcium dependent, carbohydrate-	3.40
	452907	BE256966	Hs.31652	ESTs, Moderately similar to I54374 gene	3.40
	420281	AI623693	Hs.323494	Predicted cation efflux pump	3.39
	452404	AW450675	Hs.212709	ESTs	3.39
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	3.39
10	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	3.39
	440606	AI828751		ESTs, Weakly similar to I38022 hypothe	3.38
	425474	Z48054	Hs.158084	peroxisome receptor 1	3.37
	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	3.37
	446214	AK001322	Hs.14347	hypothetical protein FLJ10460	3.36
15	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.36
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	3.36
	421633	AF121860	Hs.106260	sorting nexin 10	3.36
	438192	AI859065	Hs.293807	Homo sapiens AFG3L1 isoform 1 mRNA, part	3.36
	436511	AA721252	Hs.291502	ESTs	3.35
20	402680			Target Exon	3.35
	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	3.35
	449477	AI652602	Hs.197043	ESTs	3.35
	413686	AI469213	Hs.71404	ESTs	3.35
	401091			decay accelerating factor for complement	3.35
25	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	3.35
	433220	AI076192	Hs.131933	ESTs	3.34
	453200	AA033832	Hs.212433	ESTs	3.33
	427239	BE270447		ubiquitin carrier protein	3.33
	418355	L42563	Hs.1165	ATPase, H ⁺ transporting, nongastric, alp	3.33
30	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synthase	3.31
	441243	AI767058	Hs.193002	ESTs	3.30
	440716	AW105245	Hs.146509	ESTs	3.30
	400587			C10000649: g[7296574]gb[AAF51857.1] (AE	3.30
	401148			Target Exon	3.30
35	411752	AW236047	Hs.126497	ESTs	3.30
	433252	AB040957	Hs.151343	KIAA1524 protein	3.30
	434008	AA740878	Hs.112982	ESTs	3.30
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.30
	458067	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.30
40	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.29
	452761	BE244742	Hs.30532	CGI-77 protein	3.29
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	3.29
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	3.28
	432809	AA565509	Hs.131703	ESTs	3.27
45	449426	T92251	Hs.198882	ESTs	3.27
	425174	D87450	Hs.154978	KIAA0261 protein	3.25
	435159	AA688879	Hs.116649	ESTs	3.25
	446597	AK001334	Hs.15470	putative ring zinc finger protein NY-REN	3.25
	411554	W22895	Hs.112360	prominin (mouse)-like 1	3.25
50	447555	AI391662	Hs.160963	Homo sapiens, clone MGC:12318, mRNA, com	3.25
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KIX 4, clone HF.1	3.25
	445093	AI207197		ESTs	3.25
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.24
55	424568	AF005418	Hs.150596	cytochrome P450, subfamily XXVIA, polype	3.24
	453293	AA382267	Hs.10653	ESTs	3.24
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.23
	430552	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	3.22
	411975	AI916058	Hs.144583	ESTs	3.22
60	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.22
	403432			NM_001622:Homo sapiens alpha-2-HS-glycop	3.21
	436515	AJ278111	Hs.195292	putative tumor antigen	3.21
	456505	AA504595		ESTs	3.21
	427668	AA298760	Hs.180191	hypothetical protein FLJ14904	3.21
65	452794	AI192444	Hs.25892	ESTs, Weakly similar to I37356 epithelia	3.20
	427314	AB033024	Hs.175475	KIAA1198 protein	3.20
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.20
	452028	AK001859	Hs.27595	hypothetical protein FLJ21142	3.20
	421002	AF116030	Hs.100932	transcription factor 17	3.20
70	422225	BE245652	Hs.118261	zinc finger protein 266	3.20
	437549	AA759149	Hs.128757	gb:ah70e03.s1 Soares_testis_NHT Homo sap	3.20
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	3.20
	427642	R40761	Hs.9834	ESTs	3.20
	442765	BE567353	Hs.99480	ESTs	3.20
75	410048	W76467	Hs.343874	proline oxidase homolog	3.20
	412008	NM_001841	Hs.73037	cannabinoid receptor 2 (macrophage)	3.20
	423675	AI990509	Hs.131342	small inducible cytokine subfamily A (Cy	3.20
	453895	AA039843	Hs.61948	Homo sapiens, clone MGC:16466, mRNA, com	3.20
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	3.19
80	428612	AA770001		ESTs	3.19
	422805	AA436989	Hs.121017	H2A histone family, member A	3.19
	444371	BE540274	Hs.239	forkhead box M1	3.18
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.17
	451684	AF216751	Hs.26813	CDA14	3.17

5	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	3.17
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	3.16
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	3.16
	444823	BE262989	Hs.12045	putative protein	3.15
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	3.15
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	3.15
	447801	H88923	Hs.270247	Homo sapiens cDNA FLJ11977 fis, clone HE	3.15
	424188	AW954552	Hs.142634	zinc finger protein	3.15
10	436941	AA860383	Hs.292791	ESTs	3.15
	400592			Target Exon	3.15
	437842	AL079309		gb:Homo sapiens mRNA full length insert	3.15
	450405	AI694913	Hs.279637	ESTs	3.15
	414161	AA136106	Hs.184852	KIAA1553 protein	3.15
15	440129	AA866818		ESTs, Weakly similar to S71886 Ste20-lik	3.14
	438538	AA832203	Hs.291955	ESTs	3.14
	441013	AI125252	Hs.126419	ESTs	3.14
	450431	AW136797	Hs.266041	ESTs	3.14
	423755	AB037735	Hs.132560	hypothetical protein FLJ10312	3.13
20	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	3.13
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.12
	410704	BE076754		gb:CM1-BT0601-180290-121-b10 BT0601 Homo	3.12
	412673	AL042957	Hs.31845	ESTs	3.11
	420507	AF093408	Hs.98397	A kinase (PRKA) anchor protein 3	3.11
25	423419	R55336	Hs.23539	ESTs	3.11
	428925	AW242474	Hs.98960	ESTs	3.11
	426108	AA622037	Hs.166468	programmed cell death 5	3.10
	439398	AA284267	Hs.221504	ESTs	3.10
	449138	AW294215	Hs.195631	ESTs	3.10
30	441795	N58115	Hs.21137	AD024 protein	3.10
	456053	S57498	Hs.76252	endothelin receptor type A	3.10
	403610			C3001199:gil7494834[pir]T15308 hypothet	3.10
	421281	AI299139	Hs.17517	ESTs	3.10
	429274	AI379772	Hs.99206	ESTs	3.10
35	438243	AI581311		ESTs	3.10
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.09
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	3.08
	416443	N69469	Hs.194225	ESTs	3.08
	421230	AW958439	Hs.105633	ESTs	3.07
40	427906	AA864330	Hs.166520	ESTs	3.07
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.06
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	3.06
	445679	AI343868	Hs.301059	hypothetical protein FLJ12488	3.06
	434456	AW452621	Hs.116832	ESTs	3.05
45	433228	F28212	Hs.14953	KIAA1491 protein	3.05
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	3.05
	415227	AW821113	Hs.72402	ESTs	3.05
	421184	NM_003616	Hs.102455	survival of motor neuron protein interac	3.05
50	438869	AF075009		gb:Homo sapiens full length insert cDNA	3.05
	422726	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott sy	3.04
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.04
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	3.04
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	3.04
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	3.04
55	435726	BE535787	Hs.113170	ESTs	3.03
	426386	AA748850	Hs.125830	bladder cancer overexpressed protein	3.03
	420596	NM_002692	Hs.99185	polymerase (DNA directed), epsilon 2	3.02
	427953	AA417944	Hs.44331	ESTs	3.01
	433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3)	3.01
60	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	3.00
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cel	3.00
	434776	AA648988		gb:ns41f11.s1 NCI_CGAP_GCB1 Homo sapiens	3.00
	414132	AI801235	Hs.48480	ESTs	3.00
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	3.00
65	433493	AA594915	Hs.155087	ESTs	3.00
	452606	NA5202	Hs.90012	hypothetical protein FLJ23441	3.00
	453416	NM_003037	Hs.32970	signaling lymphocytic activation molecu	3.00

TABLE 53B

Key: Unique Eos probe set identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

75	Pkey	CAT Number	Accession
	432666	144_7	AA558585 AA565499 AI360576 AW204069 AA991648 AA884939
	423458	30480_1	BC018070 BG702493 AI204212 AA460929 AA993606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539
			BG215094 BG198867 BG196332 BG208220 BG212418
	430676	60836_2	BG433950 BE061583 T05808 BE144813 AW812038 BE144812 AW812040 AW812041 AU124350 BE061602 BE061604 BF922595 BE061603
			AI352469 BE061601 BI062752 AW818206 BF887722
80	422828	227063_1	BE671981 BE503379 AI655440 AI337054 AI288920 AI242370 AI825182 AA758081 BF855141 BF091068
	418477	4172_1	BC022538 AI990847 BF478249 BG217996 BG212702 BG182057 AW589883 BF000085 AA993969 BG479023 BG220014 BG679466 BE907092
			AI623855 AA223956 AA223917 AW022983 AW090580 AW573219 BF514491 BF445397 AA884705 AI910424
	443058	18695_17	AV752763 AI032142 N30308 N22181 H95390 AW675632
	436812	659779_1	AW978773 AW298067 AA810101 AW194180 AA731645 AI690673

427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165 AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
436899	1000797_1	AA764852 AA736937
422689	874209_1	AW954733 AA315006 AW856685
440968	518029_1	AI964001 AI634418 AW236545 AI824860 BF223710 AW139686 AI672051 AI655566 AW025712 N36327 BF222876 N34083 AA911045 N40303 AW835451
427486	684159_1	BF510715 BE673055 BE464111 AW590620 AI637939 AA404324 AW236441 AI650952 BF056796 AA974433
421974	864120_1	AA301270 AA301379 AA301366
435514	132288_1	AA683356 AW592804 AI150287
434609	14739_1	AF147390 R76593 R76594
414136	30243_1	AJ420453 AL526740 AW968449 AA459140 AA843893 AI566516 AW971760 AA430089 AI753216 AA854268 AA743075 AI864957 AA458920 AI566534 AA211796 BG615512 BE169275 BF983253 BF969462 AA766261 AI769894 AA135833 AI831542 N63376 AA214392 AI154486 AW650517 AW450072 AA464599 BE881875 AI061423 AA598549 AW439151 AA426273 Z40087 AA812434 AA135965 H04812 BF666746 D59356 BG678312 N56640 AA166861
415684	18695_18	AA917062 AA757369 AW592218
437421	978554_1	AL109688 R23665 R26578
439780	49082_1	BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H0775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R08336
453160	6028_5	AA210987 D57294 AA214584 AA207006 D56572 AK025201 AA425472 AI694282 BG057305 AA907787 AI286170 AI684577 AJ420494 AI809865 BF058095 AI478773 AI160445 AL044114 AW665529 AI129239 AW297152 AI268215 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AV759188 BI259364 BF445142 BG232065 AI141758 AI631202 AI167566 AI208445 AA889823 BF982682 N90322 BI090882 BF208005 AW953918 AL044113 AJ016793 AA382556 AW235763 AA927051 AI862075 BE886691 BE619282 AA906366 AA938956 AI910938 AW102570 AA907150 AA907120 AA737188 AI248890 AW977353 BG676155 BM000591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW969605 AI553633 BM453041 AA760783 BE218582 AI340046 AW166131 BF515854 AI630286 AA461307 AI090881 AW023059 AA155797 AA115486 AL597396 AW899004 AW937420 AA137082 AA013374 BG619478 BG401839 BE072634 BE072653 AA830615 AA214736 AA331718 AA218925 AW962081 AA354237 BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056481 W46291 H01532 H04384 H03231 AA852876 H04410 H59605 BE157601 AA113758 NM_00363 X54163 M64247 AI265781 AI760600 AI367238 BE140258 AW207185 AI657074 C03333 AI193911 C05024 C03193 AI950215 C05070 C05613 W17389 C05351 AA311399 C04180 C04896 C05502 C05482 C04456 C04543 C04558 C04551 C03114 C03103 AI369979 AI652255 T12391 T12073 W19390 C02994 C02730 C04434 W07136 R57607 C03339 AK056685 BG399272 AA187835 BF821903 AV660550 AV660556 AV660502 BG564397 BE379584 BF446861 AI653056 AW973709 AI653173 BG054997 AI266043 BI054879 AI656750 AI492830 AW021142 AI472184 AW170056 AI082443 AI167921 D59940 BI492088 H74180 AW130886 AI348677 AI278577 AA761517 AI698203 AA115535 AI264790 AW205074 AA860452 AA554902 AI000715 D62102 BE544768 AI376090 D59939 AW242249 AA525421 R34211 R34328 BF248064 BF241437 BF572759 BF218832 BI015205 AI761324 AW880937 AW880941 AA338252 AA338213 AK055746 AA039909 BE183282 W60721 AA464867 AA398986 T67280 BF995651 AI675065 BG001051 BF764727 BF766707 BF764717 BF764852 BF173139 BE010038 AA933717 BF061897 AW628327 AA641788 AA400495 BE065183 AI144398 BE05367 BF377924 NM_058166 AF220030 AL043894 AW974257 AA625445 AU153502 AI650537 AW612116 AI672377 AW772451 BE892241 BE501740 AA718936 AI650276 AI654206 BE503226 AI651327 AW873562 AW271269 AW271565 AI873518 AI207150 AI338826 AI650258 AI628362 AA227117 AI207149 AW052076 AI470776 AA588100 AW235852 AA769791 AI701653 AK027664 AI984770 AU153469 BE222316 AA609539 BE220093 AA609112 BI054316 AF080229 AF080232 U87593 U87592 U87591 U87590 AI636743 AI633818 AW206802 AI583718 AF080231 AF080234 AF080233 AL535594 AI818326 AF080230 S46404 AI970376 AA463992 AW665466 BF512210 U87595 U87589 BE550633 AI672574 BE467547 AI680633 AW614951 N29986 N25695 H69001 U87596 BE673974 AI797496 AI701526 AA703398 AW139734 H92278 N66048 BE219539 BE571665 AI624817 BE466611 AI206344 AA574397 BF593413 BG231271 BF773517 U87594 BF062180 BE466420 AI887798 BF674385 AA204735 AW496808 AA204833 AA207155 BI004756 AA206262 AI365204 H77608 AW590511 T39328 T39310 T39303 T39284 BE893356 AA625304 AI765607 AI624898 R76060 AA069651 BG998885 R35783 BF086499 AA428755 AI245055 BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236 N50454 AA620999 T16375 AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI585211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256627 BE089727 T65754 AA229658 AA229857 AK056550 AK056356 AI928212 AI742073 AW300558 BG058755 AA058343 AI554842 AW207438 BF509981 BF444954 AW026234 AI620104 AA973460 AI370934 N63066 AA493129 AW590888 AI682952 AI167202 AA631394 AI421915 AI222883 BF477519 AI208777 AA765849 AI675076 AI370922 AI339579 AA486224 AA453524 AW771805 AI492842 H54679 AA961022 AW023555 H06192 AA910222 AI660021 AI032525 AI375480 AI361860 AI032918 AA833599 BG057928 AA553913 AW235737 AA002124 AA913636 F04607 AI867699 AA648100 BE091446 AA486378 BE002022 H84627 BI059837 BF917659 BF917100 BF917043 BF917104 BF916878 BG280981 AW954251 AA757126 H11545 AA353384 N48448 AA379845 AA004943 AA379928 AA002123 BM470118 AL598847 AL598830 BG899239 R57470 BF939179 AI650642 AI758851 BF352505 W68422 W35297 H11435 AA937499 AI783995 R12500 AI919557 N30983 Z41619 H22849 AA004942 R09436 R02403 T80942 T85823 BG029683 AI248120 BI850480 AW779829 N22494 BE155042 BE155040 BE154987 BE155012 BG110129 AW749287 BE535498 AW749299 AW749293 AW749302 AW749298 AW749291 AW749294 AW749289 AW749288 AW749296 AA769294 AW749297 AW749295 AW749292 BE002573 AW813110 BF771370 BF771371 AW813113 AW003381 BI862319 AA204955 BF240507 BG212143 AW205739 BF760647 BM129481 BI760482 AW300025 AI288591 AW236114 AI302852 AI038548 AI797207 AA534496 BG188194 AA921877 BG191846 BG182959 BE620243 BF217428 BC009514 BM463015 AL529077 BM051874 BG773269 BM314351 BM314660 AW629666 AA316207 AI623431 AA504153 AA314700 BG195449 BG614101 BE999967 BF438599 AW864793 AI802899 BE815132 AW468888 AI672189 AI052004 BF112024 AA772335 AW275054 AA573845 AI144148 AI968683 AA846676 AA927355 H80424 AW973295 R88209 F29668 BE928871 AA846804 AA757581 AI050950 AI092024 AA838807

5	417553	258857_1	AL545411 AI096369 BF431750 AI130946 W60065 W80663 AA258580 W73279 W76156 W80662 AW058658 AI204699 W60115 N56751 N30878
	408065	101881_1	AI769345 R71250 AI363766 R22777 R17009 R27985 R28243
	418049	12052_4	BI603077 AW954272 BI598724 AI003154 AA059300 AA046911 BI669907 BI600966 BI669987
	430968	1237115_1	AJ314647 NM_052888 BI494693 AA835055 AI634477 AJ336578 AI807696 BF477887 AI701147 Z39187 R39879 F02234 AA984711 BI222234
	400268	840_4	AV731417 R42406 H04996 T98498 R12489 R12577 R42405
10			AW972830 AA489820 AA527647 AA570362
			U69668 AA448366 X63105 BC016514 BE694435 AI655840 AW235355 BG427984 AA612862 AA448223 BM145813 BM194565 AI870824 BE973573
			BM148408 AA448232 AA454176 AA740959 AA884391 AA808545 AW070759 BM144223 N75518 BE542983 BE241942 AI124022 AA761687
			BF908518 BF907890 R11490 AL536642 BF109180 AA953881 AI783716 BE622908 AI621005 AW148784 AI690114 AW275000 AI765790 BF222859
			AW167268 AI990460 AW300443 AA779660 AI620568 BF115024 BE504703 AW628332 AI922851 BE006636 AU158376 AI168279 AA809916
15	440606	10075_1	AI469757 AA830828 AA830388 N64324 AI049683 AA970275 BF477364 BG261301 AA326388 AU150565 AU158374 AA687967 N58510 AI650450
	427239	20459_2	AL549572 BF349280 BF349269 BM463016 AW836798 AL120958 AW836891 AW385525 BE175733 BE175727 BE175723 BF092430 BI061782
			AU135358 BE175731 BE175754 BE175756 BE841747 BF798384 AU128251 BF095246 BG223262 AW847833 AL536643 AW366516 AW391532
			BE934857 BF925057 AW438446 R86246 AW179270 BE087782 BI832144
			BC017350 BC021031 AI220219 AI828751 AW134498 BE139642 AA894554 AI278594 AV747315 BE561749 BI085890 T80117 H69682 N70904
20			AV741999 H70098
			AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881
			AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478
			AI251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839
			AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420
25	445093	175963_1	AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073465 AI334733 AI054335 BE139260
	456505	15472_2	AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427
	428612	1383189_1	BF178773 BF178645 AW074866 BE857822
	437642	77594_1	AI207197 BF773544 AW196462
	440129	2607882_1	BC017865 AW969075 AA279982 AA504511 AI219979 AA504595 AI245579 AA278181 BG485019 BI049312
30	410704	1054673_1	AA770001 AA431112 AA432126
			AL079309 AA281819
			AI732997 AA977633 AA865818
			AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
			BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866
35	438243	2532601_1	AW840571
	438869	52134_1	AI581311 AA781682 AA781678
	434776	118129_1	AF075009 R63109 R63068
			AW974599 AA648988 R98760
40	TABLE 53C		
	Pkey:	Unique number corresponding to an Eos probeset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.	
	Strand:	Indicates DNA strand from which exons were predicted.	
	NL_position:	Indicates nucleotide positions of predicted exons.	
45	Pkey	Ref	Strand
	408547	7711513	Minus
	404996	6007890	Plus
	402199	8576116	Minus
	402145	8018280	Plus
50	401837	7630990	Minus
	403780	8076989	Plus
	402299	6693370	Plus
	401435	8217934	Minus
	401464	6682291	Minus
55	402098	8117697	Minus
	404287	2326514	Plus
	406367	9256126	Minus
	403137	9211494	Minus
	402178	8575912	Plus
60	403433	9719611	Minus
	402408	9796239	Minus
	405935	6758795	Minus
	406542	7711499	Plus
	402099	8117697	Plus
65	404068	3168621	Minus
	401644	8576138	Plus
	402680	8113438	Plus
	401091	9958240	Plus
	400587	9887626	Plus
70	401148	2547238	Minus
	403432	9719611	Minus
	400592	9887642	Minus
	403610	8308266	Plus
75	TABLE 54A:		
	Pkey:	Unique Eos probeset identifier number	
	ExAccn:	Exemplar Accession number, Genbank accession number	
	UnigeneID:	Unigene number	
	Unigene Title:	Unigene gene title	
80	R1:	Ratio of normal testis to normal adult tissues	
	R2:	Ratio of "average" normal testis to "average" testicular cancer	
	Pkey	ExAccn	UnigeneID
			Unigene Title

R1

R2

	401979		C17000767.gij11990770[jemb]CAC19651.1 (A	10.08	43.3	
	421825	AA298758	Hs.183747	ESTs, Moderately similar to CALB_HUMAN C	10.35	36.8
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	5.74	32.0
	441728	AI797395	Hs.169797	Homo sapiens BOULE (BOULE) mRNA, complet	10.54	24.5
5	452215	AK002043	Hs.28472	hypothetical protein FLJ11181	4.86	22.0
	415211	R64730.	Hs.155986	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	6.93	19.8
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	4.94	18.5
	449108	AI140683	Hs.98328	hypothetical protein MGC13040	7.94	17.5
	420437	AA992768	Hs.97633	A kinase (PRKA) anchor protein 4	16.75	15.6
10	436632	AA724299	Hs.304020	ESTs, Weakly similar to CRTC_HUMAN CALRE	6.51	14.9
	418409	AA219332	Hs.120869	ESTs, Weakly similar to R107_HUMAN H-REV	4.96	14.6
	406409			Target Exon	3.98	14.3
	427050	AW378993	Hs.90286	ESTs	3.56	14.2
	427310	AI613480	Hs.47152	teklin 3	4.50	14.0
15	427166	AA431576	Hs.99154	ESTs	4.28	13.9
	427178	AA398866	Hs.97542	Homo sapiens testis-development related	10.19	13.7
	410694	AL137538	Hs.65500	Homo sapiens mRNA; cDNA DKFZp434N2019 (f	5.76	13.4
	424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.24	13.3
	427441	AA412605	Hs.343879	SPANX family, member C	10.45	12.6
20	438057	AW294544	Hs.125785	ESTs, Weakly similar to CORB_MOUSE CORNI	18.57	12.3
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	5.18	12.3
	427293	AA705799	Hs.183714	ESTs	10.79	12.1
	444963	AI916973	Hs.213603	ESTs	3.18	12.1
	426608	AI699329	Hs.99168	ESTs, Weakly similar to AF132972.1 CGI-3	15.40	11.8
25	453178	AA496086	Hs.61648	ESTs	4.13	11.8
	428618	AA865360		Target CAT	7.53	11.5
	401741			Target Exon	10.41	11.5
	422086	AW182930	Hs.250182	ESTs	4.39	10.7
30	426604	HS3354	Hs.97141	ESTs, Weakly similar to hypothetical pro	7.04	10.6
	442373	AI377758	Hs.164799	testes development-related NYD-SP17	8.23	10.3
	427455	AF173081	Hs.178215	Vertebrate LIN7 homolog 1, Tax Interacti	3.03	10.1
	437248	AW449340	Hs.93090	ESTs	9.06	10.1
	426608	AA444162	Hs.99344	hypothetical protein PRD-NT3	3.68	10.0
35	427297	AW292593	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com	9.70	9.8
	422358	AL133030	Hs.115429	Homo sapiens mRNA for KIAA1666 protein,	11.85	9.7
	451610	AW118604	Hs.207126	ESTs	5.63	9.7
	410630	BE044562	Hs.266847	ESTs, Weakly similar to KIAA1214 protein	4.38	9.5
	426677	AW949856	Hs.97165	ESTs	6.58	9.3
40	437558	AI126471	Hs.124112	ESTs, Moderately similar to HSJ2_HUMAN D	4.47	9.2
	423088	NM_006587	Hs.123530	actin-like 7A	15.07	8.9
	426476	NM_003296	Hs.2042	testis specific protein 1 (probe H4-1 p3	18.55	8.9
	421952	AA300900	Hs.98849	dynein light chain 2B (DNL2B)	13.93	8.8
	429877	W37337	Hs.103014	ESTs	6.97	8.7
45	413114	AI825838	Hs.75206	protein phosphatase 3 (formerly 2B), cat	3.78	8.6
	412026	AA383618	Hs.73073	testis-specific ankyrin motif containing	22.03	8.5
	411844	AI807681	Hs.144658	ESTs, Weakly similar to T17257 hypotheti	7.34	8.3
	436868	AA974253	Hs.120319	Homo sapiens autoimmune infertility-rela	4.18	8.2
	426599	AW183574		ESTs	6.29	8.1
50	426683	AI073430	Hs.146775	ESTs, Weakly similar to T30993 hypotheti	10.89	8.0
	426930	AA393442		ESTs	5.06	8.0
	427836	AA416642	Hs.116176	ESTs	4.79	8.0
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	5.11	7.9
	430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	21.26	7.6
55	434150	BE047007	Hs.116116	testis specific, 10	4.85	7.6
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	10.29	7.5
	422116	H64205	Hs.111850	mitochondrial capsule selenoprotein	9.12	7.5
	433724	AI827749	Hs.144924	serine/threonine protein kinase SSTK	22.24	7.4
	410187	AA860341	Hs.104680	ESTs	3.03	7.4
60	419584	AF053356	Hs.283764	F-box only protein 24	6.43	7.4
	458182	AI147996	Hs.155833	ESTs, Weakly similar to spliceosomal pro	9.90	7.3
	418665	T19204	Hs.195685	ESTs	7.14	7.3
	426646	AA392787	Hs.122713	ESTs	7.03	7.3
	420349	NM_016611	Hs.97174	potassium inwardly-rectifying channel, s	14.90	7.3
65	428624	AI125222	Hs.98712	hypothetical protein DKFZp434H0311	3.71	7.1
	420710	NM_007009	Hs.99875	zona pellucida binding protein	20.78	7.1
	434317	AI674095		ESTs	3.98	7.1
	443432	AI056863	Hs.339871	ESTs	3.46	7.0
	425709	AA383076	Hs.159274	outer dense fibre of sperm tails 1	23.21	7.0
70	426670	AA383047	Hs.310210	ESTs	6.92	7.0
	408613	AW242086	Hs.253967	ESTs	5.77	6.8
	452235	AL039743	Hs.28514	testes development-related NYD-SP21	9.23	6.7
	434133	AI655275	Hs.236635	ESTs, Weakly similar to ATHUB actin beta	7.46	6.7
	427294	AA412594	Hs.125902	ESTs	3.44	6.7
75	427262	AA448509	Hs.128652	ESTs	5.66	6.5
	429851	AA459835	Hs.120573	hypothetical protein DKFZp434K1172	9.01	6.5
	406378			NM_021247::Homo sapiens protamine 3 (PRM	3.96	6.4
	425865	AA393491	Hs.183740	ESTs	9.15	6.4
	428665	NM_017481	Hs.189184	ubiquitin 3	11.07	6.4
80	439379	AA835002	Hs.125611	ESTs	5.06	6.3
	427520	BE467881	Hs.97489	ESTs, Weakly similar to B28096 line-1 pr	9.29	6.2
	458940	BE149824	Hs.132888	KIAA1674	3.11	6.2
	426620	AW450252		ESTs	12.27	6.2
	429516	AI653299	Hs.99354	ESTs, Weakly similar to hyperpolarizatio	9.15	6.1

	426736	AA431615	Hs.130722	ESTs	3.58	6.1
	427843	AC005622	Hs.180943	hypothetical protein R30953_1	6.34	6.1
	426639	A1799059	Hs.112807	ESTs	6.93	6.0
5	438637	BE500941	Hs.126730	ESTs, Weakly similar to KIAA1214 protein	3.04	6.0
	433795	A1216583	Hs.122599	ESTs, Weakly similar to ALU7_HUMAN ALU S	10.45	5.9
	441232	A1656050	Hs.7086	hypothetical protein MGC12435	4.27	5.9
	433943	AA992805	Hs.44865	lymphoid enhancer-binding factor 1	6.87	5.8
	426955	AA393669	Hs.238094	ESTs	4.75	5.8
10	428918	AL036957	Hs.2324	protamine 2	38.40	5.8
	427851	AA846543	Hs.98257	ESTs	15.87	5.8
	428208	AA442327	Hs.104854	ESTs	6.34	5.7
	422207	A1828862	Hs.10964	ESTs	6.43	5.7
	431153	AW972342	Hs.77823	hypothetical protein FLJ21343	9.24	5.7
15	419350	AC005328		Homo sapiens chromosome 19, cosmid R2666	14.94	5.6
	427107	AA899586	Hs.180346	ESTs	6.25	5.6
	429461	A188219	Hs.99311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	3.92	5.6
	432512	NM_003284	Hs.3017	transition protein 1 (during histone to	22.03	5.6
	434451	AW445179	Hs.121438	ESTs	7.89	5.5
20	420348	AL137385	Hs.97140	Homo sapiens mRNA; cDNA DKFZp434M1126 (f	11.26	5.5
	427214	AA442240	Hs.178213	ESTs	8.41	5.5
	458658	A1301117	Hs.122055	ESTs	4.35	5.5
	457034	AA398061	Hs.296587	Homo sapiens chromosome 21 segment HS21C	11.29	5.4
	423120	AW160551	Hs.124021	soggy-1 gene	8.88	5.4
25	438983	AF085884	Hs.20029	proacrosin binding protein sp32 precursor	22.69	5.4
	426619	A1357194	Hs.119284	ESTs	7.07	5.4
	440822	A1554897		Homo sapiens clone 19187 placenta expres	3.80	5.4
	416205	AA176396	Hs.169624	ESTs	10.26	5.4
	426712	AW173177	Hs.197755	hypothetical protein MGC5356	8.17	5.3
30	427840	A1216654	Hs.98251	ESTs	6.44	5.3
	439314	AA382413	Hs.178144	ESTs	8.35	5.3
	428943	BE551631	Hs.20969	ESTs	6.31	5.2
	409209	AA460160	Hs.73217	ESTs	7.85	5.2
	441710	A187883	Hs.127510	ESTs, Weakly similar to ENC1_HUMAN ECTOD	7.73	5.1
35	420571	AA442366	Hs.98952	Human DNA sequence from clone RP1-39G22	9.39	5.1
	428563	AA431616	Hs.98660	ESTs	14.94	5.1
	433994	AL042483	Hs.335499	ESTs	6.84	5.0
	441856	A1674774	Hs.128014	ESTs	3.74	5.0
	427789	AA412428	Hs.48642	hypothetical protein FLJ23093	4.29	5.0
40	418967	NM_001725	Hs.89535	bactericidal/permeability-increasing pro	4.14	4.9
	430232	AA469940	Hs.105324	ESTs, Moderately similar to FRHJH ferrit	10.66	4.9
	421850	AW274576	Hs.121021	ESTs	12.27	4.9
	449436	AA860329	Hs.279307	hypothetical protein DKFZp434I2117	4.50	4.9
	426699	AA383337	Hs.121269	ESTs	5.67	4.9
45	426627	AF012359	Hs.195685	ESTs	20.66	4.9
	427285	AA401664	Hs.97784	ESTs	4.72	4.8
	423693	AL133633	Hs.131779	Homo sapiens mRNA; cDNA DKFZp434E2118 (f	6.03	4.8
	457019	AA421844	Hs.12830	hypothetical protein	3.87	4.8
	405264			NM_030813*:Homo sapiens suppressor of po	4.48	4.8
50	450608	A1668605	Hs.50380	ESTs, Moderately similar to ALU6_HUMAN A	3.76	4.8
	421378	L77564	Hs.103978	serine/threonine kinase 22B (spermogene	7.35	4.8
	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	8.66	4.7
	427423	BE267041	Hs.177926	exonuclease NEF-sp	19.27	4.7
	438756	AW081754	Hs.303923	hypothetical protein DKFZp434L1717	12.05	4.7
55	424197	AF096834	Hs.142989	germ cell specific Y-box binding protein	17.70	4.7
	423284	AC005764	Hs.126496	Homo sapiens chromosome 19, cosmid R3134	7.50	4.7
	432117	AL036195	Hs.2909	protamine 1	55.33	4.7
	424426	A1478416	Hs.132888	KIAA1674	5.41	4.6
	437387	A1198874	Hs.28847	AD026 protein	5.04	4.6
60	420718	NM_002301	Hs.99881	lactate dehydrogenase C	9.18	4.6
	420768	A1468780	Hs.292503	ESTs, Weakly similar to T47142 hypotheti	5.70	4.6
	423677	M86808	Hs.131361	pyruvate dehydrogenase (lipoamide) alpha	10.93	4.5
	436661	A1125270	Hs.128069	ESTs, Weakly similar to T19142 hypotheti	3.82	4.5
	427749	BE045979	Hs.98095	Homo sapiens cDNA: FLJ23052 fis, clone L	6.45	4.5
65	441830	AA383104	Hs.42954	hypothetical protein DKFZp564D0372	11.29	4.5
	427877	AW138725	Hs.178067	ESTs	4.09	4.5
	426623	AA382826	Hs.132793	ESTs	26.62	4.5
	429965	AL040379	Hs.99551	Homo sapiens cDNA FLJ11789 fis, clone HE	13.25	4.5
70	451099	RS2795	Hs.25954	interleukin 13 receptor, alpha 2	3.88	4.4
	417592	AA204664	Hs.182437	ESTs, Weakly similar to IS4383 chromosom	3.46	4.4
	421938	AA405951		gbzu66c01.r1 Soares_testis_NHT Homo sap	4.69	4.4
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	19.15	4.4
	426710	BE041517	Hs.143893	ESTs	5.57	4.4
	428710	A1890919	Hs.126780	ESTs, Weakly similar to T12519 hypotheti	11.86	4.4
75	438641	AW138484	Hs.190653	ESTs	6.19	4.4
	420614	AL110291	Hs.99364	putative transmembrane protein	6.86	4.4
	422705	NM_005686	Hs.119287	actin-like 7B	9.73	4.4
	421805	AL042716	Hs.130947	hypothetical protein DKFZp434N1415	5.89	4.4
	448963	AA459796	Hs.331247	Homo sapiens, clone IMAGE3610712, mRNA,	6.77	4.3
80	426738	AA421097	Hs.291902	ESTs	3.49	4.3
	440403	AW665135	Hs.130531	ESTs	6.97	4.3
	456085	A1184560	Hs.130352	ESTs, Weakly similar to A47582 B-cell gr	6.30	4.3
	439594	A1245026	Hs.111099	hypothetical protein MGC10974	7.85	4.3
	428909	A1190714	Hs.98945	ESTs	7.79	4.3

	426735	T78716	Hs.120445	ESTs	5.10	4.3
	438653	AW188099	Hs.131813	ESTs	5.29	4.3
	443038	AI968058	Hs.209206	ESTs, Weakly similar to S38782 actin bet	7.29	4.2
5	428677	AI657119	Hs.120036	tropoin 1, cardiac	10.73	4.2
	424220	AK000869	Hs.143251	hypothetical protein	9.13	4.2
	426299	H93373	Hs.169222	acrosomal vesicle protein 1	4.87	4.2
	428871	AA913840	Hs.98903	ESTs	3.76	4.2
	410163	AF151977	Hs.59260	NTT5 protein	7.29	4.2
10	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	5.29	4.2
	427757	AI142295	Hs.129794	ESTs	3.57	4.1
	426721	AA383588	Hs.131816	ESTs, Weakly similar to T29012 hypotheti	11.13	4.1
	401692			C16000122:gi5689527[dbj]BAA83047.1] (A	6.37	4.1
	403783			NM_031956:Homo sapiens NYD-SP14 protein	3.74	4.0
15	421611	AA459841	Hs.97309	ESTs	11.51	4.0
	404271			ENSP00000244792*:Phosphoglycerate kinase	4.02	4.0
	441800	AW027571	Hs.7973	hypothetical protein DKFZp434G156; KIAA1	8.86	4.0
	423000	AF049615	Hs.122959	Huntingtin interacting protein M	3.60	4.0
	423118	AL035460	Hs.124009	Human DNA sequence from clone RP5-860F19	4.84	4.0
20	420419	AA397796	Hs.11614	HSPC055 protein	4.07	3.9
	435897	AF269223	Hs.128322	I-complex 11 (a murine tcp homolog)	23.29	3.9
	428516	R38137	Hs.156469	ESTs, Moderately similar to KIAA0940 pro	5.28	3.9
	427179	AA400590	Hs.97543	ESTs	6.18	3.9
	426609	AL040604	Hs.99344	hypothetical protein PRD-NY3	10.07	3.9
25	452579	AA131657	Hs.23830	ESTs	5.24	3.9
	441443	BE465999	Hs.129293	ESTs	4.60	3.9
	427709	AI631811	Hs.180403	STRN protein	3.82	3.9
	435484	AA682756	Hs.88051	ESTs	5.10	3.9
	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	4.61	3.8
30	436302	AL355841	Hs.99330	hypothetical protein FLJ23588	7.14	3.8
	421620	AA446183	Hs.91885	ESTs, Weakly similar to I55214 salivary	5.20	3.8
	427086	AA436131	Hs.188781	ESTs	5.76	3.8
	420475	AW408407	Hs.187018	ESTs	3.99	3.8
	441357	AI240184	Hs.343487	ESTs	4.63	3.8
35	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	8.04	3.8
	441806	AI024442	Hs.346385	ESTs	5.48	3.8
	413209	AW083791	Hs.21263	suppressor of potassium transport defect	9.02	3.8
	414544	AA149285	Hs.115659	hypothetical protein MGC5521	10.15	3.8
	427251	AI026844	Hs.98843	ESTs, Highly similar to GRA2_HUMAN GLYCI	7.69	3.8
40	437982	N93466	Hs.121764	ESTs, Weakly similar to testicular tek1	3.46	3.7
	442589	BE405869		protein kinase, cAMP-dependent, regulato	4.50	3.7
	425841	BE262951	Hs.99052	ESTs	8.26	3.7
	410350	AA446395	Hs.62595	chromosome 9 open reading frame 9	7.64	3.7
	440487	AI203685	Hs.135763	ESTs	5.90	3.7
45	419455	AW172570	Hs.14600	ESTs	4.23	3.7
	436588	AA759233		ESTs	5.04	3.7
	421610	AA393168	Hs.90034	hypothetical protein FLJ21916	5.53	3.7
	441982	AI216902	Hs.48802	ESTs	4.79	3.6
	427288	AI139000	Hs.97792	hypothetical protein DKFZp434I099	5.17	3.6
50	414439	W45387	Hs.100007	regulatory factor X, 2 (influences HLA c	4.43	3.6
	401798			Target Exon	4.83	3.6
	433395	AF039442	Hs.160881	Homo sapiens colon cancer antigen NY-CO-	3.17	3.6
	438064	AI476330	Hs.234934	ESTs	3.56	3.6
55	426658	AA397912	Hs.115366	Human DNA sequence from clone RP4-803K15	7.26	3.6
	431986	AA536130		Novel human gene mapping to chromosome 20	6.13	3.6
	427872	AA835058	Hs.9622	Human DNA sequence from clone RP1-261G23	4.04	3.6
	437896	AA813689	Hs.123436	ESTs, Weakly similar to KIAA1205 protein	4.69	3.6
	420431	AB007131		Homo sapiens cDNA FLJ12825 fis, clone NT	4.24	3.5
	409467	Z22780	Hs.307358	cyclin, basic protein of sperm head cyt	5.13	3.5
60	422770	AL117544	Hs.120021	DKFZP434I092 protein	8.02	3.5
	437399	AI808626	Hs.121188	ESTs, Weakly similar to T29922 hypotheti	5.03	3.5
	428448	AA625766	Hs.98609	ESTs, Weakly similar to A Chain A, Coagu	4.30	3.5
	426705	AL042749	Hs.97714	ESTs	10.45	3.5
	427312	AA400657	Hs.135283	ESTs	4.47	3.5
65	423329	AF054910	Hs.127111	tek1n 2 (testicular)	4.40	3.5
	439290	AI638094	Hs.236896	ESTs	3.29	3.4
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N1923	6.18	3.4
	420500	AC005261	Hs.98338	serine/threonine kinase 13 (aurora)/PL1-	6.24	3.4
	441168	AI198850	Hs.131654	DMRT-like family B with proline-rich C-1	10.39	3.4
70	420482	X57655	Hs.98243	serine protease inhibitor, Kazal type, 2	20.38	3.4
	426988	AI208684	Hs.163960	Homo sapiens heat shock transcription fa	5.02	3.4
	444968	AW628609	Hs.148653	ESTs	5.10	3.4
	429210	AA448011	Hs.131918	ESTs	4.22	3.4
	442970	R28215	Hs.143878	Homo sapiens mRNA for FLJ00024 protein,	4.20	3.4
75	422782	AL133054	Hs.120369	hypothetical protein DKFZp434H2215	4.72	3.4
	436601	AA969884		ESTs	4.84	3.4
	421209	AJ010230	Hs.102576	rat finger protein-like 1 antisense	7.83	3.4
	415705	U06632	Hs.966	collin	6.30	3.4
80	435587	AF215924	Hs.97899	putative allantoinase	3.48	3.3
	427572	AA417291	Hs.97978	hypothetical protein MGC4766 similar to	3.54	3.3
	427541	AI798983	Hs.82921	solute carrier family 35 (CMP-sialic aci	10.33	3.3
	429404	NM_005738	Hs.201672	ADP-ribosylation factor-like 4	3.57	3.3
	415014	AW954064	Hs.24951	ESTs	4.03	3.3
	420547	AF155140	Hs.98738	gonadotroph-regulated testicular RNA he	10.76	3.3

5	412092	H43229	Hs.125201	ESTs, Weakly similar to I38022 hypotheli	5.27	3.3
	441579	AW468847	Hs.127194	ESTs	7.13	3.3
	420619	AF130255	Hs.99430	testis zinc finger protein	5.19	3.3
	425368	AB014595	Hs.155976	cullin 4B	3.07	3.3
	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	3.52	3.3
10	429938	BE296804	Hs.226377	phosphate cytidyltransferase 2, ethano	3.03	3.3
	453017	R84301	Hs.31387	DKFZP564J0123 protein	3.30	3.3
	424466	AL040420	Hs.148250	Homo sapiens mRNA; cDNA DKFZp434N1535 (f	4.81	3.3
	442084	H81173	Hs.34596	ESTs	4.78	3.3
	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	4.63	3.3
15	434183	AW104257	Hs.123426	ESTs, Weakly similar to SN1L_HUMAN PROBA	5.73	3.3
	428093	AW594506	Hs.104830	ESTs	6.95	3.3
	433982	AA724720	Hs.112941	ESTs	5.11	3.2
	429821	AL096749	Hs.225433	Homo sapiens mRNA; cDNA DKFZp434G153 (fr	4.04	3.2
	408415	AW418788		ESTs, Weakly similar to S43569 R01H10.6	3.49	3.2
20	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinas	6.77	3.2
	402857			Target Exon	3.19	3.2
	416667	AK000526	Hs.79457	hypothetical protein FLJ20519	3.69	3.2
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	14.29	3.2
	427748	AA421041		ESTs	4.57	3.2
25	422794	AJ011733	Hs.120857	synaptogyrin 4	4.23	3.2
	417488	AL046052	Hs.321046	hypothetical protein FLJ11743	3.57	3.2
	440115	R41808		ESTs, Weakly similar to B Chain B, Solut	4.67	3.2
	437143	AW204056	Hs.8917	ESTs	4.16	3.2
	417473	M55268	Hs.82201	casein kinase 2, alpha prime polypeptide	4.02	3.2
30	426594	AA884317	Hs.97130	ESTs	3.45	3.2
	428733	AA346824	Hs.191996	Homo sapiens organic cation transporter	6.29	3.2
	440864	AK382142	Hs.132104	ESTs	8.48	3.2
	427141	AW628007	Hs.97643	testis-specific protein TSP-NY	5.60	3.2
	431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp434F0919 (f	5.10	3.2
35	438670	AI275803	Hs.123428	ESTs	4.08	3.2
	412443	AW951103	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	4.26	3.2
	452251	R37132	Hs.65009	ESTs	4.01	3.1
	444141	AW629475	Hs.8977	ESTs, Weakly similar to RED1_HUMAN DOUBL	4.89	3.1
	428254	AK000542	Hs.183362	hypothetical protein FLJ20535	5.23	3.1
40	421621	AL045589	Hs.180197	ESTs	7.09	3.1
	451017	BE391847	Hs.181173	hypothetical protein MGC10771	3.57	3.1
	457138	AW140059	Hs.98579	ESTs	13.17	3.1
	428524	AA429772		ESTs	4.40	3.1
	428726	AA432195	Hs.98694	ESTs	6.47	3.1
45	431310	AW327889	Hs.252433	Homo sapiens cDNA FLJ13794 fis, clone TH	4.07	3.1
	428076	AA420979	Hs.234895	ESTs, Weakly similar to Lysozyme [H.sapi	5.97	3.1
	427532	AA442152	Hs.104744	hypothetical protein DKFZp434J0617	3.45	3.1
	424450	AL137526	Hs.147472	dynein intermediate chain 2	6.01	3.1
	433963	AI218808	Hs.187778	ESTs	5.68	3.1
50	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	3.20	3.1
	440933	AI208217		ESTs	3.44	3.1
	441854	AA215990	Hs.99841	ESTs, Weakly similar to dJ1108D11.1 [H.s	4.03	3.1
	423313	NM_014269	Hs.126838	a disintegrin and metalloproteinase doma	6.36	3.1
	428630	AA431270	Hs.140646	ESTs	3.59	3.1
55	448813	AF169802	Hs.22142	cytochrome b5 reductase b5R2	5.63	3.0
	434720	AI208541	Hs.189160	ESTs, Weakly similar to cytochrome c-lik	6.04	3.0
	436328	AI201145	Hs.122042	Human DNA sequence from clone RP4-576H24	7.10	3.0
	429293	AI767879	Hs.99214	ESTs	5.69	3.0
	427255	AA400082	Hs.343593	ESTs, Weakly similar to TD54_HUMAN TUMOR	5.37	3.0
60	440713	AA904448	Hs.126368	ESTs	6.28	3.0
	418499	AI627392	Hs.302023	hypothetical protein FKSG25	7.88	3.0
	423218	NM_015896	Hs.167380	BLU protein	6.68	3.0
	444644	AW070634	Hs.144794	ESTs	5.00	3.0
	430252	AI638774	Hs.105328	testes development-related NYD-SP20	21.75	3.0
65	427829	AI188225		ESTs	7.36	3.0
	426879	AI969340	Hs.115437	hypothetical protein MGC3048	7.24	3.0
	427362	AA625582	Hs.97752	EST	4.38	3.0
	441973	T60072	Hs.10688	ESTs, Weakly similar to HRHFB2157 [H.s	4.06	2.9
	428989	AF104260	Hs.194712	p1w1 (Drosophila)-like 1	4.45	2.9
70	438735	M76676		ESTs	3.81	2.9
	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp434K1815 (f	11.37	2.9
	427586	AA609661	Hs.190592	ESTs, Moderately similar to WASP-family	6.26	2.9
	427306	AI476743	Hs.229275	ESTs	3.00	2.9
	418725	AL117637	Hs.306094	DKFZP434I225 protein	7.13	2.9
75	456748	AW137749	Hs.125902	ubiquitin specific protease 2	3.48	2.9
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.60	2.9
	433836	AA610065	Hs.179646	ESTs	3.33	2.9
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	3.22	2.9
	437426	AW136558	Hs.125246	ESTs	4.49	2.9
80	405528			C2002647:gi4507721 ref NP_003310.1 tit	6.03	2.9
	442977	AW291731	Hs.144090	ESTs	4.23	2.9
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	13.24	2.8
	424275	AW673173	Hs.144505	DKFZP566F0546 protein	5.60	2.8
	426567	AA770016	Hs.121192	ESTs	3.64	2.8
	410202	AB023213	Hs.60177	KIAA0996 protein	3.00	2.8
	428080	AI198656	Hs.98330	ESTs	4.09	2.8
	427252	AA400069	Hs.97757	hypothetical protein FLJ13031	4.34	2.8

	458255	AW140126	Hs.132357	ESTs	3.23	2.8
	433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3)	3.95	2.8
	440582	AA993337	Hs.129082	ESTs	5.29	2.8
	435566	AK57958	Hs.80464	hepatitis B virus x-interacting protein	3.28	2.8
5	433771	AI028794	Hs.112684	ESTs	3.36	2.8
	447924	AJ817226	Hs.313413	ESTs, Weakly similar to T23110 hypothe	5.30	2.8
	426703	AJ221693	Hs.121549	ESTs	3.93	2.8
	430251	AA609246	Hs.181451	ESTs	4.04	2.8
	427184	AI969361	Hs.180471	ESTs	6.78	2.8
10	439909	AW450062	Hs.187134	ESTs, Moderately similar to AF263742 1 g	3.65	2.8
	448885	AW003686	Hs.30325	ESTs, Highly similar to AF200923 1 test	3.34	2.7
	450340	AA442322	Hs.60288	ESTs	5.39	2.7
	428100	AW665592	Hs.190413	ESTs	5.32	2.7
	449333	AJ203021		ESTs	4.35	2.7
15	429861	AI989571	Hs.99510	ESTs	3.28	2.7
	426622	AL044400	Hs.25371	ESTs, Weakly similar to A37232 mucin, tr	5.38	2.7
	427256	AL042436	Hs.97723	ESTs	4.08	2.7
	408407	AF214680	Hs.44685	C3HC4-like zinc finger protein	3.27	2.7
	403328			Target Exon	4.26	2.7
20	436264	AA707457	Hs.120014	ESTs	3.58	2.7
	427104	AA398187	Hs.104682	ESTs, Weakly similar to mitochondrial cl	3.68	2.7
	426640	AJ200981	Hs.98104	ESTs	4.60	2.7
	428789	AW296167	Hs.91930	ESTs	4.23	2.7
	435274	AA887547	Hs.150905	ESTs	4.25	2.7
25	426612	AA922067	Hs.184185	ESTs	7.17	2.7
	435110	N42688	Hs.81001	F-box only protein 25	4.85	2.7
	433792	AA778661		ESTs	4.06	2.7
	423278	AL117627	Hs.126289	Homo sapiens mRNA; cDNA DKFZp434B115 (fr	3.04	2.7
30	427284	AA400298	Hs.144696	ESTs	5.81	2.6
	423375	Z94277	Hs.127689	type 1 protein phosphatase inhibitor	3.36	2.6
	422362	Z46967	Hs.115460	calicin	4.72	2.6
	439993	T18864	Hs.144924	serine/threonine protein kinase SSTK	5.03	2.6
	409364	AI480252	Hs.137368	ESTs	7.22	2.6
35	419224	NM_012189	Hs.314452	fibrousheathin II	13.86	2.6
	428915	AI041278	Hs.87908	Snf2-related CBP activator protein	4.73	2.6
	427181	AI183653	Hs.27888	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.21	2.6
	442122	AI932330		ESTs	3.07	2.6
	424812	AF059252	Hs.153299	DOM-3 (C. elegans) homolog Z	3.80	2.6
40	430956	AI183529	Hs.2706	glutathione peroxidase 4 (phospholipid h	3.19	2.6
	427234	AA399667	Hs.104675	ESTs	3.43	2.6
	423005	AL080148	Hs.123004	DKFZP434B204 protein	3.53	2.6
	428214	AA936282	Hs.120397	ESTs	4.14	2.6
	452613	AA461599	Hs.23459	ESTs	7.78	2.6
45	410380	AL133068	Hs.62880	novel protein similar to mouse MOV10	3.45	2.6
	452537	AW247390	Hs.77735	hypothetical protein FLJ11618	3.43	2.6
	401712			Target Exon	4.51	2.6
	429188	BE503443	Hs.112095	hypothetical protein DKFZp434F1819	5.90	2.6
	438124	AA778610	Hs.122045	ESTs	3.43	2.6
50	422937	U03270	Hs.122511	centrin, EF-hand protein, 1	3.60	2.6
	410279	BE271977	Hs.61809	hypothetical protein FLJ14117	4.36	2.6
	428625	W87565	Hs.18566	ESTs	5.29	2.6
	433439	AA431176	Hs.133230	ribosomal protein S15	3.50	2.5
	433760	AW592321		ESTs	3.26	2.5
55	431219	AI190773	Hs.127204	ESTs, Weakly similar to similar to CR16,	5.10	2.5
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	8.07	2.5
	453468	W00712	Hs.32990	DKFZP566F084 protein	3.56	2.5
	445158	AI992108	Hs.127206	ESTs	3.60	2.5
	440860	R10482	Hs.132876	ESTs	4.26	2.5
60	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	3.95	2.5
	433281	N48673	Hs.146037	hypothetical protein DKFZp434C135	5.68	2.5
	429369	AI269514	Hs.129802	ESTs	3.49	2.5
	433949	AI574766	Hs.112877	ESTs	5.15	2.5
	427668	AA298760	Hs.180191	hypothetical protein FLJ14904	10.46	2.5
65	414708	AA393379	Hs.97415	ESTs, Weakly similar to T33068 hypothe	3.87	2.5
	408485	AW274294	Hs.144092	ESTs, Weakly similar to A Chain A, Sacch	6.10	2.4
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	5.64	2.4
	426956	AA393873		ESTs, Weakly similar to ALU5_HUMAN ALU S	4.68	2.4
	429152	AA447209	Hs.99099	Homo sapiens NYD-SP28 mRNA, complete cds	4.34	2.4
70	426247	U92992	Hs.98834	ESTs	5.40	2.4
	427589	T19219	Hs.97978	hypothetical protein MGC4766 similar to	3.40	2.4
	429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2 (testis)	5.85	2.4
	453353	U33055	Hs.32959	G protein-coupled receptor kinase 2 (Dro	4.82	2.4
	413372	H55532		tubulin, alpha 2	9.32	2.4
75	411737	AW160339	Hs.71791	hypothetical protein	5.26	2.4
	453868	NM_014433	Hs.35584	rhomboid tumor deletion region protein 1	3.05	2.4
	427098	AA398161	Hs.97602	ESTs	3.21	2.4
	427165	AA429709	Hs.99336	ESTs, Weakly similar to T15446 hypothe	4.27	2.4
	425808	AA364109	Hs.177990	ESTs	7.80	2.4
80	444790	AB030506	Hs.11955	B9 protein	3.32	2.4
	426718	AA383555	Hs.126413	ESTs	4.20	2.4
	411441	AL042355	Hs.70202	WD repeat domain 10	6.14	2.4
	450852	AI983354	Hs.7740	oxysterol binding protein-like 1	4.97	2.3
	427054	AA421240	Hs.97570	ESTs	3.10	2.3

5	438633	AI653327	Hs.123501	ESTs	3.46	2.3
	427199	AW015836	Hs.292919	ESTs	4.31	2.3
	440182	AA868919	Hs.250110	ESTs	3.03	2.3
	435517	AA928626	Hs.130177	ESTs	3.64	2.3
	446309	BE044261	Hs.149774	ESTs	3.52	2.3
	420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	4.23	2.3
	433829	AI190715	Hs.102021	ESTs	6.08	2.3
	429485	AW197086	Hs.99338	ESTs	3.14	2.3
	423058	AW964568	Hs.111591	ESTs	3.36	2.3
10	433822	AI218609	Hs.112772	ESTs	3.83	2.3
	442268	BE278084	Hs.8179	hypothetical protein, clone 2746033	3.00	2.3
	434298	AA860090	Hs.116290	ESTs	3.71	2.3
	440720	AW662776	Hs.336943	Human DNA sequence from clone RP11-60H7	3.08	2.3
	427554	AW246578	Hs.179615	hypothetical protein FLJ10058	3.39	2.3
15	414251	AL042306	Hs.97689	VASA protein	11.25	2.3
	430254	AI809520		ESTs	3.27	2.3
	437418	AI478954	Hs.59459	ESTs	3.43	2.2
	437522	AA983844	Hs.121383	ESTs	4.15	2.2
	422808	AA449014	Hs.121025	chromosome 11 open reading frame 5	3.09	2.2
20	436695	AA725655	Hs.120480	ESTs	5.26	2.2
	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	6.78	2.2
	421625	AA405386	Hs.178004	ESTs	3.22	2.2
	434807	AA364183	Hs.323443	hypothetical protein FLJ11806	5.51	2.2
	428174	AA913321	Hs.126778	ESTs	3.09	2.2
25	409735	AL035295	Hs.56175	H.sapiens gene from PAC 106H8, similar t	3.11	2.2
	444467	AI150368		ESTs	3.81	2.2
	433832	AA918018	Hs.172516	ESTs	6.94	2.2
	440036	AW593295	Hs.210956	ESTs	5.87	2.2
	415240	AA161411	Hs.58668	chromosome 21 open reading frame 57	3.66	2.2
30	432538	BE258332	Hs.278362	male-enhanced antigen	3.58	2.1
	440882	AI205777	Hs.129538	ESTs	3.83	2.1
	436605	AI187742		ESTs	3.41	2.1
	422990	AF035620	Hs.122764	BRCA1 associated protein	5.65	2.1
	432174	AW590264	Hs.132806	ESTs	3.05	2.1
35	409267	NM_012453	Hs.52515	transducin (beta)-like 2	5.46	2.1
	423021	AL036111	Hs.292767	ESTs	3.87	2.1
	439012	BE383814	Hs.6455	RuvB (E coli homolog)-like 2	5.25	2.1
	433812	AA725026	Hs.97165	ESTs, Weakly similar to T31611 hypotheti	3.62	2.1
	456924	AI631510	Hs.196956	ESTs, Highly similar to match to EST AA3	4.38	2.1
40	437249	AA432202	Hs.103147	hypothetical protein FLJ21347	3.38	2.1
	426038	AA368101	Hs.99052	ESTs	3.03	2.1
	427065	AA397903	Hs.236635	gb:z189f12.r1 Soares_testis_NHT Homo sap	3.23	2.1
	428824	W23624	Hs.173059	ESTs	3.07	2.1
45	428224	X54017	Hs.183088	acrosin	3.18	2.1
	436954	AA740151	Hs.130425	ESTs	3.20	2.1
	444470	AA412195	Hs.13740	ESTs	4.27	2.1
	457579	AB030816	Hs.36761	HRAS-like suppressor	5.30	2.1
	427886	AA417083	Hs.104789	ESTs	3.49	2.1
	439273	AW139099	Hs.269701	ESTs	3.83	2.1
50	434318	AW207552	Hs.116328	ESTs, Weakly similar to A39564 transcrip	4.01	2.1
	427015	AA397520		ESTs	4.28	2.1
	421598	AW630942	Hs.106061	RD RNA-binding protein	3.30	2.1
	427236	AA399959	Hs.148271	ESTs	3.07	2.1
	434520	AA205273	Hs.177011	hypothetical protein	3.19	2.0
55	456051	T85626	Hs.76239	hypothetical protein FLJ20608	3.11	2.0
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	8.41	2.0
	451807	W52854		hypothetical protein FLJ23293 similar to	3.52	2.0
	448984	AW751955	Hs.22753	hypothetical protein FLJ22318	4.73	2.0
	420484	W32963	Hs.98289	VRK3 for vaccinia related kinase 3	3.86	2.0
60	414181	AK000476	Hs.75798	hypothetical protein	3.33	2.0
	424558	AF038847	Hs.150490	FK506-binding protein 6 (36kD)	7.70	2.0

TABLE 54B

Key: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

70	Key	CAT Number	Accession
	428618	2668_1	BC017998 B1826643 BG715794 BG722597 B1460787 BG773459 H52859 AI652853 AI990773 AW665193 AW340501 AA913806 AI337099 BE045942 AW572790 AW515652 H15004 AA909115 B1465310 B1462024 B1561578 B1463075 BG722527 R86003 BG623286 H15003 B1562131 BG435272
	426599	10110_1	BE738800 BM471423 AL557221 BG763302 BF742196 BF991016 BG200112 BF920027 BG576409 BG332214 B1830957 AI827504 AW183574 AI805171 AI126491 AA448257 AI090641 AW183329 AA994873 AI203663 BE041513 AA382260 AA382261 AL554887 BE273483
75	426930	1310779_1	AI809889 AA393442 AI150574 AI200886 AI221692 AA608977 AA813213
	434317	599587_1	AI205094 AI377740 AW117382 AW182289 AI674095 AW188019 AA897352 AA931314 AA923336 AW656317 AA629314 AA776691 AA906846 AA974625 AA884357 AI808590
	426620	142987_1	AL042392 AI147451 AA758821 AW450252 AA399310 AI656343 AI636668 AW515660 AI190733 AI025812 AA723645 AA709253 AA725709 AA398244 AA382463 AI139837
80	419350	13086_1	AI218809 BC014609 BG724383 AI024359 AA904573 AI138595 AA868685 AI768931 B1828436 BG717350 BG719800 AW182303 AA448181 B1826670 B1827131 B1830254 B1824155 B1831745 T19190 B1830415
	440822	532606_1	BG207562 BG192113 AA977616 AW274024 AI554897 AI221379 AA969158 AA906867 AI873494 AI015039
	421938	863689_1	AA412383 AA300675 BG773248 AA412243 AA405951

42589	33097_2	NM_004157 X14968 BG480488 BE409869 BG723898 BG476313 AU121626 BE386516 A969297 AW172340 AA889658 R23436 AI015037 BE250558 BF590945 AW385933 BF983000 AA070235 AL556082 M78388 AW504473 AW370139 BG913697 BE899096 BG827945 BE741233 AI015465 AW370169 BE297350 AA093249 AI122828 AA909991 AA759233 AI591713 BF197609 AI985094 AW448916 AI243277 AL449630 AL449629 AW241405 AW205071 AI671586 AI652354 AI638465 AW590359 AW662771 AW594067 BE502532 AI218894 BE466416 BF056295 AI247366 AI990484 AI917746 AW665925 AI216456 AW182169 AA969884 AA723888 AI018419 BI602176 BI603138 BI459895 BI755030 AW418788 AA883999 AA724858 AI480311 AW196355 AI004813 AI651117 BE814363 AW589856 AAA48124 AA447982 BI461166 AA405629 AI208966 AA421041 AA815377 AA411954 BF980396 R51074 BF979883 AI539370 BM128735 AA993397 AI611039 AW593985 R41808 AI208080 AA442862 AA429772 AI125404 AW593312 AI247364 AI208217 AA910021 AI915307 AI190292 AI188225 AA416673 AA416596 AA952888 AA972172 AA906874 M76676 NM_022571 BG772522 BF516449 AI537485 AW517245 BF762536 AA634446 AW196331 AI203035 BG722281 AK056320 AL522040 BI793043 AW071691 AI433682 AA865414 AA702684 BI792794 H96879 R52351 AA211126 AA442875 N25725 AA482563 N33446 N25222 AI1110 N26507 N73447 N24077 N20492 AW275550 H99619 AL518306 AL522041 AW959849 AL518307 AA725907 AI655113 AI309906 F10184 BM451081 BE257595 BG721625 BI828509 BG700470 F12568 Z45396 BI829288 AA364618 AA364851 AA421448 T74231 R52350 AA482415 AI203021 T88948 AI565842 AI024286 AA769898 AA778661 AA868972 AA609524 AI932330 AI190707 AI376782 AA976847 AA609179 AW592321 AA758282 AI214437 AW072537 AA781937 BI831486 AW190479 AI472793 AA460217 AA459937 BF082576 AA393673 AA398702 NM_006001 L11645 AI205604 AI207994 AI187362 AA709190 BI462421 BG772170 BG772772 AA436991 BG771655 BI553260 BF126025 BF125857 BI462670 BG724164 BI562424 BG721652 BI559662 BG722455 BI596415 BG717561 BG722138 BG773507 BG720572 C03867 AI016802 AL042663 AA770436 AA435720 T19365 AA626698 AA759057 AI208021 BF507844 AI208058 AA412719 AA426374 AI208775 AA977217 AA758055 F34585 AA180062 BG700885 AA868017 AW341719 AA971332 AI688794 Z20462 AI808145 AW665263 AA884952 AA906136 AW663704 AI150368 AI216464 AI125340 AI125684 AI377949 AI126470 AI218351 AW665355 AI243952 AW663454 AI240603 AI187742 AA884214 AA723933 AA857437 AI968733 AI968938 AA992784 AA397520 AW235244 BM479185 AL552795 AL577722 BF038888 BM127617 BF510346 AW450652 AA865478 AW449519 BM127314 AI806539 AW449522 AA993634 BA827626 AA904788
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40	TABLE 54C
	Pkey: Unique number corresponding to an Eos probaset
	Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
	Strand: Indicates DNA strand from which exons were predicted.
	NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
401979	2828778	Minus	75693-75851,76977-77112
406409	9256384	Minus	141101-141256
401741	2982169	Plus	195686-196823,200241-200381
406378	9256142	Minus	126408-126800
405264	7329374	Plus	28556-28684
401692	3540172	Plus	26365-26510
403783	8081824	Plus	128412-128635
404271	9826129	Minus	56392-57645
401798	6730720	Plus	22831-23448
402857	9801539	Plus	13402-14133
405528	9581957	Minus	22418-22687
403328	8469086	Minus	120428-120703
401712	6682593	Minus	76410-76527,76692-76829,78737-78866,8024

60	TABLE 55A:
	Pkey: Unique Eos probaset identifier number
	ExAccn: Exemplar Accession number, Genbank accession number
	UnigeneID: Unigene number
	Unigene Title: Unigene gene title
	R1: Ratio of non-seminomatous mixed germ cell testicular cancer compared to normal adult testicular tissues

Pkey	ExAccn	UnigeneID	Unigene Title	R1
416680	AW245540	Hs.79516	brain abundant, membrane attached signal	48.80
423961	D13666	Hs.136348	perlastin(OSF-2os)	43.30
412948	BE243313	Hs.334851	UIM and SH3 protein 1	42.50
428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	36.80
424247	X14008	Hs.234734	lysosome (renal amyloidosis)	29.80
414438	AI879277	Hs.76136	thioredoxin	29.40
406658	AI920965	Hs.77961	major histocompatibility complex, class	29.25
446899	NM_005397	Hs.16426	podocalyxin-like	28.70
411573	AB029000	Hs.70823	KIAA1077 protein	28.40
432730	AI066520	Hs.131358	ESTs	28.00
418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	28.00
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	27.90
446619	AJ076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	26.80
447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	25.00
418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	24.15

	406856	AW515336	Hs.29797	ribosomal protein L10	23.66
	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	23.60
	440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (Ig),	23.60
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptide	22.35
5	417426	NM_002291	Hs.82124	laminin, beta 1	21.60
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	21.55
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	21.50
	413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	21.50
10	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	20.90
	412636	NM_004415		desmoplakin (DPI, DPII)	20.90
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	20.30
	414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	19.45
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	19.30
15	406648	AA563730	Hs.277477	major histocompatibility complex, class	19.10
	412247	AF022375	Hs.73793	vascular endothelial growth factor	17.45
	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	17.40
	424800	AL035588	Hs.153203	MyoD family inhibitor	17.20
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	16.90
20	415314	N88802	Hs.5422	glycoprotein M6B	16.80
	406656	M16714	Hs.89643	major histocompatibility complex, class	16.75
	426295	AW367283		zinc finger protein 6 (CMPX1)	16.25
	406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	16.00
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	15.85
25	417088	M54915	Hs.81170	pim-1 oncogene	15.60
	449338	H73444	Hs.394	adrenomedullin	15.51
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	15.33
	414420	AA043424	Hs.76095	immediate early response 3	15.30
	425543	R23313	Hs.334895	ribosomal protein L10a	15.10
30	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	15.00
	420754	W79431	Hs.346911	ribosomal protein L22	14.92
	410397	AF217517	Hs.63042	DKFZp564J157 protein	14.86
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	14.70
	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	14.60
35	406786	AW161678	Hs.111334	ferritin, light polypeptide	14.57
	422105	AI929700	Hs.111680	endosulfine alpha	14.57
	422714	AB018335	Hs.119387	KIAA0792 gene product	14.25
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	14.05
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	14.00
40	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	14.00
	429614	AI371172	Hs.211539	hypothetical protein MGC4248	13.95
	410185	BE294068	Hs.737	immediate early protein	13.85
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	13.60
	410611	AW954134	Hs.20924	KIAA1628 protein	13.60
45	448588	AI970276	Hs.156905	KIAA1676	13.40
	421406	AF179897	Hs.104105	Mels (mouse) homolog 2	13.10
	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	13.00
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	13.00
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	13.00
50	454413	AI653672	Hs.40092	PNAS-123	12.90
	415221	W07418	Hs.78225	annexin A1	12.89
	425535	AB007937	Hs.158287	KIAA0468 gene product	12.48
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	12.45
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	12.40
55	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	12.19
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	12.12
	445055	BE512855	Hs.109051	SH3 domain binding glutamic acid-rich pr	12.07
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	11.90
	408437	AW957744	Hs.278469	lacrimal proline rich protein	11.80
60	430542	AI557486	Hs.119122	ribosomal protein L13a	11.51
	424670	W61215	Hs.116651	epithelial V-like antigen 1	11.50
	432409	AA806538	Hs.130732	KIAA1575 protein	11.50
	425945	AW410669	Hs.184280	solute carrier family 25 (mitochondrial	11.44
	425996	W67330		hypothetical protein AL110115	11.40
65	449961	AW265634	Hs.133100	ESTs	11.40
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	11.25
	407179	AA206465		thymosin, beta 4, X chromosome	11.21
	412623	R28898	Hs.74170	metallothionein 1E (functional)	11.10
	429978	AA249027		ribosomal protein S6	11.10
70	450377	AB033091		KIAA1265 protein	11.10
	418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	11.10
	440869	NM_014297	Hs.7486	protein expressed in thyroid	11.00
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	11.00
	451106	BE382701	Hs.25960	N-MYC oncogene	10.93
75	426552	BE297660	Hs.170328	moesin	10.91
	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	10.90
	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	10.80
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	10.80
	449944	AF290512	Hs.58215	Homo sapiens, Similar to rhotekin, clone	10.75
80	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.70
	435055	AW023337	Hs.5422	glycoprotein M6B	10.70
	406743	AA911568	Hs.279860	tumor protein, translationally-controlled	10.70
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	10.65
	420676	AI434780	Hs.4248	vav 2 oncogene	10.60

	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	10.60
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	10.50
	436075	BE090176	Hs.179902	transporter-like protein	10.30
5	450139	AK001838		serum/vitellin/corticoid regulated kinase	10.30
	427691	AW194426	Hs.20726	ESTs	10.26
	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	10.15
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	10.10
	440528	BE313555	Hs.7252	KIAA1224 protein	10.06
10	423184	NM_004428	Hs.1624	ephrin-A1	10.05
	450847	NM_003155	Hs.25590	stanniocalcin 1	9.90
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [Hsapi	9.90
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mito	9.90
	421395	D90084	Hs.1023	pyruvate dehydrogenase (lipoamide) alpha	9.89
15	435918	AF263538	Hs.86232	growth differentiation factor 3	9.89
	411251	R19774	Hs.22835	HHGP protein	9.80
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	9.75
	441187	AW195237	Hs.7734	hypothetical protein FLJ22174	9.75
	425580	L11144	Hs.1907	galanin	9.60
20	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	9.60
	413813	M96956	Hs.75561	teratocarcinoma-derived growth factor 1	9.60
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	9.60
	417944	AU077195	Hs.82985	collagen, type V, alpha 2	9.53
	409963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	9.51
25	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	9.42
	416926	H03109	Hs.263395	HTO18 protein	9.41
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	9.40
	428065	AI634045	Hs.157313	ESTs	9.40
	441455	AJ271671	Hs.7854	zinc/iron regulated transporter-like	9.39
30	410325	AB023154	Hs.62264	KIAA0937 protein	9.30
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	9.30
	454038	X06374	Hs.37040	platelet-derived growth factor alpha pol	9.29
	452568	AA805634	Hs.300870	Homo sapiens mRNA: cDNA DKFZp457M072 (tr	9.24
	447211	AL161961	Hs.17767	KIAA1554 protein	9.22
35	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	9.20
	418299	AA279530	Hs.83968	Integrin, beta 2 (antigen CD18 (p95), ly	8.93
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	8.90
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.90
	422241	Y00082	Hs.170121	protein tyrosine phosphatase, receptor t	8.90
40	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	8.84
	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	8.80
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	8.70
	426215	AW963419	Hs.155223	stanniocalcin 2	8.70
45	446627	AI973016	Hs.15725	hypothetical protein SBB148	8.60
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	8.60
	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase II	8.60
	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	8.50
	445245	AB032973	Hs.12461	LCHN protein	8.50
	448776	BE302454	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	8.40
50	453855	AA804789	Hs.19447	PDZ-LIM protein mystique	8.35
	410143	AA188169		KIAA1191 protein	8.35
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	8.30
	433208	AW002834	Hs.24095	ESTs	8.30
55	423753	Y11312	Hs.132463	phosphotransferase-3-kinase, class 2, beta	8.25
	432559	AW462948	Hs.257631	ESTs	8.20
	450581	AF081513	Hs.25195	TGF-beta 4	8.10
	450157	AW961576	Hs.60178	ESTs	8.10
	444795	AI193356	Hs.160316	ESTs	8.10
	400288	X06256	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	8.05
60	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	8.00
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	8.00
	419970	AW612022		ESTs	8.00
	411975	AI916058	Hs.144583	ESTs	7.95
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	7.90
65	451831	NM_001674	Hs.460	activating transcription factor 3	7.90
	437103	AW139408	Hs.152940	ESTs	7.90
	432636	AA340864	Hs.278562	claudin 7	7.87
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	7.84
70	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	7.80
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	7.80
	450147	AW373713	Hs.146324	CGI-145 protein	7.75
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	7.70
	449571	AW016812	Hs.200266	ESTs	7.70
	429355	AW973253	Hs.292689	ESTs	7.70
75	446488	AB037782	Hs.15119	KIAA1361 protein	7.70
	414774	X02419	Hs.77274	plasminogen activator, urokinase	7.69
	422424	AI186431	Hs.296638	prostate differentiation factor	7.67
	426818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	7.65
	416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	7.65
80	451812	X81889	Hs.152151	plakophilin 4	7.65
	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	7.60
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	7.60
	422746	NM_004484	Hs.119651	glypican 3	7.60
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	7.57

	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	7.57
	426689	BE245550	Hs.171825	basic helix-loop-helix domain containing	7.55
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	7.53
5	418329	AW247430	Hs.84152	cystathionine-beta-synthase	7.50
	425246	AI085561	Hs.155321	serum response factor (c-fos serum respo	7.50
	419223	X60111	Hs.1244	CD9 antigen (p24)	7.47
	406776	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	7.44
	401466			vesicle-associated membrane protein 4	7.43
10	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	7.40
	413686	AI469213	Hs.71404	ESTs	7.40
	408805	AF025374	Hs.46465	T-cell, immune regulator 1	7.40
	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	7.30
	444838	AV651680	Hs.208558	ESTs	7.30
15	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	7.28
	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	7.20
	452924	AW580939	Hs.97199	complement component C1q receptor	7.15
	436398	H87136	Hs.5174	ribosomal protein S17	7.15
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	7.10
20	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	7.10
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	7.10
	401192			Target Exon	7.08
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	7.08
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	7.00
25	449567	AI990790	Hs.188614	ESTs	7.00
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	7.00
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	7.00
	430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	7.00
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	6.90
30	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	6.87
	424292	AA528489	Hs.234518	ribosomal protein L23	6.84
	417365	D50683	Hs.82028	transforming growth factor, beta recepto	6.80
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	6.80
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	6.80
35	435684	NM_001290	Hs.4980	LIM domain binding 2	6.80
	442685	AB033017	Hs.8594	KIAA1191 protein	6.79
	413542	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg	6.77
	411789	AF245505	Hs.72157	Adiclan	6.76
	441565	AW953575	Hs.303125	p53-induced protein PIGPC1	6.75
40	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	6.74
	444207	AI565004		cathepsin D (lysosomal aspartyl protease	6.72
	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	6.70
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytolaclin)	6.70
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	6.70
45	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	6.70
	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	6.70
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	6.70
	433271	BE621697	Hs.14317	nuclear protein family A, member 3 (H/	6.66
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	6.65
50	406858	AI865720	Hs.29797	ribosomal protein L10	6.65
	435748	AA699756	Hs.117335	ESTs	6.63
	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	6.62
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	6.62
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	6.61
55	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	6.60
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	6.55
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	6.50
	450294	HA2587	Hs.238730	hypothetical protein MGC10823	6.45
	417336	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	6.45
60	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	6.43
	402145			Target Exon	6.43
	414662	AL036058	Hs.76807	major histocompatibility complex, class	6.42
	436660	H12751	Hs.5327	PRO1914 protein	6.40
	438952	BE046594		gb:hn41c11.x1 NCL_CGAP_RDF2 Homo sapiens	6.40
65	435937	AA830893	Hs.119769	ESTs	6.40
	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	6.40
	446173	BE565849	Hs.14158	copine III	6.39
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	6.36
	412093	BE242691	Hs.14947	ESTs	6.34
70	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	6.30
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	6.30
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	6.30
	447519	U46258	Hs.339665	ESTs	6.30
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	6.30
75	434423	NM_006769	Hs.3844	LIM domain only 4	6.30
	434524	AA635931	Hs.249716	ESTs	6.30
	441970	AW959918	Hs.73737	ESTs	6.30
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	6.30
80	437374	AL359571	Hs.44054	ninein (GSK3B interacting protein)	6.25
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	6.23
	407284	AI539227	Hs.214039	hypothetical protein FLJ23556	6.20
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	6.20
	447029	AL137281	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (f	6.20
	417315	AI080042	Hs.180450	ribosomal protein S24	6.20

	418840	AJ821614	Hs.185831	ESTs	6.20
	410668	BE379794	Hs.159551	hypothetical protein	6.16
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	6.13
5	413840	AJ301558		RNA binding motif protein, X chromosome	6.13
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	6.12
	450944	AA554989		sudD (suppressor of bimD6, Aspergillus n	6.10
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	6.10
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.10
10	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	6.10
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	6.10
	408996	AJ979168	Hs.344096	glycoprotein (transmembrane) nmb	6.10
	432666	AW204059		ESTs, Weakly similar to unnamed protein	6.09
	435812	AA700439	Hs.188490	ESTs	6.06
	432805	X94630	Hs.3107	CD97 antigen	6.06
15	441283	AA927670	Hs.131704	ESTs	6.06
	417632	R20855	Hs.5422	glycoprotein M6B	6.00
	435905	AW997484	Hs.5003	KIAA0456 protein	6.00
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	5.99
	429083	Y09397	Hs.227817	BCL2-related protein A1	5.95
20	410598	AJ817130	Hs.9195	Homo sapiens cDNA FLJ13598 fis, clone PL	5.95
	425291	AA354572		gb:EST62857 Jurkat T-cells V Homo sapien	5.95
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14295 fis, clone PL	5.93
	451052	AA281504	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	5.90
	447217	BE465754	Hs.17778	neuropilin 2	5.90
25	417228	AL134324	Hs.7312	ESTs	5.86
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	5.86
	452382	N38902	Hs.211539	hypothetical protein MGC4248	5.84
	427747	AW411425	Hs.180655	serine/threonine kinase 12	5.84
	414483	R25513	Hs.10683	ESTs	5.82
30	428570	AA430321	Hs.293945	ESTs	5.81
	443194	AJ954968		matrix Gla protein	5.80
	429582	AJ569068	Hs.22247	ESTs	5.80
	414405	AJ362533		KIAA0306 protein	5.80
35	428342	AJ739168		Homo sapiens cDNA FLJ13458 fis, clone PL	5.80
	437739	AW579216	Hs.264610	ESTs, Moderately similar to lbd1 [H.sapi	5.80
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	5.80
	442821	BE391929	Hs.8752	transmembrane protein 4	5.77
	434511	R28982	Hs.18106	ESTs	5.76
40	406745	AW511970	Hs.279860	tumor protein, translationally-controlled	5.70
	453187	AJ161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	5.70
	453115	AW772041	Hs.18439	ESTs, Moderately similar to JC5238 galac	5.70
	406857	AA613726	Hs.29797	ribosomal protein L10	5.69
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	5.68
45	444273	AJ903474	Hs.230	fibromodulin	5.65
	441623	AA315805		desmoglein 2	5.63
	418300	AJ433074	Hs.85682	Homo sapiens cDNA: FLJ21578 fis, clone C	5.63
	440099	AL080058	Hs.6909	DKFZP564G202 protein	5.60
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	5.60
50	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	5.60
	422610	AF153820	Hs.1547	potassium inwardly-rectifying channel, s	5.60
	438278	BE409248	Hs.57988	hypothetical protein FLJ22357 similar to	5.58
	430451	AA836472	Hs.297939	cathepsin B	5.57
	406899	L06505	Hs.182979	ribosomal protein L12	5.53
55	458965	AA010319	Hs.60389	ESTs	5.50
	430592	AJ224864	Hs.9688	leukocyte membrane antigen(IRC1)	5.50
	433655	AL036559	Hs.3463	ribosomal protein S23	5.50
	428471	X57348	Hs.184510	stratfin	5.42
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	5.40
60	417849	AW291587	Hs.82733	nidogen 2	5.40
	408989	AW361666	Hs.49500	KIAA0746 protein	5.40
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	5.40
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	5.40
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	5.40
65	406819	AA908472		gbxog82a10.s1 NCI_CGAP_Ov8 Homo sapiens	5.39
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	5.36
	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	5.34
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	5.34
	427968	AJ857607	Hs.181301	cathepsin S	5.32
	429307	AU076592	Hs.198951	jun B proto-oncogene	5.30
70	424950	AA602917	Hs.156974	ESTs	5.30
	410619	BE512730	Hs.65114	keratin 18	5.30
	424408	AJ754813	Hs.146428	collagen, type V, alpha 1	5.27
	425430	BE185921	Hs.98073	ESTs, Moderately similar to Z195_HUMAN Z	5.27
	411165	NM_000169	Hs.69089	galactosidase, alpha	5.28
75	406701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	5.26
	435631	BE254086	Hs.29647	uncharacterized hematopoietic stem/proge	5.24
	418905	BE539574		actinin, alpha 4	5.23
	449303	AK001495	Hs.23467	hypothetical protein FLJ10633	5.22
80	440703	AL137663	Hs.7378	Homo sapiens mRNA: cDNA DKFZp434G227 (tr	5.20
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	5.20
	444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	5.20
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.20
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	5.20

	409604	AW444448	Hs.49124	ESTs	5.20
	432581	AU076465	Hs.278441	KIAA0015 gene product	5.16
	430556	AW967807	Hs.13797	ESTs	5.16
5	431315	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	5.16
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subunit	5.15
	454227	AW963897	Hs.44743	KIAA1435 protein	5.15
	429367	AB007867	Hs.278311	plexin B1	5.12
	452191	AU076408	Hs.28309	UDP-glucose dehydrogenase	5.11
10	419073	AW372170	Hs.183918	Homo sapiens cDNA FLJ12797 fis, clone NT	5.11
	442295	AJ827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	5.10
	443030	R68048	Hs.9238	hypothetical protein FLJ23516	5.10
	421878	AA298652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	5.10
	424875	AH187945	Hs.199310	ESTs	5.10
	427641	AJ270591	Hs.146116	ESTs	5.10
15	442806	AW294522	Hs.149991	ESTs	5.10
	442495	AI184717		ESTs	5.10
	439941	AI392640	Hs.18272	amino acid transporter system A1	5.09
	444981	AW855398	Hs.12210	hypothetical protein FLJ13732 similar to	5.07
	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	5.06
20	418117	AI922013	Hs.83496	linker for activation of T cells	5.06
	431824	AW972842		gb:EST384937 MAGE resequences, MAGL Homo	5.06
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	5.03
	410570	AH133096	Hs.64593	ATP synthase, H transporting, mitochondr	5.00
	431805	NM_014053	Hs.270594	FLVCR protein	5.00
25	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	5.00
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005	5.00
	419641	BE170548	Hs.118190	Homo sapiens cDNA: FLJ21081 fis, clone C	5.00
	443634	H73972	Hs.134460	ESTs	5.00
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	4.97
30	444621	AA298085	Hs.11465	glutathione-S-transferase like; glutathi	4.95
	422200	AA080895	Hs.347969	cytochrome c oxidase subunit IV	4.94
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	4.94
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	4.93
35	452063	R53185	Hs.32366	ESTs, Weakly similar to TWIST_HUMAN TWIST	4.93
	414821	M53835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.92
	429558	AJ391454	Hs.207251	nucleolar autoantigen (55kD) similar to	4.92
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	4.92
	433162	AJ025842		ESTs	4.91
40	406797	AI432224		ribosomal protein L6	4.90
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	4.90
	422392	NM_005908	Hs.115945	mannosidase, beta A, lysosomal	4.90
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	4.90
	447832	AI433357		ESTs	4.90
45	420932	AW374605	Hs.11607	ESTs, Weakly similar to T21697 hypotheti	4.90
	413593	AA205248		gb:zq78c12.r1 Stratagene hNT neuron (937	4.90
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	4.90
	441224	AU076964	Hs.7753	calumenin	4.90
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	4.90
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.90
50	417308	H60720	Hs.81892	KIAA0101 gene product	4.89
	438763	AI583207	Hs.99029	CCAAT/enhancer binding protein (C/EBP)	4.89
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.88
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	4.87
55	421748	NM_014718	Hs.107809	KIAA0726 gene product	4.86
	427486	AA974433		fibroblast growth factor 4 (heparin secr	4.82
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	4.81
	406867	AA157857	Hs.182265	keratin 19	4.81
	449378	AW664026	Hs.59892	ESTs	4.80
60	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	4.80
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	4.80
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.80
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.79
	433681	AJ004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	4.75
65	441321	H17182	Hs.7771	B-cell associated protein	4.75
	448896	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr	4.73
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	4.73
	449317	AW293413	Hs.132906	19A24 protein	4.71
	436372	AW972301	Hs.310286	ESTs	4.70
70	422082	AA016188	Hs.111244	hypothetical protein	4.70
	432465	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)	4.70
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	4.70
	446659	AI335361	Hs.226376	ESTs	4.70
	414829	AA321568	Hs.77436	pleckstrin	4.70
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	4.70
75	417677	NM_016055	Hs.82389	CGI-118 protein	4.70
	443559	AK076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	4.70
	423766	AA303799	Hs.300141	ribosomal protein L39	4.69
	432407	AA221036	Hs.13273	gb:zr0312r1 Stratagene NT2 neuronal pr	4.67
	453485	BE620712	Hs.33026	hypothetical protein PP2447	4.67
80	452973	H88409	Hs.40527	ESTs	4.67
	427816	AA159248	Hs.180909	peroxiredoxin 1	4.66
	406794	AI890243		ribosomal protein L6	4.65
	449475	AI348027	Hs.108557	hypothetical protein PP1057	4.65

	427157	U51166	Hs.173824	thymine-DNA glycosylase	4.64
	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	4.62
	407874	AI766311	Hs.289047	Homo sapiens cDNA FLJ14059 fis, clone HE	4.61
	417535	AA203569	Hs.191482	ESTs	4.61
5	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	4.61
	408491	AI088063	Hs.7882	ESTs	4.60
	428398	AI249368	Hs.98558	ESTs	4.60
	410295	AA741357		nidogen (enactin)	4.60
	407198	H91679		gb:YV04a07.s1 Soares fetal liver spleen	4.60
10	440327	R12581	Hs.191146	ESTs	4.60
	417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFpZp586F1822 (f	4.60
	426141	C05886	Hs.293972	ESTs	4.60
	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	4.59
	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	4.58
15	416987	D86957	Hs.80712	KIAA0202 protein	4.57
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.57
	416581	H66276	Hs.108268	ESTs	4.56
	440983	M20681	Hs.7594	solute carrier family 2 (facilitated glu	4.56
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	4.56
20	413663	BE247585	Hs.75462	BTG family, member 2	4.55
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity I, rec	4.54
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	4.53
	453330	AI268081	Hs.342389	peptidylprolyl isomerase A (cyclophilin	4.52
	417750	AI267720	Hs.260523	synovial sarcoma, translocated to X chro	4.51
25	440774	AI420611	Hs.153934	ESTs	4.51
	422693	BE300073	Hs.279860	tumor protein, translationally-controlle	4.51
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	4.51
	449267	AI638640	Hs.220624	ESTs	4.51
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	4.50
30	432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma	4.50
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypothe	4.50
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	4.50
	413703	BE158360		gb:PM1-HT0383-131299-001-h08 HT0383 Homo	4.50
	415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.50
35	406623	X69392	Hs.91379	ribosomal protein L26	4.49
	456642	AW451623	Hs.109752	putative c-Myc-responsive	4.47
	406653	AA574074	Hs.77961	major histocompatibility complex, class	4.47
	408307	AI761786	Hs.204674	ESTs	4.46
	428297	AA238291	Hs.183583	serine (or cysteine) proteinase inhibito	4.46
40	447286	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	4.45
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	4.45
	406870	AA075144		gb:zm86f06.s1 Stratagene ovarian cancer	4.45
	446291	BE397753	Hs.14623	Interferon, gamma-inducible protein 30	4.44
	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	4.44
45	428773	BE256238	Hs.193163	bridging integrator 1	4.43
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	4.43
	437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	4.43
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	4.43
	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	4.42
50	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	4.41
	424868	AI568170	Hs.96886	ESTs	4.41
	406380	AF123050	Hs.44532	dubiquitin	4.40
	411960	R77776	Hs.18103	ESTs	4.40
	428782	X12830	Hs.193400	interleukin 6 receptor	4.40
55	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	4.40
	456629	AW891965		histone deacetylase 3	4.40
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	4.40
	422499	AI268666	Hs.19631	ESTs, Weakly similar to I38022 hypothe	4.39
	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	4.39
60	427779	AA906997	Hs.180780	TERA protein	4.38
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	4.37
	413276	Z24725	Hs.75260	mitogen inducible 2	4.36
	452651	AI218918	Hs.30209	KIAA0854 protein	4.35
	453467	AI535997	Hs.30089	ESTs	4.35
65	435961	BE293127	Hs.283722	GTT1 protein	4.35
	415691	AW963979	Hs.24723	ESTs	4.34
	435958	AW161481	Hs.111577	integral membrane protein 3	4.34
	420099	D80011	Hs.95140	KIAA0189 gene product	4.33
	421522	R48881	Hs.102991	hypothetical protein FLJ13956	4.33
70	457073	AA233210	Hs.179943	ribosomal protein L11	4.31
	427337	Z46223	Hs.176683	Fc fragment of IgG, low affinity IIb, r	4.31
	420732	AA789133	Hs.63525	ESTs	4.30
	432731	R31178	Hs.287820	fibronectin 1	4.30
	437275	AW976035	Hs.292396	ESTs, Weakly similar to A47582 B-cell gr	4.30
75	408784	AW971350	Hs.63386	ESTs	4.30
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	4.30
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	4.30
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	4.30
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	4.30
80	413677	AW503116	Hs.301819	zinc finger protein 146	4.29
	428970	BE276891	Hs.194691	retinoic acid induced 3	4.28
	408896	AI610447	Hs.48778	niban protein	4.26
	433550	AA989061	Hs.177376	ESTs	4.26

	406230		Target Exon	4.25
	435855	AW105663	Hs.6947	4.25
	448717	R67419	Hs.21851	4.24
	437386	W52452	Homo sapiens cDNA FLJ12900 fis, clone NT	4.24
5	416759	AK000978	Hs.79741	4.23
	447341	AF106941	Hs.18142	4.22
	410423	AW402432	Hs.63489	4.22
	409453	AI885516	Hs.95612	4.22
	428453	AB011110	Hs.184367	4.22
10	444681	AJ243937	Hs.288316	4.21
	416072	AL110370	Hs.79000	4.20
	450937	R49131	Hs.26267	4.20
	447595	AW379130	Hs.18953	4.20
	418452	BE379749	Hs.85201	4.20
15	430694	AK000790	Hs.246885	4.20
	425259	AL049280	Hs.155397	4.20
	431550	BE244135	Hs.260238	4.20
	439403	BE265745	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.20
	409245	AA361037	IRNA isopentenylpyrophosphate transferas	4.18
20	437296	AA350994	Hs.20281	4.17
	406877	AA226392	Hs.179943	4.17
	419652	AL157485	Hs.91973	4.15
	406661	X66975	Hs.172550	4.15
	452432	AW206008	Hs.283378	4.14
25	448782	AL050295	Hs.283378	4.14
	407110	AA018042	Hs.252085	4.14
	422960	AW890487	Prader-Willi/Angelman syndrome-5	4.13
	432841	M93425	Hs.62	4.12
	415857	AA866115	Hs.127797	4.11
30	420298	AI199510	Hs.267912	4.11
	419726	U50330	Hs.1274	4.11
	426075	AW513691	Hs.270149	4.10
	430255	AK000703	Hs.323822	4.10
	418699	BE539639	Hs.173030	4.10
35	443035	Z45822	Hs.8906	4.10
	457415	AK000010	Hs.258798	4.10
	412220	BE350058	Hs.36787	4.10
	427509	M82505	Hs.2161	4.10
	444633	AF111713	Hs.286218	4.10
40	441384	AA447849	Hs.288660	4.09
	431958	X63629	Hs.2877	4.09
	422310	AA316622	Hs.98370	4.08
	439815	AA206079	Hs.6693	4.07
	417930	H81136	Hs.334604	4.06
45	418458	AA332941	Hs.85226	4.06
	424464	R68537	Hs.17962	4.06
	417035	AA192455	Hs.22968	4.06
	412627	BE391959	Hs.74276	4.06
	414890	BE281095	Hs.77573	4.05
50	452248	AA093668	Hs.28578	4.05
	450887	AA011518	Hs.271778	4.05
	444224	AV648599	Hs.199438	4.05
	451351	AW058261	Hs.321435	4.04
	407792	AI077715	Hs.39384	4.04
55	439864	AI720078	Hs.291997	4.04
	408745	AW936356	Hs.300925	4.03
	409132	AJ224538	Hs.50732	4.01
	410597	W16518	Hs.279518	4.01
	409485	S80990	Hs.252136	4.01
60	426398	BE256390	Hs.169718	4.01
	417777	AI823763	Hs.7055	4.01
	446979	AI654443	Hs.197683	4.00
	416000	R82342	Hs.79856	4.00
	426647	AA243464	Hs.294101	4.00
65	436394	AA531187	Hs.125705	4.00
	409956	AW103364	Hs.727	4.00
	414602	AW630088	Hs.76550	4.00
	446013	AI360167	Hs.152774	4.00
	452404	AW450675	Hs.212709	4.00
70	444736	AA533491	Hs.23317	4.00
	438590	AA811465	Hs.123375	4.00
	451838	AW005866	Hs.193969	4.00
	449832	AA694264	Hs.60049	4.00

TABLE 55B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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413787	7612_1	BC003047 S80794 NM_003405 X78138 AY007132 L08439 AW340648 AW131665 AI082748 AJ470204 BI711078 BF350700 BI496963 AI087141 AA720684 AA862331 AA605146 BM313650 AI089749 AI359738 N69107 AW995424 AI086917 AI083995 AW340217 N99662 AI829449 AI089839 AI080761 AI342365 AI199076 AA080944 AI248943 AI160053 AI191245 AI218477 AI077943 AA864930 AI310394 AA872478 AI279782 W61343 AA565955 W46596 AA126874 AA223241 AA491574 R48413 AA491520 BG055114 AI469689 BE464590 AW664539 H67097 AL534332 C21397 AI085941 AW028427 BG939820 AI697089 AI039008 AI125315 AI655561 AW150042 L20422 X57345 BI458375 AU142852 BI666601 BE888276 AU119302 BI603754 BG705953 BI598754 BE296713 BG002538 BF951911 N29226 BE909424 AV698274 AV683116 AV708195 AA127798 AI124697 D54224 F08031 AA340253 BF923383 BM467808 BI546644 BG777200 BG705941 BG468577 AU127209 AW403970 BI597630 BI458091 AV689560 BI669267 BG506219 BI837163 BI667275 AA343750 BE783112 BF671405 BF954720 H67636 H69456 AA484894 BI669271 BF998207 N31547 BF945817 BF947918 N90630 BG980194 AA156681 BI493502 AW273118 AI473820 AA608688 AI359337 AV712091 AA084101 BF592036 H13301 AI864305 AA505883 AI423953 AW084401 AI917740 R69858 AA033631 N79982 BE885276 AI635674 AA096126 AA700018 AV707753 AI082545 AU145681 AA629032 AI421367 AA740589 AA150830 AI248541 AA988608 AA150478 W65437 BM310234 AA262704 T28031 AI811116 BM272753 H21979 T15405 AA938406 F04963 AI188296 AW152629 AA905196 BG223058 AI831016 AI766457 AI811102 AA776573 AI922133 AA775958 AI261476 AA219489 AI688035 AI872093 BE537084 AW189078 D82630 AI123121 AL583492 BE350791 R69901 W65436 BE155392 BI089081 BE155394 AL120538 AW166100 AI359620 AI174338 N20527 W47413 AA155615 AI272249 H25293 BE514558 H69864 AW383484 H78021 H11617 R58892 H23204 N21530 R82499 AW383522 AA774536 AL534331 W94127 W46459 AI666231 AA513281 AA192465 H69844 W85827 AW383642 AW383529 AA171496 AL537424 BE814866 BF823254 R82553 AI089817 AI559406 M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000556 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177764 AW205789 AW951576 AW845892 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720069 BE715154 BE082584 BE080407 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 AI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177833 BF873679 AW178000 BE082526 BF476666 BF086994 BF582276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159648 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 CD4715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW84674 AW376699 AW376817 AW376897 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE866474 BE185187 BE156621 BE715089 BE713297 BE713298 BE719915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 BI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W50570 AA149181 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI605084 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI94069 AI270027 AI635878 AA128330 BG681425 BE706078 R20504 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE007786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AJ905927 BF992780 AW853812 BG954443 BI70853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337240 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177788 AA025851 BE931733 BF154837 BG949393 BE714441 AW969245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487 BE880923 BG390191 AW470082 AW014585 AI423255 BI714731 BG054894 AW780248 N31683 AW664132 AW467353 AI983152 AA617918 BF447795 AI088357 AA807328 AA576970 AI741153 AI755003 AI474016 AI222030 AI348114 AW997085 BM271753 AI363147 BM311311 AI146640 AI246771 AW512619 AI359020 BG054897 AI292234 AI215830 AI283836 C06205 AW503423 AW272680 N33205 AW873021 AA070724 AI753886 AW192487 AI087151 AA658909 AI346368 AI335677 AA825442 AW440066 AW131357 AW513210 AI082314 AI085455 BE551404 AA780704 AW008596 AI796964 AA917471 AI400531 AA668626 W72207 AI306482 AW440562 AI084687 AA347280 AA063536 BF477389 AI241662 AA931543 AA484310 AA812486 AI032216 AA665779 AI916336 AI350590 BF198108 AI433377 AI300638 AI672626 AI282741 AI351487 AW105544 AA973627 AW517914 AA715424 AA508454 BF334080 AI274618 AW367201 AW572619 AW468088 AA382095 AI368364 AI146934 AI357180 AI361181 BI911347 BI871044 AA136325 BF084010 BF084007 AA335788 AI920878 AA809614 BE932941 AI678261 C75308 AI148479 BE178174 W88513 BM013627 BM006551 AA367152 AW953705 AI631833 AW237429 AW027804 AA729038 BE503409 AI521935 BF739953 AA702982 AA557633 AA780065 AI218139 AW194264 D20120 AI082715 AI969980 BE857686 BE326711 AW953706 AI393749 AI383821 W67199 AI431759 AI796526 AI521794 AI796380 AW117545 AI749657 AI537634 N50122 BE738425 BE738323 BM126944 AW629678 AW265195 AI916735 AI394255 AI573090 AI354442 AW612857 AI339558 AI919424 AI377532 AI354441 AI308821 AA772275 AW055215 AI589705 AI336532 AA806547 AV682125 H93575 AW071172 AW769904 AI863985 AW265018 AW196655 D79662 BE042393 N75017 AW014741 C75509 BE748621 H92431 AW079261 AW901780 AA329482 AW960115 BI260621 AI767525 R31663 BI918664 AW963198 C06195 AI678018 AB033091 AL520743 BE811813 N53332 N97116 AL561910 AA280655 BE710392 AV705100 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AI886630 AA904112 AI864588 AW271985 AW078868 AA725342 BF326598 AA843572 AI082536 AA766664 AI453279 AA435673 AI619515 AA879080 AA234592 AA890223 AA766824 BI258822 AA393631 AW968840 BE940639 T83865 BE762742 AW897470 W50809 AA1323 T87376 R68544 H88711 BI087136 AK001838 AU135179 AU134241 AV651702 AV650032 AV651304 AV650101 AV651263 AV651888 AV651866 AA628554 AV651355 AV651174 AV651172 AW856145 AU117599 AU113538 BG254665 AA166919 BG483981 AW809606 BG494194 AA622811 AI676156 AA687804 AI701729 AU133725 AW961387 AU144387 AU151757 AA551031 BE675412 N34769 AA713483 AI890079 AI588918 AI361889 AI209020 AA668981 AI240990 AA741144 AA490899 AI200221 AW589574 W96201 BG154182 AV655159 AA328145 N36348 AI081357 N76715 AA693346 AA742488 AI269719 AA897483 AI866459 AU155873 H04255 AW243986 AA557749 AI286227 R68691 R33453 AW388097 BE005398 AA628622 AA994155 AK000357 AI571830 AA579613 AA668790 BF939495 BF196886 AI990982 BF591561 AI809189 AW410232 BF739769 AI144392 BF438721 AI707495 AI423359 N52903 BE85784 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426295	510_1	
425996	138046_1	
429978	35194_2	
450377	12109_1	
444060	6315_1	
450139	34017_1	
434280	1474904_1	
410143	MH1244_8	

			AI581622 AI361357 AA468498 AW008694 AA903275 AI187724 AI187718 AA890505 BF092771 AI066555 BE714172 BG289028 AW080390 BE001197 BF132049 AK055270 BE348291 AI190289 AW612022 AI269506 AI266578 AI269675 AW271406 BE879851 BF574163 BI497126 AW903775 BI917368 AW150900 BF244813 H79201 AK074047 AI144342 AW014280 BM145128 N28267 AW206231 AA989041 H93197 AW594063 BG236296 AW236606 AW081031 AA765843 BM144372 AA989341 AI824838 AI963970 AI637671 AW196330 BG427526 BM148789 BF893644 BF861946 AA947566 BE739425 AA514221 AA865491 AI828293 AA470456 AI276739 AA169357 BE932464 AA514889 AW819039 AW819083 BE843048 AI432496 AI70335 AI247243 BG533994 AA513783 AI887309 AA528036 AW972006 AW873028 AI924914 AI818810 AW152378 AW084946 AI521413 AI669583 BE932521 AI581370 BE180238 AW089750 AW771461 AW089714 AI590949 AI819148 AA731056 BF815234 BF911506 AA235803 AA485373 AI735658 AW393133 AW073080 AI076373 BF353320 BE843111 AW819036 AW393135 BG697291 AV648670 AV654332 AV687530 BG566864 AI807430 AI676072 AA837010 AI452482 AI625817 AW241750 BE048616 AI290928 AI680714 AA485530 BE175687 AV648513 AW130312 AI000556 AA632893 BE674169 BF001208 AA948166 BE175650 AA524664 AA490345 AI244948 AA602956 AA483492 AA918178 AW802049 BG675859 AV658871 BG678060 AI565004 AW819026 BE843092 AV686437 AV723049 BG616948 AI911647 AI743490 AI091096 BE857251 AI962074 AA040027 AW769317 AA343477 AA640112 BF876213 R82948 H26425 H82876 BE843095 BE843140 BG536641 BG617830 AA235802 BE774985 BE006682 BF342375 AA903144 BF338083 BF984258 AV657996 AI749532 BE768614 BE857252 BE932516 BE768573 AV657993 AV657777 AV752631 BE774974 T55847 BF095761 BF911511 BE710793 BE180119 BG617338 H45942 T55897 AV657718 BG563497 BE177661 H08215 BE144709 BE144829 AI207343 BF813684 BF928775 AA828585 BC020284 AW953495 AW402677 BF890739 Z44378 AI660081 AI769242 T84954 C05886 AI224851 AI568340 AI024026 AW015010 AI032051 AA505095 AA830304 H98001 H63431 BG249610 AI284792 AA205732 AI598130 AW516813 AI123905 AA132557 AI140199 H53399 AA928496 AI200299 AI400044 BE940512 BE940609 H28028 BF913688 AI301558 D79095 AI762695 AA311547 AI673408 AI673002 N67358 AA885913 AI288094 N67347 Z40311 T94918 BF722693 AW170339 AW975566 AA452774 AA504759 AA370643 T79706 AA721603 BF858887 BG982917 AI343373 AW236167 BE568091 BF747959 BF241262 BE940663 AI435278 R05794 AW027091 AI860259 AI268890 T94871 AW182884 N67183 AW149083 H42473 AI678254 R26706 AI19684 R24095 AW388568 AW363261 N31299 H63489 AW195475 AA452592 BE844216 T91205 H64955 BF858811 AW962779 AW388295 BF857615 BF856552 BF858548 BF857611 AW866752 BG926557 AW965540 R76280 AA335645 BF370246 BE835794 AA725102 AW152576 BF055494 AI743398 BE464853 AI391675 AI453078 BE017970 AI803141 AI417070 AA489486 BE835818 AW050475 BE835826 AI015220 AW300496 AA343881 H98062 AA554969 N32774 AA012825 BF989549 AL76463 W60527 AW576215 N32300 AA450065 AW137525 AI290944 T16431 T50379 AA830657 N78847 T51070 AW050528 AI446370 AA100986 AA824552 BE835780 AA770659 BF370223 H03890 R76557 AA558585 AA565499 AI360576 AW204069 AA991648 AA864939 AI744949 AW062361 BF919486 AW813419 AW816041 AA354572 BI754027 BF696071 AI351939 BG151298 AI919334 AI01620 BI770165 W72057 T96158 T29478 AA181252 BG927793 AA714431 AA600749 AA181247 AA614756 AA081092 H52207 BG926934 BF222579 BG899001 N64245 AA953040 AI832406 AA102441 BG928081 AA993445 AA916041 AA987847 AA983329 AA737219 AA916443 AW128994 AI492560 AI761847 BC005272 NM_000900 X53331 M58549 BI758966 AL598829 BI754530 BG699770 BE439699 BE440148 AV704365 AV733652 BG212015 BG184149 BG200180 BG212690 BI761222 BG182079 AW338822 AI925631 AI423041 AW071181 AI889836 AW129112 BG925339 AI017633 AA568964 BF725690 AI004210 AI809799 BE083097 BG896220 AW997681 BF668788 BE083134 AW631281 BG193052 BG183095 BE440088 BG185728 AI499579 AA188162 AA864282 BI493352 AA155854 AA836749 AA836844 AA985478 AW082299 AI816747 AA450221 AA971294 BE327509 AI719662 BG576669 AI479382 BF824747 AI741800 BG982962 AI088473 AA916151 AW473324 BG901177 BE439998 AW023269 BE813871 AW999947 BE839108 AV707983 AA368722 AW796627 AW980608 AI341771 AA302459 BI493353 AA366332 AA371104 AA367277 AL547972 BG928011 AI678903 AI699886 AI956165 AA484893 AA643953 AW591063 BG203275 BG211093 AI334791 AA916589 AW058266 AI362370 AI143352 AA508721 AI928079 D57214 BE045265 AA541785 BG219510 BG201686 BG195572 AW019904 AW089242 AA953322 AI686698 F27562 AA614749 D56845 F20774 F30660 F25646 AW023542 AA827300 AA582214 AI701289 AA228293 AI906950 AA230156 AA384572 AW438988 AA742516 BI490938 AA731082 BF665869 BG190518 AW041568 BE439643 AA910666 AA155913 AA923097 AA975721 AA985555 BG927032 AA948389 AA451625 AI527219 AV707258 AW083733 AA128053 AI953789 AI911993 AA421798 BG429150 AI915306 Z30130 AA126929 BG926630 AA081013 AA553696 AA916094 BG924321 AI039722 AI954968 AI372839 AI401406 AI538215 AL047596 AA393792 AI670731 AI037957 AW874364 AI038137 N62286 AI241379 BE501096 AW090696 AI927369 AI669226 AI369437 AI371075 AW612409 AI866711 AI183289 AA477717 AI076122 AA635190 AA700984 AA781508 D81020 BF575223 AI356183 D79312 AI375558 H61111 BG283489 BE090666 BE090664 BE090662 H26545 AK056315 AI016524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 AI392620 Z40708 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061672 BI059498 AA134476 AW084888 AA036967 AW370823 T55263 BI002756 AA489684 BF827261 W74741 BF963166 BC022413 BE395396 BF754175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853 AW371849 BE153241 BC017410 AI337912 AI090244 AW090300 BE219837 AI623661 BE501576 BE501734 AI742232 AI023964 AI584824 AA975373 AI288904 AI984583 AA890325 N32562 AI358102 AW241694 AI038448 AI672071 AI018369 AA576391 AA977874 AW189392 W37448 AA612894 AI277548 H89561 AI699774 H89365 AA315805 AW579186 BC014584 BC014581 AW870125 AI672414 BE328145 AW600919 BF031306 AW172758 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522 BM129822 AI122760 BE718200 AW887496 AA149420 BE706307 BE539395 BE478765 AI373653 R75904 BF979185 BF691393 BG495595 BI094458 BE708702 BG496559 BF248373 BG494800 AA908472 BM469076 AA530327 AI127512 AI368802 AA533141 AA700560 AW576028 AI610851 AI435361 BM129172 AW474544 BM128899 AI814292 AW502039 AA531243 BF941858 AW502037 AA702337 AI419854 AA662755 AA934364 AI300510 AI291136 AA505263 AI144527 AI076919 AI633534 AI242473 AA938561 BG055372 AA512894 AI671356 AA862403 BF808010 AA663911 AA847056 AA513301 AA369069 AA377265 BG291206 AA402298 AA885766 AW801002 AA302290 AI305842 AW800873 AA302492 AA478427 AI817291 AW801104 AW801028 AA865744 BF155979 AI374743 AA478431 AI159846 AI369757 AI800672 BF435788 AA255451 AI937707 AW006198 AI280363 BF062434 AW801115 AI919181 F28413 W04214 AW152380 AW901567 AW901570 AA886371 AA384251 AI302846 BE701902 AA931606 H42673 R33703 AW901556 AA009816 AW901568 AW352200 AA256558 H15928 BI087170 AW800530 AA369068 N98562 H28652 H34644 H196150 H00956 W70039 AI142831 AA009817 F37136 N70289 AA531347 R72374 H27488 R66605 AI184717 AW518883 AF121173 AW972842 AA516061 AA630205 AI742311 AI025842 AA578843 AI432224 AW276890 AI489346 AA937014 AA653573 AI318525 AI246219 AA961591 AI270640 R36075 R36167 AI366546 AI628543 AI433357 AW772732 AA205248 AA204737 AA130658 BF510715 BE673055 BE464111 AW590620 AI637939 AA404324 AW238441 AI650952 BF056796 AA974433 AI890243 BG402852 BG545066 AA150252 AL036760 AA452480 AI033256 W68776 W93372 N31248 AI052219 AI367635 W69374 N88610 R58194 BI524854 BI497111 BF940043 AI129268 AI359798 AI056480 AA121421 AI042150 AW449003 AI418180 AI419420 AI356058 BF832243 AI349330 AI359448 W76647 BF477170 AA099163 BF994549 AW508256 AA045418 H03770 AL574791 AW069455 BE302148 AW02281 AW590273 AA121268
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 N21313 BF674610 H02874 AW957523 R16904 AA328030 AA054671 R79546 BF832310 A1249109
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 AA075144
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 AW801688 BE003837 AW801621 AW385721 AW385742 AW385714 AW604757 W87409 AW604738 AW385757 AW580796 AW801247 BE003239
 BE003183 AA847112 AW580975 AW604760 AW385727 BE164590 BE003090 AW362791 AW604759 AW866589 AW604758 H44337 A1378548
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 AA248197 AW381373 AW177325 AW806879 AA935217 BE067498 BE083742 BE067470 AW894935 BE082529 A1248811 BE179917 BE002200
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 A1688683 A1688894 AW009660 AW601421 AW360793 BE066524 BE083901 AW369847 AW381871 AW935435 AW664582 AW607775 AW838449
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 BE011715 BE167842 BE011718 BE011724 AW363639 AW878658 AW878662 AW894887 BE082356 AW389211 AW804286 AW610312 A1904717
 AW610318 AW996909 AW610296 AW901923 AW880003 A1762171 AW062582 AW368713 AW602593 AW176663 AW842064 AW842089
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 A1524921 F02989 Z39328 F02705 F01414 T88678 A1215165 H87220 AW374781
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 BE768511 BG940948 W37195 BF372041 BE883798 BF372082 BF367329 BF909744 AW966003 AV714014 B1492868 B1495144 AA921845
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 H16217 H21980 H22651 H88179 H87354 H44052 H25165 H44128
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 R73937 AA127680 AW044037 A1096437 AA384077 BF941499 T93764 BG003285
 BF090249 AW954947 AW890487 A1305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 A1350279 AA879119
 AA319510 BE702077 BE699015 BE702046 AW901293 T93919 D81708 BF475488 D60383 D81751 BE599260

TABLE 55C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
401466	6682292	Plus	28748-29023
401192	9719502	Minus	69559-70101
402474	7547175	Minus	53526-53628, 55755-55920, 57530-57757
402145	8018280	Plus	113086-114800
406230	4760409	Plus	71716-72515

TABLE 56A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of seminomatous testicular cancer compared to normal adult testicular tissues

Pkey	ExAccn	UnigenelD	Unigene Title	R1
414438	A1879277	Hs.76136	thioredoxin	47.30

	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	44.80
	438091	AW373062		nuclear receptor subfamily 1, group I, m	40.10
	412948	BE243313	Hs.334851	LIM and SH3 protein 1	34.90
5	417088	M54915	Hs.81170	pim-1 oncogene	31.10
	430542	AI557486	Hs.119122	ribosomal protein L13a	29.60
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	29.10
	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	28.15
	406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	28.13
10	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	28.10
	406658	AI920965	Hs.77961	major histocompatibility complex, class	27.85
	416680	AW245540	Hs.79516	brain abundant, membrane attached signal	27.70
	446526	AW967069	Hs.211556	hypothetical protein MGCS487	27.20
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	26.30
15	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	25.80
	429978	AA249027		ribosomal protein S6	25.40
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	24.60
	440207	AI371978	Hs.128326	ESTs	24.50
	425543	R23313	Hs.334895	ribosomal protein L10a	24.30
20	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	24.10
	444562	AA186715	Hs.336429	RIKEN cDNA 913042N19 gene	24.05
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	24.00
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	22.90
	420367	AA259090	Hs.257028	ESTs	22.90
25	406856	AW515336	Hs.29797	ribosomal protein L10	22.77
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	22.75
	412636	NM_004415		desmoplakin (DPI, DPL)	22.40
	420676	AI434780	Hs.4248	vav 2 oncogene	21.40
	440869	NM_014297	Hs.7486	protein expressed in thyroid	21.20
30	446627	AI973016	Hs.15725	hypothetical protein SBB148	21.10
	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	20.98
	420754	W79431	Hs.346911	ribosomal protein L22	20.90
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	20.80
	440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (Ig),	20.40
35	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	19.50
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	19.15
	422714	AB018335	Hs.119387	KIAA0792 gene product	19.00
	430253	AK001514	Hs.236844	hypothetical protein FLJ10852	18.50
	413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	18.50
40	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	18.00
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	17.90
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	17.70
	448588	AI970276	Hs.156905	KIAA1676	17.50
45	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	17.40
	428782	X12830	Hs.193400	interleukin 6 receptor	17.20
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	17.15
	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	17.10
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	17.06
	440528	BE313555	Hs.7252	KIAA1224 protein	17.05
50	410143	AA188169		KIAA1191 protein	16.90
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	16.70
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020.1 E2IG5	16.70
	429183	AB014604	Hs.197955	KIAA0704 protein	16.60
	450937	R49131	Hs.26267	ATP-dependent interferon response protei	16.50
55	449571	AW016812	Hs.200266	ESTs	16.20
	432730	AI066520	Hs.131358	ESTs	16.15
	426295	AW367283		zinc finger protein 6 (CMPX1)	15.90
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	15.80
60	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	15.80
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	15.70
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	15.50
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	14.90
	428928	BE409838	Hs.194557	cadherin 1, type 1, E-cadherin (epitheli	14.90
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	14.85
65	406656	M16714	Hs.89643	major histocompatibility complex, class	14.71
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	14.70
	450377	AB033091		KIAA1265 protein	14.60
	425996	W67330		hypothetical protein AL110115	14.60
	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	14.42
70	427691	AW194426	Hs.20726	ESTs	14.35
	429614	AI371172	Hs.211539	hypothetical protein MGC4248	14.21
	451106	BE382701	Hs.25960	N-MYC oncogene	14.13
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	13.90
	436860	H12751	Hs.5327	PRO1914 protein	13.90
75	446899	NM_005397	Hs.16426	podocalyxin-like	13.75
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	13.70
	408380	AF123050	Hs.44532	diubiquitin	13.40
	447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	13.30
	427521	AW973352		ESTs	13.25
80	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	13.23
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	13.23
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	12.70
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	12.69
	426562	BE297660	Hs.170328	moesin	

	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	12.55
	436398	H87136	Hs.5174	ribosomal protein S17	12.50
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	12.30
5	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	12.30
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	12.28
	414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	12.25
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	12.25
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	12.20
10	419384	AA490866	Hs.39429	ESTs	12.20
	410185	BE294068	Hs.737	Immediate early protein	12.15
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10534 fis, clone OV	12.05
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	12.00
	406743	AA911568	Hs.279860	tumor protein, translationally-controlle	11.90
	408989	AW361666	Hs.49500	KIAA0746 protein	11.80
15	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	11.80
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	11.80
	410325	AB023154	Hs.62264	KIAA0537 protein	11.70
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	11.70
20	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	11.61
	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	11.60
	454413	AI653672	Hs.40092	PNAS-123	11.60
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	11.40
	428065	AI634046	Hs.157313	ESTs	11.40
25	432805	X94630	Hs.3107	CD97 antigen	11.36
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	11.35
	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	11.30
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-in	11.30
	409963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	11.11
30	402474			NM_004079:Homo sapiens cathepsin S (CTSS	11.00
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.00
	406786	AW161678	Hs.111334	ferritin, light polypeptide	10.95
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	10.90
	444656	AI277924	Hs.145199	ESTs	10.90
35	453856	AA804789	Hs.19447	POZ-LIM protein mystique	10.85
	440774	AI420611	Hs.153934	ESTs	10.82
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	10.80
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	10.80
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	10.80
40	418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	10.70
	437374	AL359571	Hs.44054	rheln (GSK3B interacting protein)	10.65
	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	10.60
	450719	AI096837	Hs.21349	ESTs, Weakly similar to RB8B_HUMAN RAS-R	10.43
	424800	AL035588	Hs.153203	MyoD family inhibitor	10.40
45	446682	AW205632	Hs.211198	ESTs	10.40
	447211	AL161981	Hs.17767	KIAA1554 protein	10.31
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	10.30
	422105	AI929700	Hs.111680	endosulfine alpha	10.21
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	10.20
50	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	10.20
	452651	AI218918	Hs.30209	KIAA0854 protein	10.15
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	10.11
	426995	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	10.10
	427761	AA412205	Hs.140996	ESTs	10.10
55	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	9.90
	402145			Target Exon	9.82
	413686	AI469213	Hs.71404	ESTs	9.80
	446488	AB037782	Hs.15119	KIAA1361 protein	9.80
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	9.80
60	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	9.80
	407179	AA206465		thymosin, beta 4, X chromosome	9.72
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	9.70
	430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	9.70
	446795	AI797713	Hs.156471	ESTs	9.70
65	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	9.65
	451864	N20370	Hs.69547	ESTs	9.65
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	9.60
	419904	AA974411	Hs.18672	ESTs	9.60
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	9.60
70	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	9.52
	424950	AA602917	Hs.156974	ESTs	9.50
	447534	AW953935	Hs.288655	ESTs	9.50
	419223	X60111	Hs.1244	CD9 antigen (p24)	9.41
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	9.40
75	422960	AW890487		cadherin 13, H-cadherin (heart)	9.33
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein Interac	9.32
	408784	AW971350	Hs.63386	ESTs	9.30
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [Hsapi	9.30
	432409	AA806538	Hs.130732	KIAA1575 protein	9.30
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	9.30
80	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	9.22
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	9.20
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	9.20
	434524	AA635931	Hs.249716	ESTs	9.20

	450294	H42587	Hs.238730	hypothetical protein MGC10823	9.20
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	9.10
	434442	AA737415		ESTs	9.10
5	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	9.03
	447519	U46258	Hs.339665	ESTs	9.00
	433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	8.98
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	8.90
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypotheti	8.90
10	442806	AW294522	Hs.149991	ESTs	8.90
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H	8.89
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	8.81
	408437	AW957744	Hs.278469	lacrima proline rich protein	8.80
	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	8.80
15	431187	AW971146	Hs.293187	ESTs	8.80
	421098	AI697901	Hs.192425	ESTs	8.70
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	8.70
	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	8.62
	401091			decay accelerating factor for complement	8.60
20	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	8.60
	438089	W05391		nuclear receptor subfamily 1, group I, m	8.60
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	8.59
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	8.56
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	8.50
25	411979	X85134	Hs.72984	retinoblastoma-binding protein 5	8.50
	414829	AA321568	Hs.77436	pleckstrin	8.50
	430162	AW450843	Hs.346348	ESTs	8.50
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	8.45
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	8.43
30	407833	AW955632	Hs.66666	ESTs, Weakly similar to S19660 proline-r	8.40
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	8.40
	433208	AW002834	Hs.24095	ESTs	8.38
	428970	BE276891	Hs.194691	retinoic acid induced 3	8.33
	425284	AF155568		NS1-associated protein 1	8.33
35	437108	AA434054	Hs.80624	hypothetical protein MGC2560	8.30
	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	8.30
	426827	AW067805	Hs.172665	methylene tetrahydrofolate dehydrogenase	8.30
	453716	AA037675	Hs.152675	ESTs	8.20
	418840	AI821614	Hs.185831	ESTs	8.20
40	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	8.20
	449656	AA002008	Hs.188633	ESTs	8.17
	425535	AB007937	Hs.158287	KIAA0468 gene product	8.13
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	8.10
	432559	AW452948	Hs.257631	ESTs	8.10
45	436797	AA731491	Hs.334477	hypothetical protein MGC14879	8.01
	420099	D80011	Hs.95140	KIAA0189 gene product	8.00
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	8.00
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	8.00
	434423	NM_006769	Hs.3844	LIM domain only 4	8.00
50	437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	7.92
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	7.89
	433655	AL036559	Hs.3463	ribosomal protein S23	7.89
	435968	AW161481	Hs.111577	integral membrane protein 3	7.88
	434511	R28982	Hs.18106	ESTs	7.86
55	423523	AW299828	Hs.193580	ESTs	7.84
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	7.80
	411960	R77776	Hs.18103	ESTs	7.80
	434159	AW135214	Hs.191828	ESTs	7.80
	447500	AI381900	Hs.159212	ESTs	7.75
60	406699	L06505	Hs.182979	ribosomal protein L12	7.68
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	7.66
	426759	AI590401	Hs.21213	ESTs	7.62
	406776	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	7.60
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	7.60
65	444795	AI193356	Hs.160316	ESTs	7.59
	406663	U24683		immunoglobulin heavy constant mu	7.56
	442821	BE391929	Hs.8752	transmembrane protein 4	7.52
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	7.50
	407252	AA659037	Hs.163780	ESTs	7.50
70	414405	AI362533		KIAA0306 protein	7.50
	427395	AW298741	Hs.97861	ESTs, Moderately similar to I38022 hypot	7.50
	425999	AI761902	Hs.99597	ESTs	7.50
	441436	AW137772	Hs.185980	ESTs	7.50
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	7.46
75	420943	AI718702	Hs.279930	major histocompatibility complex, class	7.43
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	7.42
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	7.41
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	7.40
	437134	AA349944	Hs.48924	ARP2 (actin-related protein 2, yeast) ho	7.40
80	408912	AB011084	Hs.93304	KIAA0512 gene product; ALEX2	7.40
	419839	U24577	Hs.252748	phospholipase A2, group VII (platelet-ac	7.40
	431427	AK000401	Hs.15514	Homo sapiens cDNA FLJ20394 fis, clone KA	7.40
	437469	AW753112	Hs.157106	hypothetical protein MGC3260	7.40
	432598	AI341227		ESTs	7.38

	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	7.34
	441612	AJ802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	7.30
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	7.30
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	7.30
5	437103	AW139408	Hs.152940	ESTs	7.30
	442495	AJ184717		ESTs	7.30
	445929	AJ089660	Hs.323401	dpy-30-like protein	7.30
	446013	AJ360167	Hs.152774	ESTs	7.30
10	436075	BE090176	Hs.179902	transporter-like protein	7.20
	450139	AK001838		serum/glucocorticoid regulated kinase	7.20
	423905	AW579950	Hs.135150	lung type-I cell membrane-associated gly	7.17
	406819	AA908472		gb:cg82a10.s1 NCL CGAP_Ov8 Homo sapiens	7.16
	407719	AW963866	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,	7.12
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	7.10
15	413888	AW958264	Hs.103832	similar to yeast Upf3, variant B	7.10
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	7.10
	424677	U09414		zinc finger protein 137 (clone pHZ-30)	7.10
	427254	AL121523	Hs.97774	ESTs	7.10
20	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	7.10
	438980	AW502384		gb:U1-HF-BR0p-aka-4-12-O-Ulr1 NIH_MGC_5	7.10
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	7.10
	441878	AJ801869	Hs.127982	ESTs	7.09
	443247	BE614387	Hs.333893	c-Myc target JPO1	7.04
25	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	7.00
	417315	AJ080042	Hs.180450	ribosomal protein S24	7.00
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	7.00
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	7.00
	445245	AB032973	Hs.12461	LCHN protein	7.00
30	414812	X72755	Hs.77367	monokine Induced by gamma Interferon	7.00
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	6.97
	410397	AF217517	Hs.63042	DKFZp564J157 protein	6.96
	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	6.96
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	6.95
35	418134	AA397769	Hs.86617	ESTs	6.90
	424768	AA353895	Hs.152983	HUS1 (S. pombe) checkpoint homolog	6.90
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	6.90
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypothi	6.89
	451838	AW005866	Hs.193969	ESTs	6.88
40	425367	BE271188	Hs.155875	protein tyrosine phosphatase, receptor t	6.87
	453485	BE620712	Hs.33026	hypothetical protein PP2447	6.85
	401466			vesicle-associated membrane protein 4	6.84
	457073	AA233210	Hs.179943	ribosomal protein L11	6.83
	412093	BE242691	Hs.14947	ESTs	6.83
45	442492	AA528489	Hs.234518	ribosomal protein L23	6.83
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	6.83
	431773	BE409442	Hs.268557	pleckstrin homology-like domain, family	6.82
	416401	N80139	Hs.268916	ESTs	6.80
	426501	AW043782	Hs.293616	ESTs	6.80
50	435080	AJ831760	Hs.155111	hypothetical protein FLJ14428	6.80
	436876	AJ124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	6.80
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.80
	432666	AW204069		ESTs, Weakly similar to unnamed protein	6.79
	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	6.77
55	425277	NM_001241	Hs.155478	cyclin T2	6.72
	425246	AJ085561	Hs.155321	serum response factor (c-fos serum respo	6.70
	428728	NM_016625	Hs.191381	hypothetical protein	6.70
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	6.70
	433735	AA608955	Hs.109653	ESTs	6.70
60	430556	AW967807	Hs.13797	ESTs	6.69
	417535	AA203569	Hs.191482	ESTs	6.69
	418117	AJ922013	Hs.83496	linker for activation of T cells	6.67
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	6.65
	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	6.62
65	447341	AF106941	Hs.18142	arrestin, beta 2	6.61
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	6.60
	442460	NM_014135	Hs.8345	PRO0641 protein	6.60
	428818	AJ131291	Hs.102308	potassium inwardly-rectifying channel, s	6.59
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	6.57
70	415221	W07418	Hs.78225	annexin A1	6.56
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	6.54
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	6.51
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	6.50
	441224	AU076964	Hs.7753	catumenin	6.50
75	443749	R38828	Hs.143463	ESTs	6.50
	448094	H24387	Hs.32061	ESTs, Weakly similar to 138022 hypothi	6.50
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	6.40
	418259	AA215404		ESTs	6.40
	421633	AF121860	Hs.106260	sorting nexin 10	6.40
80	435937	AA830893	Hs.119769	ESTs	6.40
	445612	N94126	Hs.12969	hypothetical protein	6.40
	451653	W18193		ESTs, Moderately similar to HERC2 (Hsap	6.40
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	6.40
	422693	BE300073	Hs.279860	tumor protein, translationally-controlle	6.39

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	434817	AA082118	Hs.102737	goliath protein	6.38
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	6.35
	425410	AA310974	Hs.155828	Homo sapiens cDNA FLJ10522 fis, clone NT	6.34
5	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	6.33
	435812	AA700439	Hs.188490	ESTs	6.31
	401113			solute carrier family 22 (organic cation	6.30
	408418	AW963897	Hs.44743	KIAA1435 protein	6.30
	412220	BE350058	Hs.36787	chromodomain helicase DNA binding protei	6.30
10	426780	BE242284	Hs.172199	adenylate cyclase 7	6.30
	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	6.30
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	6.30
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	6.30
	449576	AW014631	Hs.225068	ESTs	6.30
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	6.30
15	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	6.27
	411975	AI916058	Hs.144583	ESTs	6.26
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	6.25
	433162	AI025842		ESTs	6.23
	449322	AI638616	Hs.196566	ESTs	6.22
20	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	6.20
	440327	R12581	Hs.191146	ESTs	6.20
	442832	AW206560	Hs.253569	ESTs	6.20
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	6.20
25	427968	AI857607	Hs.181301	cathepsin S	6.18
	414662	AL036058	Hs.76807	major histocompatibility complex, class	6.16
	418113	AI272141	Hs.83484	SRV (sex determining region Y)-box 4	6.16
	406870	AA075144		gb:zm86f06.s1 Stratagene ovarian cancer	6.15
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	6.15
30	445493	AI915771		metallothionein 1E (functional)	6.15
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.14
	427477	AW973119	Hs.178391	ribosomal protein L44	6.14
	422499	AI268666	Hs.19631	ESTs, Weakly similar to I38022 hypotheti	6.13
	443441	AW291196	Hs.92195	ESTs	6.12
35	413677	AW503116	Hs.301819	zinc finger protein 146	6.11
	406797	AI432224		ribosomal protein L6	6.10
	406857	AA613726	Hs.29797	ribosomal protein L10	6.10
	410387	AI277367	Hs.47094	ESTs	6.10
	410503	AW975746	Hs.188662	KIAA1702 protein	6.10
40	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	6.10
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	6.08
	406877	AA226392	Hs.179943	ribosomal protein L11	6.07
	407784	AW139585	Hs.12708	ESTs	6.05
	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	6.05
45	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	6.01
	412949	AI471639	Hs.71913	ESTs	6.00
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	6.00
	435756	AI418466	Hs.33665	ESTs	6.00
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	6.00
50	441623	AA315805		desmoglein 2	5.98
	416926	H03109	Hs.263395	HT018 protein	5.96
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subuni	5.95
	441244	BE612935	Hs.184052	PP1201 protein	5.95
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.95
55	430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	5.94
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	5.92
	408605	AF025374	Hs.46465	T-cell, immune regulator 1	5.91
	433891	AA613792		gb:mo97h03.s1 NCL CGAP_Pr2 Homo sapiens	5.90
	406542			C19000728:gil12585552[sp]Q9Y2Q1J2257_HU	5.90
60	406858	AI865720	Hs.29797	ribosomal protein L10	5.90
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.90
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	5.90
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	5.90
	455263	AW961702		Homo sapiens cDNA FLJ14028 fis, clone HE	5.90
65	441321	H17182	Hs.7771	B-cell associated protein	5.88
	429083	Y08397	Hs.227817	BCL2-related protein A1	5.87
	406806	AW088535		ribosomal protein, large, P0	5.87
	416987	D86957	Hs.80712	KIAA0202 protein	5.86
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	5.83
70	428773	BE256238	Hs.193163	bridging integrator 1	5.83
	406794	AI890243		ribosomal protein L6	5.82
	457752	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	5.82
	435511	AA683336	Hs.189046	ESTs	5.81
	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	5.80
75	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	5.80
	412528	AI123478	Hs.32112	ESTs	5.80
	424875	AI187945	Hs.199310	ESTs	5.80
	426981	AL044675	Hs.173081	KIAA0530 protein	5.80
	447711	AI459554	Hs.161286	ESTs	5.80
80	449961	AW265634	Hs.133100	ESTs	5.80
	416759	AK000978	Hs.79741	hypothetical protein FLJ10116	5.80
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JCS238 galactosy	5.79
	422773	AB028962	Hs.301552	KIAA1039 protein	5.78
	441455	AJ271671	Hs.7854	zinc/ferron regulated transporter-like	5.78

	414774	X02419	Hs.77274	plasminogen activator, urokinase	5.77
	449317	AW293413	Hs.132906	19A24 protein	5.75
	425787	AA363867	Hs.155029	ESTs	5.73
5	414890	BE281095	Hs.77573	uridine phosphorylase	5.72
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne)	5.71
	435961	BE293127	Hs.283722	GTT1 protein	5.71
	419378	R24922	Hs.90078	nucleotide-sugar transporter similar to	5.70
	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	5.70
10	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	5.70
	446659	AI335361	Hs.226376	ESTs	5.70
	457250	AA811987	Hs.125779	ESTs	5.70
	414150	AA136026		gb:zn88d07.r1 Stratagene lung carcinoma	5.68
	439924	AI985897	Hs.125293	ESTs	5.67
15	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	5.66
	451812	X81889	Hs.152151	plakophilin 4	5.65
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	5.63
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [Hs	5.63
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	5.60
20	431770	BE221880	Hs.268555	5'-3' exonuclease 2	5.60
	436511	AA721252	Hs.291502	ESTs	5.60
	446630	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr	5.60
	406623	X69392	Hs.91379	ribosomal protein L26	5.60
	452382	N38902	Hs.211539	hypothetical protein MGC4248	5.57
25	416047	BE439894	Hs.78991	DNA segment, numerous copies, expressed	5.56
	437296	AA350994	Hs.20281	KIAA1700	5.56
	453985	N44545	Hs.251865	ESTs	5.56
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	5.55
	448877	AI583696	Hs.253313	ESTs	5.53
30	435748	AA699756	Hs.117335	ESTs	5.52
	420732	AA789133	Hs.63525	ESTs	5.51
	421818	AW992976	Hs.50098	NM_002489: Homo sapiens NADH dehydrogenas	5.50
	430915	AA488953		gb:aa65e05.r1 NCI_CGAP_GCB1 Homo sapiens	5.50
	436716	AI433540		gb:bf69g05.x1 NCI_CGAP_Kid11 Homo sapien	5.50
35	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	5.50
	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	5.50
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	5.50
	451287	AK002158	Hs.26194	likely homolog of mouse immunity-associat	5.50
	433701	AW445023	Hs.15155	ESTs	5.49
40	427640	AF058293	Hs.180015	D-dopachrome tautomerase	5.47
	420552	AK000492	Hs.98806	hypothetical protein	5.45
	449338	H73444	Hs.394	adrenomedullin	5.42
	427176	AW381569	Hs.40334	ESTs	5.42
	409945	AW015935	Hs.122642	ESTs	5.40
45	421568	W85858	Hs.98804	ESTs	5.40
	423961	D13666	Hs.136348	perforin (OSF-2os)	5.40
	440719	AA150869	Hs.26267	ATP-dependant interferon response protel	5.40
	443035	Z45822	Hs.8906	Homo sapiens clone 24889 mRNA sequence	5.40
	458659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	5.40
50	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	5.40
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	5.39
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	5.38
	439815	AA206079	Hs.6693	hypothetical protein FLJ20420	5.37
	452432	AW206008	Hs.283378	Homo sapiens cDNA: FLJ21778 fis, clone H	5.37
55	457465	AW301344	Hs.122908	DNA replication factor	5.37
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.36
	409485	S80990	Hs.252136	ficollin (collagen/fibrinogen domain-cont	5.35
	430283	BE391688		RAB7, member RAS oncogene family	5.33
	406814	AA642947	Hs.119122	ribosomal protein L13a	5.33
60	409019	AW385412		myosin regulatory light chain 2, smooth	5.30
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	5.30
	412623	R28898	Hs.74170	metallothionein 1E (functional)	5.30
	417450	AA314435	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	5.30
	418702	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	5.30
65	419826	AW900992	Hs.93796	DKFZP586D2223 protein	5.30
	422900	AA641201	Hs.222051	ESTs	5.30
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	5.30
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	5.30
	427774	AA278583	Hs.180737	Homo sapiens clone Z3664 and Z3905 mRNA	5.30
70	430177	AW969233	Hs.302746	MSTP028 protein	5.30
	430835	AI240006	Hs.192326	ESTs	5.30
	433009	AA761668		gb:zn24c08.s1 NCI_CGAP_GCB1 Homo sapiens	5.30
	439776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	5.30
	447082	T85314	Hs.54629	thioredoxin-like	5.30
75	415995	NM_004573		phospholipase C, beta 2	5.29
	424578	AK001973	Hs.150890	hypothetical protein	5.27
	441303	AW293081	Hs.241801	ESTs	5.27
	427816	AA159248	Hs.180909	peroxiredoxin 1	5.27
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	5.26
80	450273	AW296454	Hs.24743	hypothetical protein FLJ20171	5.24
	444708	AW971049	Hs.11774	protein (peptidyl-prolyl cis/trans isome	5.23
	415121	D60971	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	5.21
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.21
	405086			NM_006662*: Homo sapiens Snf2-related CBP	5.20

	413401	AI361861	Hs.118659	ESTs	5.20
	418459	R85436	Hs.268814	ESTs	5.20
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.20
	426496	D31765	Hs.170114	KIAA0061 protein	5.20
5	431749	AL049263	Hs.306292	Homo sapiens mRNA; cDNA DKFZp564F133 (fr	5.20
	434372	AA631373		gb:np86c01.s1 NCI_CGAP_Thy1 Homo sapiens	5.20
	436812	AW298067		gb:U1-H-BW0-ajp-g-09-0-U1.s1 NCI_CGAP_Su	5.20
	441390	AI692560	Hs.131175	ESTs	5.20
	449419	R34910	Hs.119172	ESTs	5.20
10	453127	AI696671	Hs.294110	ESTs	5.20
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	5.19
	417750	AI267720	Hs.260523	synovial sarcoma, translocated to X chro	5.18
	451814	AA847992	Hs.137003	ESTs	5.18
	410423	AW402432	Hs.63469	protein tyrosine phosphatase, non-recept	5.16
15	406799	AA908548		gb:cg83g12.s1 NCI_CGAP_Ov8 Homo sapiens	5.15
	413963	R84282	Hs.75643	nuclear factor (erythroid-derived 2), 45	5.14
	422293	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	5.12
	432465	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)	5.12
	414768	AW376989	Hs.259855	elongation factor-2 kinase	5.12
20	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	5.11
	430478	NM_014349	Hs.241535	apolipoprotein L, 3	5.11
	420151	AA255931	Hs.186704	ESTs	5.10
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	5.10
	419317	AA236282	Hs.172318	ESTs	5.10
25	424699	AW206227	Hs.287727	hypothetical protein FLJ23132	5.10
	428403	AI393048	Hs.326159	leucine rich repeat (in FLJ) interactin	5.10
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	5.10
	431709	AF220185	Hs.267923	uncharacterized hypothalamus protein HT0	5.10
	436137	AI056769	Hs.133512	ESTs	5.10
30	440948	AW188311	Hs.128619	ESTs	5.09
	448497	BE613269	Hs.21893	hypothetical protein DKFZp761N0624	5.09
	416655	AW968613	Hs.79428	9CL2/adenovirus E1B 19kD-interacting pro	5.09
	417228	AL134324	Hs.7312	ESTs	5.08
	424868	AI568170	Hs.96886	ESTs	5.08
35	418905	BE539674		actinin, alpha 4	5.07
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.06
	442618	R56222	Hs.26514	ESTs	5.06
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.06
	406813	AW276131		ribosomal protein L13a	5.05
40	454128	AL031259	Hs.41639	programmed cell death 2	5.05
	440709	AW797724	Hs.130350	ESTs	5.05
	436372	AW972301	Hs.310286	ESTs	5.05
	446173	BE565849	Hs.14158	copine III	5.04
45	453330	AI268081	Hs.342389	peptidylprolyl isomerase A (cyclophilin	5.03
	418876	AA740616		gb:ny97f11.s1 NCI_CGAP_GCB1 Homo sapiens	5.00
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	5.00
	410570	AI133095	Hs.64593	ATP synthase, H transporting, mitochondr	5.00
	410800	BE280421	Hs.94499	ESTs	5.00
	431451	AA761378	Hs.192013	ESTs	5.00
50	432879	AW815932	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.00
	435655	AW105663	Hs.6947	HSPC089 protein	5.00
	435919	AI052189	Hs.114104	ESTs	5.00
	436394	AA531187	Hs.126705	ESTs	5.00
55	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	5.00
	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	5.00
	442685	AB033017	Hs.8594	KIAA1191 protein	5.00
	444454	BE018316	Hs.11183	sorting nexin 2	5.00
	444670	H58373	Hs.332938	hypothetical protein MGC5370	5.00
	447197	R36075		gb:yn88b01.s1 Soares placenta Nb2HP Homo	5.00
60	450113	AI683098	Hs.200866	ESTs, Moderately similar to ALU7_HUMAN A	5.00
	450511	R07423	Hs.85092	thyroid hormone receptor interactor 11	5.00
	450887	AA011518	Hs.271778	ESTs, Weakly similar to I38022 hypotheti	5.00
	452056	AW955065	Hs.101150	Homo sapiens, clone IMAGE:4054156, mRNA,	5.00
	457068	X69391		ribosomal protein L6	4.97
65	406793	AW264291	Hs.5662	guanine nucleotide binding protein (G pr	4.95
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	4.94
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.92
	440638	AI376551		gb:ta64e10.x1 Soares_NFL_T_GBC_S1 Homo s	4.91
	400281			Eos Control	4.90
70	414420	AA043424	Hs.76095	Immediate early response 3	4.90
	415799	AA653718	Hs.225841	DKFZP434D193 protein	4.90
	434666	AF151103	Hs.112259	T cell receptor gamma locus	4.90
	449057	AB037784	Hs.22941	KIAA1363 protein	4.90
	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	4.90
75	451598	N28102	Hs.118078	ESTs	4.88
	409686	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp434L0827 (f	4.88
	410597	W16518	Hs.279518	amyloid beta (A4) precursor-like protein	4.86
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	4.86
	447150	AA439011	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-r	4.85
80	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	4.85
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	4.84
	437186	AA338305	Hs.5472	hypothetical protein FLJ20173	4.84
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	4.84

	406781	AA639388		gb:nq88b06.s1 NCI_CGAP_Co9 Homo sapiens	4.83
	449810	AB008881	Hs.23994	activin A receptor, type IIB	4.82
	410323	A1241708	Hs.296322	Homo sapiens cDNA: FLJ22844 fis, clone K	4.81
5	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subun	4.81
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	4.81
	400424	AJ276316	Hs.287374	zinc finger protein 304	4.80
	411573	AB029000	Hs.70823	KIAA1077 protein	4.80
	421045	BE144608	Hs.55533	ESTs	4.80
10	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.80
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.80
	438590	AA811465	Hs.123375	ESTs	4.80
	442071	BE048433	Hs.276043	ESTs	4.80
	449567	AI990790	Hs.188614	ESTs	4.80
15	453213	AA082650	Hs.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	4.80
	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	4.78
	437802	AI475995	Hs.122910	ESTs	4.77
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	4.77
	421932	W51778	Hs.323949	kangal 1 (suppression of tumorigenicity	4.74
20	428453	AB011110	Hs.184357	GTPase activating protein-like	4.74
	413441	AI929374	Hs.75367	Src-like-adaptor	4.74
	446560	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	4.73
	435541	AA687361	Hs.221318	ESTs	4.71
	410557	AA085803	Hs.192997	ESTs, Moderately similar to I78885 serin	4.70
25	412766	BE544475	Hs.54347	ESTs	4.70
	415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.70
	418973	AA233056	Hs.191518	ESTs	4.70
	421433	AI829192	Hs.223380	ESTs	4.70
	432925	AA878324	Hs.264750	ESTs	4.70
30	438869	AF075009		gb:Homo sapiens full length insert cDNA	4.70
	442233	AW967149	Hs.28439	ESTs, Weakly similar to I38022 hypotheti	4.70
	447198	D61523	Hs.283435	ESTs	4.70
	446552	AW973653	Hs.20104	hypothetical protein FLJ00052	4.70
	444681	AJ243937	Hs.288316	chromosome 6 open reading frame 9	4.66
35	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	4.66
	447817	BE620775	Hs.4866	Homo sapiens cDNA FLJ14387 fis, clone HE	4.65
	416062	AA724811	Hs.334791	Homo sapiens cDNA FLJ14609 fis, clone NT	4.65
	406661	X66975	Hs.172550	polypyrimidine tract binding protein (he	4.64
	424582	AF026849	Hs.150922	BCS1 (yeast homolog)-like	4.64
40	411165	NM_000169	Hs.69089	galactosidase, alpha	4.63
	435905	AW997484	Hs.5003	KIAA0456 protein	4.63
	445776	NM_001310	Hs.13313	cAMP responsive element binding protein-	4.62
	424730	NM_003358	Hs.23703	ESTs, Moderately similar to CEGT_HUMAN C	4.62
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	4.62
45	410668	BE379794	Hs.159651	hypothetical protein	4.61
	406774	AW518383	Hs.177592	ribosomal protein, large, P1	4.60
	406648	AA563730	Hs.277477	major histocompatibility complex, class	4.60
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	4.60
	415682	AI347128	Hs.191870	ESTs	4.60
50	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	4.60
	419970	AW612022		ESTs	4.60
	420012	AW857965	Hs.99014	Homo sapiens, clone IMAGE:3632168, mRNA	4.60
	431574	AW572659	Hs.261373	hypothetical protein dJ434014.3	4.60
	432586	AA568548		ESTs	4.60
55	437438	AL359620	Hs.14217	hypothetical protein DKFZp762P2111	4.60
	441355	AI822034	Hs.137097	ESTs	4.60
	444539	AI955765	Hs.146907	ESTs, Weakly similar to 2004399A chromos	4.60
	458965	AA010319	Hs.60389	ESTs	4.60
	406655	M21533	Hs.277477	major histocompatibility complex, class	4.60
60	414915	NM_002462	Hs.76391	myxovirus (Influenza) resistance 1, homo	4.60
	414821	M83835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.59
	423766	AA303799	Hs.300141	ribosomal protein L39	4.59
	451351	AW058261	Hs.321435	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.56
	450043	AA885699	Hs.24332	CGI-26 protein	4.56
65	447742	AF113925	Hs.19405	caspase recruitment domain 4	4.54
	433339	AF019226	Hs.8036	glioblastoma overexpressed	4.54
	426395	BE151985		hypothetical protein FLJ23316	4.53
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	4.53
	423799	AW026300	Hs.132906	19A24 protein	4.53
70	445093	AI207197		ESTs	4.52
	428044	AA093322	Hs.301404	RNA binding motif protein 3	4.52
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	4.51
	414194	BE175494	Hs.75811	N-acetylserine/threonine hydrolase (acid c	4.50
	427747	AW411425	Hs.180655	serine/threonine kinase 12	4.50
75	406745	AW511970	Hs.279860	tumor protein, translationally-controlled	4.50
	407013	U35637	Hs.83870	gb:Human nebulin mRNA, partial cds	4.50
	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	4.50
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	4.50
	429687	AI675749	Hs.211608	nucleoporin 153kD	4.50
80	436566	BE545586	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	4.50
	437634	AW293046	Hs.255158	ESTs	4.50
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	4.50
	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	4.50
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	4.50

5	450497	H64159	Hs.15328	ESTs	4.50
	417497	AW402482	Hs.82212	CD53 antigen	4.50
	447667	AL117611	Hs.19150	Homo sapiens mRNA; cDNA DKFZp564A2164 (f	4.49
	413856	D13639	Hs.75586	cyclin D2	4.49
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	4.49
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	4.48
	427157	U51166	Hs.173824	thymine-DNA glycosylase	4.48
	446021	BE389213	Hs.286	ribosomal protein L4	4.47
10	413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.46
	412819	T25829	Hs.24048	FK506 binding protein precursor	4.46
	448717	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	4.45
	401846			NM_000988*:Homo sapiens ribosomal protei	4.44
	422303	AW410382	Hs.27556	hypothetical protein FLJ22405	4.43
15	442358	BE567985	Hs.18585	ESTs, Moderately similar to ALU4_HUMAN A	4.43
	436623	AI417073	Hs.107265	ESTs	4.42
	412146	M92444	Hs.73722	APEX nuclease (multifunctional DNA repai	4.42
	437042	AK000702	Hs.5420	hypothetical protein FLJ20695	4.42
	416754	H07145	Hs.6799	ESTs, Weakly similar to T12483 hypothe	4.41
20	436671	AW137159	Hs.183291	ESTs	4.40
	410079	U94362	Hs.58589	glycogenin 2	4.40
	420150	AA648712	Hs.29798	KIAA1712 protein	4.40
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	4.40
	428931	AA994979	Hs.98967	ATPase, H ⁺ -transporting, lysosomal, non	4.40
25	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	4.40
	430280	AA361258	Hs.237868	Interleukin 7 receptor	4.40
	438330	AW450572	Hs.257316	ESTs	4.40
	438962	BE046594		gb:hm41c11.x1 NCI_CGAP_RDF2 Homo sapiens	4.40
30	444794	AI419991	Hs.145225	ESTs	4.40
	445100	AW188205	Hs.12311	Homo sapiens clone 23570 mRNA sequence	4.40
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	4.40
	449832	AA694264	Hs.60049	ESTs	4.40
	452404	AW450675	Hs.212709	ESTs	4.40
35	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	4.39
	425097	NM_014247		PDZ domain containing guanine nucleotide	4.37
	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	4.37
	406742	AI468091	Hs.279860	tumor protein, translationally-controlle	4.35
	425095	AW014160	Hs.182585	KJAA1276 protein	4.34
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity 1, rec	4.34
40	442333	AI650877	Hs.129302	ESTs	4.33
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.32
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.32
	437386	W52452		ribosomal protein L10	4.31
45	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	4.30
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	4.30
	409604	AW444448	Hs.49124	ESTs	4.30
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.30
	419423	D26488	Hs.90315	KIAA0007 protein	4.30
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	4.30
50	422797	AB033064	Hs.236463	KIAA1238 protein	4.30
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	4.30
	432290	AK001099	Hs.274273	Homo sapiens cDNA FLJ10237 fis, clone HE	4.30
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	4.30
	436138	H53323	Hs.25717	Homo sapiens cDNA: FLJ23454 fis, clone H	4.30
55	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	4.30
	445217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	4.30
	452994	AW962597	Hs.31305	KJAA1547 protein	4.30
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.29
	437250	BE257342	Hs.94576	hypothetical protein MGC3062	4.29
60	440910	H97875	Hs.117974	ESTs	4.28
	406853	AA614563	Hs.252259	hypothetical protein FLJ23059	4.28
	432295	BE091049	Hs.343665	ribosomal protein S15a	4.28
	400244			Eos Control	4.28
65	413518	BE149455	Hs.75415	beta-2-microglobulin	4.27
	409132	AJ224538	Hs.50732	protein kinase, AMP-activated, beta 2 no	4.27
	406746	AA580395	Hs.279860	tumor protein, translationally-controlle	4.26
	400395	AF111167		v-fos FBJ murine osteosarcoma viral onco	4.26
	443229	AI057129	Hs.133396	ESTs	4.25
	450201	T97838	Hs.25722	ESTs	4.25
70	409636	AA305729	Hs.18272	amino acid transporter system A1	4.25
	422082	AA016188	Hs.111244	hypothetical protein	4.24
	444099	D87432	Hs.10315	solute carrier family 7 (cationic amino	4.24
	453902	BE502341	Hs.3402	ESTs	4.24
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	4.22
75	404854			Target Exon	4.21
	406653	AA574074	Hs.77961	major histocompatibility complex, class	4.20
	400440	X83957	Hs.83870	nebulin	4.20
	415049	N67334	Hs.50158	ESTs	4.20
80	418304	AA215702		gb:cz97g10.r1 NCI_CGAP_GC81 Homo sapiens	4.20
	423180	AF068302	Hs.125031	choline/ethanolaminephosphotransferase	4.20
	424684	AW752714	Hs.5174	ribosomal protein S17	4.20
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	4.20
	438141	AW946871		gb:RC2-ET0022-080500-012-d02 ET0022 Homo	4.20
	438607	AW080237	Hs.252884	ESTs	4.20

5	451952	AL120173	Hs.301663	ESTs	4.20
	455397	AW936332		gb:QV4-DT0021-281299-070-g01 DT0021 Homo	4.20
	417116	Z43916	Hs.7634	hypothetical protein FLJ12287 similar to	4.19
	453247	T80198	Hs.111806	ESTs	4.19
	430451	AA836472	Hs.297939	cathepsin B	4.19
	414283	AW960011	Hs.154993	ESTs	4.18
	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	4.18
	450746	D82673	Hs.278589	general transcription factor II, I	4.16
	444797	AB018333	Hs.12002	KIAA0790 protein	4.16
10	445718	H79791	Hs.15227	ESTs	4.15
	425783	AI026740	Hs.1948	ribosomal protein S21	4.15
	414837	U24266	Hs.77448	aldehyde dehydrogenase 4 family, member	4.15
	406710	AI708347	Hs.184014	ribosomal protein L31	4.15
	424436	AW818428	Hs.4953	golgi autoantigen, golgin subfamily a, 3	4.14
15	422343	AI628633	Hs.346823	gb:ty77d05.x1 NCL_CGAP_Kid11 Homo sapien	4.13
	416207	NM_014745	Hs.79077	Homo sapiens, clone MGC:2908, mRNA, comp	4.13
	406724	C14071	Hs.234518	ribosomal protein L23	4.12
	449475	AJ348027	Hs.108557	hypothetical protein PP1057	4.12
20	413828	L19067		v-rel avian reticuloendotheliosis viral	4.11
	416819	U77735	Hs.80205	pim-2 oncogene	4.11
	436674	AA725002	Hs.272018	low molecular mass ubiquitinone-binding pr	4.11
	405266			Target Exon	4.10
	408996	AJ979168	Hs.344096	glycoprotein (transmembrane) nmb	4.10
25	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	4.10
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.10
	423096	AA732684	Hs.278428	progesterone induced protein	4.10
	428328	AA426080	Hs.292812	ESTs, Weakly similar to I38022 hypotheti	4.10
	429355	AW973253	Hs.292689	ESTs	4.10
30	433308	AA582718	Hs.291650	ESTs	4.10
	443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	4.10
	450850	AA648885	Hs.151999	ESTs	4.10
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	4.10
	406854	AA613705	Hs.252259	ribosomal protein S3	4.10
35	410768	AF038185	Hs.65187	Homo sapiens clone 23700 mRNA sequence	4.09
	419612	AJ498267	Hs.110613	KIAA0421 protein	4.09
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.08
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	4.08
	441374	AA043696	Hs.7822	Homo sapiens mRNA; cDNA DKFZp564C1216 (f	4.08
40	443415	AI056523	Hs.133472	ESTs	4.08
	424338	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-	4.07
	422305	AI928242	Hs.293438	ESTs, Highly similar to AF198488 1 trans	4.07
	400233			Eos Control	4.06
	421959	AW751497	Hs.98370	cytochrome P450, subfamily IIS, polypept	4.06
45	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	4.06
	424795	AW102850	Hs.153177	ribosomal protein S28	4.05
	446231	NM_002163	Hs.14453	interferon consensus sequence binding pr	4.05
	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fls, clone H	4.05
	427681	AB018263	Hs.180338	tumor necrosis factor receptor superfam	4.03
50	409061	AI204994	Hs.7874	Homo sapiens cDNA: FLJ21435 fls, clone C	4.03
	413891	BE271020		tumor suppressor deleted in oral cancer-	4.02
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	4.02
	417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	4.02
	410584	AB011112		KIAA0540 protein	4.01
55	417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.00
	423645	AI215632	Hs.147487	ESTs	4.00
	430048	T65054	Hs.73605	ESTs	4.00
	431113	AK000673	Hs.274337	hypothetical protein FLJ20666	4.00
	434170	AA626509	Hs.122329	ESTs	4.00
60	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fls, clone NT	4.00
	435391	AA704588	Hs.58934	ESTs	4.00
	446768	AV660305	Hs.110286	ESTs	4.00
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	4.00
	451831	NM_001674	Hs.460	activating transcription factor 3	4.00

TABLE 56B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey CAT Number Accession

438091 22448_1 AK054860 AV652188 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184
 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW853629 BM263546 BE550772 AA701084 AJ681352 AA358689
 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183
 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720
 AW510698 AA987230 BE467708 AW898628 AW898544 AJ146984 AW043642 AJ288245 AI186932 AI635262 AI139455 AI298739 AI813854
 AJ024768 BE699445 BE699444 AJ07807 OS2654 AI214518 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AJ334784 BF108411
 AI061126 BF362770 AI268939 AJ435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AJ334784 BF108411
 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762
 AI922204 AW898625 BE699458 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244
 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552

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			AA969444 AI080438 AA552500 AW237538 AA481050 AI246378 AA565227 AA398921 AA207051 AA721378 BF438608 AI086295 AI886630 AA904112 AI864588 AW271985 AW078868 AA725342 BF326598 AA843572 AI082536 AA766664 AA53279 AA435673 AI619515 AA879080 AA234592 AA890223 AA766824 BI259822 AA393631 AW968840 BE940639 T83865 BE762742 AW897470 W05809 N41323 T87376 R68544 H88711 BI087136 BE177661 H06215 BE144709 BE144829 AA947566 AI074047 AI144342 AW014280 BM145128 N28267 AW206231 AA989041 H93197 AW594063 BG236296 AW236606 AW081031 AA765843 BM144372 AA89341 AI824838 AI963970 AI637671 AW196330 BG427526 BM148789 BF893644 BF681946 BF090249 AW954947 AW890487 AI305236 D06045 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 AI350279 AA879119 AA319510 BE702077 BE699015 BE702046 AW901293 T99319 D81708 BF475488 D60383 D81751 BE699260 BE005398 AA628622 AA994155 AA662701 AA633929 AA737415 BG427950 AA826016 AI903441 BG939868 AW979154 AA640872 BG547134 AA457091 AW368860 W88852 R94779 AA088823 BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899664 H91240 R60548 N41701 BM476120 BE672181 AI697653 AA938187 AI280879 AW340123 AI912727 AI081775 AI089556 AI191349 AI871604 AI631607 AI890800 AI701917 AW771624 AA663041 AI991576 AI160622 AA771753 BE089784 BE089788 AI222942 AW418516 AA329211 AI095736 BE550294 AA738345 BE218683 BE670548 BG149505 BF061776 D19821 BE005786 BE178892 BE005728 BF841237 BE005648 R27634 AW954733 AA315006 AW856665 ALD47596 AA393792 AI670731 AI037957 AW874364 AI038137 N62286 AI241379 BE501096 AW090696 AI927369 AI669226 AI369437 AI371075 AW612409 AI686711 AI183289 AA477717 AI076122 AA635190 AA700984 AA781508 D81020 BF575223 AI356183 D79312 AI375558 H61111 BG283489 BE090666 BE090664 BE090662 H26545 AI184717 AW518883 AF121173 AK001838 AU135179 AU134241 AV651702 AV650032 AV651304 AV650101 AV651263 AV651888 AV651866 AA628554 AV651355 AV651174 AV651172 AW856145 AU117599 AU135388 BG254665 AA166919 BG483981 AW809606 BG494194 AA622811 AI676156 AA687804 AI701729 AU133725 AW961387 AU144387 AU151757 AA551031 BE675412 N34769 AA713483 AI890079 AI588918 AI361889 AI209020 AA668981 AI240990 AA741144 AA490899 AI200221 AW589574 W96201 BG154182 AV655159 AA328145 N36348 AI081357 N76715 AA693346 AA742488 AI269719 AA897483 AI886459 AU155873 H04255 AW243986 AA557749 AI286227 R68691 R33453 AW388097 AA908472 U09414 NM_Q03438 AA503545 AI022449 AA043458 AW766074 AA765442 AA805052 AI028211 AW609708 AW502384 AA828822 AI982587 BE072881 AI762181 BE072946 AA558585 AA565499 AI360576 AW204069 AA991648 AA864939 BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969 BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563 AA459408 AA459633 AA418444 W23607 BG940150 AI493445 AW054729 AI221929 AI868744 AA215405 AA766713 AA621546 BF928317 BE464132 AI990909 AW271459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 R69057 BF766886 BE769254 W05240 BG119563 AW975776 BG498478 BE245304 AW450934 BF508792 AA599489 AA599477 AI805268 AA055489 AI128758 AA761425 AA731858 AI302271 BE219432 AA687294 AA018972 AW629429 Z45675 AW961626 T30940 R34554 T84712 BG986694 AI742311 AI025842 AA578843 AA075144 AV711317 AI809938 AI808768 AI240593 AI915771 AI432224 AW276890 AI499346 AA937014 AA653573 AI318525 AI246219 AA961591 AI270640 BC022413 BE395396 BF764175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853 AW371849 BE153241 BC017410 AI337912 AI090244 AW090300 BE219837 AI623661 BE501576 BE501734 AI742232 AI023964 AI58424 AA975373 AI288904 AI984583 AA890325 N32562 AI358102 AW241694 AI038448 AI672071 AI018389 AA576391 AA977874 AW189392 W37448 AA612894 AI277548 H89551 AI699774 H89365 AA315805 AW579186 BC014584 BC014581 AW780125 AI672414 BE328145 AW600919 BF031306 AW172758 BE708322 AA345875 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522 BM128822 AI122760 BE718200 AW887486 AA149420 BE706307 BE539395 BE748765 AI373653 R75904 BF979185 BF691393 BG495595 BI094458 BE706702 BG496559 BF248373 BG494800 BE219720 BF475241 AI571723 BE219848 BI789268 AI224899 AA724864 AW771467 AA480255 AW845616 AI440295 H52800 BE218790 AI681575 AW300064 AW262133 H21568 AI363015 AI884914 H86948 AW182329 AA613792 T05304 AW858385 BG216963 BG164885 BG213710 BG204771 BG193014 BG197556 BG217481 BG198185 BG183594 BI596425 AA115605 AI589156 BF439839 BG188832 AI359615 BG190473 AI024233 BF439574 AW118065 AI672797 AA610042 BG212008 AI204382 R70913 AA033534 AA781036 AI527278 AA307285 AA034218 BG482749 AW162429 BI602460 AA721969 AA476516 AA476416 AA903019 BF110864 AA307286 AA115471 AW964555 AA423826 AA115129 AI419107 AW088535 AI889321 AA954221 AI337552 R42581 AW194670 AA064862 AW001147 AA864374 AA630699 AW276176 AA676615 AA857965 AI625428 AA580792 AA582038 AA581668 AA658065 AA828156 AA857160 AA936103 AI149335 AA936925 AA581684 AA954198 AW238461 AI281504 AI265812 AA583267 AW236162 AA876535 AW304286 AW474334 AI559415 AI589241 AI660952 AA641137 AI431696 AI688844 AA552513 AA564954 AW090553 AI205612 AI245753 AA954883 AA947909 AI866014 AI890243 AW971213 AA493925 AA493567 AA876839 AA934462 T40644 AA136139 AA136026 BG425760 BF997600 N48516 W73454 BF816344 BF997601 AA488953 AI433540 AA804581 AA728984 BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360 BC013728 BI084032 BF090365 BE410706 N36391 WB0436 BF813124 R90857 R62778 H00591 H02329 AA355285 AK000826 BC008721 BG744004 BG479141 BG823656 BG479061 AU121103 AU138176 BG702567 BI599840 BG422775 BG700944 BE280747 AU138529 BE269929 BG704110 AU123329 AU122058 AU138135 BG723106 BG722291 BG831041 BG705239 BE740517 BE207133 BE252867 AU139772 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5	438141 455397 413828	1173217_1 1163608_1 9453_1	AA778849 AW946871 AW946782 AW946955 AW936332 AW936341 BC011603 BG479117 AU124990 BG829759 AU143705 BG701663 BG699781 AU131718 BE515064 AU121812 BG898850 AL558461 BM151867 AU128758 BM263692 AU099013 AI241350 U88316 AW058398 AW469340 BF683967 AI470140 AU150993 AA633376 AW150821 AA536142 AU148749 AI620647 AU151769 AU153404 AW070666 AI457758 AU153077 N99966 AW050940 BG055674 AA506657 AW301529 AI918846 AI611235 AI266081 AI334542 AW071277 AI312434 AW303114 AI436544 AI436466 R22872 AI472887 N77886 AW072883 AA318683 O19761 AW050566 AI312433 AA328444 R72435 AA430721 AI142599 AA582290 AU148896 AA721233 AW628132 R39335 AA100710 BI520773 AI934172 BG222461 H85359 AW074639 AA017117 BI026412 AL582142 AA443547 AA586793 AA777535 AA693844 AI018661 AA577422 AA522800 BF054818 AA102378 AA757993 AA687769 R55540 AA505784 BI820705 BI767939 10 410704 1054673_1 AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 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BG481705 BG104314 BM464565 BI261500 BG831857 BG831684 BG829852 BG765030 BG760419 BG760268 BG749762 BG480900 BG419627 BG248771 BF975542 BM042233 BI161149 BG831302 BG830033 BG829626 BM050064 BI193014 BI181360 BG822729 BE395269 BG832027 BG831469 BG490895 BM413638 BG943529 BG831012 BG829471 BG686284 BG337575 BG336551 BF206677 BI258301 BI160946 BG105893 BF183072 BM459542 BI193881 BG832043 BG831323 BI194545 BI160968 BG755930 BG706018 BE743865 BM465145 25 BG831227 BG774290 BF683451 BE907161 BM045391 BI194396 BI161269 BG747091 BG546643 BF984863 BI160206 BI226402 BI226336 AW328236 BG339458 BF972634 BE909808 BI160988 BI160251 BG828764 BG826860 BG758360 BF568228 BI818282 BI457127 BG831491 BG759884 AI830010 BF568381 BE907238 BI161172 BI116773 BG827153 BG825088 BG335419 BG109404 AI929068 BE906354 BE408564 BM045000 BG339617 BG827794 BG335767 BE907263 BF568921 BG829961 BG479305 BG260397 AI922228 BE301975 AW516055 BG480919 30 BG480626 AW196817 BG336261 BE906157 BE395717 BE391427 BI192954 BG829757 BG476379 BE301536 BE394727 BE257695 BE905344 AI433577 BE894416 BE886992 BE409223 BF034756 BE904077 BG830886 BE909163 BE907998 BE395767 AI871751 BE744523 BI192663 BG831669 AI000225 BE743836 BE272515 AA628078 BM463802 BE393375 BE393033 AW170187 BE730961 BE395410 BE744572 BE392297 BE391448 BE390780 BE388821 BE258477 BE905970 BE901567 BE898833 BE880326 BF726889 BE910504 BE390753 BE390131 AA650542 BE744156 BE394125 BE742207 BE395265 BE392942 BE894336 BE378222 BE906926 BE904650 BE393704 BE620999 BE515162 BE378753 35 BE741570 BE907458 BE612801 BE392484 BE907636 BE907353 BE910491 BE909798 BE905331 AW248173 AI683576 BE908826 BE620180 BF037570 BE908312 BE615015 BE256977 BE746875 BE394133 BE391478 BE910068 BE907185 BE742109 AA955746 BE561195 BE908825 BE906472 BE906509 BE906017 BE910442 BE514657 BI261969 BE741707 BE392216 BM042793 BF570283 BI262119 BE395707 BE378298 AW327827 BE394422 BF569178 BE263240 AI700512 BG830290 BF669308 BF569156 BI194587 BE390831 BG745096 AI681675 BE395674 40 413891 823_1 AA136372 BE279892 AA442822 BE384898 AA313519 AI878866 AA305904 F33366 BE394852 F29153 F33618 AI133637 AA300009 F34063 F29455 AU099691 AI905085 AI906656 AA343249 BE388691 AW404280 AA379888 F29022 BF089981 F31013 F24305 BE271020 AI925430 AI806151 AW129911 AA288002 AW003539 BE042625 AI287859 AW778973 AI621173 AI991000 AA846016 AW150029 AW169748 AA649945 AI358496 AI470921 BF434211 AW513748 AW451232 AI953739 AI249448 AI040580 AI655280 AI637976 AW194345 AW611997 AI367197 BF064039 F29558 AI537342 BF346057 AI763358 AW003726 AI139045 AI570748 AW237602 T57492 BE887212 AI969311 45 410584 35319_1 AA426653 AA480106 AW243290 BF513102 BF346057 AI763358 AW003726 AI139045 AI570748 AW237602 T57492 BE887212 AI969311 AA133045 F23464 AA576416 T15590 AI650891 AI950958 AI983931 AW515101 AI650820 H81989 AA508473 BF828833 AI968217 AI651409 AI760574 AI147562 AW001418 AI146791 AI650589 AI952939 AI432373 AI964094 AI963870 AI420438 AI336803 AA809634 BF590826 AA741075 BI712639 AL134637 BM264338 AA527993 AI867208 AI439038 AI684987 AI631696 AI587126 AI637622 AI651931 AI867525 AI783674 AI638281 AI825752 AI339197 AI653411 AI341372 AI673213 AI673191 AW779768 AI627934 AI921836 AI741634 AI382284 AI741624 AI401569 AW190430 AW196390 AI829182 AI523816 AI760522 BE505014 AI917343 BG818909 AW009307 AA927544 AA825621 50 AA829400 AA527307 AI887999 AI865022 AA885063 AA653458 AA483816 AA836167 AA505879 AA421004 AA252626 AI380678 AW195980 AA649133 AI742276 AW015700 AA595019 AA877835 AI701658 AA729793 AA535004 AA926792 AA505113 AA603726 W68390 N90130 AA489461 AA830462
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55	TABLE 56C
	Pkey: Unique number corresponding to an Eos probe set
	Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
	Strand: Indicates DNA strand from which exons were predicted.
60	Nt_position: Indicates nucleotide positions of predicted exons.

65	Pkey	Ref	Strand	Nt_position
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	402145	8018280	Plus	113086-114800
	401091	9958240	Plus	94760-94898
	401466	6682292	Plus	28748-29023
	401113	8966541	Minus	19419-19959
	406542	7711499	Plus	117335-118473
	405086	8072509	Plus	73664-73841,74081-74217,74610-74779,7492
	401846	7712190	Minus	82775-82823,82912-83022
70	404854	7143420	Plus	14260-14537
	405266	4156171	Minus	63337-63552

75 TABLE 57A: 703 genes upregulated in testicular cancer relative to normal body tissues

80 Table 57A lists about 703 genes upregulated in testicular cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probe set obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of having oncogenic function or of transducing intracellular signals, or of being modifiable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar accession number, GenBank accession number
	UniGeneID:	UniGene number
5	Pred.Protdomains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
	UniGene Title:	UniGene gene title
	R1	95th percentile of testicular cancer AIs divided by the 50th percentile of normal tissues AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator
10	Pkey; ExAccn; UniGeneID; Unigene Title; Pred.Protdomains; R1	
		424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase); matrix metalloproteinase 9 (gelatinase B; 31.23
		440119; AA855455; Hs.125331; ESTs, Moderately similar to unknown [H.sapiens]; ESTs, Moderately similar to unknown [H.s.; 27.37
15		421241; X91817; Hs.102866; transketolase-like 1; transketolase-like 1; 26.89
		431840; AA534908; Hs.2860; POU domain, class 5, transcription factor 1; POU domain, class 5, transcription factor 1; 25.03
		435918; AF263538; Hs.86232; growth differentiation factor 3; growth differentiation factor 3; 19.88
		432666; AW204069; Hs.351118; ESTs, Weakly similar to unnamed protein product [H.sapiens]; ESTs, Weakly similar to unnamed protein; 17.74
		419556; U29515; Hs.91093; chitinase 1 (chitotriosidase); chitinase 1 (chitotriosidase); 17.64
20		452838; U65011; Hs.30743; preferentially expressed antigen in melanoma; preferentially expressed antigen in melanoma; 17.06
		417886; AA214584; ; ESTs; ESTs; 15.95
		412265; AA101325; Hs.86154; hypothetical protein FLJ12457; hypothetical protein FLJ12457; 15.93
		425572; AB011076; Hs.158307; undifferentiated embryonic cell transcription factor 1; undifferentiated embryonic cell transcript; 15.82
		423905; AW579960; Hs.135150; lung type-I cell membrane-associated glycoprotein; lung type-I cell membrane-associated gly; 15.11
25		419741; NM_007019; Hs.93002; ubiquitin carrier protein E2-C; ubiquitin carrier protein E2-C; 15.08
		427584; BE410293; Hs.179718; v-myb avian myeloblastosis viral oncogene homolog-like 2; v-myb avian myeloblastosis viral oncogene; 14.17
		418696; AW594333; Hs.326290; hypothetical protein FLJ12581; hypothetical protein FLJ12581; 13.58
		416819; U77735; Hs.80205; pim-2 oncogene; pim-2 oncogene; 13.20
		414034; U89277; Hs.305985; early development regulator 1 (homolog of polyhomeotic 1); early development regulator 1 (homolog o; 12.93
30		454077; AC005952; Hs.37062; insulin-like 3 (Leydig cell); insulin-like 3 (Leydig cell); 12.90
		432730; AI066520; Hs.131358; ESTs; ESTs; 12.84
		446293; AI420213; Hs.149722; LIM domain transcription factor LIM-1 (hLIM-1) mRNA; LIM domain transcription factor LIM-1 (h; 12.74
		423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alpha 2/delta subunit 2; calcium channel, voltage-dependent, alph; 12.46
		450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta 4; 12.42
35		450719; AI096837; Hs.21349; ESTs, Weakly similar to R88B_HUMAN RAS-RELATED PROTEIN RAB-8B [H.sapiens]; ESTs, Weakly similar to R88B_HUMAN RAS-R; 12.26
		431462; AW583672; Hs.256311; granin-like neuroendocrine peptide precursor; granin-like neuroendocrine peptide precu; 11.96
		431354; BE046956; Hs.251673; DNA (cytosine-5-)-methyltransferase 3 beta; DNA (cytosine-5-)-methyltransferase 3 be; 11.91
		402199; ; Target Exon; Target Exon; 11.85
		424578; AK001973; Hs.150890; hypothetical protein; hypothetical protein; 11.81
40		416350; AF188635; Hs.189507; phospholipase A2, group IID; phospholipase A2, group IID; 11.67
		439979; AW600291; Hs.6823; hypothetical protein FLJ10430; hypothetical protein FLJ10430; 11.57
		410048; W76467; Hs.343874; proline oxidase homolog; proline oxidase homolog; 11.42
		442573; H93366; Hs.7567; branched chain aminotransferase 1, cytosolic; branched chain aminotransferase 1, cytos; 11.42
		414812; X72755; Hs.77357; monokine induced by gamma interferon; monokine induced by gamma interferon; 11.38
45		421917; AB028943; Hs.109445; KIAA1020 protein; KIAA1020 protein; 11.15
		440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF-1-like; NALP2 protein; PYRIN-Containing APAF-1-li; 10.92
		414683; S78296; Hs.76888; hypothetical protein MGC12702; hypothetical protein MGC12702; 10.91
		423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage elastase); matrix metalloproteinase 12 (macrophage; 10.74
		433800; AI034361; Hs.135150; lung type-I cell membrane-associated glycoprotein; lung type-I cell membrane-associated gly; 10.68
50		429120; AK001673; Hs.196530; hypothetical protein FLJ10811; hypothetical protein FLJ10811; 10.48
		444371; BE540274; Hs.239; forkhead box M1; forkhead box M1; 10.46
		441553; AA281219; Hs.121296; ESTs; ESTs; 10.37
		426534; U58096; Hs.2051; testis specific protein, Y-linked; testis specific protein, Y-linked; 10.28
		414878; AI801869; Hs.127982; ESTs; ESTs; 10.06
55		432117; AL036195; Hs.2909; prolamine 1; prolamine 1; 10.01
		425427; AI652662; Hs.317432; branched chain aminotransferase 1, cytosolic; branched chain aminotransferase 1, cytos; 9.97
		416201; AA467752; Hs.195161; ESTs; ESTs; 9.97
		410929; H47233; Hs.30643; ESTs; ESTs; 9.91
		427486; AA974433; Hs.362432; fibroblast growth factor 4 (heparin secretory transforming protein 1, Kaposi sarcoma oncogene); fibroblast growth factor 4 (heparin secr; 9.81
60		427239; BE270447; Hs.356512; ubiquitin carrier protein; ubiquitin carrier protein; 9.68
		402680; ; Target Exon; Target Exon; 9.68
		409208; Y00093; Hs.172631; integrin, alpha X (antigen CD11C (p150), alpha polypeptide); Integrin, alpha X (antigen CD11C (p150); 9.46
		443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; chromosome 20 open reading frame 1; 9.42
		440207; AI371978; Hs.128326; ESTs; ESTs; 9.41
65		433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; clone HQ0310 PRO0310p1; 9.41
		447534; AW953935; Hs.288655; ESTs; ESTs; 9.33
		442333; AI650877; Hs.129302; ESTs; ESTs; 9.28
		421307; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFp43480425 (from clone DKFp43480425); Homo sapiens mRNA; cDNA DKFp43480425 (f; 9.24
		423458; AI204212; Hs.351113; ESTs; ESTs; 9.23
70		431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placental); cadherin 3, type 1, P-cadherin (placenta; 9.23
		422938; NM_001809; Hs.1594; centromere protein A (17kD); centromere protein A (17kD); 9.21
		411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor, ; 9.21
		425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); topoisomerase (DNA) II alpha (170kD); 9.18
		428664; AK001666; Hs.189095; similar to SALL1 (sal (Drosophila)-like; similar to SALL1 (sal (Drosophila)-like; 9.17
75		428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabotropic glutamate family GPCR; retinoic acid induced 3(RAIG1); metabo; 9.11
		447733; AF157482; Hs.19400; MAD2 (mitotic arrest deficient, yeast, homolog)-like 2; MAD2 (mitotic arrest deficient, yeast, h; 9.11
		422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypept; 9.10
		449722; BE280074; Hs.23960; cyclin B1; cyclin B1; 8.86
		441560; F13386; Hs.7888; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (HER4); v-erb-a avian erythroblastic leukemia vi; 8.86
80		440983; M20681; Hs.7594; solute carrier family 2 (facilitated glucose transporter), member 3; solute carrier family 2 (facilitated glu; 8.86
		409342; AU077058; Hs.54089; BRCA1 associated RING domain 1; BRCA1 associated RING domain 1; 8.83
		420367; AA259090; Hs.257028; ESTs; ESTs; 8.82
		415947; U04045; Hs.78934; mutS (E. coli) homolog 2 (colon cancer, nonpolyposis type 1); mutS (E. coli) homolog 2 (colon cancer, ; 8.73
		418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase kinase 1; mitogen-activated protein kinase kinase ; 8.71

- 417407; AA923278; Hs.290905; ESTs, Weakly similar to protease [H.sapiens]; ESTs, Weakly similar to protease [H.sapi]; 8.64
 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor; 8.58
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-conjugating enzyme; HSPC150 protein similar to ubiquitin-con; 8.55
 412140; AA219591; Hs.73625; RAB6 interacting, kinesin-like (rabkinesin 6); RAB6 interacting, kinesin-like (rabkines); 8.52
 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, member 3; nuclear receptor subfamily 1, group I, m; 8.51
 424800; AL035588; Hs.153203; MyoD family inhibitor; MyoD family inhibitor; 8.45
 447188; H65423; Hs.17631; hypothetical protein DKFZp434E2135; hypothetical protein DKFZp434E2135; 8.45
 430056; X97548; Hs.228059; KRAB-associated protein 1; KRAB-associated protein 1; 8.42
 417389; BE260964; Hs.82045; midkine (neurotrophin growth-promoting factor 2); midkine (neurotrophin growth-promoting factor); 8.40
 430676; AF084866; Hs.372585; gb:Homo sapiens envelope protein R1C-3 (env) gene, complete cd; gb:Homo sapiens envelope protein R1C-3 (; 8.38
 420759; T11832; Hs.127797; Homo sapiens cDNA FLJ11381 f1s, clone HEMBA1000501; Homo sapiens cDNA FLJ11381 f1s, clone HE; 8.38
 406621; X57809; Hs.181125; Immunoglobulin lambda locus; Immunoglobulin lambda locus; 8.37
 453914; NM_000507; Hs.574; fructose-1,6-bisphosphatase 1; fructose-1,6-bisphosphatase 1; 8.25
 423198; M81933; Hs.1634; cell division cycle 25A; cell division cycle 25A; 8.19
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit); integrin, beta 2 (antigen CD18 (p95), ly; 8.17
 453968; AA847843; Hs.62711; High mobility group (nonhistone chromosomal) protein 4; High mobility group (nonhistone chromoso; 8.16
 453985; AA4545; Hs.251865; ESTs; ESTs; 8.14
 451108; BE382701; Hs.25960; N-MYC oncogene; N-MYC oncogene; 8.10
 420347; AL033539; Hs.97124; Human DNA sequence from clone RP1-309H15 on chromosome 6p22.1-22.3 Contains a gene similar to HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like)), ESTs, STSs, GSSs and a CpG Is; Human DNA sequence from clone RP1-309H15; 8.03
 415857; AA866115; Hs.127797; Homo sapiens cDNA FLJ11381 f1s, clone HEMBA1000501; Homo sapiens cDNA FLJ11381 f1s, clone HE; 8.02
 425601; AW629485; Hs.140720; GSK-3 binding protein FRAT2; GSK-3 binding protein FRAT2; 7.90
 421016; AA504583; Hs.101047; transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47); transcription factor 3 (E2A immunoglobul; 7.89
 432407; AA221036; ; gb:zr03f12.1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 5' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN ; mRNA sequence; gb:zr03f12.1 Stratagene NT2 neuronal pr; 7.83
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1); neutrophil cytosolic factor 1 (47kD, chr; 7.80
 433228; F28212; Hs.14953; KIAA1491 protein; KIAA1491 protein; 7.73
 446528; AU076640; Hs.15243; nucleolar protein 1 (120kD); nucleolar protein 1 (120kD); 7.71
 447350; Hs.172634; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (HER4); v-erb-a avian erythroblastic leukemia vi; 7.71
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moiety X)-type motif 1; nudix (nucleoside diphosphate linked mot; 7.71
 430253; AK001514; Hs.236844; hypothetical protein FLJ10652; hypothetical protein FLJ10652; 7.70
 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodiesterase 1 (Plasma-cell membrane glycoprotein PC-1); ectonucleotide pyrophosphatase/phosphodi; 7.62
 443537; D13305; Hs.203; cholecystokinin B receptor; cholecystokinin B receptor; 7.57
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; Interferon, gamma-inducible protein 30; 7.55
 410006; AW732308; Hs.57783; eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD); eukaryotic translation initiation factor; 7.53
 430255; AK000703; Hs.323822; Homo sapiens mRNA for KIAA1551 protein, partial cds; Homo sapiens mRNA for KIAA1551 protein; ; 7.52
 411975; A1916058; Hs.144583; 3'UTR of: dead ringer (Drosophila)-like 1; 3'UTR of: dead ringer (Drosophila)-like; 7.50
 439864; A1720078; Hs.291997; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell gr; 7.47
 440773; AA352702; Hs.37747; Homo sapiens, Similar to RIKEN cDNA 2700083B06 gene, clone MGC:4669, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 2700; 7.47
 417705; AW134952; Hs.175220; hypothetical protein FLJ14541; hypothetical protein FLJ14541; 7.47
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor type, C-associated protein; protein tyrosine phosphatase, receptor t; 7.47
 407710; AW022272; Hs.23616; ESTs; ESTs; 7.45
 445093; A1207197; Hs.374149; ESTs; ESTs; 7.41
 418113; A1272141; Hs.83484; SRY (sex determining region Y)-box 4; SRY (sex determining region Y)-box 4; 7.39
 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevisiae, homolog); CDC20 (cell division cycle 20, S. cerevi; 7.37
 429469; M84590; Hs.111801; glycine dehydrogenase (decarboxylating); glycine decarboxylase, glycine cleavage system protein P; glycine dehydrogenase (decarboxylating); ; 7.33
 422726; U11690; Hs.1572; faciolgenital dysplasia (Aarskog-Scott syndrome); faciolgenital dysplasia (Aarskog-Scott sy; 7.33
 430504; H52761; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, com; 7.32
 448981; A1968719; Hs.185387; ESTs; ESTs; 7.28
 413762; AW411479; Hs.846; FK506-binding protein 4 (59kD); FK506-binding protein 4 (59kD); 7.26
 435092; AL137310; Hs.4749; Homo sapiens mRNA; cDNA DKFZp761E13121 (from clone DKFZp761E13121); partial cds; Homo sapiens mRNA; cDNA DKFZp761E13121 ; 7.25
 434414; A1798376; gb:345b07.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ; mRNA sequence; gb:345b07.x1 NCL_CGAP_Ov23 Homo sapiens; 7.24
 428977; AK001404; Hs.194698; cyclin B2; cyclin B2; 7.19
 434274; AA265539; Hs.57783; ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Moderately similar to ALU1_HUMAN A; 7.19
 446700; AW206257; Hs.156326; Human DNA sequence from clone RP11-145L22 on chromosome 6p21.32-22.2. Contains the gene for myelin oligodendrocyte glycoprotein MOG, (part of) the gene for a novel KRAB box containing C2H2 type zinc f; Human DNA sequence from clone RP11-145L2; 7.16
 420524; AB010575; Hs.98547; amiloride-sensitive cation channel 3, testis; amiloride-sensitive cation channel 3, te; 7.15
 439053; BE244588; Hs.6456; chaperonin containing TCP1, subunit 2 (beta); chaperonin containing TCP1, subunit 2 (b; 7.14
 445076; A1206888; Hs.154131; ESTs; ESTs; 7.14
 448588; A1970276; Hs.156905; KIAA1676; KIAA1676; 7.13
 429486; AF155827; Hs.203963; hypothetical protein FLJ10339; hypothetical protein FLJ10339; 7.10
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog (E. coli RacA homolog); RAD51 (S. cerevisiae) homolog (E. coli Ra; 7.04
 433914; AF108138; Hs.112160; Homo sapiens DNA helicase homolog (PIF1) mRNA, partial cds; Homo sapiens DNA helicase homolog (PIF1); 7.02
 413278; BE563085; Hs.833; Interferon-stimulated protein, 15 kDa; Interferon-stimulated protein, 15 kDa; 7.02
 423765; R23858; Hs.143375; Homo sapiens, clone IMAGE:3840937, mRNA, partial cds; Homo sapiens, clone IMAGE:3840937, mRNA; 6.96
 416658; U03272; Hs.79432; fibrillin 2 (congenital contractural arachnodactyly); fibrillin 2 (congenital contractural ara; 6.92
 438450; A1050866; Hs.65853; nodal, mouse, homolog; nodal, mouse, homolog; 6.90
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2); neutrophil cytosolic factor 2 (65kD, chr; 6.90
 444381; BE387335; Hs.283713; hypothetical protein BC014245; hypothetical protein BC014245; 6.89
 447582; BE293520; Hs.18910; prostate cancer overexpressed gene 1; prostate cancer overexpressed gene 1; 6.89
 424779; AL046851; Hs.153053; CD37 antigen; CD37 antigen; 6.89
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding protein; TYRO protein tyrosine kinase binding pro; 6.84
 427298; AA400496; ; ESTs; ESTs; 6.82
 414732; AW410976; Hs.77152; minichromosome maintenance deficient 1 (S. cerevisiae) 7; minichromosome maintenance deficient (S.; 6.81
 424959; NM_005781; Hs.153937; activated p21cdc42Hs kinase; activated p21cdc42Hs kinase; 6.81
 428666; U02330; Hs.172816; neuregulin 1; neuregulin 1; 6.80
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CDC28 protein kinase 2; 6.80
 427521; AW973352; ; ESTs; ESTs; 6.75
 430397; A1924533; Hs.105607; bicarbonate transporter related protein 1; bicarbonate transporter related protein ; 6.75
 427719; A1393122; Hs.134726; ESTs; ESTs; 6.74

- 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; thyroid hormone receptor interactor 13; 6.72
 453348; BE272318; Hs.8595; hypothetical protein FLJ12438; hypothetical protein FLJ12438; 6.71
 446113; AW967553; Hs.323518; Homo sapiens mRNA for FLJ00083 protein, partial cds; Homo sapiens mRNA for FLJ00083 protein, partial cds; 6.70
 445363; NM_005993; Hs.12570; tubulin-specific chaperone d; tubulin-specific chaperone d; 6.70
 433701; AW445023; Hs.15155; ESTs; ESTs; 6.69
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; lysyl oxidase-like 2; 6.63
 441031; A110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen, B beta polypeptide; 6.62
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell gr; 6.59
 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); protein kinase Chk2 (CHEK2); 6.58
 414821; M53835; Hs.77424; Fc fragment of IgG, high affinity Ia, receptor for (CD64); Fc fragment of IgG, high affinity Ia, re; 6.58
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; acid phosphatase 5, tartrate resistant; 6.57
 414161; AA136106; Hs.184852; KIAA1553 protein; KIAA1553 protein; 6.57
 437437; AA226869; Hs.351623; hypothetical protein DKFZp762L0311; hypothetical protein DKFZp762L0311; 6.55
 425769; U72513; Hs.159486; Human RPL13-2 pseudogene mRNA, complete cds; Human RPL13-2 pseudogene mRNA, complete; 6.55
 452363; A1582743; Hs.94953; Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279, mRNA, complete cds; Homo sapiens, Similar to complement comp; 6.55
 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (survivin); baculoviral IAP repeat-containing 5 (sur; 6.51
 409893; AW247090; Hs.57101; minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin); minichromosome maintenance deficient (S.; 6.50
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell receptor; CD2 antigen (p50), sheep red blood cell; 6.49
 417911; AA333387; Hs.82916; chaperonin containing TCP1, subunit 6A (zeta 1); chaperonin containing TCP1, subunit 6A; 6.44
 427747; AW411425; Hs.180655; serine/threonine kinase 12; serine/threonine kinase 12; 6.43
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; SMC4 (structural maintenance of chromoso; 6.42
 430280; AA361258; Hs.237868; Interleukin 7 receptor; Interleukin 7 receptor; 6.42
 432938; T27013; Hs.3132; steroidogenic acute regulatory protein; steroidogenic acute regulatory protein; 6.42
 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; hypothetical protein FLJ10549; 6.40
 427578; A1591305; Hs.169084; ESTs, Highly similar to TUL3_HUMAN TUBBY RELATED PROTEIN 3 [H.sapiens]; ESTs, Highly similar to TUL3_HUMAN TUBBY; 6.40
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypeptide E; small nuclear ribonucleoprotein polypept; 6.39
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cys-X-Cys), member 10; small inducible cytokine subfamily B (Cy; 6.39
 441384; AA447849; Hs.288660; retinoic acid induced 3; retinoic acid induced 3; 6.38
 438915; AA280174; Hs.285681; Williams-Beuren syndrome chromosome region 14; Williams-Beuren syndrome chromosome regi; 6.34
 416773; AK000340; Hs.79828; hypothetical protein FLJ20333; hypothetical protein FLJ20333; 6.34
 451999; AW176401; Hs.27424; DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase); DEAD/H (Asp-Glu-Ala-Asp/His) box polypept; 6.31
 444159; AF116846; Hs.10431; dead ringer (Drosophila)-like 2 (bright and dead ringer); dead ringer (Drosophila)-like 2 (bright; 6.31
 425274; BE281191; Hs.155462; minichromosome maintenance deficient (mis5, S. pombe); minichromosome maintenance deficient (mi; 6.31
 434649; AA738254; Hs.165390; ESTs, Highly similar to A40350 transcription repressor protein YY1 [H.sapiens]; ESTs, Highly similar to A40350 transcrip; 6.30
 420507; AF093408; Hs.98397; A kinase (PRKA) anchor protein 3; A kinase (PRKA) anchor protein 3; 6.30
 415829; AW450198; Hs.163742; ESTs; ESTs; 6.28
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; Fc fragment of IgE, high affinity I, rec; 6.26
 446839; BE091926; Hs.16244; mitotic spindle coiled-coil related protein; mitotic spindle coiled-coil related prot; 6.25
 457465; AW301344; Hs.122908; DNA replication factor; DNA replication factor; 6.25
 428918; AL036867; Hs.2324; protamine 2; protamine 2; 6.24
 443523; AK001575; Hs.9535; hypothetical protein FLJ10713; hypothetical protein FLJ10713; 6.19
 424415; NM_001975; Hs.146580; enolase 2, (gamma, neuronal); enolase 2, (gamma, neuronal); 6.19
 407245; X90568; Hs.172004; titin; titin; 6.18
 458627; AW088642; Hs.97984; SRY (sex determining region Y)-box 17 (SOX17); SRY (sex determining region Y)-box 17 (S; 6.18
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cys-X-Cys), member 11; small inducible cytokine subfamily B (Cy; 6.16
 435099; AC004770; Hs.4756; flap structure-specific endonuclease 1; flap structure-specific endonuclease 1; 6.13
 424308; AW975531; Hs.154443; minichromosome maintenance deficient (S. cerevisiae) 4; minichromosome maintenance deficient (S.; 6.12
 430521; NM_016383; Hs.242183; HOM-TES-85 tumor antigen; HOM-TES-85 tumor antigen; 6.10
 444823; BE262989; Hs.12045; putative protein; putative protein; 6.10
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino acid transporter, y system), member 5; solute carrier family 7 (cationic amino; 6.09
 402260; ; NM_001436; Homo sapiens fibrinogen (FBL), mRNA. transcript (F8A), mRNA; NM_001436; Homo sapiens fibrinogen (FBL); 6.09
 441321; H17182; Hs.7771; B-cell associated protein; B-cell associated protein; 6.05
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevisiae, homolog)-like; CDC45 (cell division cycle 45, S.cerevis; 6.04
 431629; AU077025; Hs.265827; Interferon, alpha-inducible protein (clone IFI-16); interferon, alpha-inducible protein (clo; 6.04
 402678; ; Target Exon; Target Exon; 6.03
 453884; AA355925; Hs.36232; KIAA0186 gene product; KIAA0186 gene product; 6.01
 439753; BE262233; Hs.7423; hypothetical protein from EUROMIMAGE 2168212; hypothetical protein from EUROMIMAGE 2168; 6.01
 420596; NM_002692; Hs.99185; polymerase (DNA directed), epsilon 2; polymerase (DNA directed), epsilon 2; 6.01
 420676; A1434780; Hs.4248; vav 2 oncogene; vav 2 oncogene; 6.00
 418756; AA252254; Hs.226949; ESTs; ESTs; 5.99
 454438; AA224053; Hs.172405; cell division cycle 27; cell division cycle 27; 5.98
 407818; AL021938; Hs.40154; jumonji (mouse) homolog; jumonji (mouse) homolog; 5.98
 413313; NM_002047; Hs.293885; glycyl-tRNA synthetase; glycyl-tRNA synthetase; 5.96
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lysozyme (renal amyloidosis); 5.95
 417777; A1823763; Hs.7055; ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; ESTs, Weakly similar to I78885 serine/th; 5.94
 449569; A1656634; Hs.195389; ESTs; ESTs; 5.92
 436576; AA458213; Hs.77542; ESTs; ESTs; 5.90
 438746; A1885815; Hs.184727; Human melanoma-associated antigen p97 (melanotransferrin) mRNA, 3' flank; Human melanoma-associated antigen p97 (m; 5.89
 420005; AW271106; Hs.133294; ESTs; ESTs; 5.89
 417208; S67773; Hs.81665; v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog; v-kit Hardy-Zuckerman 4 feline sarcoma v; 5.88
 403171; ; C2001472; gi5809678|gb|AAB41848.2| (U64675) sperm membrane protein BS-63 [Homo sapiens]; C2001472; gi5809678|gb|AAB41848.2| (U64; 5.87
 448730; AB032983; Hs.21894; KIAA1157 protein; KIAA1157 protein; 5.87
 406137; ; NM_000179; Homo sapiens mutS (E. coli) homolog 6 (MSH6), mRNA. VERSION NM_000178.1 GI; NM_000179; Homo sapiens mutS (E. coli) h; 5.85
 423787; A1295745; Hs.236204; nuclear pore complex protein; nuclear pore complex protein; 5.85
 425126; N32759; Hs.172944; chorionic gonadotropin, beta polypeptide; chorionic gonadotropin, beta polypeptide; 5.84
 452796; AB011100; Hs.30656; KIAA0528 gene product; KIAA0528 gene product; 5.84
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase); cyclin-dependent kinase inhibitor 3 (CDK; 5.80
 447359; NM_012093; Hs.18268; adenylylate kinase 5; adenylylate kinase 5; 5.79
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; putative G protein-coupled receptor; 5.78
 420297; A1628272; Hs.128757; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU1_HUMAN ALU S; 5.75
 414761; AU077228; Hs.77256; enhancer of zeste (Drosophila) homolog 2; enhancer of zeste (Drosophila) homolog 2; 5.75

- 430287; AW182459; Hs.125759; ESTs, Weakly similar to LEU5_HUMAN LEUKEMIA ASSOCIATED PROTEIN 5 [H.sapiens]; ESTs, Weakly similar to LEU5_HUMAN LEUKE; 5.74
436251; BE515055; Hs.295585; nucleolar protein (KKE/D repeat); nucleolar protein (KKE/D repeat); 5.73
421535; AB002359; Hs.105478; phosphoribosylformylglycinamide synthase (FGAR amidotransferase); phosphoribosylformylglycinamide synth; 5.71
414883; AA926960; Hs.348669; CDC28 protein kinase 1; CDC28 protein kinase 1; 5.69
5 425159; NM_004341; Hs.154868; carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase; carbamoyl-phosphate synthetase 2, aspart; 5.69
401704; ; NM_021195; Homo sapiens claudin 6 (CLDN6), mRNA, VERSION NM_020982.1 G; NM_021195; Homo sapiens claudin 6 (CLDN6); 5.66
425358; AL079658; Hs.338207; FK506 binding protein 12-rapamycin associated protein 1; FK506 binding protein 12-rapamycin assoc; 5.65
402677; ; NM_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA. alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM_000478; Homo sapiens
alkaline phosphat; 5.64
10 409264; NM_014937; Hs.52463; KIAA0966 protein; KIAA0966 protein; 5.63
432185; AA221032; Hs.272838; hypothetical protein FLJ10494; hypothetical protein FLJ10494; 5.63
409012; AL117435; Hs.49725; DKFZP434I216 protein; DKFZP434I216 protein; 5.63
430252; AJ638774; Hs.105328; testes development-related NYD-SP20; testes development-related NYD-SP20; 5.61
419359; AL043202; Hs.90073; chromosome segregation 1 (yeast homolog)-like; chromosome segregation 1 (yeast homolog); 5.61
15 452816; AA131789; Hs.61509; ESTs; ESTs; 5.60
402679; ; NM_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA. alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM_000478; Homo sapiens
alkaline phosphat; 5.59
414291; AJ289619; Hs.13040; G protein-coupled receptor 86; G protein-coupled receptor 86; 5.58
453028; AB006532; Hs.31442; RacQ protein-like 4; RacQ protein-like 4; 5.58
20 453905; NM_002314; Hs.35566; LIM domain kinase 1; LIM domain kinase 1; 5.56
411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associated kinesin); kinesin-like 6 (mitotic centromere-assoc; 5.55
419660; BE280337; Hs.194693; solute carrier family 7 (cationic amino acid transporter, y system), member 7; solute carrier family 7 (cationic amino ; 5.55
446979; AI654443; Hs.197683; ESTs; ESTs; 5.54
424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kinase; lymphocyte-specific protein tyrosine kin; 5.53
25 418962; AA714835; Hs.271863; ESTs; ESTs; 5.53
447388; AW630534; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, comp; 5.52
427247; AW504221; Hs.174103; Integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide); Integrin, alpha L (antigen CD11A (p180);
5.52
30 449322; AI638616; Hs.196566; ESTs; ESTs; 5.51
428450; NM_014791; Hs.184339; KIAA0175 gene product; KIAA0175 gene product; 5.51
415141; AA189099; Hs.268171; ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar
to ALU7_HUMAN ALU S; 5.48
454048; H05626; Hs.6921; ESTs; ESTs; 5.46
35 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; interleukin 1 receptor antagonist; 5.45
434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fts, clone HEMBB1001304; Homo sapiens cDNA FLJ11980 fts, clone HE; 5.44
414334; AA824298; Hs.21331; hypothetical protein FLJ10036; hypothetical protein FLJ10036; 5.44
452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; CDC7 (cell division cycle 7, S. cerevisiae; 5.44
438564; AA381553; Hs.198253; major histocompatibility complex, class II, DQ alpha 1; major histocompatibility complex, class ; 5.44
427668; AA288760; Hs.180191; hypothetical protein FLJ14904; hypothetical protein FLJ14904; 5.43
40 449437; AT702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fts, clone KAT05581; Homo sapiens cDNA: FLJ22902 fts, clone K; 5.41
453633; AA357001; Hs.34045; hypothetical protein FLJ20764; hypothetical protein FLJ20764; 5.40
450746; D82673; Hs.278589; general transcription factor II, t; general transcription factor II, t; 5.40
425966; NM_001761; Hs.1973; cyclin F; cyclin F; 5.39
418134; AA397769; Hs.86617; ESTs; ESTs; 5.38
45 432141; BE410964; Hs.272736; nuclear receptor binding protein; nuclear receptor binding protein; 5.37
417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, member 3; nuclear receptor subfamily 1, group H, m; 5.36
428329; AA426091; Hs.98453; ESTs, Moderately similar to R27328 2 [H.sapiens]; ESTs, Moderately similar to R27328 2 [H.; 5.35
406811; U82979; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor, ; 5.34
50 415819; AU077330; Hs.360791; transcription elongation factor A (SII), 1; transcription elongation factor A (SII); 5.33
448133; AA723157; Hs.73769; folate receptor 1 (adult); folate receptor 1 (adult); 5.33
424762; AL119442; Hs.183884; eukaryotic translation initiation factor 4 gamma, 2; eukaryotic translation initiation factor; 5.32
421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypept; 5.32
429271; AF039850; Hs.198515; dead ringer (Drosophila)-like 1; dead ringer (Drosophila)-like 1; 5.32
55 456373; BE247706; Hs.86693; membrane-spanning 4-domains, subfamily A, member 2 (CD20 antigen); membrane-spanning 4-domains, subfamily A; 5.30
414907; X90725; Hs.77597; polo (Drosophila)-like kinase; polo (Drosophila)-like kinase; 5.30
422997; BE018212; Hs.122908; DNA replication factor; DNA replication factor; 5.29
440014; AW960782; Hs.6856; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; ash2 (absent, small, or homeotic, Drosop; 5.28
418399; AF131781; Hs.84753; hypothetical protein FLJ12442; hypothetical protein FLJ12442; 5.26
60 416178; AB08527; Hs.192822; serologically defined breast cancer antigen NY-BR-81; serologically defined breast cancer anti; 5.21
450377; AB033091; Hs.355925; KIAA1265 protein; KIAA1265 protein; 5.20
409670; AJ368109; Hs.375604; KIAA1856 protein; KIAA1856 protein; 5.20
429083; Y09397; Hs.227817; BCL2-related protein A1; BCL2-related protein A1; 5.20
449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; chemokine (C-C motif) receptor 5; 5.20
65 408908; BE296227; Hs.250822; serine/threonine kinase 15; serine/threonine kinase 15; 5.19
429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD); lymphocyte cytosolic protein 2 (SH2 doma; 5.19
438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, member 3; nuclear receptor subfamily 1, group I, m; 5.16
437623; D63880; Hs.5719; chromosome condensation-related SMC-associated protein 1; chromosome condensation-related SMC-assoc; 5.15
448181; AF272833; Hs.279763; hypothetical protein FLJ10504; hypothetical protein FLJ10504; 5.15
70 436540; BE397032; Hs.14468; hypothetical protein MGC14226; hypothetical protein MGC14226; 5.14
422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor type, C; protein tyrosine phosphatase, receptor t; 5.14
426752; X69490; Hs.172004; tlin; tlin; 5.13
415007; BE244332; Hs.77770; adaptor-related protein complex 3, mu 2 subunit; adaptor-related protein complex 3, mu 2; 5.13
400263; ; Hs.75309; Eos Control; Eos Control; 5.13
75 437099; N77793; Hs.48659; ESTs, Highly similar to S14458 laminin alpha-1 chain precursor [H.sapiens]; ESTs, Highly similar to S14458 laminin alpha; 5.12
427209; H06509; Hs.92423; KIAA1566 protein; KIAA1566 protein; 5.10
407347; AA829847; ; gbcd40d07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1370413 3' similar to contains Alu repetitive element, mRNA sequence.; gbcd40d07.s1
NCL_CGAP_GCB1 Homo sapiens; 5.10
80 458933; AI638429; Hs.24763; RAN binding protein 1; RAN binding protein 1; 5.10
450431; AW136797; Hs.266041; ESTs; ESTs; 5.09
434608; AA805443; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 5.08
410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-receptor type 6; protein tyrosine phosphatase, non-recept; 5.08
417829; R27219; Hs.74647; Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds; Human T-cell receptor active alpha-chain; 5.05
417273; AA648459; Hs.335951; hypothetical protein AF301222; hypothetical protein AF301222; 5.05

- 447321; AW271217; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 5.03
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; collagen, type XI, alpha 1; 5.03
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; Musashi (Drosophila) homolog 1; 5.02
 433592; NM_004642; Hs.3436; deleted in oral cancer (mouse, homolog) 1; deleted in oral cancer (mouse, homolog); 5.02
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort 1, Importin alpha 1); karyopherin alpha 2 (RAG cohort 1, impor; 5.00
 425237; U07695; Hs.155227; EphB4; EphB4; 5.00
 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); transferrin receptor (p90, CD71); 4.99
 402145; ; Target Exon; Target Exon; 4.99
 432126; AA865239; Hs.37196; ESTs; ESTs; 4.99
 408279; AF216965; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, com; 4.98
 419525; T79257; Hs.1259; asialoglycoprotein receptor 2; asialoglycoprotein receptor 2; 4.97
 424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; ligase I, DNA, ATP-dependent; 4.97
 427667; AK001279; Hs.180171; Homo sapiens cDNA FLJ10417 fis, clone NT2RP1000112; Homo sapiens cDNA FLJ10417 fis, clone NT; 4.96
 457313; AF047002; Hs.241520; transcriptional coactivator; transcriptional coactivator; 4.96
 448569; BE382657; Hs.21486; signal transducer and activator of transcription 1, 91kD; signal transducer and activator of trans; 4.94
 426427; M86699; Hs.169840; TTK protein kinase; TTK protein kinase; 4.91
 440129; AA865818; Hs.369523; ESTs, Weakly similar to S71886 Ste20-like protein kinase [H.sapiens]; ESTs, Weakly similar to S71886 Ste20-like; 4.91
 453922; AF053306; Hs.35708; budding uninhibited by benzimidazoles 1 (yeast homolog), beta; budding uninhibited by benzimidazoles 1; 4.90
 435602; AF217515; Hs.283532; uncharacterized bone marrow protein BM039; uncharacterized bone marrow protein BM03; 4.89
 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; chemokine (C-C motif) receptor 1; 4.88
 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to ras-related protein RAB17; hypothetical protein FLJ12538 similar to; 4.88
 437162; AW005505; Hs.5464; thyroid hormone receptor coactivating protein; thyroid hormone receptor coactivating pr; 4.87
 41600; AA939347; Hs.127223; Homo sapiens cysteine knot protein (ZS/GS1) mRNA, complete cds; Homo sapiens cysteine knot protein (ZS/G; 4.87
 421350; AW301608; Hs.278188; ESTs, Moderately similar to IS4374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to IS4374 gene; 4.87
 409093; BE243834; Hs.50441; CGI-04 protein; CGI-04 protein; 4.86
 424304; NM_001395; Hs.144879; dual specificity phosphatase 9; dual specificity phosphatase 9; 4.86
 437696; Z83844; Hs.5790; hypothetical protein dJ37E16.5; hypothetical protein dJ37E16.5; 4.86
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase transporters), member 1; solute carrier family 23 (nucleobase tra; 4.84
 416445; AL043004; Hs.79337; KIAA0135 protein; KIAA0135 protein; 4.83
 448939; BE267795; Hs.22595; hypothetical protein FLJ10637; hypothetical protein FLJ10637; 4.82
 413566; AW604451; Hs.285814; sprouty (Drosophila) homolog 4; sprouty (Drosophila) homolog 4; 4.82
 424081; NM_006413; Hs.139120; ribonuclease P (30kD); ribonuclease P (30kD); 4.81
 425474; Z48054; Hs.158084; peroxisome receptor 1; peroxisome receptor 1; 4.81
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (glycosylation-inhibiting factor); macrophage migration inhibitory factor (gly; 4.81
 422689; AW856655; Hs.299797; gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapiens cDNA, mRNA sequence; gb:RC3-CT0297-290100-013-d03 CT0297 Homo; 4.80
 409101; NM_004297; Hs.50612; guanine nucleotide binding protein (G protein), alpha 14; guanine nucleotide binding protein (G pr; 4.79
 412760; AW379030; Hs.41324; ESTs; ESTs; 4.79
 447250; AJ878909; Hs.17883; protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; protein phosphatase 1G (formerly 2C), ma; 4.79
 429345; R11141; Hs.199695; hypothetical protein; hypothetical protein; 4.78
 448950; AF286887; Hs.9275; CGI-152 protein; CGI-152 protein; 4.78
 412926; AJ879076; Hs.75061; macrophage myristoylated alanine-rich C kinase substrate; macrophage myristoylated alanine-rich C; 4.78
 412641; M16660; Hs.74335; heat shock 90kD protein 1, beta; heat shock 90kD protein 1, beta; 4.76
 420261; AW206093; Hs.748; fibroblast growth factor receptor 3 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 3 (fms; 4.76
 421905; AI660247; Hs.32699; ESTs, Weakly similar to LIV-1 protein [H.sapiens]; ESTs, Weakly similar to LIV-1 protein [H; 4.75
 413880; AI660842; Hs.110915; interleukin 22 receptor; interleukin 22 receptor; 4.75
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related kinase 2 (NEK2); NIMA (never in mitosis gene a)-related k; 4.74
 418355; L42563; Hs.1165; ATPase, H⁺ transporting, nongastric, alpha polypeptide; ATPase, H⁺ transporting, nongastric, alp; 4.74
 435905; AW997484; Hs.5003; KIAA0456 protein; KIAA0456 protein; 4.74
 428024; Z29057; Hs.22336; NIMA (never in mitosis gene a)-related kinase 3; NIMA (never in mitosis gene a)-related k; 4.74
 421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; protein kinase C substrate 80K-H; 4.72
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ryanodine receptor 1 (skeletal); 4.72
 437296; AA350994; Hs.20281; KIAA1700; KIAA1700; 4.70
 450142; AW207469; Hs.24485; chondroitin sulfate proteoglycan 6 (barnacan); chondroitin sulfate proteoglycan 6 (barnac; 4.70
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism); fibroblast growth factor receptor 3 (ach; 4.69
 449475; AJ348027; Hs.129826; hypothetical protein PP1057; hypothetical protein PP1057; 4.69
 420062; AW111096; Hs.94785; TGF(beta)-induced transcription factor 2; TGF(beta)-induced transcription factor 2; 4.69
 429336; AB005038; Hs.199270; cytochrome P450, subfamily XXVIB (25-hydroxyvitamin D-1-alpha-hydroxylase), polypeptide 1; cytochrome P450, subfamily XXVIB (25-hy; 4.69
 436856; AI469355; Hs.127310; ESTs; ESTs; 4.68
 406937; U14622; ; gb:Human transketolase-like protein gene, partial cds.; gb:Human transketolase-like protein gene; 4.67
 411295; BE207307; Hs.10114; growth suppressor 1; growth suppressor 1; 4.67
 426726; AA488915; Hs.171955; trophinin associated protein (tastin); trophinin associated protein (tastin); 4.67
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 non-catalytic subunit; protein kinase, AMP-activated, beta 2 no; 4.67
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; melanoma cell adhesion molecule; 4.66
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; hypothetical protein FLJ20371; 4.65
 443623; AA345519; Hs.9641; complement component 1, q subcomponent, alpha polypeptide; complement component 1, q subcomponent; 4.65
 441595; AW206035; Hs.356457; ESTs; ESTs; 4.64
 423419; R55336; Hs.23539; ESTs; ESTs; 4.64
 415724; NM_003580; Hs.78687; neutral sphingomyelinase (N-SMase) activation associated factor; neutral sphingomyelinase (N-SMase) activ; 4.63
 435045; BE297155; Hs.143698; ESTs; ESTs; 4.62
 424441; X14850; Hs.147097; H2A histone family, member X; H2A histone family, member X; 4.62
 414972; BE263782; Hs.77695; KIAA0008 gene product; KIAA0008 gene product; 4.62
 436885; W28661; Hs.5288; Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245); Homo sapiens mRNA; cDNA DKFZp434M245 (fr; 4.62
 449515; AI653378; Hs.302012; ESTs; ESTs; 4.61
 425998; AU076629; Hs.165950; fibroblast growth factor receptor 4; fibroblast growth factor receptor 4; 4.61
 420027; AF009746; Hs.94395; ATP-binding cassette, sub-family D (ALD), member 4; ATP-binding cassette, sub-family D (ALD); 4.61
 436469; AK001455; Hs.51598; Down syndrome critical region gene 2; Down syndrome critical region gene 2; 4.61
 413441; AJ929374; Hs.75367; Src-like adapter; Src-like adapter; 4.60
 456847; AJ360456; Hs.86088; ESTs; ESTs; 4.58
 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; thymidine kinase 1, soluble; 4.57
 426935; NM_000088; Hs.172928; collagen, type I, alpha 1; collagen, type I, alpha 1; 4.57
 428782; X12830; Hs.193400; interleukin 6 receptor; interleukin 6 receptor; 4.56
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; splicing factor, arginine/serine-rich 5; 4.56
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L ORF; similar to vaccinia virus HindIII K4L OR; 4.55

- 443068; AI188710; Hs.374480; ESTs; ESTs; 4.55
 441607; NM_005010; Hs.7912; neuronal cell adhesion molecule; neuronal cell adhesion molecule; 4.54
 453227; AW135862; Hs.243991; ESTs; ESTs; 4.52
 438459; T49300; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; Homo sapiens cDNA FLJ13655 fis, clone PL; 4.51
 422565; BE259035; Hs.118400; singed (Drosophila)-like (sea urchin fascin homolog like); singed (Drosophila)-like (sea urchin fas); 4.51
 453613; F06838; Hs.374476; ESTs; ESTs; 4.50
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein); stress-induced-phosphoprotein 1 (Hsp70/H); 4.50
 412507; L36645; Hs.73964; EphA4; EphA4; 4.50
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; hemopoietic cell kinase; 4.49
 413431; AW246428; Hs.75355; ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13); ubiquitin-conjugating enzyme E2N (homolo); 4.49
 406547; ; Target Exon; Target Exon; 4.49
 443216; W80487; Hs.324521; hypothetical protein DC50; hypothetical protein DC50; 4.48
 417497; AW402482; Hs.82212; CD53 antigen; CD53 antigen; 4.47
 448595; AB014544; Hs.21572; KIAA0644 gene product; KIAA0644 gene product; 4.47
 445350; AF052112; Hs.12540; lysophospholipase I; lysophospholipase I; 4.46
 446236; NM_006293; Hs.301; TYRO3 protein tyrosine kinase; TYRO3 protein tyrosine kinase; 4.46
 429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; smoothened (Drosophila) homolog; 4.46
 420340; NM_000734; Hs.97087; CD32 antigen, zeta polypeptide (TIT3 complex); CD32 antigen, zeta polypeptide (TIT3 com); 4.46
 413426; U88837; Hs.75354; GCN1 (general control of amino-acid synthesis 1, yeast)-like 1; GCN1 (general control of amino-acid synt); 4.44
 421819; NM_013403; Hs.108665; zinedin; zinedin; 4.44
 409512; AW979187; Hs.293591; melanoma differentiation associated protein-5; melanoma differentiation associated prot; 4.44
 428995; AW004975; Hs.194716; MAD (mothers against decapentaplegic, Drosophila) homolog interacting protein, receptor activation anchor; MAD (mothers against decapentaplegic, Drosophila) homolog interacting protein, receptor activation anchor; 4.43
 434551; BE387162; Hs.280858; ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 [Hsapiens]; ESTs, Highly similar to A35661 DNA excis; 4.43
 418295; AW970043; Hs.238039; hypothetical protein FLJ11090; hypothetical protein FLJ11090; 4.42
 409243; AB037761; Hs.51743; KIAA1340 protein; KIAA1340 protein; 4.42
 437103; AW139408; Hs.152940; ESTs; ESTs; 4.42
 413186; AU077141; Hs.374548; solute carrier family 16 (monocarboxylic acid transporters), member 1; solute carrier family 16 (monocarboxylic); 4.42
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 4.40
 424078; AB006625; Hs.139033; paternally expressed 3; paternally expressed 3; 4.39
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2; HMT1 (hnRNP methyltransferase, S. cerevi); 4.37
 410134; U68140; Hs.58927; nuclear VCP-like; nuclear VCP-like; 4.36
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; membrane-spanning 4-domains, subfamily A; 4.35
 400440; X83957; Hs.83870; nebulin; nebulin; 4.35
 437218; AL117497; Hs.58185; ESTs, Weakly similar to T42727 proliferation potential-related protein - mouse [M.musculus]; ESTs, Weakly similar to T42727 prolifera; 4.34
 430478; NM_014349; Hs.241535; apolipoprotein L 3; apolipoprotein L 3; 4.34
 432744; AA988835; Hs.38664; ESTs; ESTs; 4.33
 423173; AA442655; Hs.124942; protein phosphatase 2A 48 kDa regulatory subunit; protein phosphatase 2A 48 kDa regulatory; 4.33
 415995; NM_004573; Hs.355888; phospholipase C, beta 2; phospholipase C, beta 2; 4.33
 408728; AL137379; Hs.47125; hypothetical protein FLJ13912; hypothetical protein FLJ13912; 4.30
 431222; X56777; Hs.273790; zona pellucida glycoprotein 3A (sperm receptor); zona pellucida glycoprotein 3A (sperm re); 4.30
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily, member 7; tumor necrosis factor receptor superfam; 4.29
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mRNA, 3'UTR; Human proteinase activated receptor-2 mR; 4.29
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, receptor for (CD16); Fc fragment of IgG, low affinity IIb, r; 4.29
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; pyruvate dehydrogenase phosphatase; 4.29
 412314; AA825247; Hs.356084; downstream of: G protein-coupled receptor 27 (GPR27) (SREB1); downstream of: G protein-coupled receptor; 4.28
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor type, U; protein tyrosine phosphatase, receptor t; 4.28
 426108; AA622037; Hs.166468; programmed cell death 5; programmed cell death 5; 4.28
 428820; AA436187; Hs.172631; Integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide); Integrin, alpha M (complement component; 4.27
 437908; AJ082424; Hs.351043; ESTs; ESTs; 4.27
 444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-STYX; map kinase phosphatase-like protein MK-S; 4.27
 429002; AW248439; Hs.2340; junction plakoglobin; junction plakoglobin; 4.26
 439334; AI148976; Hs.112062; ESTs; ESTs; 4.26
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan receptor 2; receptor tyrosine kinase-like orphan rec; 4.25
 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; interleukin 2 receptor, beta; 4.25
 453648; W21493; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 4.24
 447200; BE543145; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 4.24
 447528; AJ612027; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, comp; 4.23
 452721; AJ269523; Hs.301871; solute carrier family 37 (glycerol-3-phosphate transporter), member 1; solute carrier family 37 (glycerol-3-pho); 4.22
 449810; AB008681; Hs.23994; activin A receptor, type IIB; activin A receptor, type IIB; 4.22
 447198; D61523; Hs.283435; ESTs; ESTs; 4.22
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated alpha); CD79A antigen (immunoglobulin-associated); 4.22
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 145kD; inositol polyphosphate-5-phosphatase, 14; 4.22
 422605; H16646; Hs.118666; hypothetical protein PP591; hypothetical protein PP591; 4.21
 444535; AF011466; Hs.122575; EDG-4 (endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4); EDG-4(endothelial differentiation, lys; 4.21
 417088; M54915; Hs.81170; pim-1 oncogene; pim-1 oncogene; 4.20
 421707; NM_014921; Hs.107054; lectomedin-2; lectomedin-2; 4.20
 408717; AF045458; Hs.47061; unc-51 (C. elegans)-like kinase 1; unc-51 (C. elegans)-like kinase 1; 4.20
 438465; W57578; Hs.378718; RAB7, member RAS oncogene family; RAB7, member RAS oncogene family; 4.19
 419452; U33633; Hs.90572; PTK7 protein tyrosine kinase 7; PTK7 protein tyrosine kinase 7; 4.18
 418755; Y14443; Hs.88219; zinc finger protein 200; zinc finger protein 200; 4.18
 417212; AW952823; Hs.351547; NS1-binding protein; NS1-binding protein; 4.17
 413686; AJ469213; Hs.71404; ESTs; ESTs; 4.17
 419344; U94905; Hs.277445; diacylglycerol kinase, zeta (104kD); diacylglycerol kinase, zeta (104kD); 4.16
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fusin); chemokine (C-X-C motif), receptor 4 (fus); 4.16
 408482; NM_000676; Hs.45743; adenosine A2b receptor; adenosine A2b receptor; 4.16
 422391; D63479; Hs.115907; diacylglycerol kinase, delta (130kD); diacylglycerol kinase, delta (130kD); 4.15
 409421; AA199883; Hs.67624; ESTs; ESTs; 4.15
 415938; BE383507; Hs.78921; A kinase (PRKA) anchor protein 1; A kinase (PRKA) anchor protein 1; 4.14
 415198; AW009480; Hs.943; natural killer cell transcript 4; natural killer cell transcript 4; 4.14
 424685; W21223; Hs.151734; nuclear transport factor 2 (placental protein 15); nuclear transport factor 2 (placental pr; 4.13

- 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to M; cell division cycle 2, G1 to S and G2 to M; 4.13
 423728; AW891294; Hs.132136; solute carrier family 4, sodium bicarbonate cotransporter, member 8; solute carrier family 4, sodium bicarbonate; 4.13
 433435; BE545277; Hs.340959; Ts translation elongation factor, mitochondrial; Ts translation elongation factor, mitochondrial; 4.13
 420253; A1656055; Hs.96200; neighbor of A-kinase anchoring protein 95; neighbor of A-kinase anchoring protein 9; 4.12
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 2489 expressed sequence; DNA segment on chromosome 12 (unique) 24; 4.12
 400205; Hs.81848; NM_006265; Homo sapiens RAD21 (S. pombe) homolog (RAD21), mRNA. (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), mRNA; NM_006265; Homo sapiens RAD21 (S. pombe); 4.12
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic polypeptide; protein kinase, DNA-activated, catalytic; 4.11
 419607; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; Homo sapiens clone 23783 mRNA sequence; 4.10
 459035; AW291109; Hs.332563; ESTs, Weakly similar to T31611 hypothetical protein Y50E8A.g - *Caenorhabditis elegans* [C.elegans]; ESTs, Weakly similar to T31611 hypothetical protein; 4.10
 432512; NM_003284; Hs.3017; transition protein 1 (during histone to protamine replacement); transition protein 1 (during histone to protamine replacement); 4.10
 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 1177 expressed sequence; DNA segment on chromosome 19 (unique) 11; 4.09
 423804; AW403448; Hs.1706; interferon-stimulated transcription factor 3, gamma (48kD); interferon-stimulated transcription factor 3, gamma (48kD); 4.09
 413745; AW247252; Hs.75514; nucleoside phosphorylase; nucleoside phosphorylase; 4.09
 442091; AW770493; Hs.182874; guanine nucleotide binding protein (G protein) alpha 12; guanine nucleotide binding protein (G protein) alpha 12; 4.09
 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease (APEX nuclease)-like 2 protein; apurinic/apyrimidinic endonuclease (APEX); 4.08
 421859; AA356620; Hs.108947; KIAA0050 gene product; KIAA0050 gene product; 4.08
 432841; M93425; Hs.62; protein tyrosine phosphatase, non-receptor type 12; protein tyrosine phosphatase, non-receptor type 12; 4.08
 452059; AB028949; Hs.183994; KIAA1026 protein; KIAA1026 protein; 4.08
 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-related subfamily, beta member 2; potassium voltage-gated channel, shaker-related; 4.07
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic acid transporters), member 3; solute carrier family 16 (monocarboxylic acid transporters), member 3; 4.07
 424517; A1539443; Hs.137447; Homo sapiens cDNA FLJ12169 f1s, clone MAMMA100643; Homo sapiens cDNA FLJ12169 f1s, clone MAMMA100643; 4.07
 434224; AA380731; Hs.84; interleukin 2 receptor, gamma (severe combined immunodeficiency); interleukin 2 receptor, gamma (severe combined immunodeficiency); 4.06
 446791; A1632278; Hs.195922; ESTs; ESTs; 4.06
 432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catalytic subunit; protein phosphatase 4 (formerly X), catalytic; 4.06
 431194; D43704; Hs.250712; calcium channel, voltage-dependent, beta 3 subunit; calcium channel, voltage-dependent, beta 3 subunit; 4.06
 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma); phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma); 4.06
 425923; NM_005028; Hs.162808; phosphoinositide-3-kinase, catalytic, delta polypeptide; phosphoinositide-3-kinase, catalytic, delta polypeptide; 4.05
 408692; AL040127; Hs.34074; dipeptidylpeptidase VI; dipeptidylpeptidase VI; 4.04
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrate 1; hematopoietic cell-specific Lyn substrate 1; 4.04
 439176; A1446444; Hs.190394; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; 4.04
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule 1); selectin L (lymphocyte adhesion molecule 1); 4.04
 410068; A1633888; Hs.58435; FYN-binding protein (FYN-120/130); FYN-binding protein (FYN-120/130); 4.03
 410639; BE269047; Hs.65234; hypothetical protein FLJ20596; hypothetical protein FLJ20596; 4.03
 427716; L38951; Hs.180446; karyopherin (importin) beta 1; karyopherin (importin) beta 1; 4.03
 451050; AW937420; Hs.351869; ESTs; ESTs; 4.02
 449667; AB023227; Hs.23860; KIAA1010 protein; KIAA1010 protein; 4.02
 448499; BE613280; Hs.77550; p53-regulated DDA3; p53-regulated DDA3; 4.01
 437527; A1241019; Hs.145644; ESTs; ESTs; 4.01
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase (NAD dependent), methylenetetrahydrofolate dehydrogenase (NAD dependent); methylene tetrahydrofolate dehydrogenase (NAD dependent), methylenetetrahydrofolate dehydrogenase (NAD dependent); 4.00
 451931; AK000208; Hs.27267; Homo sapiens cDNA FLJ20201 f1s, clone COLF1210; Homo sapiens cDNA FLJ20201 f1s, clone COLF1210; 4.00
 412939; AW411491; Hs.75059; eukaryotic translation elongation factor 1 gamma; eukaryotic translation elongation factor 1 gamma; 4.00
 409581; U66243; Hs.55039; mitogen-activated protein kinase 12; mitogen-activated protein kinase 12; 3.99
 433577; AW007080; Hs.284192; ESTs; ESTs; 3.99
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase, isoform 1b, gamma subunit (29kD); platelet-activating factor acetylhydrolase, isoform 1b, gamma subunit (29kD); 3.99
 418629; BE247550; Hs.88659; growth factor receptor-bound protein 7; growth factor receptor-bound protein 7; 3.99
 448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin, gamma 1; 3.98
 402398; ; ; C19000263; gi108023[gb]AAC15755.1 [AC004659] BC62940.2 [Homo sapiens] [156335; C19000263; gi108023[gb]AAC15755.1 [AC004659] BC62940.2 [Homo sapiens] [156335; 3.97
 408414; A114688; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; 3.97
 415012; NM_004383; Hs.77793; c-src tyrosine kinase; c-src tyrosine kinase; 3.97
 416084; L16991; Hs.79008; deoxythymidylate kinase (thymidylate kinase); deoxythymidylate kinase (thymidylate kinase); 3.95
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; 3.95
 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine protease; caspase 8, apoptosis-related cysteine protease; 3.95
 430770; AA765694; Hs.123296; ESTs; ESTs; 3.94
 442994; A1026718; Hs.16954; ESTs; ESTs; 3.94
 420333; AJ001383; Hs.97084; lymphocyte antigen 94 (mouse) homolog (activating NK-receptor, NK-p46); lymphocyte antigen 94 (mouse) homolog (activating NK-receptor, NK-p46); 3.94
 438456; AA913381; Hs.279763; ESTs; ESTs; 3.94
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) expressed in; non-metastatic cells 1, protein (NM23A) expressed in; 3.93
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; cyclin-dependent kinase 4; 3.93
 424829; NM_002507; Hs.1827; nerve growth factor receptor (TNFR superfamily, member 16); nerve growth factor receptor (TNFR superfamily, member 16); 3.93
 447574; AF162666; Hs.18895; tousel-like kinase 1; tousel-like kinase 1; 3.93
 425797; AF002986; Hs.159545; platelet activating receptor homolog; platelet activating receptor homolog; 3.93
 421910; NM_014586; Hs.109437; hormonally upregulated neu tumor-associated kinase; hormonally upregulated neu tumor-associated kinase; 3.92
 413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase 1; IMP (inosine monophosphate) dehydrogenase 1; 3.92
 434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 f1s, clone NT2RP4002075; Homo sapiens cDNA FLJ13221 f1s, clone NT2RP4002075; 3.92
 400262; ; Hs.75309; Eos Control; Eos Control; 3.90
 424977; AA349289; Hs.100057; Homo sapiens cDNA: FLJ22902 f1s, clone KAT05581; Homo sapiens cDNA: FLJ22902 f1s, clone KAT05581; 3.90
 409799; D11928; Hs.76846; phosphoserine phosphatase-like; phosphoserine phosphatase-like; 3.90
 435206; A1432364; Hs.160594; ESTs; ESTs; 3.90
 439863; BE547830; Hs.375208; paired immunoglobulin-like receptor beta; paired immunoglobulin-like receptor beta; 3.90
 413627; BE182082; Hs.246973; intron of Bicaudal D homolog 1; intron of Bicaudal D homolog 1; 3.90
 426265; AA421069; Hs.97896; ESTs; ESTs; 3.89
 451063; AW163702; Hs.25911; HLA-B associated transcript-2; HLA-B associated transcript-2; 3.89
 407013; U35637; Hs.83870; gb:Human nebulin mRNA, partial cds; gb:Human nebulin mRNA, partial cds; 3.89
 437239; AW503395; Hs.5541; ATPase, Ca transporting, ubiquitous; ATPase, Ca transporting, ubiquitous; 3.88
 400261; ; Hs.1802; Eos Control; Eos Control; 3.88
 450447; AF212223; Hs.25010; hypothetical protein P15-2; hypothetical protein P15-2; 3.88
 422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); 3.87
 414251; AL042306; Hs.97689; VASA protein; VASA protein; 3.87
 417767; BE242241; Hs.82542; acylxyacyl hydrolase (neutrophil); acylxyacyl hydrolase (neutrophil); 3.87
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor, beta polypeptide; platelet-derived growth factor receptor, beta polypeptide; 3.87

- 444099; D87432; Hs.10315; solute carrier family 7 (cationic amino acid transporter, y system), member 6; solute carrier family 7 (cationic amino ; 3.86
 419596; BE378320; Hs.91448; MKP-1 like protein tyrosine phosphatase; MKP-1 like protein tyrosine phosphatase; 3.86
 427022; AW245839; Hs.173255; small nuclear ribonucleoprotein polypeptide A; small nuclear ribonucleoprotein polypeptide; 3.86
 443661; AA336609; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.85
 408056; AA312329; Hs.42331; ephrin-A4; ephrin-A4; 3.85
 410552; X66945; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms); 3.85
 450778; U81375; Hs.25450; solute carrier family 29 (nucleoside transporters), member 1; solute carrier family 29 (nucleoside tr; 3.85
 416978; T85295; Hs.268605; ESTs; ESTs; 3.84
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory subunit 1 (p35); cyclin-dependent kinase 5, regulatory su; 3.84
 442980; AA857025; Hs.8878; kinesin-like 1; kinesin-like 1; 3.84
 447232; AW499834; Hs.327; Interleukin 10 receptor, alpha; interleukin 10 receptor, alpha; 3.84
 434689; AF154115; Hs.4076; CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1; CTD (carboxy-terminal domain, RNA polyme; 3.83
 432539; AL138169; Hs.278378; karyopherin beta 2b, transportin; karyopherin beta 2b, transportin; 3.83
 415684; D59356; Hs.374480; sorbitol dehydrogenase; sorbitol dehydrogenase; 3.83
 451598; N29102; Hs.79658; ESTs; ESTs; 3.82
 449433; A1672096; Hs.9012; ESTs, Weakly similar to S26650 DNA-binding protein 5 [H.sapiens]; ESTs, Weakly similar to S26650 DNA-bind; 3.82
 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.81
 435160; AB002374; Hs.4791; KIAA0376 protein; KIAA0376 protein; 3.80
 443402; U77846; Hs.9295; elastin (supravalvular aortic stenosis, Williams-Beuren syndrome); elastin (supravalvular aortic stenosis, ; 3.80
 422753; A1928995; Hs.1575; small nuclear ribonucleoprotein D3 polypeptide (18kD); small nuclear ribonucleoprotein D3 polyp; 3.79
 421508; NM_004833; Hs.105115; absent in melanoma 2; absent in melanoma 2; 3.79
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; phosphatidylserine synthase 1; 3.79
 428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone LNG15735; Homo sapiens cDNA: FLJ23602 fis, clone L; 3.79
 421654; AW163267; Hs.106469; suppressor of var1 (S.cerevisiae) 3-like 1; suppressor of var1 (S.cerevisiae) 3-like; 3.79
 439568; A1091277; Hs.302634; frizzled (Drosophila) homolog 8; frizzled (Drosophila) homolog 8; 3.79
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; cytochrome b-245, alpha polypeptide; 3.78
 429170; NM_0010394; Hs.2359; dual specificity phosphatase 4; dual specificity phosphatase 4; 3.78
 425354; U62027; Hs.155935; complement component 3a receptor 1; complement component 3a receptor 1; 3.78
 423909; AJ223183; Hs.135194; immunoglobulin superfamily, member 6; immunoglobulin superfamily, member 6; 3.78
 429687; A1875749; Hs.211608; nucleoporin 153kD; nucleoporin 153kD; 3.77
 414177; A1351355; Hs.356303; uncharacterized hypothalamus protein HARP11; uncharacterized hypothalamus protein HAR; 3.77
 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; dual specificity phosphatase 5; 3.77
 445817; NM_003642; Hs.13340; histone acetyltransferase 1; histone acetyltransferase 1; 3.77
 410422; AL042014; Hs.63348; Homo sapiens, clone MGC:15203, mRNA, complete cds; Homo sapiens, clone MGC:15203, mRNA, com; 3.76
 412146; M92444; Hs.73722; APEX nuclease (multifunctional DNA repair enzyme); APEX nuclease (multifunctional DNA repair; 3.76
 413011; AW068115; Hs.821; biglycan; biglycan; 3.76
 428157; A1738719; Hs.198427; hexokinase 2; hexokinase 2; 3.76
 400288; X06256; Hs.149609; Integrin, alpha 5 (fibronectin receptor, alpha polypeptide); Integrin, alpha 5 (fibronectin receptor, ; 3.75
 427378; BE515037; Hs.177556; melanoma antigen, family D, 1; melanoma antigen, family D, 1; 3.75
 405484; ; C3002124*gi|12737280|ref|XP_006682.2| keratin 18 [Homo sapiens][6633; C3002124*gi|12737280|ref|XP_006682.2| k; 3.75
 450999; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; splicing factor 3b, subunit 4, 49kD; 3.75
 432460; H12912; Hs.274691; adenylate kinase 3; adenylate kinase 3; 3.75
 428816; AA004986; Hs.193852; ATP-binding cassette, sub-family C (CFTR/MRP), member 2; ATP-binding cassette, sub-family C (CFTR; 3.74
 431884; AA521246; Hs.210792; ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar
 45 to ALU8_HUMAN ALU S; 3.74
 453329; T97205; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell ; 3.74
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glucose transporter), member 1; solute carrier family 2 (facilitated glu; 3.74
 438330; AW450572; Hs.257316; ESTs; ESTs; 3.74
 419911; L15301; Hs.1276; BNS1 (BHK21) temperature sensitivity complementing; BNS1 (BHK21) temperature sensitivity com; 3.74
 452695; AW780199; Hs.30327; mitogen-activated protein kinase-activated protein kinase 5; mitogen-activated protein kinase-activat; 3.73
 442233; AW967149; Hs.28439; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; ESTs, Weakly similar to I38022 hypotheti; 3.73
 451295; A1557212; Hs.17132; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to I54374 gene ; 3.73
 410772; BE275297; Hs.194685; Homo sapiens clone 24675 mRNA sequence; Homo sapiens clone 24675 mRNA sequence; 3.73
 426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54), human rhinovirus receptor; intercellular adhesion molecule 1 (CD54); 3.72
 449843; R85337; Hs.24030; solute carrier family 31 (copper transporters), member 2; solute carrier family 31 (copper transpor; 3.71
 423523; AW299828; Hs.193580; ESTs; ESTs; 3.71
 413407; A1356293; Hs.75339; inositol polyphosphate phosphatase-like 1; inositol polyphosphate phosphatase-like ; 3.71
 448336; R53848; Hs.44976; ESTs; ESTs; 3.70
 422083; NM_001141; Hs.111256; arachidonate 15-lipoxygenase, second type; arachidonate 15-lipoxygenase, second typ; 3.70
 416087; AF045184; Hs.79008; SKI-INTERACTING PROTEIN; SKI-INTERACTING PROTEIN; 3.70
 442200; AW590572; Hs.235768; ESTs; ESTs; 3.70
 414280; BE410769; Hs.75873; zyxin; zyxin; 3.69
 409354; N68188; Hs.159472; Homo sapiens cDNA: FLJ22224 fis, clone HRC01703; Homo sapiens cDNA: FLJ22224 fis, clone H; 3.69
 415276; U88666; Hs.78353; SFRS protein kinase 2; SFRS protein kinase 2; 3.69
 439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA; leucine-rich repeat-containing G protein; 3.69
 446522; NM_003876; Hs.15196; putative receptor protein; putative receptor protein; 3.69
 422785; A1824114; Hs.289088; heat shock 90kD protein 1, alpha; heat shock 90kD protein 1, alpha; 3.68
 401083; ; NM_016582*Homo sapiens peptide transporter 3 (LOC51295), mRNA, VERSION NM_016579.1 GI; NM_016582*Homo sapiens peptide transpor; 3.68
 413048; M53221; Hs.75182; mannose receptor, C type 1; mannose receptor, C type 1; 3.68
 452690; A1536070; Hs.15085; ESTs; ESTs; 3.68
 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar
 70 to ALU2_HUMAN ALU S; 3.68
 415010; NM_004203; Hs.77783; membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase; membrane-associated tyrosine- and threon; 3.68
 428579; NM_005756; Hs.184942; G protein-coupled receptor 64; G protein-coupled receptor 64; 3.68
 446430; AA346837; Hs.15075; hypothetical protein DKFZp434E2216; hypothetical protein DKFZp434E2216; 3.66
 442013; AA506476; Hs.375009; Human DNA sequence from clone RP11-353C18 on chromosome 20 Contains ESTs, STSs, GSSs and CpG Islands. Contains the NIFS gene for
 75 cysteine desulfurase, two genes for novel proteins and the gene for the; Human DNA sequence from clone RP11-353C1; 3.66
 416602; NM_006159; Hs.367895; Protein kinase C-binding protein NELL2; Protein kinase C-binding protein NELL2; 3.65
 441226; BE563042; Hs.118820; Homo sapiens, Similar to RIKEN cDNA 0610012G03 gene, clone MGC:14132, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 0610;
 80 3.65
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; wee1 (S. pombe) homolog; 3.65
 429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; ESTs, Weakly similar to S65657 alpha-1C; 3.65
 452060; W26980; Hs.349089; ATP-binding cassette, sub-family F (GCN2), member 2; ATP-binding cassette, sub-family F (GCN2; 3.65

- 451558; NM_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1), member 3; ATP-binding cassette, sub-family A (ABC1); 3.65
 414774; X02419; Hs.77274; plasminogen activator, urokinase; plasminogen activator, urokinase; 3.65
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin, beta 1; 3.65
 450295; AL041949; Hs.24758; hepatocyte growth factor-regulated tyrosine kinase substrate; hepatocyte growth factor-regulated tyrosine kinase substrate; 3.64
 437669; AI358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA667999 [H.sapiens]; ESTs, Weakly similar to match to ESTs AA; 3.64
 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dependent); mannose-6-phosphate receptor (cation dep); 3.64
 444388; AB033058; Hs.11101; KIAA1232 protein; KIAA1232 protein; 3.64
 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; CCAAT-box-binding transcription factor; 3.63
 451484; AV648898; Hs.283771; hypothetical protein; hypothetical protein; 3.63
 444613; H29627; Hs.79092; hypothetical protein FLJ14427; hypothetical protein FLJ14427; 3.63
 447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-inducing factor); programmed cell death 8 (apoptosis-induc); 3.62
 408101; AW968504; Hs.278346; CDC2-related protein kinase 7; CDC2-related protein kinase 7; 3.62
 424732; D80001; Hs.152629; KIAA0179 protein; KIAA0179 protein; 3.62
 411165; NM_000169; Hs.69089; galactosidase, alpha; galactosidase, alpha; 3.62
 422112; BE540240; Hs.111783; Lsm1 protein; Lsm1 protein; 3.62
 453020; AL162039; Hs.31422; Homo sapiens mRNA; cDNA DKFZp434M229 (from clone DKFZp434M229); Homo sapiens mRNA; cDNA DKFZp434M229 (fr; 3.61
 438795; AA825792; Hs.377119; gb:cd84b11.s1 NCL CGAP_Ov2 Homo sapiens cDNA clone, mRNA sequence; gb:cd84b11.s1 NCL CGAP_Ov2 Homo sapiens; 3.61
 445515; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457003, mRNA; Homo sapiens, clone IMAGE:3457003, mRNA; 3.61
 407797; AK000524; Hs.39850; hypothetical protein FLJ20517; hypothetical protein FLJ20517; 3.60
 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive); collagen, type VII, alpha 1 (epidermolys; 3.60
 444985; AI677737; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 3.60
 433764; AW753676; Hs.39982; zinc finger protein RINZF (NM_023929); zinc finger protein RINZF (NM_023929); 3.59
 427857; AL133017; Hs.288679; hypothetical protein FLJ22865; hypothetical protein FLJ22865; 3.59
 415020; BE249915; Hs.293533; Human DNA sequence from clone RP11-127L20 on chromosome 10. Contains ESTs, STSs, GSSs and CpG islands. Contains the gene for a novel
 glutathione-S-transferase and five novel genes; Human DNA sequence from clone RP11-127L2; 3.59
 415149; X12451; Hs.78056; cathepsin L; cathepsin L; 3.57
 458715; AK000973; Hs.1706; hypothetical protein FLJ10111; hypothetical protein FLJ10111; 3.57
 423576; NM_000383; Hs.129829; autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy); autoimmune regulator (autoimmune polyen; 3.57
 440270; NM_015986; Hs.7120; cytokine receptor-like molecule 9; cytokine receptor-like molecule 9; 3.57
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; hypothetical protein MGC12959; 3.57
 404976; ; NM_014323* Homo sapiens zinc finger protein 278 (ZNF278), transcript variant 1, mRNA; NM_014323* Homo sapiens zinc finger prot; 3.57
 449656; AA002008; Hs.188633; ESTs; ESTs; 3.56
 413795; AL040178; Hs.142003; ESTs; ESTs; 3.56
 406859; AI581134; Hs.181357; laminin receptor 1 (67kD, ribosomal protein SA); laminin receptor 1 (67kD, ribosomal prot; 3.56
 411030; BE387193; Hs.67896; 7-60 protein; 7-60 protein; 3.56
 447079; AA280057; Hs.105280; ESTs, Weakly similar to dJ963K23.2 [H.sapiens]; ESTs, Weakly similar to dJ963K23.2 [H.s]; 3.56
 424263; M77640; Hs.1757; L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs)
 syndrome, spastic paraplegia 1); L1 cell adhesion molecule (hydrocephalus; 3.55
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affinity glutamate transporter), member 3; solute carrier family 1 (glial high affi; 3.55
 443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible IkappaB kinase; IKK-related kinase epsilon; inducible Ik; 3.55
 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase); uridine monophosphate synthetase (orotat; 3.55
 450931; N25158; Hs.25648; tumor necrosis factor receptor superfamily, member 5; tumor necrosis factor receptor superfam; 3.55
 425836; AW955696; Hs.90960; ESTs; ESTs; 3.54
 441054; AA913591; Hs.126480; ESTs; ESTs; 3.54
 440592; AL137268; Hs.7285; KIAA0759 protein; KIAA0759 protein; 3.54
 458946; AA009716; Hs.42311; ESTs; ESTs; 3.53
 449027; AJ271218; Hs.22880; dipeptidylpeptidase III; dipeptidylpeptidase III; 3.53
 421662; NM_014141; Hs.106552; cell recognition molecule Caspr2; cell recognition molecule Caspr2; 3.53
 422732; AA577455; Hs.24937; transformer-2 alpha (htra-2 alpha); transformer-2 alpha (htra-2 alpha); 3.53
 424870; T15545; Hs.244624; ESTs; ESTs; 3.52
 442794; AI744130; Hs.356753; hypothetical protein MGC2975; hypothetical protein MGC2975; 3.52
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); protein C receptor, endothelial (EPCR); 3.51
 419971; AA400027; Hs.296234; ESTs, Weakly similar to T31613 hypothetical protein Y508A.I - Caenorhabditis elegans [C.elegans]; ESTs, Weakly similar to T31613 hypotheti; 3.51
 410257; BE244044; Hs.61469; hypothetical protein; hypothetical protein; 3.51
 424837; BE276113; Hs.333034; N-acetyltransferase, homolog of S. cerevisiae ARD1; N-acetyltransferase, homolog of S. cerev; 3.51
 421921; H83363; Hs.355993; translocase of inner mitochondrial membrane 10 (yeast) homolog; translocase of inner mitochondrial membr; 3.50
 454128; AL031259; Hs.367900; programmed cell death 2; programmed cell death 2; 3.50
 434049; AA501430; Hs.5771; amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2; amyotrophic lateral sclerosis 2 (juvenil; 3.50
 453641; AA444140; Hs.90960; ESTs; ESTs; 3.50
 429592; AB029041; Hs.209646; KIAA1118 protein; KIAA1118 protein; 3.49
 430647; AC003682; Hs.127988; ESTs, Weakly similar to Z211_HUMAN ZINC FINGER PROTEIN 211 [H.sapiens]; ESTs, Weakly similar to Z211_HUMAN ZINC; 3.47
 410855; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; RAD54 (S.cerevisiae)-like; 3.44
 413372; H55532; Hs.349695; tubulin, alpha 2; tubulin, alpha 2; 3.07
 437224; AL117628; Hs.97808; ESTs; ESTs; 2.77
 430439; AL133561; ; DKFZP434B061 protein; DKFZP434B061 protein; 2.76
 435897; AF269223; Hs.128322; t-complex 11 (a murine top homolog); t-complex 11 (a murine top homolog); 2.53
 417592; AA204664; Hs.182437; ESTs, Weakly similar to I54383 chromosome segregation protein smc1 [H.sapiens]; ESTs, Weakly similar to I54383 chromosom; 2.46
 412026; AA383618; Hs.73073; testis-specific ankyrin motif containing protein; testis-specific ankyrin motif containing; 2.35
 422789; AK001113; Hs.120842; hypothetical protein FLJ10251; hypothetical protein FLJ10251; 2.33
 426627; AF012359; Hs.195685; ESTs; ESTs; 2.12
 438983; AF085884; Hs.20029; proacrosin binding protein sp32 precursor; proacrosin binding protein sp32 precursor; 2.07
 425709; AA383076; Hs.159274; outer dense fibre of sperm tails 1; outer dense fibre of sperm tails 1; 1.99
 433724; AI827749; Hs.144924; serine/threonine protein kinase SSTK; serine/threonine protein kinase SSTK; 1.68
 420710; NM_007009; Hs.99875; zona pellucida binding protein; zona pellucida binding protein; 1.54

TABLE 57B

Pkey:	Unique Eos probeset identifier number	
CAT number:	Gene cluster number	
Accession:	Genbank accession numbers	
Pkey	CAT Number	Accession

417886 1031334_1 AA210987 D57294 AA214584 AA207006 D56572
 432407 MH1429_12 BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104
 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AJ732411 BG778834 BG283641 BE748279
 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849
 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AJ075321 L13823 AA216700 BF771864 AW861859
 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928
 AW861687 AW821826 B1055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
 AF134164 BF809407 AA218567 BF842853 AJ267168 BF876178 BG999253 AW861851 AW858352 AJ817548 BF771300 AA113928 AA223422
 AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298
 AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AJ694265 AA045564 BG950256 AI293309 BG987850 BE093175
 BF854337
 427298 115241_1 AA933717 BF061897 AW628327 AA641788 AA400495
 427521 513212_1 AW973352 BF222929 AW016853 BF059130 AJ651829 BE551767 AA558414 AJ339359 BF069601 AI961162 AJ341422 AI206248 AI206165
 407347 810943_1 T23514 AI655785
 430439 6750_2 AL133561 AL117481 AL122069 AW439292 AI968826 AL041090

TABLE 57C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402199	8576116	Minus	84187-84744
402680	8113438	Plus	137634-137768, 139702-139893, 140475-14059
402260	3399665	Minus	113765-113910, 115653-115765, 116808-11694
402678	8113438	Plus	37395-37514, 37866-37981
403171	9838164	Minus	74502-74703
406137	9166422	Minus	30487-31058
401704	3097841	Plus	24712-25374
402677	8113438	Plus	22135-22309, 23063-23238
402679	8113438	Plus	132079-132216
402145	8018280	Plus	113086-114800
406547	7711513	Minus	172780-174358
402398	4092817	Minus	24019-24973
405484	5922025	Plus	199214-199579, 199672-199920, 200262-20049
401083	3242744	Plus	33192-33360
404976	3419864	Minus	139625-140632

TABLE 58A: 434 genes upregulated in bladder cancer relative to normal body tissues

Table 58A lists about 434 genes upregulated in bladder cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymatrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.ProL.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1: 90th percentile of bladder tumor AIs divided by the 50th percentile of normal tissue AIs

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.ProL.Domains; R1

430630; AW269920; Hs.2621; cystatin A (stafin A); cystatin; TM=M; 35.25
 422282; AF019225; Hs.114309; apolipoprotein L; MoIA_ExbB; TM=Y; SS=M; 33.25
 414555; N98569; Hs.76422; phospholipase A2, group IIA (platelets, ; phoslip; TM=M; SS=Y; 31.68
 415192; D17793; Hs.78183; aldo-keto reductase family 1, member C3; aldo_ket_red; TM=M; 31.04
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazarot; none, none; 28.50
 439180; AJ393742; Hs.199087; v-erb-b2 avian erythroblastic leukemia v; Furin-like, pkinase, Recep_L_domain, Furin-like, pkinase, Recep_L_domain, Peptidase_M24; 27.43
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; SS=M; 25.98
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT; none; 25.38
 418818; AA228899; Hs.101307; Homo sapiens HUT11 protein mRNA, partial; UT; none; 25.28
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB, DNA_topoisomIV, HATPase_c; SS=M; 23.58
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (ach; lg, pkinase; TM=Y; SS=M; 21.24
 424006; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm_1; TM=Y; SS=M; 20.45
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none, none; 19.78
 408243; Y00787; Hs.624; Interleukin 8; HLH.PAS.IJ8; TM=M; 18.90
 427450; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase; TM=M; 18.75
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase; SS=M; 18.63
 444381; BE387335; Hs.283713; ESTs, Weakly similar to S64054 hypohalit; Collagen; TM=M; SS=M; 18.60
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; lg, Rhabd_glycop; TM=Y; SS=M; 18.55
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4, LIM; TM=M; 18.25

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- 413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent, catalytic); PKI;SS=M; 17.73
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, γ 2; Ig;TM=Y;SS=M; 17.68
 450746; D82673; Hs.278589; general transcription factor II, τ ; none;SH3,PX; 17.12
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase;PLAT;TM=M; 16.88
 420981; L40904; Hs.100724; peroxisome proliferative activated recep; hormone_rec,zf-C4;TM=M; 16.78
 439941; A1392640; Hs.18272; amino acid transporter system A1; Aa_trans;TM=Y; 16.75
 431846; BE018924; Hs.271580; uroplakin 1B; transmembrane4;TM=Y;SS=M; 16.56
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys,lg,FAD_Synth,Ihh,Kth_C,kinase;SS=M; 16.43
 414883; AA926960; ; CDC28 protein kinase 1; CKS; 16.20
 438091; AW373062; ; nuclear receptor subfamily 1, group 1, m; hormone_rec,zf-C4,none; 15.80
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase; PAF-AH,IIb,Lipase_GDSL;TM=M; 15.70
 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,kinase;TM=M; 15.63
 422278; AF072873; Hs.114216; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 15.45
 434293; NM_004445; Hs.3796; EphB6; EPH_Ibd,fn3,kinase,SAM;TM=Y;SS=M; 15.43
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule); EGF,lectin_c,sushi;TM=M;SS=M; 15.28
 433991; NM_002250; Hs.10082; potassium intermediate/small conductance; CaMBD,SK_channel,ion_trans;TM=Y;SS=M; 15.10
 416305; AU076628; Hs.79187; coxsackie virus and adenovirus receptor; ig;TM=Y;SS=M; 14.90
 432306; Y18207; Hs.303090; protein phosphatase 1, regulatory (inhib); CBM_21;TM=M; 14.80
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=M; 14.73
 428345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 14.58
 449230; BE613348; Hs.211579; melanoma cell adhesion molecule; Ig,Isohd,Ribosomal_L6,F-box;TM=Y;SS=M; 14.55
 421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN,HIN;TM=M; 14.53
 446006; NM_004403; Hs.13530; deafness, autosomal dominant 5; none;TM=M;SS=M; 14.35
 429556; AW139399; Hs.98988; ESTs; none;TM=M; 14.18
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium binding; ehnd;SS=M; 14.13
 428673; AA884407; Hs.211595; protein tyrosine phosphatase, non-recept; Y_phosphatase,Band_41,PDZ;SS=M; 13.90
 426657; NM_015865; Hs.171731; solute carrier family 14 (urea transport); UT;TM=Y; 13.83
 428157; A1738719; Hs.198427; hexokinase 2; hexokinase,hexokinase2,none; 13.80
 400843; ; NM_003105; Homo sapiens sortilin-related; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 13.78
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,CoaE;TM=M; 13.38
 432314; AA533447; Hs.312989; ESTs; Xlink,none; 13.25
 413109; AW389845; Hs.110855; ESTs; PHO4,none; 13.15
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank,kinase;TM=M; 13.13
 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; PAC,PAS;TM=M; 12.93
 426158; NM_001982; Hs.199067; v-erb-b2avian erythroblastic leukemia v; Furin-like,kinase,Recep_L_domain,Furin-like,kinase,Recep_L_domain,Peptidase_M24; 12.43
 440249; A1246590; Hs.249175; ESTs; TatD_DNase,kinase,death,none; 12.38
 425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none;SS=M; 12.38
 404942; U30825; ; splicing factor, arginine/serine-rich 9; CD36;TM=Y;SS=M; 12.03
 439569; AW062166; Hs.222399; CEGP1 protein; EGF,TNFR_c6,granulin,CUB,Keratin_B2,TIL;TM=M;SS=M; 11.93
 443195; BE148235; Hs.193063; Homo sapiens cDNA FLJ14201 f1s, clone NT; Aa_trans,none; 11.88
 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (230/240kD); ehnd,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,FlD,bZIP,Tropomyosin,Myc-LZ,M,Ihh_C,CH,AIP3;TM=M; 11.88
 412182; AA205588; Hs.155160; Splicing factor, arginine/serine-rich, 4; rrm,hormone_rec,zf-C4,sugar_tr; 11.85
 433470; AW960564; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 11.80
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb-DNA-binding,THF_DHG_CYH,THF_DHG_CYH_C,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,M,xan_ur_permease,HCO3_cotransp;TM=M; 11.69
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm_1,7tm_2;TM=Y;SS=M; 11.50
 426761; A1015709; Hs.172089; Homo sapiens mRNA; cDNA DKFZp586i2022 (f; none;TM=Y;SS=M; 11.48
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDNA; IMPDH_C,IMPDH_N,CBS,integrin_B,Ricin_B,Jedlin; 11.38
 446742; BE148235; Hs.16085; putative G-protein coupled receptor; none;TM=Y;SS=M; 11.23
 436729; BE621807; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 11.18
 409960; BE261944; Hs.339673; hexokinase 1; none,none; 11.02
 426539; AB011155; Hs.170290; discs, large (Drosophila) homolog 5; SH3,PDZ,Guanylate_kin;TM=M; 10.78
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; coflin_ADF;SS=M; 10.63
 427654; AA410183; Hs.137475; ESTs; ion_trans,vwc,IGFBP_tsp_1; 10.58
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh;TM=M;SS=M; 10.53
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (SH3,PH,RhoGEF;TM=M; 10.53
 449437; A1702038; Hs.100057; Homo sapiens cDNA: FLJ22902 f1s, clone K; none,none; 10.52
 436856; A1469355; Hs.127310; ESTs; pkinase,rrm;TM=M; 10.48
 451035; AU076785; Hs.430; plastin 1 (I isoform); ehnd,CH,Adaptin_N;SS=M; 10.38
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), β 2); integrin_B,EGF,PSI;TM=Y;SS=M; 10.35
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit); vwa,Integrin_A,FG-GAP;TM=Y;SS=M; 10.34
 440006; AK000517; Hs.6844; hypothetical protein FLJ20510; AAA,NB-ARC,PAAD_DAPIN;NA;NA; 10.25
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 10.18
 437852; BE001836; Hs.256897; ESTs, Weakly similar to dJ365O12.1 (HLSa; GPS,7tm_2;TM=Y; 10.13
 400752; ; NM_003105; Homo sapiens sortilin-related; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 10.08
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPE;TM=M; 10.05
 426728; NM_007118; Hs.171957; triple functional domain (PTPRF interact; SH3,lg,kinase,PH,spectrin,RhoGEF;TM=M; 10.05
 400496; ; ENSP00000224716; GTP-binding protein SAR; none;TM=Y; 10.01
 413899; AF083892; Hs.75608; tight junction protein 2 (zona occludens); SH3,PDZ,Guanylate_kin;TM=M; 10.00
 404568; ; NM_022071; Homo sapiens hypothetical protein; SH2;TM=M; 10.00
 444823; BE262989; Hs.12045; putative protein; Mir1,MBOAT;TM=M;SS=Y; 9.93
 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; ehnd,kazal,arf,ras,7tm_1;TM=M; 9.90
 413441; A1929374; Hs.75367; Src-like-adaptor; SH2,SH3;TM=M; 9.90
 424954; NM_000546; Hs.1846; tumor protein p53 (Li-Fraumeni syndrome); P53,WD40,JRK;TM=M; 9.88
 452289; BE568205; Hs.28827; mitogen-activated protein kinase kinase ; pkinase;TM=M; 9.85
 439223; AW238299; Hs.250618; UL16 binding protein 2; tdl_recept_a,PKD,MHC_I;TM=M;SS=Y; 9.83
 429238; NM_002849; Hs.198288; protein tyrosine phosphatase, receptor t; Y_phosphatase;TM=Y;SS=M; 9.80
 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPE,Y_phosphatase;TM=M; 9.73
 452239; AW379378; Hs.170121; protein tyrosine phosphatase, receptor t; none,none; 9.73
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase,DSPE;TM=M; 9.72
 403912; ; C5000394; gij12737280[ref]XP_006682.2[k; none;TM=M; 9.70
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none,spectrin,SH3,PH,CH; 9.70

- 428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xc); pkinase;TM=M; 9.68
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin,fn3,Y_phosphatase;TM=M; 9.63
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M; 9.63
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic; PI3_P14_kinase,FAT,FATC;TM=M; 9.55
 430259; BE550182; Hs.127826; RafGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 9.50
 428520; AA331901; Hs.184736; hypothetical protein FLJ10097; none;TM=M; 9.50
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M; 9.50
 448913; AA194422; Hs.22564; myosin VI; rm,zf-RanBP,pkinase,GST_C,Eis,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFIIS,AT_hook,SAM;TM=M; 9.50
 414911; NM_000107; Hs.77602; damage-specific DNA binding protein 2 (4; WD40,homobox,UIM;TM=M; 9.48
 451295; A1557212; Hs.17132; ESTs, Moderately similar to I54374 gene; pkinase,DAG_PE-bind,pkinase_C,OPR;none; 9.45
 402328; ; Target Exon; pkinase;TM=M; 9.44
 443710; A1928136; Hs.9691; Homo sapiens cDNA: FLJ23249 fls, clone C; G-alpha;none; 9.42
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M; 9.42
 434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase,ATP-sulfurylase,PRK,Thymidylate_kin;SS=M; 9.40
 418827; BE327311; Hs.47166; HT021; none;TM=M; 9.40
 440675; AW005054; Hs.47883; ESTs, Weakly similar to KCC1_HUMAN CALCI; pkinase;none; 9.35
 433376; A1249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20;SS=M; 9.28
 410668; BE379794; Hs.65403; hypothetical protein; death,TNFR_c6;TM=Y;SS=M; 9.25
 430024; A1808780; Hs.227730; Integrin, alpha 6; Integrin_A,FG-GAP;TM=Y;SS=M; 9.23
 452696; A1826645; Hs.211534; ESTs; ArfGap,PH,ank,Guanylate_kin,PDZ,SH3; 9.13
 434263; N34895; Hs.44648; ESTs; Ig;none; 9.13
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell; Ribosomal_S14,ank,pkinase,death;none; 9.10
 429332; AF030403; Hs.199263; Ste-20 related kinase; pkinase,metalho;TM=M;SS=M; 9.08
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,Integrin_B;SS=M; 9.08
 443951; F13272; Hs.111334; ferritin, light polypeptide; PMP22,Claudin;none; 9.07
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE; 8.98
 451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M; 8.93
 438000; A1825880; Hs.5985; non-kinase Cdc42 effector protein SPEC2; none;TM=M; 8.90
 446620; AA128808; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 8.90
 436075; BE090176; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 8.88
 437056; A1147061; ; gbok33a11.s1 Soares_NSF_F8_9W_OT_PA_P_S; none,spectrin,SH3,PH,CH; 8.78
 445496; AB007860; Hs.12802; development and differentiation enhancer; SH3,ank,PH,ArfGap;TM=M; 8.78
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 8.75
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none;TM=M; 8.70
 445033; AV652402; Hs.72901; mucin 13, epithelial transmembrane; ank; 8.68
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); none;TM=M;SS=M; 8.65
 432841; M93425; Hs.62; protein tyrosine phosphatase, non-recept; Y_phosphatase;SS=M; 8.65
 430397; A1924533; Hs.105607; bicarbonate transporter related protein; HCO3_cotransp;TM=Y; 8.64
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD;TM=M; 8.60
 442994; A1026718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal_S14; 8.60
 429109; AL008637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3,OPR,PX;TM=M; 8.60
 455439; AW945484; Hs.184252; ESTs, Weakly similar to ALU8_HUMAN ALU S; none,7tm_1; 8.55
 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1; TIMP,pkinase,DAG_PE-bind,RBD; 8.43
 417035; AA192455; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA se; none;none; 8.40
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank; 8.39
 448209; AW160489; Hs.20709; tetraspan 5; transmembrane4;TM=Y;SS=M; 8.33
 450139; AK001838; Hs.296323; serum/glucocorticoid regulated kinase; none;none; 8.33
 445350; AF052112; Hs.12540; lysophospholipase 1; abhydrolase_2;TM=M; 8.31
 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a I; 7tm_1;TM=Y;SS=M; 8.30
 445633; A1453386; Hs.17287; ESTs, Weakly similar to S26689 hypothei; IRK;none; 8.28
 446719; W39500; Hs.301872; hypothetical protein MGC4840; AAA,SK1;TM=M; 8.23
 424762; AL119442; Hs.183684; eukaryotic translation initiation factor; none;none; 8.20
 427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, for; Ig,pkinase;TM=Y;SS=M; 8.18
 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none;none; 8.15
 419262; AA834664; Hs.29131; nuclear receptor coactivator 2; PAS,zf-C2H2,SET; 8.15
 417386; AL037228; Hs.82043; D123 gene product; NUDIX,secY,E1_dehydrog,transkel_pyr;TM=Y;SS=M; 8.13
 431236; AV656840; Hs.285115; interleukin 13 receptor, alpha 1; fn3;TM=Y;SS=M; 8.10
 439658; AA332057; Hs.6639; hypothetical protein MGC15440; none;TM=M;SS=M; 8.09
 425424; NM_004954; Hs.157199; ELK1, motif kinase; pkinase,UBA,KA1;TM=M; 8.08
 422573; AW297985; Hs.295726; Integrin, alpha V (vitronectin receptor; FG-GAP,Integrin_A;none; 8.05
 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo_seg;TM=M;SS=M; 8.03
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; pkinase;SS=M; 8.03
 404891; ; Target Exon; none;none; 7.95
 414278; AA330116; Hs.77273; Human glucose transporter pseudogene; none;none; 7.93
 452888; AW955454; Hs.30942; ephrin-B2; Ephrin,fn2;TM=Y;SS=M; 7.93
 433211; H11850; Hs.12808; MARK; pkinase,UBA,KA1;SS=M; 7.91
 438485; W57578; Hs.237955; RAB7, member RAS oncogene family; pkinase,ABC1;none; 7.90
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fls, clone PL; HLH,death,TNFR_c6,Acyl-CoA_hydro; 7.90
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase tra; xan_ur_permease,RA; 7.88
 427122; AW057738; Hs.323910; HER2 receptor tyrosine kinase (c-erb-b2; Furin-like,pkinase,Recep_L_domain,YLP;TM=Y;SS=M; 7.86
 405036; ; NM_021628; Homo sapiens arachidonate lip; lipoxygenase,complex_L_49kd,PLAT;TM=M; 7.83
 418529; AW005695; Hs.250897; TRK-fused gene; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M; 7.83
 431912; A1660552; Hs.76549; ESTs, Weakly similar to A56154 Abl subst; none,Acyl-CoA_dh,Acyl-CoA_dh_M,Acyl-CoA_dh_N; 7.80
 432981; NM_002733; Hs.3138; protein kinase, AMP-activated, gamma 1 r; CBS,AA_trans;TM=M; 7.78
 422940; BE077458; gbRC1-BT0606-090500-015-b04 BT0606 Homo; Sec7,PH,ANF_receptor,Ig_chan,WD40,IRK; 7.78
 446636; AC002563; Hs.15767; citron (rho-interacting, serine/threonin; CNH,DAG_PE-bind,PH,Involutcrin,M;TM=M; 7.78
 431183; NM_006855; Hs.250696; KDE1 (Lys-Asp-Glu-Leu) endoplasmic retic; ER_Juman_recept;TM=M;SS=M; 7.78
 400845; ; NM_003105; Homo sapiens sortilin-related; EGF,fn3,kd_recept_a,kd_recept_b,granulin,BNR;TM=Y;SS=M; 7.73
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran,M,SMC_N,SMC_C,DUF164;none; 7.73
 437192; AW975788; Hs.75355; ubiquitin-conjugating enzyme E2N (homolo; UQ_con_Y_phosphatase,SH2; 7.70
 403212; ; NM_019595; Homo sapiens intersectin 2 (IT; SH3,efhand,C2,PH,RhoGEF;TM=M; 7.70
 441190; H09073; Hs.25046; ESTs; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase;none; 7.68

- 409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7tm_1,zf-C3HC4,f,n3,SPRY,KRAB,zf-C2H2,ve,zf-8_box;TM=Y;SS=M; 7.68
 428840; M15990; Hs.194148; v-yes-1 Yamaguchi sarcoma viral oncogene; SH2,SH3,pkinase;SS=M; 7.65
 447898; AW969638; Hs.112318; 6.2 kd protein; none;none; 7.65
 425289; AW139342; Hs.155530; Interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN;SS=M; 7.63
 401927; ; C17000914*gi|8394367|ref|NP_058549.1|s; none; 7.60
 407347; AA829847; ; gb:od40d07.s1 NCI_CGAP_GCB1 Homo sapiens; RhoGAP,SH2,pkinase,POLO_box;none; 7.58
 449924; W30681; Hs.146233; Homo sapiens cDNA: FLJ22130 fis, clone H; SH3;none; 7.57
 429952; AF080158; Hs.226573; Inhibitor of kappa light polypeptide gen; pkinase,ubiquitin,Enterotoxin_A,PHO4,pkinase,ubiquitin; 7.55
 445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase, ty; none;none; 7.55
 421489; AI922821; Hs.32433; ESTs; none,PI-PLC-X,PI-PLC-Y,C2; 7.53
 430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none;TM=Y;SS=M; 7.53
 431605; AW972407; Hs.124370; gb:EST384498 MAGE resequences, MAGL Homo; adenylatekinase,SRP54;TM=M; 7.50
 430570; AI417881; Hs.292464; ESTs; 7tm_2,Fz,Frizzled;none; 7.50
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y; 7.48
 420676; AA34780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG_PE-bind;none; 7.48
 444252; R21135; Hs.54985; ESTs; none;none; 7.47
 414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT,FATC,PI3_P14_kinase;TM=M; 7.47
 443426; AF089158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M; 7.45
 418546; AA224827; ; gb:nc32g04.s1 NCI_CGAP_Pr2 Homo sapiens ; vwa,Integrin_A,FG-GAP;none; 7.45
 437860; AA333063; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none;NA;NA; 7.43
 452007; AA426234; Hs.34906; ESTs, Weakly similar to T17210 hypothet; none,pkinase; 7.40
 432407; AA221036; ; gb:z03f12.r1 Stratagene NT2 neuronal pr; DEAD,helicase_C,rm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,Rlla,abhydrolase,TGF-beta,DUF139,TPR,OSPC,isp_1,Ribosomal_S21,rvp;TM=M; 7.40
 424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,DENN,uDENN;TM=M; 7.40
 421429; NM_014922; Hs.104305; death effector filament-forming Ced-4-l; LRR,PAAD_DAPIN,AAA,CARD,NB-ARC;NA;NA; 7.38
 417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, m; hormone_rec,zf-C4;SS=M; 7.38
 430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX,EXS;TM=Y; 7.38
 422813; AV658571; Hs.121068; transmembrane 4 superfamily member 6; transmembrane4;TM=Y;SS=M; 7.32
 433390; AA586950; Hs.260180; Homo sapiens mRNA; cDNA DKFZp761G18121 (; none,spectrin,SH3,PH,CH; 7.25
 409213; U81412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase;TM=M; 7.24
 444745; AF117754; Hs.11861; thyroid hormone receptor-associated prot; none;TM=M; 7.23
 452817; AA322859; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; pkinase,PBD;TM=M; 7.19
 407591; NM_000910; Hs.37125; neurotrophin Y receptor Y2; 7tm_1;TM=Y; 7.18
 427231; AW851989; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 7.18
 450285; AW383256; Hs.24752; spectrin SH3 domain binding protein 1; SH3;TM=M; 7.18
 403344; ; NM_000341:Homo sapiens solute carrier fa; alpha-amylase;TM=Y; 7.15
 427268; X78520; Hs.174139; chloride channel 3; CBS,voltage_CLC;TM=Y; 7.14
 442213; N36110; Hs.305971; solute carrier family 2 (facilitated glur; sugar_br;TM=Y;SS=M; 7.14
 404875; ; NM_022819:Homo sapiens phospholipase A2; phospho;SS=M; 7.11
 433618; AA602539; Hs.345494; ESTs; G-alpha_A_deaminase; 7.10
 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_transp,STAS,HMG_box; 7.08
 413073; AL038165; Hs.75187; translocase of outer mitochondrial membr; MAS20,zf-A20,VPS9;TM=M;SS=M; 7.05
 426655; AL049589; Hs.171723; neuronal cell death-related protein; TFIID-31;TM=M; 7.05
 423387; AJ012074; ; vasoactive intestinal peptide receptor 1; 7tm_2,HRM,CSD;TM=Y;SS=M; 7.03
 400211; ; NM_003899:Homo sapiens PAK-interactin; SH3,PH,RhoGEF,Terpene_synth;TM=M; 7.03
 438150; AA037534; Hs.342874; transforming growth factor, beta recepto; zona_pellucida;none; 6.93
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome;TM=M; 6.93
 405275; AB028989; ; mitogen-activated protein kinase 8 inter; Cys_knot,TGF-beta,vwa,vwc,vwd,TIL,DUF139;SS=M; 6.93
 415392; Z44067; Hs.10957; ESTs; PIP5K;none; 6.89
 429355; AW973253; Hs.292689; ESTs; pkinase,bZIP,Armadoillo_seg;none; 6.88
 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic; ; C2,PLA2_B;TM=M; 6.85
 427832; AF038362; Hs.180930; TBP-associated factor 172; SNF2_N,helicase_C,Armadoillo_seg,HEAT;TM=M; 6.83
 447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M; 6.80
 400158; ; ENSP00000244302:C.DNA FLJ11591 fis, clone; Sm;SS=M; 6.78
 401917; AL050149; ; RAN binding protein 3; Orexin,SH2,STAT,STAT_bind,STAT_prot,lon_trans,PAC,PAS;none; 6.78
 400844; ; NM_003105:Homo sapiens sortilin-related; EGF,f,n3,kd1_recept_a,kd1_recept_b,granulin,BNR;TM=Y;SS=M; 6.73
 457239; U07358; Hs.211601; mitogen-activated protein kinase kinase ; pkinase; 6.73
 404440; ; NM_021048:Homo sapiens melanoma antigen; ; MAGE;TM=M; 6.73
 424241; AW995948; Hs.182339; Homo sapiens pyruvate dehydrogenase kina; Els,SAM_PNT;TM=M; 6.70
 426746; J03626; Hs.2057; uridine monophosphate synthetase (protat; Pribosyllran,OMPDecase;TM=M; 6.70
 429429; AA829725; Hs.334437; hypothetical protein MGC4248; none,transmembrane4; 6.65
 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate_kin;SS=M; 6.64
 408638; AW451353; Hs.173328; ESTs; B56;none; 6.63
 408058; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 6.61
 401057; BE563186; ; eukaryotic translation elongation factor; lon_trans,IQ;TM=Y; 6.60
 446526; H89616; Hs.296290; Homo sapiens cDNA FLJ13357 fis, clone PL; none;none; 6.60
 400528; ; NM_020975:Homo sapiens ret proto-oncoge; cadherin,pkinase;TM=Y;SS=M; 6.58
 418562; R60669; Hs.124831; CGI-67 protein; none,Skp1,AAA; 6.57
 453826; AL138129; ; gb:DKFZp547F152_r1 547 (synonym: htfb1); PK,PK_C;none; 6.55
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (tr; ABC_tran,GTP_EFTU,ABC_membran;none; 6.54
 415088; AI077288; Hs.296323; serum/glucocorticoid regulated kinase; none;none; 6.50
 453489; AA300067; Hs.33032; hypothetical protein DKFZp434N185; F5_F8_type_C,pkinase,Els,F5_F8_type_C,pkinase,Els; 6.47
 439866; AA280717; Hs.6727; Ras-GTPase activating protein SH3 domain; rrm,NTF2;TM=M; 6.46
 456376; AA663904; Hs.89862; TNFRSF1A-associated via death domain; death;TM=M; 6.46
 441712; AW391927; Hs.7946; KIAA1288 protein; ALP3;TM=M; 6.44
 414557; AA340111; Hs.100009; acyl-Coenzyme A oxidase 1, palmitoyl; pkinase,7tm_1; 6.43
 432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY_C;TM=M; 6.43
 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 6.40
 438941; AF075047; Hs.31864; ESTs; Ca_channel_B,SH3,arf;none; 6.40
 441466; AW673081; Hs.54828; ESTs; pkinase,zf-C2H2,KRAB;none; 6.33
 438698; AW279755; Hs.125815; ESTs, Weakly similar to I38022 hypothet; lipoxigenase,PLAT;none; 6.33
 433255; AJ274270; Hs.96840; KIAA1527 protein; MHCK_EF2_kinase;TM=M;SS=M; 6.33
 427801; AW979155; Hs.298275; amino acid transporter 2; Aa_trans;TM=M;SS=M; 6.32

- 407970; AW403814; Hs.41714; BCL2-associated athanogene; ubiquitin, BAG, Tropomyosin; 6.30
 438464; AA669735; Hs.324743; protein phosphatase 4 regulatory subunit; none, none; 6.30
 453977; AA886006; Hs.250427; ESTs; pkinase, P2X_receptor, E1-E2_ATPase, Hydrolase; 6.30
 412491; W31589; Hs.73957; RAB5A, member RAS oncogene family; ras, raf, PP2C; TM=M; 6.30
 413235; BE243445; Hs.75248; topoisomerase (DNA) II beta (180kD); DNA_gyraseB, DNA_topoisolV, HATPase_c, DNA_gyraseB, DNA_topoisolV, HATPase_c; 6.29
 404342; ; C7002192; gi|7299207|gb|AAAF54404.1| (AEO; none; TM=M; 6.27
 409274; NM_003930; Hs.52644; SKAP55 homologue; SH3, PH; SS=M; 6.25
 419693; AA133749; Hs.301350; FXD domain-containing ion transport reg; ATP1G1, PLM, MAT8; TM=Y; SS=M; 6.23
 405429; ; Target Exon; Y_phosphatase, none; 6.23
 404975; AL042279; ; uncharacterized hypothalamus protein HTQ; kringle; TM=Y; SS=M; 6.20
 452929; AW954983; Hs.172816; neuregulin 1; Neuregulin, EGF, Jg, Neuregulin, EGF, Jg; 6.18
 446883; AW452756; Hs.16364; hypothetical protein FLJ10955; DEAD, helicase_C, rm, Ndr, Cys_knot, TIL, vwa, vwc, vwd, IQ, RIIa, abhydrolase, TGF-beta, DUF139, TPR, DSPc, lrp_1, Ribosomal_S21, rvp; TM=M; 6.18
 433233; AB040927; Hs.301804; KIAA1494 protein; SH3, zf-C3HC4; TM=M; 6.15
 458791; BE615453; Hs.346509; dedicator of cyto-kinesis 1; none; TM=Y; 6.15
 421836; AF109219; Hs.108787; phosphatidylinositol glycan, class N; none, none; 6.14
 447727; AA421079; tumor necrosis factor receptor superfamily; none, synaptobrevin; 6.13
 410536; ; NM_002530; Homo sapiens neurotrophic tyrosine kinase, type 3, class I; ig, pkinase, LRR, LRRNT, LRRCT; TM=M; SS=M; 6.11
 444317; AI140566; Hs.143436; ESTs, Weakly similar to PLHU plasmin [H]; PAN, kringle, trypsin, PI-PLC-X, C2, SH2, PH, SH3, PI-PLC-Y, PAN; 6.10
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6, ET, PLA2_inh; SS=M; 6.08
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2; TM=M; 6.08
 450107; AI873287; Hs.257812; ESTs; ICE_p20, DED; TM=M; 6.05
 418175; AW967054; Hs.206312; ESTs, Weakly similar to I38022 hypotheli; zf-C2H2, BTB, K_tetra, Synlaxin; none; 6.05
 408983; NM_000492; Hs.663; cystic fibrosis transmembrane conductance; ABC_tran, ABC_membrane, PRK, Bac_export_3; TM=Y; 6.05
 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema, PSI, integrin_B; TM=Y; 6.03
 427625; AF008216; Hs.285013; putative human HLA class II associated p; none, none; 6.03
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc, Rhodanese; none; 6.03
 446650; AB016825; Hs.15813; solute carrier family 22 (organic cation; sugar_tr; TM=Y; SS=M; 6.03
 405102; ; C15001220; gi|4469558|gb|AAD21311.1| (AF; DAG_PE-bind, PH, RhoGEF, DC1; SS=M; 6.03
 400121; ; Eos Control; SH3, PH, RhoGEF, Terpene synth; TM=M; 6.03
 415327; H22769; ; gb|ym54c02.r1 Soares infant brain 1N1B H; SH3, PDZ, Guanylate_kin; SS=M; 6.03
 404148; ; NM_002944; Homo sapiens v-ros avian UR2; ; fn3, pkinase, DUF139; TM=Y; SS=M; 6.03
 405531; ; Target Exon; PDZ, CARD, Guanylate_kin; TM=M; 6.00
 433363; AA584829; Hs.275163; non-metastatic cells 2, protein (NM23B); NDK; none; 6.00
 427270; HA7921; Hs.174139; chloride channel 3; voltage_CLC, CBS; none; 5.99
 423774; L39064; Hs.1702; Interleukin 9 receptor; none; TM=M; SS=M; 5.98
 424124; AA335809; Hs.7589; ESTs, Weakly similar to A46010 X-linked; pkinase, TBQ; 5.98
 411040; AF007393; Hs.177574; protein-kinase, Interferon-inducible dou; HLH; TM=M; 5.95
 423422; AC005175; Hs.128425; NY-REN-24 antigen; Sulfotransfer, 7tm_1; none; 5.88
 453902; BE502341; Hs.3402; ESTs; none, none; 5.88
 409636; AA305729; Hs.18272; amino acid transporter system A1; Aa_trans; TM=Y; 5.86
 436154; AA764950; Hs.119898; ESTs; ehand, DAG_PE-bind, DAGKa, PHD, DAGKc, PSI; none; 5.85
 455358; AW902641; ; gb|CV3-NN1024-100500-181-d08 NN1024 Homo; Sulfatase, Somatomedin_B, Phosphodiesterase; none; 5.83
 414108; AI267592; Hs.75761; SFRS protein kinase 1; ank, PH, Oxysterol_BP, pkinase; TM=M; 5.82
 452547; AA335295; Hs.74120; adipose specific 2; LEA; TM=M; 5.82
 415204; T27434; ; gb|hbc2294 Human pancreatic islet Homo s; Na_Ca_Ex_Cab-beta; none; 5.80
 435663; AF210317; Hs.95497; solute carrier family 2 (facilitated glu; sugar_tr; TM=Y; 5.78
 456097; C15702; Hs.288028; ESTs, Moderately similar to I54374 gene; dsrm, FKBP; 5.78
 422445; M23114; Hs.1526; ATPase, Ca transporting, cardiac muscle; E1-E2_ATPase, CaATPase_N, Hydrolase; TM=Y; 5.77
 436246; AW450963; Hs.119991; ESTs; none, DNA_gyraseB, DNA_topoisolV, HATPase_c; 5.75
 422953; AA488860; Hs.245043; hypothetical protein FLJ14297; ABC_tran, PRK; TM=Y; SS=M; 5.75
 425854; AA749190; ; ESTs; RhoGAP, SH2, pkinase, POLO_box; none; 5.74
 424160; T74062; ; gb|ycb1f01.r1 Soares infant brain 1N1B H; ROK; none; 5.70
 417389; BE260964; Hs.82045; midkine (neurtic growth-promoting factor; PTN_MK; TM=M; SS=Y; 5.69
 437613; R19892; Hs.10267; MIL1 protein; none, none; 5.68
 410820; BE391493; Hs.16475; Human DNA sequence from clone RP5-852M4; TBQ; SS=M; 5.68
 423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase, PBD; TM=M; 5.66
 426500; NM_014638; Hs.170155; KIAA0450 gene product; C2, PI-PLC-Y; TM=M; 5.63
 406930; U04691; ; gb|Human olfactory receptor (OR17-219) g; none; TM=Y; SS=M; 5.60
 401044; ; Target Exon; none, ICE_p20, ICE_p10, CARD, Peptidase_M1; 5.56
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase, ICE_p10, ICE_p20; TM=M; SS=M; 5.55
 421970; AF227156; Hs.110103; RNA polymerase I transcription factor RR; aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DOT, PI3_P14_kinase, FAT, FATC, BclA, RUN; TM=M; 5.53
 426248; T18988; Hs.293668; ESTs; pkinase, none; 5.50
 418426; NM_003804; Hs.296327; receptor (TNFRSF)-interacting serine-thr; pkinase, death; TM=M; 5.43
 417085; AA194446; ; ESTs, Weakly similar to S55024 nebulin; ank, death, ZU5, EGF, kringle, trypsin, Nebulin, LIM; SS=M; 5.43
 447437; U07225; Hs.339; purinergic receptor P2Y, G-protein coupl; 7tm_1, SH2; TM=Y; SS=M; 5.40
 412247; AF022375; Hs.73793; vascular endothelial growth factor; PDGF; SS=M; 5.40
 434938; AW500718; Hs.8115; Homo sapiens, clone MGC:16169, mRNA, com; pkinase, TBQ, Rhodanese; TM=M; 5.38
 419355; AA428520; Hs.90061; progesterone binding protein; heme_1; TM=Y; SS=M; 5.35
 411188; BE161168; ; gb|PMO-HT0425-170100-002-a10 HT0425 Homo; adenylylase, none; 5.35
 422461; NM_003417; Hs.117077; zinc finger protein 264; zf-C2H2, KRAB, TFIIS; TM=M; 5.28
 426348; BE465586; Hs.17433; hypothetical protein FLJ20967; none, none; 5.25
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese, DSPc, Y_phosphatase, Ribosomal_S3_N; TM=M; 5.23
 429592; AB029041; Hs.209646; KIAA1118 protein; Troponin, Exo_endo_phos, IQ; TM=M; 5.22
 434821; AA159111; Hs.284281; Human putative ribosomal protein S1 mRNA; ER_lumen_recept, Ribosomal_L11, Ribosomal_L11_N; TM=Y; SS=M; 5.21
 434368; AW519020; Hs.73893; dopamine receptor D2; pkinase, SH3; none; 5.15
 405586; ; NM_000299; Homo sapiens pleckstrin 1 (ec; Armadillo_seg; TM=M; 5.13
 408176; AK001553; Hs.43436; adenylylase kinase 3 alpha like; adenylylase kinase, none; 5.12
 407443; AF227138; ; gb|Homo sapiens candidate taste receptor; none; TM=Y; SS=M; 5.11
 416817; AA398045; Hs.104679; ESTs; Furin-like, pkinase, Recept_L_domain, fn3; none; 5.10
 401886; ; NM_021783; Homo sapiens XEDAR (XEDAR); mR; TNFR_c6; TM=M; SS=M; 5.08
 410314; AW860708; Hs.18851; hypothetical protein FLJ10875; myb_DNA-binding, PAH, BAH, bromodomain, PHD, SET; TM=M; 5.08

- 401579; AL031447; ; Homo sapiens, clone IMAGE:4053044, mRNA; ; Neur_chan_LBD, Neur_chan_memb, none; 5.05
- 445873; AA250970; Hs.251946; poly(A)-binding protein, cytoplasmic 1-t; PABP, rrm, pkinase, 14-3-3; 5.05
- 417529; AA203634; ; gb:zx58b09.r1 Soares_fetal_liver_spleen; ; pkinase, UBA, KA1, none; 5.03
- 417527; AA203524; ; gb:zx56e10.r1 Soares_fetal_liver_spleen; ; SH3; SS=M; 4.98
- 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinas; ptkB; TM=M; 4.96
- 431321; AW136372; Hs.1852; acid phosphatase, prostate; acid_phosphat, none; 4.93
- 404298; ; C6001238*gi121715|sp|P26697|GTA3_CHICK; none, GST_C, GST_N, pkinase; 4.85
- 407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE:4299322, mRNA; ; none; TM=M; 4.82
- 424099; AF071202; Hs.139336; ATP-binding cassette, sub-family C (CFTR; ABC_tran, ABC_membrane; TM=Y; 4.73
- 422366; TB3882; Hs.97927; ESTs; pkinase, none; 4.64
- 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase; TM=M; 4.48
- 426925; NM_001196; Hs.131589; Homo sapiens cDNA: FLJ22373 fis, clone H; Esterase, enolase, Peptidase_S9; TM=M; 4.45
- 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1; TM=Y; SS=M; 4.40
- 400749; ; NM_003105; Homo sapiens sortilin-related; EGF, fn3, ldl_recept_a, ldl_recept_b, granulin, BNR; TM=Y; SS=M; 4.38
- 425721; AC002115; Hs.159309; uroplakin 1A; transmembrane4; TM=Y; SS=M; 4.33
- 444006; BE395085; Hs.10086; type I transmembrane protein Fn14; ldl_recept_a, PKD, MHC_1; TM=M; SS=Y; 4.31
- 400751; ; NM_003105; Homo sapiens sortilin-related; EGF, fn3, ldl_recept_a, ldl_recept_b, granulin, BNR; TM=Y; SS=M; 4.18
- 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase; SS=M; 3.90
- 422152; AA909249; Hs.112282; solute carrier family 30 (zinc transport; none, none; 3.88
- 458760; AL498631; Hs.111334; ferritin, light polypeptide; cystatin, ferritin, histone, HCO3_cotransp, SH3, RhoGAP, xan_ur_permease, FCH; SS=M; 3.85
- 441218; BE327561; Hs.202345; ESTs; none, WD40, E1-E2_ATPase, Cation_ATPase_N, Hydrolase; 3.78
- 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death, ZU5; SS=M; 3.76
- 451385; AA017656; ; gb:ze39h01.r1 Soares retina N2b4HR Homo ; Atrophin-1, enolase, Atrophin-1_Y_phosphatase, SH2, fibrinogen_C, TIM; 3.60
- 412604; AW978324; Hs.1904; protein kinase C, iota; pkinase, DAG_PE-bind, pkinase_C, OPR; TM=M; 3.30
- 409582; R27430; Hs.271565; ESTs; none, Neur_chan_LBD, Neur_chan_memb; 3.28
- 441155; AW161008; Hs.7719; GABA(A) receptor-associated protein; MAP1_LC3; SS=M; 3.23
- 436740; AW975133; ; gb:EST387239 MAGE resequences, MAGN Homo; none, EPH_b, fn3, pkinase, SAM; 3.20
- 418319; AW611703; Hs.190173; ESTs, Weakly similar to A46010 X-linked; none, IRK; 3.20
- 409744; AW675258; Hs.56265; Homo sapiens mRNA; cDNA DKFZp586P2321 (f; none, NA; NA; 3.13
- 418764; N30531; Hs.42215; protein phosphatase 1, regulatory subunit; none, none; 3.10
- 400846; ; sortilin-related receptor, L(DLR class); EGF, fn3, ldl_recept_a, ldl_recept_b, granulin, BNR; TM=Y; SS=M; 3.09
- 422005; BE266556; Hs.110702; Homo sapiens mRNA; cDNA DKFZp761E212 (fr; none, Na_H_Exchange; 3.03
- 426440; BE382758; Hs.169902; solute carrier family 2 (facilitated glc; sugar_tr; TM=Y; SS=M; 3.02
- 424187; AA336561; Hs.17287; ESTs, Weakly similar to S26689 hypothet; IRK; none; 2.98
- 425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member; death, TNFR_c6; TM=Y; SS=M; 2.93
- 401279; ; C13000351*gi2494033|sp|Q64398|KGD_MES; none, none; 2.88
- 406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte growth fa; Sema, pkinase, TIG, PSI; none; 2.83
- 447081; Y13898; Hs.17287; potassium inwardly-rectifying channel, s; IRK; TM=Y; 2.80
- 453619; H87648; Hs.33922; Homo sapiens, clone MGC:9084, mRNA, comp; pkinase; TM=M; 2.75
- 441699; AW511126; Hs.127572; ESTs; none, Aa_trans; 2.73
- 458781; AL444821; Hs.63085; ESTs, Weakly similar to MPP3_HUMAN MAGUK; SH3, PDZ, Guanylate_kin, L27; TM=M; 2.73
- 446913; AA430650; Hs.16529; transmembrane 4 superfamily member (tet; transmembrane4; TM=Y; SS=M; 2.70
- 453487; R31770; Hs.56562; ESTs; 7tm_1, none; 2.68
- 421279; AW664878; Hs.106645; ESTs; pkinase, none; 2.68
- 419720; AA249131; Hs.337778; hypothetical protein FLJ11068; none, none; 2.65
- 452345; AA293279; Hs.29173; hypothetical protein FLJ20515; DSPc; TM=M; 2.63
- 422247; U18244; Hs.113602; solute carrier family 1 (high affinity a; SDF; TM=Y; 2.62
- 425212; AW962253; Hs.171618; ESTs; pkinase, none; 2.60
- 427344; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin) receptor; Neur_chan_LBD, Neur_chan_memb; TM=Y; SS=M; 2.58
- 423629; AW021173; Hs.18612; Homo sapiens cDNA: FLJ21909 fis, clone H; voltage_CLC, CBS; none; 2.55
- 456737; BE247203; Hs.124831; CGI-67 protein; abhydrolase_2; TM=M; SS=M; 2.53
- 421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2; 7tm_1; TM=Y; SS=M; 2.53
- 424028; AF055084; Hs.153692; Homo sapiens cDNA FLJ14354 fis, clone Y7; none, none; 2.50
- 448324; AL571356; Hs.34174; ESTs, Moderately similar to ALU8_HUMAN A; ICE_p20, CARD, ICE_p10, none; 2.50
- 402256; ; Target Exon; pkinase, UBA, none; 2.43
- 452258; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fis, clone HE; GDI, 7tm_1, none; 2.40
- 419169; AW851980; Hs.262346; ESTs, Weakly similar to S72482 hypothet; none, spectrin, SH3, PH, CH; 2.40
- 420634; S42457; Hs.1323; cyclic nucleotide gated channel alpha 1; cNMP_binding, lon_trans; TM=Y; 2.35
- 419630; W57756; ; gb:zd20g10.r1 Soares_fetal_heart_NbHH19W; z-C3HC4, none; 2.35
- 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1; TM=Y; SS=M; 2.35
- 400704; ; Target Exon; lig_chan, SBP_bac_3, ANF_receptor; TM=Y; SS=M; 2.33
- 400149; ; Eos Control; acid_phosphat; TM=Y; SS=M; 2.30
- 459327; AW149706; Hs.7859; gb:zd41d02.x1 NCL_CGAP_Bm50 Homo sapien; PHD, PWWP, SET, pkinase, ig; 2.30
- 452220; BE158006; Hs.212296; ESTs; integrin_A, FG-GAP, none; 2.25
- 416890; H84078; Hs.108551; ESTs; pkinase, none; 2.23
- 408354; AL382803; Hs.159235; ESTs; none, none; 2.23
- 452203; X57522; ; transporter 1, ATP-binding cassette, sub; ABC_tran, ABC_membrane, SRP54, Thymidylate_kin; TM=Y; SS=M; 2.21
- 405093; ; C12001101*gi17522643|pir|T32733 AMPA g; none, none; 2.20
- 412723; AA648459; Hs.335951; hypothetical protein AF301222; none; TM=M; 2.20
- 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none, none; 2.18
- 417185; NM_002484; Hs.81469; nucleotide binding protein 1 (E.coli Min; ParA, far4_NiH, ArsA_ATPase; TM=M; 2.18
- 433222; AW514472; Hs.238415; dickkopf (Xenopus laevis) homolog 4; none, PHO4; 2.18
- 413627; BE182082; Hs.246973; ESTs; Armadillo_seg, IB8; TM=M; 2.18
- 407415; AF073328; ; gb:Homo sapiens tetracycline transporter; none, none; 2.15
- 450592; AL701555; Hs.202562; ESTs; pkinase, none; 2.15
- 428767; AL421972; Hs.98802; ESTs, Moderately similar to T14342 NSD1 ; none, pkinase, ig; 2.15
- 429012; AW629596; Hs.194726; BCL2-associated athanogene 4; Sm, BAG; SS=M; 2.15
- 419122; AL401360; Hs.44410; ESTs; ABC_tran, ABC_membrane, none; 2.10
- 446420; AW016693; Hs.135614; ESTs; lon_trans, none; 2.05
- 420076; AA827860; Hs.293717; ESTs; DUF59, pkinase; 2.05
- 409416; AW388359; Hs.10667; ESTs; transmembrane4; TM=Y; SS=M; 2.03
- 428768; AA477989; Hs.98800; ESTs; TPR, 7tm_1; 2.03
- 427001; NM_006482; Hs.173135; dual-specificity tyrosine-(Y)-phosphoryl; pkinase; TM=M; 2.03

453709; AL119133; ; protein kinase C substrate 80K-H; none,histone; 2.03
 423341; AW242394; Hs.108660; ESTs; none,none; 2.00
 456772; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; Ig;TM=Y;SS=M; 1.88
 427786; BE407863; Hs.256871; ESTs; none,FG-GAP,7tm_1; 1.65
 423508; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; Ig;TM=Y;SS=M; 1.00
 447993; AW139525; Hs.170362; ESTs; none,none; 1.00

TABLE 58B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

414883	8371_2	AF274943 BG494894 A1719075 AA908763 A1935150 A1422691 AA910644 AA583187 BM272167 A1828996 AA527373 AW972459 A1831360 AA772418 A1033892 AA100926 AU154749 A1459432 A123513 A1094597 A1740817 A1991988 A1090262 A1312104 B1256707 AA459522 AA416871 A1075239 A1339996 AA701623 A1139549 A1336880 AA633648 A1989380 A1362835 AA399239 A1146955 BF514270 N92892 A1348243 A1278887 AA459292 A1494230 BF507531 A1492600 AA862596 AW613002 AA293140 AA235549 BF108854 AA954344 N49682 A1457100 AW589407 AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 A1537692 A1203723 A1857576 AA584410 AW371667 BM172363
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 A1681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 A1905821 X56196 BE938355 AA628440 BE833808 BF224205 AA709126 BE673807 A1923886 AA947932 A1276125 A1185720 AW510698 AA987230 BE467708 AW898628 AW698544 A1146984 AW043642 A1288245 A1186932 A1635262 A1139455 A1298739 A1813854 A1024768 BE699445 BE699444 A1707807 D52654 A1214518 A1004723 A1698085 AW087420 A1565133 AA845571 AW898622 BF110144 AW513280 A1061126 BF362770 A1268939 A1436818 BF475318 A1024767 BE174213 AA757598 AA513019 AA902959 A1860794 A1334784 BF108411 BM310532 AW513771 A1951391 A1337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 A1922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D62477 D55017 BF955933 BG623563 AV646254 AA463522 B1003244 A1299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 A1091537 BF096583 AA345570 H48870 H08720 T83523 B1039626 B1037700 R00353 BF155184 N98343 N79072 H01812 T55581 X75684 AL573167 A1445461 A1453743 A1983655 A1564844 AA977180 A1694111 A1591358 AW071625 A1678712 A1720939 A1927769 BE439796 A1963432 AA292956 AW192593 A1865838 A1596905 A1424384 A1161312 A1911921 A1597801 B1494959 A1240988 A1492554 AW262737 BE044033 AW008570 AW629505 B1494958 AA088439 A1706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 A1799814 AA128575 A1671727 A170033 BE646195 AW779725 AA903050 AA147228 AA404570 A1075878 W38161 A1972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 A1990245 AA662517 T32487 A1800106 A1333170 A1859160 W45410 A1990827 AW275048 AA182640 AA478328 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C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 A1377596 C06111 AW088968 BE811404 BE811472 A1865912 A1925607 A1871950 A1093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 B1044896 A1744233 AW984527 C17504 BF843883 A1248307 BE773463 A1567995 W60075 BF941183 A1738844 BE811458 BE773481 A1262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 A1344943 A1348877 A1334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 B1755027 BG505731 BG008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 B1259821 BG741786 B1868522 AU135866 B1552770 B1259210 B1256520 B1255569 BG485098 B1258228 BG498501 BM044512 AU133984 AL556586 BE745111 B1222633 AU133917 BG288151 B1260715 B1550550 BG500773 B1551761 BG707601 B1818593 BF691383 BG721129 BG541578 BE906666 BG751098 B1224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 B1260895 AW651691 BM048974 BM043805 BG142185 AA315188 A1446615 C06300 BG497644 AA088544 A1815887 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 B1870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 X75684 AL573167 A1445461 A1453743 A1983655 A1564844 AA977180 A1694111 A1591358 AW071625 A1678712 A1720939 A1927769 BE439796 A1963432 AA292956 AW192593 A1865838 A1596905 A1424384 A1161312 A1911921 A1597801 B1494959 A1240988 A1492554 AW262737 BE044033 AW008570 AW629505 B1494958 AA088439 A1706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 A1799814 AA128575 A1671727 A170033 BE646195 AW779725 AA903050 AA147228 AA404570 A1075878 W38161 A1972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 A1990245 AA662517 T32487 A1800106 A1333170 A1859160 W45410 A1990827 AW275048 AA182640 AA478328 A1298935 AW085158 AW471421 AW103470 AW300456 AW191997 A1823466 AA962397 AA136658 A1251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 A1769516 AW772283 AA010631 A1692846 A1061065 H080983 R79933 A1950693 A1245632 A1349390 AA148284 A1798502 AA487893 A1621320 AW194272 C06365 AA953883 BE858936 A1918523 A1872628 A1927217 A1453453 A1189366 AW338678 A1261359 A1500576 BF477735 A1032569 A1972899 A1985583 Z28771 A1363829 A1693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 A1650338 BE773499 A1745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 A1582462 A1686240 BE773500 A1244845 A1565439 A1918453 A1472527 A1446740 AA035576 AA191414 AW674145 C05782 A1589264 D57558 A1468237 A1432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 A1928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 A1377596 C06111 AW088968 BE811404 BE811472 A1865912 A1925607 A1871950 A1093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 B1044896 A1744233 AW984527 C17504 BF843883 A1248307 BE773463 A1567995 W60075 BF941183 A1738844 BE811458 BE773481 A1262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 A1344943 A1348877 A1334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 B1755027 BG505731 BG008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 B1259821 BG741786 B1868522 AU135866 B1552770 B1259210 B1256520 B1255569 BG485098 B1258228 BG498501 BM044512 AU133984 AL556586 BE745111 B1222633 AU133917 BG288151 B1260715 B1550550 BG500773 B1551761 BG707601 B1818593 BF691383 BG721129 BG541578 BE906666 BG751098 B1224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 B1260895 AW651691 BM048974 BM043805 BG142185 AA315188 A1446615 C06300 BG497644 AA088544 A1815887 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 B1870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 X75684 AL573167 A1445461 A1453743 A1983655 A1564844 AA977180 A1694111 A1591358 AW071625 A1678712 A1720939 A1927769 BE439796 A1963432 AA292956 AW192593 A1865838 A1596905 A1424384 A1161312 A1911921 A1597801 B1494959 A1240988 A1492554 AW262737 BE044033 AW008570 AW629505 B1494958 AA088439 A1706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 A1799814 AA128575 A1671727 A170033 BE646195 AW779725 AA903050 AA147228 AA404570 A1075878 W38161 A1972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 A1990245 AA662517 T32487 A1800106 A1333170 A1859160 W45410 A1990827 AW275048 AA182640 AA478328 A1298935 AW085158 AW471421 AW103470 AW300456 AW191997 A1823466 AA962397 AA136658 A1251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 A1769516 AW772283 AA010631 A1692846 A1061065 H080983 R79933 A1950693 A1245632 A1349390 AA148284 A1798502 AA487893 A1621320 AW194272 C06365 AA953883 BE858936 A1918523 A1872628 A1927217 A1453453 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BE811453 BE614379 BF844522 B1044896 A1744233 AW984527 C17504 BF843883 A1248307 BE773463 A1567995 W60075 BF941183 A1738844 BE811458 BE773481 A1262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 A1344943 A1348877 A1334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 B1755027 BG505731 BG008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 B1259821 BG741786 B1868522 AU135866 B1552770 B1259210 B1256520 B1255569 BG485098 B1258228 BG498501 BM044512 AU133984 AL556586 BE745111 B1222633 AU133917 BG288151 B1260715 B1550550 BG500773 B1551761 BG707601 B1818593 BF691383 BG721129 BG541578 BE906666 BG751098 B1224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 B1260895

			AW651691 BM048974 BM043805 BG142185 AA315188 AA466115 C06300 BG497644 AA088544 A1815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308635 F00242 AA376086 AA316988 AA343799 B1870221 BE910282 BG538748 AW860564 AV732879 D18654 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 AW976398 A1147061 AA765223 AA743380 A1803927 BC012771 BG397153 BF366196 AA337277 AA319285 AW843252 B1030997 AA921874 AW188822 B1027862 A1347618 A1361453 A1088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 B1007625 B1027864 B1009100 B1006275 B1006270 B1031000 B1028864 B1006277 B1007627 B1006266 B1006991 B1006990 B1007763 B1007762 BG997377 AA150780 B1033518 B1027818 BG015789 B1033807 AA341445 T23514 A1655785 T59708 AA224827 T59843 BE156903 BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG861122 AA224498 AA308542 AW821833 BF902155 A1732411 BG778834 BG283641 BE748279 AA418798 BM129553 BM129126 BM129292 BM128865 A1808418 A1689932 A1806573 BF431808 AW872985 AW166269 H73241 T16182 A1264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 A1797007 BE045543 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 B1022902 B1673932 B1910138 NM_003899 D63476 AA778936 AA452871 A1052466 AW014138 AA448725 BE673088 AW026198 B1856378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 A1032663 AA704686 AA652189 AA179463 AL535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE246232 D17055 AW013876 AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 AL044534 AA258853 B1037915 AA448037 BM461769 B1825965 BE763352 AW167531 Z45588 AV721881 AA527273 A1573219 AA457036 AW439651 AW264418 AA577618 A1802954 AA902292 AA468752 A1380374 AA722690 A1867708 AA916982 A1291576 AW190427 A1338089 A1653744 A1036665 AW513541 AW440077 A1370014 AA904269 AW188378 A1671644 AW193386 A1261832 AA775336 BF436811 A1582703 A1278635 BE440186 AA617898 AA648948 B1491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 A1369564 AW503675 AA777194 BE501048 BF222087 AA042973 A1868087 AA911460 Z41274 A1919082 T16746 AA447634 A1282427 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916696 AW444935 M78398 AW581147 AW608258 AA651910 AA132152 AW806295 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW964920 AA325930 B1833627 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG988685 AA456880 BG001842 BF809452 AW892083 BF944342 T49551 W69981 BF764519 T15869 AA132030 BC000486 BC001930 U15008 NM_004597 BG326561 AV761269 BF212132 BG113313 B1838038 BG944198 BG255198 BG164334 BM013507 AV682717 BF028761 BG755489 BG030141 BG105499 BE440103 BF727449 BM454228 BG912181 BM015197 BG395995 A126579 AW248204 B1857394 B1857319 BG944205 BG323958 B1092930 AV756576 AA280959 BF033076 BE539360 AW247174 BG107836 BE796975 BG170920 A1148142 A1082009 A136349 AV713409 BF685591 BE616029 AV713166 BE909458 BE743868 BM018218 A1340153 BE792567 BE206806 A1159916 A1184271 BE208585 B1862286 C18760 BC219364 A122677 BE207297 BF754798 AA314384 BE873951 BG207294 A1148198 A1336189 A1141094 A1308985 BF220098 A1143289 BE856397 AA644001 BE575402 A1364708 A1052809 A140082 BF081542 A1342428 A1479625 AA278456 A1750163 BE707501 BG944510 AA314616 AA315774 BF360721 BE738404 AA814194 AA477195 AA932107 F36858 AA363159 BE865458 AA354147 AW904224 A1055855 AA380365 F28474 D59140 AA341946 AA993339 AA323350 F24344 AA374436 BG942081 AA636015 AA852919 T31486 F36334 BG943190 T30319 BG943153 BG941836 T32569 T31160 AA311749 BE710086 BE709911 W23826 BG941639 BF769034 A0026407 AA229555 AV755340 AV714380 AL138129 BG003205 AL138179 B1021773 BE064231 AL520734 B1666852 BF870571 BF945361 BF945354 A1770086 B1861138 A1421079 AL043200 BG683612 AW946265 NM_003899 D63476 BM456434 AA778936 AA452871 A1052466 AW014138 AA448725 BE673088 AW028198 B1856378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 A1032663 AA704686 AA652189 AA179463 AL535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE246232 D17055 AW013876 AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 AL044534 AA258853 B1037915 AA448037 BM461769 B1825965 BE763352 AW167531 Z45588 AV721881 AA527273 A1573219 AA457036 AW439651 AW264418 AA577618 A1802954 AA902292 AA468752 A1380374 AA722690 A1867708 AA916982 A1291576 AW190427 A1338089 A1653744 A1036665 AW513541 AW440077 A1370014 AA904269 AW188378 A1671644 AW193386 A1261832 AA775336 BF436811 A1582703 A1278635 BE440186 AA617898 AA648948 B1491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 A1369564 AW503675 AA777194 BE501048 BF222087 AA042973 A1868087 AA911460 Z41274 A1919082 T16746 AA447634 A1282427 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916696 AW444935 M78398 AW581147 AW608258 AA651910 AA132152 AW806295 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW964920 AA325930 B1833627 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG988685 AA456880 BG001842 BF809452 AW892083 BF944342 T49551 W69981 BF764519 T15869 AA132030 BM048470 BG983877 N92089 Z43545 F05783 R35182 H22769 H71928 H63921 R94394 AW195830 AA630220 F02030 R60760 R08204 H71929 BE484731 R62558 H63520 H77840 A1515501 F01971 T71768 N55275 AA883505 AW606824 AA704682 N74193 W57593 AW573776 H60439 A1076352 R31485 BE160931 AW130730 BE180869 AW580256 AW902073 BE702158 AW382079 N76884 BF431013 H38156 AV648937 H80573 AW902569 AW902557 AW902654 AW902641 AW902650 AW902741 AW902644 Z25288 R85077 F00323 D82802 T27434 BF184345 AA364846 B1494468 AA775693 BF195801 AA749190 A1480223 BE327332 A1470017 AW628345 A1917472 A1972264 A1375571 A1652583 A1656167 A1983110 BE550378 AW015085 BE552318 A1631475 A1433447 AA534540 A1865480 A1468119 BF110875 AW512059 W58721 AA827482 R59357 AW370493 AA923304 A1660828 AA502611 B1017370 AA039704 W65393 BE938514 W65295 BF919626 B1759440 B1838879 AA336207 F12441 BF171187 BE185031 T74062 AW904410 AA280078 BF919629 AK056605 AK056969 AW380724 AA195950 F21243 Z17422 AA176595 AA176955 AA194390 BC005933 BC017866 AA196396 Z24810 AA181361 A1193115 AA086465 F25194 F30130 AA180013 A1346143 F20589 F20620 F29371 F32439 F25153 F32146 F26110 F28506 F25307 F27533 F20375 F32370 AA653078 BF574897 Z24852 F00172 T30560 AW449825 A1620346 BG986374 BE706521 C02691 A1596834 F31902 F26078 AA670099 BF475555 F30818 F37524 A1346558 F28050 F17933 F13637 C03413 A1092152 AA180743 AA085730 F21998 F20854 F18944 F31180 F37937 F37738 AA193162 Z17344 AA192546 AW821260 BE162466 BE161168 AA203634 AA203524 W88451 AA019761 AA017656 AA017374 AW975133 AA805813 AA729943 BF223647 AA204668 AA256086 BF574707 W57756 AA249070 B1096494 AA248011 BC003160 NM_001610 X12548 BG386585 B1760866 B1559619 BG323829 AU135543 B1834101 AU142120 AU124511 AU124889 A1558171 AU117286 B1824000 BG386610 B1753285 B1223475 AU134828 BM126369 BE206493 BF751498 AL544274 AY007137 B182892 BE870130 BF771242 B1835451 B1765655 B1820955 B1223344 BG015924 B1758984 AL527413 BF310588 B13870 N23974 BE514914 T48863 AW860257 BF334625 AA883860 AU144168 AA442562 AU159491 AU148353 AA584123 A148667 A1377256 AW664004 A1871712 A141486 A1332351 A1339094 BE206109 AW19033 A1817729 A1332490 A149455 A1857411 A1763154 A1751608 A1377222 A1081956 AW664229 A1275872 AW168546 AA975270 A1367408 A1687729 A1269164 AW105344 BM193081 BE550930 A1082116 AA854691 A1056249 A1221082 A1290113 D51818 AA732409 BG055125 N85878 AU156121
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5	452203	2630_1	BF093671 AA053070 T28548 AL570460 B1006862 B1007207 AA373620 W95069 AA629136 AA708164 A1014886 AW168697 D51623 AA577168 A1094208 AA028946 AA975078 R16815 BG151132 A1276297 D51676 BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 B1823519 B1770023 AL554969 B1489906 A1304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 A1569694 AW073296 A1361433 AA584644 AA487429 BE858232 AA838610 A1539114 A1719375 A1829129 BG057675 A1423422 AU158860 BE300655 AW170777 AA586956 AL571889 AL556850 AL576404 AL582800 B1256544 BF342301 BG875994 AA054458 AA353161 A1940434 BE816522 AL577636 A1479650 AW150377 AU154395 AW951271 A1032220 A1819778 A1346733 AW771150 AW512525 A1249904 AA279809 A1352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 B1819184 AV660190 AL556475 A1620020 AW089888 AW079179 Z21518 AA687601 F04651 A1783961 T57198 A1433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 A1266514 A1538823 A1475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 A1682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601 AA587842 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 B1560216 B1753586 AK057669 AK054977 AL519747 BE893744 BM313248 BG913430 H80793 BF813504 N36311 N39276 H95973 BF791919 BE739392 BE144239 AA074615 A1291059 A1681053 AA702355 BF439899 AW055166 A1096957 BF223853 AL119659 A1692209 BM312961 A1869297 BE466252 A1292024 AA402764 A1214620 AA765312 BF380770 AA442682 AL519746 AW295039 A1037878 AW473433 A1499437 A1401618 A1130831 AA427406 A1042138 BG272488 A1828769 A1828764 A1189390 W84635 AA398496 AA761672 AA699520 A1200406 N68093 A1143913 AA993133 AA613306 A1050971 AA661905 AA722687 A1749977 AA829345 BG057324 BF001339 AA910169 AA765133 A1360722 A1701849 A1365083 H95974 A1830377 A1312866 A1370491 BE858907 N62185 AA705746 BE379632 W38303 A1440333 AW367670 AW367640 N77131 BF993216 A1858263 W52329 N68106 R83113 R85153 BE380058 AA082537 AA729731 W23495 W31190 BF995236 BF968827 BF355168 N24508 AA215711 BF170735 AA280395 BE738851 AW367707 AA630879 AA428420 R76236 BG567847 N25931 AA173568 A1073567 AA004957 A1539585 N95093 H99798 H95072 H96853 AA215712 AA034214 R85096 H82051 H80794 R44954 AA278972 H68352 H68346 R94750 R89010 R67951 H65817 N24891 AA173731 A1693577 BE181027 AA709461 BE181002 W60239 BF987598 BF995279 H17483 R76237 AL119133 BF964815 AW663315 H65903 H17591 R20167 AA310039 R58734 R58506	
10	453709	59915_1	AK057669 AK054977 AL519747 BE893744 BM313248 BG913430 H80793 BF813504 N36311 N39276 H95973 BF791919 BE739392 BE144239 AA074615 A1291059 A1681053 AA702355 BF439899 AW055166 A1096957 BF223853 AL119659 A1692209 BM312961 A1869297 BE466252 A1292024 AA402764 A1214620 AA765312 BF380770 AA442682 AL519746 AW295039 A1037878 AW473433 A1499437 A1401618 A1130831 AA427406 A1042138 BG272488 A1828769 A1828764 A1189390 W84635 AA398496 AA761672 AA699520 A1200406 N68093 A1143913 AA993133 AA613306 A1050971 AA661905 AA722687 A1749977 AA829345 BG057324 BF001339 AA910169 AA765133 A1360722 A1701849 A1365083 H95974 A1830377 A1312866 A1370491 BE858907 N62185 AA705746 BE379632 W38303 A1440333 AW367670 AW367640 N77131 BF993216 A1858263 W52329 N68106 R83113 R85153 BE380058 AA082537 AA729731 W23495 W31190 BF995236 BF968827 BF355168 N24508 AA215711 BF170735 AA280395 BE738851 AW367707 AA630879 AA428420 R76236 BG567847 N25931 AA173568 A1073567 AA004957 A1539585 N95093 H99798 H95072 H96853 AA215712 AA034214 R85096 H82051 H80794 R44954 AA278972 H68352 H68346 R94750 R89010 R67951 H65817 N24891 AA173731 A1693577 BE181027 AA709461 BE181002 W60239 BF987598 BF995279 H17483 R76237 AL119133 BF964815 AW663315 H65903 H17591 R20167 AA310039 R58734 R58506	
15	TABLE 58C			
20	Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495. Strand: Indicates DNA strand from which exons were predicted. NL_position: Indicates nucleotide positions of predicted exons.			
25	Pkey	Ref	Strand	NL_position
30	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807
35	404942	7382153	Plus	92095-92252
40	400752	7331445	Minus	36215-36461
45	400496	9743564	Plus	41515-41695
50	404568	9966995	Minus	92893-93116
55	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
60	402328	4464283	Minus	13758-13922,14558-14752
65	404891	7329392	Plus	84974-85125
70	405036	7543748	Minus	121957-122129
75	400845	9188605	Plus	34428-34612
80	403212	7630897	Minus	156037-156210
85	401927	3873185	Minus	112000-112137
90	Table 59A lists about 1170 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos HuO3 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 8.2. The "average" prostate cancer level was set to the 75 th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 50 th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10 th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.			
95	TABLE 59A: ABOUT 1170 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES			
100	Pkey:	Unique Eos probeset identifier number		
105	ExAccn:	Exemplar Accession number, Genbank accession number		
110	UnigeneID:	Unigene number		
115	Unigene Title:	Unigene gene title		
120	R1:	Ratio of prostate tumor to normal adult body tissue		
125	Pkey	ExAccn	Unigene ID	Unigene Title
130	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,
135	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen
140	420923	AF097021	Hs.273321	differentially expressed in hematopoietic
145	416854	H40184	Hs.80296	Purkinje cell protein 4
150	425075	AA506324	Hs.1852	acid phosphatase, prostate
155	431103	M57399	Hs.44	ptelotrophin (heparin binding growth fac
160	434666	AF151103	Hs.112259	T cell receptor gamma locus
165	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom
170	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina
175	420154	A1093155	Hs.95420	JM27 protein
180	428336	AA503115	Hs.183752	microsaminoprotein, beta-
185	400287	S39329	Hs.181350	kallikrein 2, prostatic
190	416602	NM_006159	Hs.79389	nel (chicken)-like 2
195	428398	A1249368	Hs.98558	ESTs
200	432441	AW292425	Hs.163484	ESTs
205	414569	AF109298	Hs.118258	prostate cancer associated protein 1
210	417771	AA804698	Hs.82547	retinoic acid receptor responder (lazarus
215	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and

	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	49.6
	446057	AJ420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	48.0
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	46.8
5	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	45.0
	427674	NM_003528	Hs.2178	H2B histone family, member Q	44.9
	432374	W58815	Hs.301885	Homo sapiens cDNA FLJ111346 fis, clone PL	44.5
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	44.5
	415314	N88802	Hs.5422	glycoprotein M6B	43.2
10	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	41.9
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	41.1
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	40.5
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	39.5
	439176	AJ464444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	39.3
15	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	39.0
	447726	AL137638	Hs.19368	matrin 2	38.6
	426174	AA547959	Hs.115838	ESTs	38.1
	425071	NM_013989	Hs.154424	delodilase, lodothyronine, type II	38.0
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	37.5
20	414217	AJ309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fs, clone L	37.0
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	35.5
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	35.1
	453086	AW294631	Hs.11325	ESTs	35.1
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	34.9
25	427665	AF134803	Hs.180141	cofilin 2 (muscle)	34.9
	415539	AJ733881	Hs.72472	BMP-R1B	34.9
	428411	AW291464	Hs.10338	ESTs	34.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	34.3
	401424			NM_001172:Homo sapiens arginase, type II	34.0
30	452114	N22687	Hs.8236	ESTs	34.0
	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	33.8
	448045	AJ297436	Hs.20166	prostate stem cell antigen	33.1
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	32.9
	432101	AJ918950	Hs.123642	EphA3	32.7
35	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	32.4
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	32.4
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	32.4
	414591	AJ888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	32.3
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	31.9
40	408380	AF123050	Hs.44532	diubiquitin	31.6
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	31.4
	453370	AJ470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.3
	408369	R38438	Hs.182575	solute carrier family 15 (H777 transport	31.2
	408001	AA046458	Hs.95296	ESTs	30.8
45	440274	R24595	Hs.7122	scrapie responsive protein 1	30.7
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	30.3
	442993	BE018582	Hs.166196	ATPase, Class I, type 8B, member 1	30.2
	433404	T32982	Hs.102720	ESTs	29.6
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	29.6
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	29.3
	459290	NM_001546	Hs.34853	Inhibitor of DNA binding 4, dominant neg	29.2
	418827	BE327311	Hs.47166	HT021	29.0
	410330	AW023830	Hs.46786	ESTs	28.6
	450377	AB033091	Hs.74313	KIAA1265 protein	28.6
55	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	28.5
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	28.2
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	27.7
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	27.7
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	27.6
60	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.4
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	27.4
	407202	N58172	Hs.109370	ESTs	27.4
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	27.4
	442870	N45018	Hs.8769	hypothetical protein DKFZp761J17121	27.3
65	403047			NM_005656:Homo sapiens transmembrane pr	27.2
	407709	AA456135	Hs.23023	ESTs	27.0
	433444	AW975324	Hs.129816	ESTs	26.8
	415989	AJ267700	Hs.317584	ESTs	26.8
	430539	AK001489	Hs.242894	ADP-ribosylation factor-like 1	26.5
70	408221	AA912183	Hs.47447	ESTs	26.5
	448519	AW175665	Hs.278695	Homo sapiens protein mRNA, complete cds	26.4
	437179	AA393508	Hs.300642	serologically defined colon cancer antig	26.4
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	26.2
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	26.2
75	400292	AA250737	Hs.72472	BMP-R1B	26.0
	433647	AA603367	Hs.222294	ESTs	26.0
	429220	AW207206	Hs.136319	ESTs	25.8
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	25.6
	448106	AI800470	Hs.171941	ESTs	25.5
80	415992	C05837	Hs.145807	hypothetical protein FLJ13593	25.5
	452792	AB037765	Hs.30652	KIAA1344 protein	25.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	25.2
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	24.9
	418961	AW967646	Hs.23023	ESTs	24.8

	451027	AW519204	Hs.40808	ESTs	24.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	24.5
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	24.4
5	418396	AJ765805	Hs.26691	ESTs	24.1
	412088	AJ689496	Hs.108932	ESTs	24.1
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	24.0
	411644	H92064	Hs.278626	Arg/Abi-interacting protein ArgBP2	24.0
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	23.9
10	433466	AA508353	Hs.105314	relaxin 1 (H1)	23.7
	431657	AJ345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	23.6
	440995	T57773	Hs.10263	ESTs	23.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	23.2
	428695	AJ355647	Hs.189999	purinergic receptor (family A group 5)	23.1
	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	22.9
15	440260	AJ972867	Hs.7130	copine IV	22.5
	443622	AJ911527	Hs.11805	ESTs	22.2
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	22.0
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	21.9
20	450642	R39773	Hs.7130	copine IV	21.9
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	21.8
	435981	H74319	Hs.188620	ESTs	21.8
	450693	AW450461	Hs.203965	ESTs	21.7
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	21.7
25	423242	AL039402	Hs.125783	DEME-6 protein	21.7
	408621	AJ970672	Hs.46638	chromosome 11 open reading frame 8	21.6
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	21.5
	404210			NM_005936:Homo sapiens myeloid/lymphoid	21.5
	417622	AW298163	Hs.82318	WAS protein family, member 3	21.5
30	419526	AJ821895	Hs.193481	ESTs	21.5
	442799	AJ564739	Hs.68505	ESTs	21.4
	424846	AU077324	Hs.1832	neuropeptide Y	21.3
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	21.3
	429922	Z97630	Hs.226117	H1 histone family, member 0	21.3
35	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	21.3
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	21.2
	431474	AL133990	Hs.190642	ESTs	21.2
	430887	N66801	Hs.260287	KIAA1841 protein	21.1
	416655	AW968813	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	21.1
40	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	21.1
	445133	AW157646	Hs.153506	ESTs	21.0
	421513	X00949	Hs.105314	relaxin 1 (H1)	21.0
	413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	20.8
	446795	AJ797713	Hs.156471	ESTs	20.7
45	440774	AJ420611	Hs.127832	ESTs	20.7
	407168	R45175	Hs.117183	ESTs	20.6
	417511	AL049176	Hs.82223	chordin-like	20.6
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein	20.6
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	20.6
50	411800	N39342	Hs.103042	microtubule-associated protein 1B	20.5
	446469	BE094848	Hs.15113	homogenisate 1,2-dioxygenase (homogeni	20.5
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	20.5
	409758	AW474950	Hs.182258	ESTs, Weakly similar to I78885 serine/th	20.5
	424897	D63216	Hs.153684	frizzled-related protein	20.5
55	430280	AA361258	Hs.237868	interleukin 7 receptor	20.4
	401197			ENSP00000229263*-HSPC213.	20.3
	452814	AJ092790	Hs.334703	hypothetical protein FLJ14529	20.3
	429918	AW873986	Hs.119383	ESTs	20.2
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Or	20.2
60	453469	AB014533	Hs.33010	KIAA0633 protein	20.2
	444922	AJ921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	20.0
	436396	AJ683487	Hs.152213	wingless-type MMTV integration site fami	20.0
	419440	AB020689	Hs.50419	KIAA0882 protein	20.0
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	19.9
65	441690	R81733	Hs.33106	ESTs	19.9
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	19.8
	423044	AA320829	Hs.97266	protocadherin 18	19.8
	410929	H47233	Hs.30643	ESTs	19.7
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	19.7
70	431556	AF016028	Hs.183428	sarcomspan (Kras oncogene-associated gene	19.6
	409632	V74001	Hs.55279	serine (or cysteine) proteinase inhibito	19.6
	444190	AJ878918	Hs.10526	cysteine and glycine-rich protein 2	19.6
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	19.5
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	19.4
75	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	19.4
	430187	AJ799909	Hs.158989	ESTs	19.3
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	19.3
	434423	NM_006769	Hs.3844	UIM domain only 4	19.2
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	19.1
80	409062	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	19.0
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	18.9
	436032	AA150797	Hs.109276	latxin protein	18.9
	413548	AJ834273	Hs.9711	novel protein	18.9
	418565	AK001529	Hs.86149	phosphoinositol 3-phosphate-binding prot	18.9

	445929	AI089660	Hs.323401	dpy-30-like protein	18.8
	453160	AI263307	Hs.239884	H2B histone family, member L	18.8
	439897	NM_015310	Hs.6763	KIAA0942 protein	18.8
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	18.8
5	434987	AW975114	Hs.293273	ESTs	18.7
	407690	R47799	Hs.266957	hypothetical protein FLJ14281	18.7
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	18.7
	418819	AA228776	Hs.191721	ESTs	18.7
10	450831	R37974	Hs.25255	ESTs	18.7
	415691	AW963979	Hs.24723	ESTs	18.7
	417124	BE122762	Hs.25338	ESTs	18.7
	445162	AB011131	Hs.12376	piccolo (presynaptic cytomatrix protein)	18.6
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	18.5
	410099	AA081630	Hs.169387	KIAA0036 gene product	18.5
15	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	18.5
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	18.5
	436420	AA443966	Hs.31595	ESTs	18.4
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	18.4
20	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	18.3
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	18.3
	444931	AV652066	Hs.75113	general transcription factor IIIA	18.2
	437446	AA788946	Hs.16869	ESTs, Moderately similar to CA1C RAT COL	18.2
	439569	AW602166	Hs.222399	CEGP1 protein	18.1
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	18.1
25	424682	AW604804	Hs.151717	KIAA0437 protein	18.0
	432435	BE218886	Hs.282070	ESTs	17.9
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	17.8
	431121	AW971157		gb:EST383245 MAGE resequences, MAGL Homo	17.8
30	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	17.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	17.7
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	17.7
	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	17.6
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	17.6
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	17.5
35	430487	D87742	Hs.241552	KIAA0268 protein	17.4
	419355	AA428520	Hs.90061	progesterone binding protein	17.4
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	17.3
	423943	AF163570	Hs.135756	polymerase (DNA directed) kappa	17.3
40	434217	AW014795	Hs.23349	ESTs	17.3
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	17.2
	447809	AW207605	Hs.164230	ESTs, Highly similar to JC7266 3',5'-cyc	17.2
	430177	AW969233	Hs.302746	MSTP028 protein	17.2
	432473	AI202703	Hs.152414	ESTs	17.1
	421823	N40850	Hs.28625	ESTs	17.1
45	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	17.0
	420092	AA814043	Hs.88045	ESTs	17.0
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	17.0
	417426	NM_002291	Hs.82124	laminin, beta 1	17.0
50	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	17.0
	401747			Homo sapiens keratin 17 (KRT17)	17.0
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	17.0
	442369	AI565071	Hs.159983	ESTs	16.9
	432966	AA650114	Hs.325198	ESTs	16.9
55	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	16.8
	419536	AA603305		gb:np12d11.s1 NCL_CGAP_P13 Homo sapiens	16.8
	443745	AB039670	Hs.9728	ALEX1 protein	16.8
	438899	AF085833	Hs.136624	ESTs	16.8
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	16.8
60	442064	AI422867	Hs.88594	ESTs	16.8
	409385	AA071267		gb:zm61g01.r1 Stralagene fibroblast (937	16.5
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	16.4
	443801	AW206942	Hs.253594	ESTs	16.3
	437536	X91221	Hs.144465	ESTs	16.3
65	409196	NM_001874	Hs.334873	carboxypeptidase M	16.3
	438337	AK002058	Hs.6166	hypothetical protein FLJ11196	16.3
	416239	AL038450	Hs.48948	ESTs	16.3
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	16.2
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	16.2
70	409060	AI815867	Hs.50130	necdin (mouse) homolog	16.1
	442571	C06338	Hs.165464	ESTs	16.1
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	16.1
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	16.0
	450164	AI239923	Hs.30098	ESTs	16.0
75	429663	M68874	Hs.211597	phospholipase A2, group IVA (cytosolic,	16.0
	408990	AL022395	Hs.49526	F-box and leucine-rich repeat protein 4	16.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	16.0
	436024	AI800041	Hs.190555	ESTs	16.0
	412652	AI801777	Hs.6774	ESTs	16.0
80	456516	BE172704	Hs.222746	KIAA1610 protein	16.0
	452576	AB023177	Hs.29900	KIAA0960 protein	15.9
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	15.9
	434792	AA649253	Hs.132458	ESTs	15.9
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	15.9

	442787	W93048	Hs.250723	hypothetical protein MGC2747	15.9
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	15.9
	402812			NM_004930*:Homo sapiens capping protein	15.8
5	447313	U92981	Hs.18081	Homo sapiens clone DT1P186 mRNA, CAG rep	15.8
	413597	AW302885	Hs.117183	ESTs	15.7
	439677	R82331	Hs.164599	ESTs	15.7
	432527	AW975028	Hs.102754	ESTs	15.7
	413654	AA331881	Hs.75454	peroxiredoxin 3	15.7
10	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	15.7
	426501	AW043782	Hs.293616	ESTs	15.7
	435056	AW023337	Hs.5422	glycoprotein M6B	15.7
	414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	15.6
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	15.6
	434988	AI418055	Hs.161160	ESTs	15.6
15	435380	AA679001	Hs.192221	ESTs	15.6
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	15.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	15.6
	446377	AW014022	Hs.170953	ESTs	15.5
20	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	15.5
	415672	N53097	Hs.193579	ESTs	15.5
	450325	AI935962	Hs.26289	ESTs	15.5
	400294	N95796	Hs.278695	Homo sapiens prostate mRNA, complete cds	15.4
	443674	AI081330	Hs.145008	ESTs	15.4
25	415263	AA948033	Hs.130853	ESTs	15.4
	442081	AA401863	Hs.22380	ESTs	15.3
	415788	AW628686	Hs.78851	KIAA0217 protein	15.3
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	15.3
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	15.3
30	418693	AI750878	Hs.87409	thrombospondin 1	15.3
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	15.3
	443180	R15875	Hs.258576	claudin 12	15.2
	432437	W07088	Hs.293685	ESTs	15.2
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	15.2
35	446091	AW022192	Hs.200197	ESTs	15.2
	409341	AI963376	Hs.12532	chromosome 1 open reading frame 21	15.2
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	15.1
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	15.1
	453698	AA037615	Hs.42746	ESTs	15.1
40	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	15.1
	427707	NM_005578	Hs.180398	LIM domain-containing preferred transloc	15.1
	453308	AW959731	Hs.323099	ESTs	15.1
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	15.1
	433927	AI557019	Hs.116467	small nuclear protein PRAC	15.0
45	443162	TA9951	Hs.9029	DKFZP434G032 protein	15.0
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	15.0
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	15.0
	443912	R37257	Hs.184780	ESTs	15.0
	410297	AA148710	Hs.79914	lumican	15.0
50	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	14.9
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	14.9
	451652	AA018968	Hs.133536	ESTs	14.9
	406038	Y14443	Hs.88219	zinc finger protein 200	14.8
	408784	AW971350	Hs.63386	ESTs	14.8
55	453510	AI699482	Hs.42151	ESTs	14.8
	407894	AJ278313	Hs.41143	phospholipase-specific phospholipase	14.8
	433908	AW298141	Hs.157975	ESTs	14.8
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	14.8
	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	14.8
60	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	14.7
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	14.7
	447752	M73700	Hs.105938	lactotransferrin	14.7
	426044	AA502490	Hs.336695	ESTs	14.7
	403362			NM_001615*:Homo sapiens actin, gamma 2,	14.7
65	427982	NM_016156	Hs.181326	KIAA1073 protein	14.7
	407634	AW016569	Hs.136414	UDP-GlcNAc6betaGal beta-1,3-N-acetylgluc	14.7
	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 siml	14.7
	433226	AW503733	Hs.9414	KIAA1488 protein	14.6
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	14.6
70	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	14.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	14.6
	409264	NM_014937	Hs.52463	KIAA0966 protein	14.6
	432729	AK000292	Hs.278732	hypothetical protein FLJ20285	14.5
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (prol	14.5
75	410339	AI916499	Hs.298258	ESTs	14.5
	431992	NM_002742	Hs.2891	protein kinase C, mu	14.5
	424432	AB037821	Hs.146858	protocadherin 10	14.5
	431933	AI187057	Hs.132554	ESTs	14.5
	440749	W22335	Hs.7392	hypothetical protein MGC3199	14.5
80	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	14.5
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	14.5
	407021	U52077		gb:Human mariner1 transposase gene, comp	14.5
	413786	AW613780	Hs.13500	ESTs	14.5
	437866	AA156781	Hs.74170	metallothionein 1E (functional)	14.5

	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	14.4
	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	14.4
	443280	AA299688	Hs.24183	ESTs	14.4
	416836	D54745	Hs.80247	cholecystokinin	14.4
5	436860	H12751	Hs.5327	PRO1914 protein	14.3
	425174	D87450	Hs.154978	KIAA0261 protein	14.3
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	14.3
	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chain	14.3
	418994	AA296520	Hs.89545	selectin E (endothelial adhesion molecule)	14.2
10	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	14.2
	437718	AI927288	Hs.196779	ESTs	14.2
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeldt-Jakob)	14.2
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta)	14.2
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	14.2
15	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl)	14.2
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	14.1
	446494	AA63276	Hs.288906	WW Domain-Containing Gene	14.1
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	14.0
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	14.0
20	426423	NM_012446	Hs.169833	single-stranded-DNA-binding protein	14.0
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	14.0
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	13.9
	418848	AI820961	Hs.193465	ESTs	13.9
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	13.9
25	439518	W76326		gbzsd60d04.r1 Soares_fetal_heart_NbHH19W	13.9
	443967	AW294013	Hs.200942	ESTs	13.9
	424775	AB014540	Hs.153026	SWAP-70 protein	13.9
	411190	AA306342	Hs.69171	protein kinase C- α 2	13.9
	447384	AI377221	Hs.40528	ESTs	13.9
30	444880	AW118683	Hs.154150	ESTs	13.9
	433409	AI278802	Hs.25661	ESTs	13.9
	423201	NM_000163	Hs.125180	growth hormone receptor	13.9
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	13.9
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	13.8
35	429165	AW009886	Hs.118258	prostate cancer associated protein 1	13.8
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	13.8
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	13.8
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	13.8
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	13.8
40	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	13.8
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	13.8
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	13.8
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	13.7
	408622	AA056050	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	13.7
45	428054	AI948688	Hs.266619	ESTs	13.7
	444636	T96667	Hs.17877	ESTs	13.7
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	13.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	13.7
	452260	AA453208	Hs.28726	RAB9, member RAS oncogene family	13.7
50	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	13.7
	450316	W84446	Hs.226434	hypothetical protein MGC4643	13.7
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	13.7
	443634	H73972	Hs.134460	ESTs	13.7
	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	13.7
55	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	13.7
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	13.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	13.6
	416795	AI497778	Hs.20509	HBV pX associated protein-8	13.6
	410001	AB041036	Hs.57771	kallikrein 11	13.6
60	452242	R50956	Hs.159993	glycosyltransferase	13.6
	413231	D87461	Hs.75244	BCL2-like 2	13.6
	404641			NM_021965*:Homo sapiens phosphoglucomula	13.6
	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfam1	13.6
	414279	AW021691	Hs.101067	GCN5 (general control of amino-acid synt	13.6
65	411573	AB029000	Hs.70823	KIAA1077 protein	13.5
	417632	R20855	Hs.5422	glycoprotein M6B	13.5
	431467	N71831	Hs.256398	Homo sapiens mRNA: cDNA DKFZp434E0528 (f	13.5
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	13.5
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	13.5
70	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN !!!!	13.5
	418663	AK001100	Hs.41690	desmocollin 3	13.5
	452277	AL049013	Hs.28783	KIAA1223 protein	13.5
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	13.5
	447082	T85314	Hs.42644	thioredoxin-like	13.5
75	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	13.4
	415443	T07353	Hs.7948	ESTs	13.4
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	13.4
	442113	BE622187	Hs.99670	ESTs, Weakly similar to I38022 hypothei	13.3
	433517	AW022133	Hs.189638	ESTs	13.3
80	430829	AW451999	Hs.194024	ESTs	13.3
	453111	AB014598	Hs.31720	hephaestin	13.3
	435839	AF249744	Hs.25951	Rho guanine nucleotide exchange factor (13.3
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	13.3

5	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	13.3
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	13.3
	437323	AA371145	Hs.226627	leptin receptor	13.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	13.2
	433037	NM_014158	Hs.279938	HSPC067 protein	13.2
10	407938	AA905097	Hs.85050	phospholamban	13.2
	400860			Target Exon	13.2
	411031	W37943	Hs.34892	KIAA1323 protein	13.2
	436797	AA731491	Hs.336454	hypothetical protein MGC14879	13.2
	409277	T05558	Hs.156880	ESTs	13.2
15	434036	AI659131	Hs.197733	hypothetical protein MGC2849	13.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.2
	450755	AA010984	Hs.159464	ESTs	13.1
	450649	NM_001429	Hs.25272	E1A binding protein p300	13.1
	408495	W68796	Hs.237731	ESTs	13.1
20	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	13.1
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	13.1
	416987	D86957	Hs.80712	KIAA0202 protein	13.0
	453006	AI362575	Hs.167133	ESTs	13.0
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	13.0
25	415752	BE314524	Hs.78776	putative transmembrane protein	13.0
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	13.0
	417318	AW953937	Hs.12891	ESTs	13.0
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	12.9
	426034	AI276989	Hs.56123	Homo sapiens cDNA FLJ13443 fis, clone PL	12.9
30	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	12.9
	428218	AA424266	Hs.123642	EphA3	12.9
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	12.9
	448779	BE042877	Hs.177135	ESTs	12.8
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	12.8
35	417315	AI080042	Hs.336901	ribosomal protein S24	12.8
	428697	AW296451	Hs.24605	ESTs	12.8
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	12.8
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	12.8
	451099	R52795	Hs.25954	Interleukin 13 receptor, alpha 2	12.8
40	424806	AA382523	Hs.105689	MSTP031 protein	12.7
	442343	AA992480	Hs.129874	ESTs	12.7
	432244	AI669973	Hs.200574	ESTs	12.7
	459513	AI032946		gb:ox06g09.s1 Soares_fetal_liver_spleen_	12.7
	452512	AW363486	Hs.337635	ESTs	12.7
45	415079	R43179	Hs.22895	hypothetical protein FLJ23548	12.7
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	12.7
	411067	AI681006	Hs.71721	ESTs	12.7
	442501	AA315267	Hs.23128	ESTs	12.7
	434466	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	12.7
50	437052	AA861697	Hs.120591	ESTs	12.7
	433234	AB040928	Hs.65366	KIAA1495 protein	12.6
	453830	AA534296	Hs.20953	ESTs	12.6
	409995	AW960597	Hs.30164	ESTs	12.6
	414290	AI568801	Hs.71721	ESTs	12.6
55	417248	AA329449	Hs.247302	twisted gastrulation	12.6
	418624	AI734080	Hs.104211	ESTs	12.6
	412654	AI093480	Hs.29263	hypothetical protein FLJ11896	12.6
	450253	AL133047	Hs.24715	Homo sapiens mRNA; cDNA DKFZp434D0215 (f	12.6
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.5
60	427078	AI676062	Hs.111902	ESTs	12.5
	420838	AW118210	Hs.5244	ESTs	12.5
	449784	AW161319	Hs.12915	ESTs	12.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	12.5
	415276	U88666	Hs.78353	SFRS protein kinase 2	12.5
65	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	12.5
	400301	X03635	Hs.1657	estrogen receptor 1	12.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	12.5
	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced trans	12.5
	420345	AW295230	Hs.25231	ESTs	12.4
70	432205	AI805683	Hs.125291	ESTs	12.4
	451893	AW192083	Hs.290855	ESTs	12.4
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	12.4
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	12.4
	404642			NM_021965*-Homo sapiens phosphoglucomuta	12.4
75	414241	AA425085	Hs.4007	Sarcotermal-associated protein	12.4
	429716	R25685	Hs.211933	collagen, type XII, alpha 1	12.4
	420871	AA702972	Hs.65300	ESTs	12.4
	448072	AI459306	Hs.24908	ESTs	12.4
	441269	AW015206	Hs.178784	ESTs	12.3
80	427761	AA412205	Hs.140996	ESTs	12.3
	425322	U83630	Hs.155637	protein kinase, DNA-activated, catalytic	12.3
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	12.3
	436521	AW203986	Hs.213003	ESTs	12.3
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	12.3
	446332	AK001635	Hs.14838	hypothetical protein FLJ10773	12.2
	453994	BE180964	Hs.165590	ribosomal protein S13	12.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	12.2

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	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	12.2
	442562	BE379584	Hs.34789	dolichyl-diphosphooligosaccharide-protei	12.2
	400880			NM_000611*:Homo sapiens CD59 antigen p18	12.2
5	425920	AL049977	Hs.162209	claudin 8	12.2
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	12.1
	414222	AL135173	Hs.878	sorbitol dehydrogenase	12.1
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	12.1
	452994	AW962597	Hs.31305	KIAA1547 protein	12.1
10	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	12.1
	437124	AA554458	Hs.197751	KIAA0666 protein	12.1
	411450	H49619	Hs.127301	ESTs	12.1
	421559	NM_014720	Hs.105751	Ste20-related serine/threonine kinase	12.1
	449625	NM_014253	Hs.23796	odc (odd Oz/ten-m, Drosophila) homolog 1	12.1
	419459	AW291128	Hs.278422	DKFZP586G1122 protein	12.1
15	426252	BE176980	Hs.28917	ESTs	12.1
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	12.1
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	12.0
	435047	AA454985	Hs.54973	cadherin-like protein VR20	12.0
20	417625	U59305	Hs.44708	Ser-Thr protein kinase related to the my	12.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	12.0
	443646	AI085198	Hs.164228	ESTs	12.0
	434874	N62448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	12.0
	443837	AI984625	Hs.9884	spindle pole body protein	12.0
25	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	11.9
	424232	AB015982	Hs.143460	protein kinase C, nu	11.9
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	11.9
	446874	AW968304	Hs.56156	ESTs	11.9
	454119	BE549773	Hs.40510	uncoupling protein 4	11.9
30	436746	AA730045	Hs.187866	ESTs	11.9
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	11.8
	416508	R39769	Hs.206088	ESTs, Moderately similar to ALU8_HUMAN A	11.8
	444758	AL044878	Hs.11899	3-hydroxy-3-methylglutaryl-Coenzyme A re	11.8
	413991	H44725	Hs.42683	ESTs	11.8
35	431645	AF078849	Hs.266483	dynein light chain-A	11.8
	421406	AF179897	Hs.104105	Meis (mouse) homolog 2	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.8
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypothe	11.8
	412977	AA125910	Hs.191461	ESTs	11.8
40	426981	AL044675	Hs.173081	KIAA0530 protein	11.7
	410853	H04588	Hs.30469	ESTs	11.7
	444670	H58373	Hs.332938	hypothetical protein MGC5370	11.7
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	11.7
	434398	AA121098	Hs.3838	serum-inducible kinase	11.7
	438032	BE045624	Hs.152992	ESTs	11.7
45	433212	BE218049	Hs.121820	ESTs	11.6
	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 fis, clone PL	11.6
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	11.6
	430929	AA489166	Hs.156933	ESTs	11.6
	423782	AA72209	Hs.323117	ESTs	11.6
50	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	11.6
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	11.6
	430200	BE613337	Hs.234896	germinin	11.5
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	11.5
55	411098	U80034	Hs.68583	mitochondrial intermediate peptidase	11.5
	422805	AA436989	Hs.121017	H2A histone family, member A	11.5
	422538	NM_006441	Hs.118131	5,10-methenyltetrahydrofolate synthetase	11.5
	412677	AW029608	Hs.17384	ESTs	11.5
	421896	N62293	Hs.45107	ESTs	11.5
60	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	11.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	11.5
	415293	R49462	Hs.106541	ESTs	11.5
	443161	AI038316		gb:ox48c08.x1 Soares_total_fetus_Nb2HF8_	11.5
	420185	AL044056	Hs.158047	ESTs	11.5
65	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	11.5
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	11.5
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	11.5
	449919	AI674685	Hs.200141	ESTs	11.5
	414844	AA296874	Hs.77494	deoxyguanosine kinase	11.5
70	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	11.4
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	11.4
	407786	AA687538	Hs.38972	tetraspan 1	11.4
	414407	AA147026	Hs.76704	ESTs	11.4
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	11.4
75	456804	AI421645	Hs.139851	caveolin 2	11.4
	422546	AB007969	Hs.301478	KIAA0500 protein	11.4
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	11.4
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	11.4
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.4
80	433577	AW007080	Hs.8817	ESTs	11.4
	453935	AI633770	Hs.42572	ESTs	11.4
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEFS_HUMAN TRANS	11.4
	425710	AF030880	Hs.159275	solute carrier family, member 4	11.3
	448766	AI473827	Hs.31793	ESTs	11.3

	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	11.3
	410108	AA081659	Hs.318775	OSBP-related protein 6	11.3
	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	11.3
5	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	11.3
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	11.3
	414212	AA136569	Hs.10848	KIAA0187 gene product	11.3
	401519			C15000476-gi12737279refXP_012163.1	11.3
	458509	AA654650	Hs.282906	ESTs	11.2
10	416913	AW934714		gb:RC1-DT0001-031299-011-e11 DT0001 Homo	11.2
	452784	BE463857	Hs.151258	hypothetical protein FLJ21052	11.2
	436758	AW977167	Hs.155272	ESTs	11.2
	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	11.2
	434715	BE005346	Hs.116410	ESTs	11.2
15	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	11.2
	428342	AI739168	Hs.131798	Homo sapiens cDNA FLJ13458 fis, clone PL	11.2
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	11.2
	430519	AF129534	Hs.49210	F-box only protein 4	11.2
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	11.1
20	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	11.1
	434158	T86534	Hs.14372	ESTs	11.1
	414341	D80004	Hs.75909	KIAA0182 protein	11.1
	414650	AA150435	Hs.72063	ESTs	11.1
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	11.1
25	437575	AW954355	Hs.36529	hypothetical protein MGC11242	11.1
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	11.1
	425289	AW139342	Hs.155530	Interferon, gamma-inducible protein 16	11.1
	452598	AI831594	Hs.68547	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	11.0
30	438379	N23018	Hs.171391	C-terminal binding protein 2	11.0
	433230	AW136134	Hs.220277	ESTs	11.0
	412622	AW664708	Hs.171959	ESTs	11.0
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	11.0
	434349	NM_015678	Hs.3821	neurobeactin	11.0
35	430261	AA305127	Hs.237225	hypothetical protein HT023	11.0
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	11.0
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	11.0
	442082	R41823	Hs.7413	ESTs	11.0
	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	11.0
40	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	11.0
	450244	AA007534	Hs.125062	ESTs	11.0
	417169	R13550	Hs.246773	ESTs	11.0
	421481	AW391972	Hs.104696	KIAA1324 protein	10.9
45	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	10.9
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	10.9
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.9
	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	10.9
	433658	L03678	Hs.156110	immunoglobulin kappa constant	10.9
50	428364	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	10.9
	441540	C01367	Hs.127128	ESTs	10.9
	431154	AW971228	Hs.290259	ESTs, Weakly similar to I38022 hypotheti	10.9
	416777	AF146760	Hs.79844	DKFZP564M1416 protein	10.9
	439556	AI623752	Hs.163603	ESTs	10.9
55	428280	H05541	Hs.183428	sarcomspan (Kras oncogene-associated gene	10.8
	453942	AW190920	Hs.19828	hypothetical protein SP329	10.8
	447982	H22953	Hs.137551	ESTs	10.8
	422779	AA317036	Hs.118787	transforming growth factor, beta-induced	10.8
	447595	AW379130	Hs.18953	phosphodiesterase 9A	10.8
60	427115	AW972853	Hs.112237	ESTs	10.8
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	10.8
	419326	W94915	Hs.42419	ESTs	10.8
	435163	AA668884	Hs.19155	ESTs	10.8
	417578	T91443	Hs.193963	ESTs	10.8
65	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	10.8
	450206	AI796450	Hs.201600	ESTs	10.8
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	10.8
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	10.8
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	10.8
	408243	Y00787	Hs.624	interleukin 8	10.8
70	439492	AF086310	Hs.103159	ESTs	10.8
	413492	D87470	Hs.75400	KIAA0280 protein	10.8
	436962	AW377314	Hs.5364	DKFZP564I052 protein	10.8
	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	10.8
	422583	AA410506	Hs.27973	KIAA0874 protein	10.8
75	417665	AW852858	Hs.22862	ESTs	10.7
	433285	AW975944	Hs.237396	ESTs	10.7
	419693	AA133749	Hs.301350	FXD domain-containing ion transport reg	10.7
	424878	H57111	Hs.221132	ESTs	10.7
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	10.7
80	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	10.7
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	10.7
	452241	AL050204	Hs.28540	Homo sapiens mRNA: cDNA DKFZp586F1223 (f	10.7
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	10.7
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	10.7

	433923	AI823453	Hs.146625	ESTs	10.7
	418196	AI745849	Hs.26549	KIAA1708 protein	10.7
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	10.7
	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	10.7
5	429350	AI754634	Hs.131987	ESTs	10.7
	418601	AA279490	Hs.86368	calmegin	10.6
	437267	AW511443	Hs.258110	ESTs	10.6
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	10.6
10	421982	AF206019	Hs.110347	REV1 (yeast homolog)- like	10.6
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	10.6
	418662	AI801098	Hs.151500	ESTs	10.6
	449685	AW298669	Hs.66095	ESTs	10.6
	441111	AI806867	Hs.126594	ESTs	10.6
15	436671	AW137159	Hs.146151	ESTs	10.6
	447974	R76886		gb:yi64b03.s1 Soares placenta Nb2HP Homo	10.6
	417916	NM_008416	Hs.82921	solute carrier family 35 (CMP-sialic aci	10.6
	424562	AI420859	Hs.150557	basic transcription element binding prot	10.6
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	10.6
20	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.6
	439584	AA838114	Hs.221612	ESTs	10.6
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	10.6
	420929	AI694143	Hs.296251	programmed cell death 4	10.6
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.6
25	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	10.6
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	10.6
	424433	H04607	Hs.9218	ESTs	10.6
	420230	AL034344	Hs.284186	forkhead box C1	10.6
	419441	AW023731	Hs.274358	MSTP032 protein	10.6
30	426011	AW996096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	10.6
	451900	AB023199	Hs.27207	KIAA0982 protein	10.6
	424692	AA429834	Hs.151791	KIAA0092 gene product	10.6
	439999	AA115811	Hs.6638	ras homolog gene family, member E	10.5
	424368	AB037766	Hs.146085	KIAA1345 protein	10.5
35	402076			C5002020*.[g]1082876[pir]S55467 tropomy	10.5
	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	10.5
	445041	T64183	Hs.282982	solute carrier	10.5
	428927	AA441837	Hs.90250	ESTs	10.5
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	10.5
40	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	10.5
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	10.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	10.5
	438913	AI380429	Hs.172445	ESTs	10.5
	443684	AI681307	Hs.55098	ESTs	10.5
45	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	10.5
	421040	AA715026	Hs.135280	ESTs	10.5
	425277	NM_001241	Hs.155478	cyclin T2	10.5
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	10.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	10.5
50	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	10.5
	419972	AL041465	Hs.182982	golgin-67	10.5
	416182	NM_004354	Hs.79069	cyclin G2	10.4
	418365	AW014345	Hs.161690	ESTs	10.4
	452286	AI358570	Hs.123933	ESTs, Weakly similar to ZN91_HUMAN ZINC	10.4
55	430361	AI033965	Hs.239926	sterol-C4-methyl oxidase-like	10.4
	446716	AA436575	Hs.16602	ESTs	10.4
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo saplen	10.4
	433023	AW864793	Hs.87409	thrombospondin 1	10.4
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	10.4
60	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	10.4
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	10.4
	443228	W24781	Hs.293798	KIAA1710 protein	10.4
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	10.4
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	10.4
65	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	10.4
	428728	NM_016625	Hs.191381	hypothetical protein	10.4
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	10.4
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	10.3
	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	10.3
70	411359	H86088	Hs.22635	ESTs	10.3
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	10.3
	412262	W26406	Hs.295923	seven in absentia (Drosophila) homolog 1	10.3
	419875	AA853410	Hs.93557	proenkephalin	10.3
	414422	AA147224	Hs.337232	Homeo box A13	10.3
75	426581	AB040956	Hs.135890	KIAA1523 protein	10.3
	424649	BE242035	Hs.151461	embryonic ectoderm development	10.3
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	10.3
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	10.3
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	10.3
80	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	10.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	10.3
	451593	AF151879	Hs.26706	CG-121 protein	10.3
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box	10.3
	438157	AW137011	Hs.49576	ESTs	10.3

	443181	AI039201	Hs.283316	ESTs	10.3
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	10.2
	411479	AW848047		gbdL3-CT0214-291299-052-A12 CT0214 Homo	10.2
5	446553	AB021179	Hs.15299	HMBA-inducible	10.2
	418278	AI088489	Hs.83937	hypothetical protein	10.2
	419791	AI579909	Hs.105104	ESTs	10.2
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	10.2
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	10.2
10	445564	AB028957	Hs.12896	KIAA1034 protein	10.2
	435021	AA922182	Hs.54709	ESTs	10.2
	457498	AI732230	Hs.191737	ESTs	10.2
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	10.2
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13445 fis, clone PL	10.2
15	446162	AI631319	Hs.63841	hypothetical protein DKFZp434E2318	10.2
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	10.2
	427393	AB029018	Hs.177635	KIAA1095 protein	10.1
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	10.1
	437743	AI383497	Hs.131811	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
20	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	10.1
	448172	N75276	Hs.135904	ESTs	10.1
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	10.1
	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATI	10.1
	413450	Z99716	Hs.75372	N-acetylglactosaminidase, alpha-	10.1
25	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	10.1
	410150	AW382942	Hs.6774	ESTs	10.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	10.1
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	10.1
	443476	AW088594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOT	10.1
30	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	10.1
	423681	AB023215	Hs.131525	Homo sapiens mRNA; cDNA DKFZp434E199 (fr	10.1
	450205	AI219748	Hs.11356	ESTs	10.1
	408374	AW025430	Hs.155591	forkhead box F1	10.0
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	10.0
35	432589	AL135725	Hs.131708	ESTs	10.0
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	10.0
	411997	AW673478	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	10.0
	419672	AA465113	Hs.23853	ESTs, Weakly similar to A34615 profilagg	10.0
	444564	AI167877	Hs.143716	ESTs	10.0
40	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	10.0
	451424	AI862026	Hs.302810	Novel human gene mapping to chromosome 20	10.0
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	10.0
	431616	AA508562	Hs.195839	ESTs, Weakly similar to I38022 hypothe	10.0
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	10.0
45	425683	AB037813	Hs.159200	hypothetical protein DKFZp762K222	10.0
	442760	BE075297	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.0
	418884	AA230228	Hs.59197	ESTs	10.0
	444821	AA053564	Hs.12040	STE20-like kinase	9.9
	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	9.9
50	439731	AI953135	Hs.45140	hypothetical protein FLJ114084	9.9
	453127	AI696671	Hs.294110	ESTs	9.9
	435706	W31254	Hs.7045	GL004 protein	9.9
	410748	BE383816	Hs.12532	chromosome 1 open reading frame 21	9.9
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	9.9
55	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	9.9
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	9.9
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	9.9
	432887	AI926047	Hs.162859	ESTs	9.9
	430291	AV660345	Hs.238126	CGI-49 protein	9.9
60	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	9.9
	412350	AI559306	Hs.73826	protein tyrosine phosphatase, non-recept	9.9
	428825	AI084336	Hs.128783	ESTs, Weakly similar to I38022 hypothe	9.9
	441054	AA913591	Hs.126480	ESTs	9.9
	415875	AA894876	Hs.5687	protein phosphatase 1B (formerly 2C), ma	9.9
65	453078	AF053551	Hs.31584	metaxin 2	9.8
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	9.8
	446720	AI439136	Hs.140546	ESTs	9.8
	418475	AI858732	Hs.30443	sentrin/SUMO-specific protease	9.8
	417708	N74392	Hs.50495	ESTs	9.8
70	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	9.8
	420568	F09247	Hs.247735	protocadherin alpha 10	9.8
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	9.8
	453548	AL079983	Hs.116774	integrin, alpha 1	9.8
	427308	D26067	Hs.174905	KIAA0033 protein	9.8
75	434579	T55958		gb:yc35i05.r1 Stratagene fetal spleen (9	9.8
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	9.8
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	9.8
	413174	AA723564	Hs.191343	ESTs	9.8
	443250	AI041530	Hs.132107	ESTs	9.8
80	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	9.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypothe	9.8
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	9.8
	427635	BE397988	Hs.179982	tumor protein p53-binding protein	9.8
	416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	9.8

	439091	AA830144	Hs.135613	ESTs, Moderately similar to I38022 hypot	9.8
	418575	AA225313	Hs.222686	ESTs, Weakly similar to TRHY_HUMAN TRICH	9.7
	432426	AW973152	Hs.31050	ESTs	9.7
	404571			NM_015902*:Homo sapiens progesterin induce	9.7
5	444427	H25094	Hs.293663	ESTs, Moderately similar to I38022 hypot	9.7
	439183	AW970600	Hs.303261	ESTs	9.7
	432686	BE159028	Hs.279704	chromatin accessibility complex 1	9.7
	432689	AB018320	Hs.278626	Arg/Abi-Interacting protein ArgBP2	9.7
10	417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	9.7
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	9.7
	412324	AW978439	Hs.69504	ESTs	9.7
	422072	AB018255	Hs.111138	KIAA0712 gene product	9.7
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-lin	9.7
15	417171	BE613486	Hs.81412	lipin 1	9.7
	421709	AA159394	Hs.107056	CED-6 protein	9.7
	415156	X84908	Hs.78060	phosphorylase kinase, beta	9.7
	436446	AW016809	Hs.323795	ESTs	9.7
	447482	AB033059	Hs.18705	KIAA1233 protein	9.7
20	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	9.7
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	9.7
	409190	AU076536	Hs.50984	sarcoma amplified sequence	9.6
	419111	AA234172	Hs.137418	ESTs	9.6
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	9.6
25	416039	AA376989	Hs.78989	alcohol dehydrogenase 5 (class III), chi	9.6
	408239	AA053401	Hs.271827	ESTs, Moderately similar to ALU7_HUMAN A	9.6
	419241	AA523939	Hs.165258	ESTs	9.6
	409752	AW963990		gb:EST376063 MAGE resequences, MAGH Homo	9.6
	453894	AW537825	Hs.56847	Homo sapiens cDNA FLJ12874 fis, clone NT	9.6
30	439671	AW162840	Hs.6641	kinesin family member 5C	9.6
	407230	AA157857	Hs.182265	keratin 19	9.6
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	9.6
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	9.6
	434263	N34895	Hs.44648	ESTs	9.6
35	412766	BE544475	Hs.54347	ESTs	9.6
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	9.6
	443970	AI280341	Hs.166571	ESTs	9.6
	424534	D87682	Hs.150275	KIAA0241 protein	9.6
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	9.6
40	447889	AW469180	Hs.170651	ESTs	9.5
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	9.5
	433165	AA578904	Hs.292437	ESTs	9.5
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	9.5
	440282	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	9.5
45	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	9.5
	408915	NM_016651	Hs.48950	heptacellular carcinoma novel gene-3 pro	9.5
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	9.5
	432682	AI376400	Hs.159588	ESTs	9.5
	435803	Z44194	Hs.4994	transducer of ERBB2, 2	9.5
50	437444	H48008	Hs.31518	ESTs	9.5
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	9.5
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	9.5
	449226	AB002365	Hs.23311	KIAA0367 protein	9.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	9.4
55	420969	AI636310	Hs.28310	ESTs	9.4
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	9.4
	434415	BE177494		gb:RC6-HT0596-270300-011-C05 HT0596 Homo	9.4
	420805	L10333	Hs.99947	reticulon 1	9.4
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	9.4
60	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	9.4
	445280	AW055063	Hs.306088	v-crk avian sarcoma virus CT10 oncogene	9.4
	425657	T89839	Hs.119471	ESTs	9.4
	428250	AW809208	Hs.183297	DKFZP566F2124 protein	9.4
	453293	AA382267	Hs.10653	ESTs	9.4
65	412446	AI768015	Hs.92127	ESTs	9.4
	441102	AA973905	Hs.331328	intermediate filament protein syncollin	9.4
	421689	N87820	Hs.106826	KIAA1696 protein	9.4
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	9.4
	422244	Y08890	Hs.113503	karyopherin (importin) beta 3	9.4
70	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	9.4
	441499	AW298235	Hs.101689	ESTs	9.4
	420184	AA188408	Hs.95665	hypothetical protein	9.4
	420061	AW024937	Hs.29410	ESTs	9.4
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	9.4
75	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	9.3
	450580	N40087	Hs.15248	ESTs	9.3
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	9.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	9.3
	412639	AW961284	Hs.296235	ESTs	9.3
80	429786	AL080232	Hs.220696	Homo sapiens mRNA; cDNA DKFZp586A061 (fr	9.3
	446131	NM_000929	Hs.290	phospholipase A2, group V	9.3
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	9.3
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	9.3
	425139	AW630488	Hs.325820	protease, serine, 23	9.3

	448807	AI571940	Hs.7549	ESTs	9.3
	412505	AA974491	Hs.21734	ESTs	9.3
	412314	AA825247	Hs.250899	heat shock factor binding protein 1	9.3
5	445704	AI493742	Hs.165210	ESTs, Moderately similar to I38022 hypot	9.3
	402855			NM_001839*:Homo sapiens calponin 3, acid	9.3
	428465	AW970976	Hs.293653	ESTs	9.3
	422564	AI148006	Hs.222120	ESTs	9.3
	430027	AB023197	Hs.227743	KIAA0980 protein	9.2
10	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	9.2
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	9.2
	433862	D86960	Hs.3610	KIAA0205 gene product	9.2
	429227	AI961456	Hs.21275	hypothetical protein FLJ11011	9.2
	401558			ENSP00000220478*:SECRETAGRANIN III.	9.2
15	428634	AA811845	Hs.106290	Kelch motif containing protein	9.2
	437678	AA829860	Hs.122834	ESTs	9.2
	416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.2
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.2
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	9.2
20	431187	AW971146	Hs.293187	ESTs	9.2
	421202	AF193339	Hs.102506	eukaryotic translation initiation factor	9.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	9.1
	430669	AW969657	Hs.291029	ESTs	9.1
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	9.1
25	448822	BE149845	Hs.289038	hypothetical protein MGCA126	9.1
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	9.1
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (9.1
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	9.1
30	434361	AF129755	Hs.117772	ESTs	9.1
	443247	BE614387	Hs.333893	c-Myc target JPO1	9.1
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	9.1
	411928	AA886624	Hs.197289	rab3 GTPase-activating protein, non-cata	9.1
	448704	AW080932	Hs.249247	heterogeneous nuclear protein similar to	9.1
	448430	AI500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	9.1
35	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	9.1
	418821	AA436002	Hs.183161	ESTs	9.1
	427213	AW007211	Hs.16131	hypothetical protein FLJ12876	9.1
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	9.1
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	9.1
40	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	9.1
	447033	AI357412	Hs.157601	ESTs	9.0
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	9.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Droso	9.0
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	9.0
45	444984	H15474	Hs.132898	fatty acid desaturase 1	9.0
	445674	BE410347	Hs.13063	transcription factor CA150	9.0
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	9.0
	419852	AW503756	Hs.286184	hypothetical protein dJ55102.5	9.0
	440349	AA884196	Hs.31476	Homo sapiens cDNA FLJ113872 fis, clone TH	9.0
50	432161	AK000400	Hs.292807	ESTs, Weakly similar to envelope [H.sapi	9.0
	405523			C8001409*:gil7441226[pilr]S31212 collage	9.0
	416662	T25853	Hs.7538	ESTs	9.0
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	9.0
	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	9.0
55	432897	AF155099	Hs.279780	NY-REN-18 antigen	9.0
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	8.9
	448523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	8.9
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.9
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.9
60	414917	CD4863	Hs.47191	ESTs	8.9
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	8.9
	441805	AA285136	Hs.301914	neuronal specific transcription factor D	8.9
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	8.9
	424683	N87519	Hs.27196	ESTs	8.9
65	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	8.9
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	8.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	8.9
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	8.9
	441079	AW150697	Hs.107418	ESTs	8.9
70	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	8.9
	431316	AA502663	Hs.145037	ESTs	8.9
	403137			NM_005381*:Homo sapiens nucleolin (NCL),	8.9
	433628	AI821784	Hs.188578	ESTs	8.9
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	8.9
75	453344	BE349075	Hs.44571	ESTs	8.9
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	8.9
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	8.9
	408161	AW952912	Hs.300383	hypothetical protein MGCC3032	8.9
	420495	AJ338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	8.9
80	433213	AW665130	Hs.137190	ESTs	8.9
	451573	AW130351	Hs.243549	ESTs	8.9
	408393	AW015318	Hs.23165	ESTs	8.8
	434725	AK000796	Hs.4104	hypothetical protein	8.8
	418876	AA740616		gb:ny97111.s1 NCL_CGAP_GCB1 Homo sapiens	8.8

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	444558	AW181975	Hs.165892	ESTs	8.8
	417355	D13168	Hs.82002	endothelin receptor type B	8.8
	424084	A1940675	Hs.20914	hypothetical protein FLJ23056	8.8
5	431706	A1816086	Hs.296341	adenylyl cyclase-associated protein 2	8.8
	424956	AW198103	Hs.158154	ESTs, Weakly similar to granule cell mar	8.8
	441866	BE464341	Hs.21201	nectin 3; DKFZP666B0846 protein	8.8
	444647	H14718	Hs.11506	Human clone 23589 mRNA sequence	8.8
	444858	A1199738	Hs.208275	ESTs, Weakly similar to ALUA_HUMAN !!!!	8.8
10	409643	AW450866	Hs.257359	ESTs	8.8
	428647	AA830050	Hs.124344	ESTs	8.8
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	8.8
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	8.8
	425465	L18964	Hs.1904	protein kinase C, iota	8.8
15	424113	A1743880	Hs.12876	ESTs	8.8
	459324	AW080953		gb:cc28c12.x1 NCI_CGAP_Co18 Homo sapiens	8.8
	451684	AF216751	Hs.26813	CDA14	8.8
	451244	AW008798	Hs.267448	hypothetical protein FLJ20039	8.8
	439170	AA332365	Hs.165639	ESTs, Weakly similar to I38022 hypotheti	8.8
20	424238	AA337401	Hs.137635	ESTs	8.8
	449686	AW072813	Hs.270868	ESTs, Moderately similar to ALUA_HUMAN A	8.8
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	8.8
	410870	U81599	Hs.66731	homeo box B13	8.8
	458229	A1929602	Hs.177	phosphatidylinositol glycan, class H	8.8
25	429831	AA564489	Hs.137526	ESTs	8.8
	453468	W00712	Hs.32990	DKFZP566F084 protein	8.8
	428340	AF261088	Hs.154721	aconitase 1, soluble	8.8
	453345	AA302862	Hs.90063	neurocalcin delta	8.8
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	8.8
30	440486	BE243513	Hs.7212	hypothetical protein PP1044	8.7
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	8.7
	408949	AF189011	Hs.49163	putative ribonuclease III	8.7
	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	8.7
	412719	AW016610	Hs.129911	ESTs	8.7
35	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	8.7
	408242	AA251594	Hs.43913	PIBF1 gene product	8.7
	430848	AW021726		gb:df27e02.y1 Morton Fetal Cochlea Homo	8.7
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	8.7
40	449893	T97999	Hs.18214	ESTs, Weakly similar to B34087 hypotheti	8.7
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	8.7
	425913	AA365799	Hs.50785	SEC22, vesicle trafficking protein (S. c	8.7
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	8.7
	427723	A1356260	Hs.279789	histone deacetylase 3	8.7
45	441683	BE564214	Hs.102946	ESTs	8.7
	447335	BE617695	Hs.286192	hypothetical protein FLJ20940	8.7
	428259	AA424793	Hs.24144	ESTs	8.7
	433104	AL043002	Hs.128246	ESTs, Moderately similar to unnamed prot	8.7
	420041	AB005142	Hs.94592	klotho	8.7
	432432	AA541323	Hs.115831	ESTs	8.7
50	452335	AW188944	Hs.61272	ESTs	8.7
	412673	AL042957	Hs.31845	ESTs	8.7
	430335	D80007	Hs.239499	KIAA0185 protein	8.7
	419904	AA974411	Hs.18672	ESTs	8.6
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	8.6
55	433759	AA680003	Hs.109368	Homo sapiens cDNA: FLJ23603 fis, clone L	8.6
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	8.6
	401785			NM_002275: Homo sapiens keratin 15 (KRT1	8.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	8.6
	419647	AA348947	Hs.91816	hypothetical protein	8.6
60	425907	AA365752	Hs.155965	ESTs	8.6
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	8.6
	424434	H87028	Hs.146861	hypothetical protein FLJ20580	8.6
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	8.6
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	8.6
	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.6
65	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	8.6
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	8.6
	441790	AW294909	Hs.132208	ESTs	8.6
	441124	T97717	Hs.119563	ESTs	8.6
70	438160	AA779332	Hs.122671	ESTs	8.6
	433264	D85782	Hs.3229	cysteine dioxygenase, type I	8.6
	434851	AA806164	Hs.116502	ESTs	8.6
	420608	BE548277	Hs.103104	ESTs	8.6
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	8.6
75	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	8.5
	454058	A1273419	Hs.135146	hypothetical protein FLJ13984	8.5
	435614	R09718	Hs.20403	ESTs	8.5
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	8.5
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	8.5
80	447894	AW204253	Hs.21912	ESTs	8.5
	452682	AA456193	Hs.9071	progesterone membrane binding protein	8.5
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	8.5
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	8.5
	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	8.5

5	434747	AA837085	Hs.220585	ESTs	8.5
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	8.5
	450813	A1739625	Hs.203376	ESTs	8.5
	413956	A1821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.5
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	8.5
	440840	AW629666	Hs.283713	ESTs, Weakly similar to S64054 hypothetical	8.5
	407891	AA486620	Hs.41135	endomucin-2	8.5
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	8.5
10	432620	AA777749	Hs.5978	LIM domain only 7	8.5
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	8.5
	408170	AW204516	Hs.31835	ESTs	8.5
	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	8.5
	450516	AA902656	Hs.21943	NIF3 (Ngg1 interacting factor 3, S.pombe	8.5
15	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	8.5
	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	8.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	8.4
	418120	AA213437	Hs.192249	ESTs	8.4
	419436	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	8.4
20	432600	A1821085		gb:ns95a12.y5 NCI_CGAP_Pr3 Homo sapiens	8.4
	448474	A1792014	Hs.13809	hypothetical protein FLJ10648	8.4
	434384	AA631910	Hs.162849	ESTs	8.4
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothetical	8.4
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	8.4
25	421622	A8037748	Hs.106204	KIAA1327 protein	8.4
	431160	AW971174	Hs.324330	ESTs	8.4
	449567	A1990790	Hs.188614	ESTs	8.4
	411088	BE247593	Hs.145053	ESTs	8.4
	452186	AA120761	Hs.28307	VW domain binding protein 4 (formin bind	8.3
30	437872	AJ002015	Hs.5887	RNA binding motif protein 7	8.3
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	8.3
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	8.3
	438440	AA807228	Hs.225161	ESTs	8.3
	431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	8.3
35	422295	AF051151	Hs.114408	toll-like receptor 5	8.3
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	8.3
	425242	D13635	Hs.155287	KIAA0010 gene product	8.3
	432769	AA620814	Hs.144959	ESTs	8.3
	433615	AA732582	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.3
40	427229	A1799751	Hs.5635	ESTs	8.3
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	8.3
	403149			NM_001450:Homo sapiens four and a half L	8.3
	436679	A1127483	Hs.120451	ESTs, Weakly similar to unnamed protein	8.3
	421991	NM_014918	Hs.110488	KIAA0990 protein	8.3
45	436476	AA326108	Hs.33829	bHLH protein DEC2	8.3
	434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	8.3
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypothetical	8.3
	453121	A1968264	Hs.232286	ESTs	8.3
	420630	AL133101	Hs.99508	Homo sapiens mRNA; cDNA DKFZp434O0921 (f	8.3
50	426101	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (f	8.2
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	8.2
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	8.2
	440080	AW051597	Hs.143707	ESTs	8.2
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	8.2
55	430154	AW583058	Hs.234726	sarime (or cysteine) proteinase inhibitor	8.2
	432695	D63480	Hs.278634	KIAA0146 protein	8.2
	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	8.2
	408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	8.2
	418051	AW192535	Hs.19479	ESTs	8.2
60	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	8.2
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN IIII	8.2
	417958	AA767382	Hs.193417	ESTs	8.2
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypothetical	8.2
	430468	NM_004673	Hs.241519	angiotensin-like 1	8.2
65	407802	D84145	Hs.39913	novel RGD-containing protein	8.2
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	8.2
	414138	AA135884	Hs.3772	ESTs	8.2
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	8.2
	408267	AW380525	Hs.32675	tubulin-specific chaperone e	8.2
70	429692	N48422	Hs.9977	ESTs, Weakly similar to B34087 hypothetical	8.2
	408108	AI580492	Hs.42743	hypothetical protein	8.2
	408418	AW963897	Hs.44743	KIAA1435 protein	8.2
	430334	A1824719	Hs.328700	ESTs	8.2
75	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	8.2

TABLE 598

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
409385	112523_1	AA071267 T65940 T64515 AA071334

409752	115301_1	AW963990 AA078196 AW749482 AA077468 BE151571 AA376917
411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905
		AW848214
411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
418866	179788_1	T65754 AA229857 AA229658
418876	179960_1	AA740616 AA654854 AA229923
419536	185688_1	AA603305 AA244095 AA244183
419544	185760_2	AI909154 AA526337 AA244193 AI909153
423800	232161_1	AA331156 AA331157 AA331155
426413	266650_1	AA377823 AW954494 AI022688
429163	300543_1	AA884766 AW974271 AA592975 AA447312
430848	324621_1	AW021726 AA487752 AA488085
431121	328275_1	AW971157 AA492575 AA492520
432189	342819_1	AA527941 AI810608 AI620190 AA635266
432600	350959_1	AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
434415	385931_1	BE177494 AW276909 AA632849
434579	38916_1	T55958 T57205 AF147346
439518	47334_1	W76326 AF086341 W72300
443161	561305_1	AI038316 AI344631 AI261653
447974	745643_1	R76886 AI453674 R77049

TABLE 59C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400860	9757499	Minus	151830-152104,152649-152744
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
402076	8117410	Plus	128316-128627
402812	6010110	Plus	25026-25091,25844-25920
402855	9662953	Minus	59763-59909
403047	3540153	Minus	59793-59968
403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
403149	9799833	Plus	25034-25185
403362	8571772	Plus	64099-64260
404210	5006246	Plus	169926-170121
404571	7249169	Minus	112450-112648
404641	9796810	Minus	32247-32362
404642	9796810	Plus	102999-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217

Table 60A lists about 1166 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 60A: ABOUT 1166 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	Ratio of prostate tumor to normal adult body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	56.6
419626	AI821895	Hs.193481	ESTs	56.2
420154	AI093155	Hs.95420	JM27 protein	44.0
432441	AW292425	Hs.163484	ESTs	41.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	39.9
431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	37.9
400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	36.0
446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	32.9
425075	AA506324	Hs.1852	acid phosphatase, prostate	31.1
400298	AA032279	Hs.61635	sbx transmembrane epithelial antigen of	30.0
439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 linc-1 pr	29.8

	400302	N48066		isolate hydrolase (prostate-specific memb	28.9
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	27.9
	432101	AJ918950	Hs.123642	EphA3	26.3
5	408369	R38438	Hs.182575	solute carrier family 15 (H7??) transport	26.2
	453096	AW294631	Hs.11325	ESTs	25.7
	400287	S39329	Hs.181350	kalikrein 2, prostatic	25.5
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	24.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	24.5
	401424			NM_001172:Homo sapiens arginase, type II	24.5
10	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	22.4
	400292	AA250737	Hs.72472	BMP-R1B	22.3
	407202	N58172	Hs.109370	ESTs	22.3
	415989	AI267700		ESTs	20.2
	407709	AA456135	Hs.23023	ESTs	20.0
15	407168	R45175	Hs.117183	ESTs	19.6
	433444	AW975324	Hs.129816	ESTs	19.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	19.1
	428336	AA503115	Hs.183752	microseminoprotein, beta-	18.7
	410929	H47233	Hs.30643	ESTs	18.0
20	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	17.9
	418961	AW967646	Hs.23023	ESTs	17.7
	452792	AB037765	Hs.30652	KIAA1344 protein	17.5
	403047			NM_005656*:Homo sapiens transmembrane pr	17.3
25	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3
	418396	AI765805	Hs.26691	ESTs	17.1
	433647	AA603367	Hs.222294	ESTs	16.9
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	16.7
	430487	D87742	Hs.241552	KIAA0268 protein	16.5
	440260	AI972867	Hs.7130	copine IV	16.0
30	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	15.7
	429220	AW207206		ESTs	15.7
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	15.3
	418819	AA228776	Hs.191721	ESTs	14.8
	421513	X00949	Hs.105314	relaxin 1 (H1)	14.8
35	429918	AW873986	Hs.119383	ESTs	14.5
	420092	AA814043	Hs.88045	ESTs	14.5
	432473	AI202703	Hs.152414	ESTs	14.4
	450693	AW450461	Hs.203965	ESTs	14.4
40	431548	AI834273	Hs.9711	novel protein	14.4
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	14.3
	430187	AI799909	Hs.158989	ESTs	14.3
	441690	R81733	Hs.33106	ESTs	14.3
	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	14.2
45	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	13.7
	450642	R39773	Hs.7130	copine IV	13.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	13.4
	432966	AA650114	Hs.325198	ESTs	13.4
	410330	AW023630	Hs.159425	ESTs	13.4
50	434666	AF151103	Hs.112259	T cell receptor gamma locus	13.1
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	13.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	12.8
	431474	AL133990	Hs.190642	ESTs	12.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	12.5
55	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	12.5
	434217	AW014795	Hs.23349	ESTs	12.3
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	12.3
	428398	AI249368	Hs.98558	ESTs	12.2
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	12.2
60	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	12.2
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	12.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	12.1
	436032	AA150797	Hs.109276	lactoxin protein	12.0
	432527	AW975028	Hs.102754	ESTs	12.0
65	434792	AA649253	Hs.132458	ESTs	12.0
	420424	AB033036	Hs.97594	KIAA1210 protein	11.9
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.9
	424846	AU077324	Hs.1832	neuropeptide Y	11.9
	448519	AW175665	Hs.278595	Homo sapiens prostasin mRNA, complete cds	11.9
70	418339	AA639502	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	11.8
	432600	AI821086		gb:ms95a12.y5 NCL_CGAP_Pr3 Homo sapiens	11.8
	413597	AW302885	Hs.117183	ESTs	11.8
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	11.7
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	11.6
75	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	11.6
	432435	BE218886	Hs.282070	ESTs	11.5
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	11.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	11.5
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	11.5
80	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.5
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	11.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	11.0
	407021	U52077		gb:Human mariner1 transposase gene, comp	11.0
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	10.8

	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.6
	400301	X03635	Hs.1657	estrogen receptor 1	10.5
	419536	AA603305		gb:np12d11.s1 NCL CGAP_Pr3 Homo sapiens	10.5
5	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	10.5
	415539	AI733881	Hs.72472	BMP-R1B	10.4
	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN IIII	10.4
	424432	AB037821	Hs.146858	protocadherin 10	10.3
	439518	W76326		gb:zd60d04.r1 Soares_fetal_hear_LNbHH19W	10.3
10	434036	AI659131	Hs.197733	hypothetical protein MGC2849	10.3
	415263	AA948033	Hs.130853	ESTs	10.2
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	10.2
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	10.1
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	10.0
15	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	10.0
	432244	AI669973	Hs.200574	ESTs	10.0
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.9
	450164	AI239923	Hs.63931	ESTs	9.8
20	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	9.8
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	9.7
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	9.6
	433234	AB040928	Hs.65366	KIAA1495 protein	9.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	9.5
25	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.5
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	9.4
	433927	AI557019	Hs.116467	small nuclear protein PRAC	9.4
	444670	H58373	Hs.332938	hypothetical protein MGC5370	9.4
	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	9.4
30	450325	AI935962	Hs.26289	ESTs	9.4
	427761	AA412205	Hs.140996	ESTs	9.4
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	9.3
	416795	AI497778	Hs.20509	HBV pX associated protein-8	9.3
	422805	AA436989	Hs.121017	H2A histone family, member A	9.2
35	418848	AI820961	Hs.193465	ESTs	9.2
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	9.2
	415788	AW628686	Hs.78851	KIAA0217 protein	9.2
	404641			NM_021965*:Homo sapiens phosphoglucomuta	9.1
	432437	W07088	Hs.293685	ESTs	9.1
40	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	9.1
	436962	AW377314	Hs.5364	DKFZP564I052 protein	9.1
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	9.0
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	9.0
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	9.0
45	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	8.8
	442082	R41823	Hs.7413	ESTs	8.8
	436671	AW137159	Hs.146151	ESTs	8.7
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	8.7
	440774	AI420611	Hs.153934	ESTs	8.7
50	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	8.7
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	8.6
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.6
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	8.6
	443646	AI085198	Hs.164226	ESTs	8.6
55	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	8.5
	428728	NM_016625	Hs.191381	hypothetical protein	8.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.5
	437162	AW005505	Hs.54464	thyroid hormone receptor coactivating pr	8.5
	437866	AA156781		metallothionein 1E (functional)	8.5
60	453006	AI362575	Hs.303171	ESTs	8.4
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	8.3
	421040	AA715026	Hs.135280	ESTs	8.3
	414212	AA135669	Hs.10848	KIAA0187 gene product	8.3
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	8.2
65	440749	W22335	Hs.7392	hypothetical protein MGC3199	8.2
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kd)	8.2
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	8.2
	447156	AW274731	Hs.157920	ESTs	8.1
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	8.1
70	417412	X16896	Hs.82112	Interleukin 1 receptor, type I	8.0
	424692	AA429834	Hs.151791	KIAA0092 gene product	8.0
	435981	H74319	Hs.188620	ESTs	7.9
	442081	AA401863	Hs.22380	ESTs	7.9
	434988	AI418055	Hs.161160	ESTs	7.9
75	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	7.8
	420345	AW295230	Hs.25231	ESTs	7.8
	412324	AW978439	Hs.69504	ESTs	7.8
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	7.8
	408374	AW025430	Hs.155591	forkhead box F1	7.8
80	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	7.8
	453160	AI263307	Hs.239884	H2B histone family, member L	7.7
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	7.7
	416182	NM_004354	Hs.79069	cyclin G2	7.7
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	7.6

	451099	R52795	Hs.25954	Interleukin 13 receptor, alpha 2	7.6
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	7.5
	443180	R15875	Hs.258576	claudin 12	7.5
5	454119	BE549773	Hs.40510	uncoupling protein 4	7.5
	418693	AJ750878	Hs.87409	thrombospondin 1	7.5
	426581	AB040956	Hs.135890	KIAA1523 protein	7.5
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	7.5
	439569	AW602166	Hs.222399	CEGP1 protein	7.4
10	416140	AJ918035	Hs.301198	roundabout (axon guidance receptor, Dros	7.4
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	7.4
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	7.4
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	7.4
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.3
15	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	7.3
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	7.3
	424649	BE242035	Hs.151461	embryonic ectoderm development	7.3
	428218	AA424266	Hs.123642	EphA3	7.3
	434158	T86534	Hs.14372	ESTs	7.3
20	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	7.3
	430261	AA305127	Hs.237225	hypothetical protein HT023	7.3
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.3
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	7.2
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kn	7.2
25	420871	AA702972	Hs.65300	ESTs	7.2
	418278	AI088489	Hs.83937	hypothetical protein	7.1
	456516	BE172704	Hs.222746	KIAA1610 protein	7.1
	417511	AL049176	Hs.82223	chordin-like	7.1
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	7.1
30	414422	AA147224	Hs.249195	Homeo box A13	7.1
	407118	AA156790	Hs.262036	ESTs, Weakly similar to ZZZ2_HUMAN ZINC	7.1
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.0
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	7.0
	437872	AK002015	Hs.5887	RNA binding motif protein 7	7.0
35	448148	NM_016578	Hs.20509	HBV pX associated protein-8	7.0
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.9
	431657	AJ345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	6.9
	457728	AW974811		gb:EST386916 MAGE resequences, MAGN Homo	6.9
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	6.9
40	421977	W94197	Hs.110165	ribosomal protein L26 homolog	6.9
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	6.9
	432887	AI926047	Hs.162859	ESTs	6.8
	444931	AV652066	Hs.75113	general transcription factor IIIA	6.8
	421823	N40850	Hs.28625	ESTs	6.8
45	426981	AL044675	Hs.173081	KIAA0530 protein	6.8
	425170	AJ077315	Hs.154970	transcription factor CP2	6.8
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	6.8
	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	6.8
50	439492	AF086310	Hs.103159	ESTs	6.8
	449919	AI674685	Hs.200141	ESTs	6.8
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	6.8
	431555	AI815470	Hs.260024	Cdc42 effector protein 3	6.7
	441111	AI808867	Hs.126594	ESTs	6.7
	457498	AI732230	Hs.191737	ESTs	6.7
55	415293	R49462	Hs.106541	ESTs	6.7
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	6.7
	433908	AW298141	Hs.157975	ESTs	6.7
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.7
60	431770	BE221880	Hs.268555	5'-3' exonuclease 2	6.7
	418575	AA225313	Hs.222866	ESTs, Weakly similar to TRHY_HUMAN TRICH	6.6
	443745	AB039670	Hs.9728	ALEX1 protein	6.6
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	6.6
	447805	AW627832	Hs.302421	gemin4	6.6
	440995	T57773	Hs.10263	ESTs	6.6
65	422173	BE385828	Hs.250619	phorbol-in-like protein MDS019	6.6
	431992	NM_002742	Hs.2891	protein kinase C, mu	6.6
	437052	AA861697	Hs.120591	ESTs	6.6
	444030	AW021254	Hs.135055	ESTs	6.6
	416836	D64745	Hs.80247	cholecystokinin	6.6
70	447033	AI357412	Hs.157601	ESTs	6.5
	428927	AA441837	Hs.90250	ESTs	6.5
	432189	AA527941		gb:mh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	6.5
	448779	BE042877	Hs.177135	ESTs	6.4
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	6.4
75	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.4
	432682	AJ376400	Hs.159588	ESTs	6.4
	441499	AW298235	Hs.101689	ESTs	6.4
	441676	BE564206	Hs.49889	ESTs	6.4
	421077	AK000061	Hs.101590	hypothetical protein	6.4
80	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	6.4
	452055	AJ377431	Hs.141693	hypothetical protein MGC10858	6.4
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	6.3
	452277	AL049013	Hs.28783	KIAA1223 protein	6.3

	412953	Z45794	Hs.238809	ESTs	6.3
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieli	6.3
	453390	AA862496	Hs.28482	ESTs	6.3
5	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	6.3
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	6.3
	425704	U79293	Hs.159264	Human clone Z3948 mRNA sequence	6.3
	433610	AA806822	Hs.112547	ESTs	6.3
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	6.3
10	412977	AA125910	Hs.191461	ESTs	6.3
	441217	A1922183	Hs.213246	ESTs	6.3
	443912	R37257	Hs.184780	ESTs	6.3
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	6.2
	435021	AA922192	Hs.54709	ESTs	6.2
15	425465	L18964	Hs.1904	protein kinase C, iota	6.2
	418821	AA436002	Hs.183161	ESTs	6.2
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	6.2
	448106	A1800470	Hs.171941	ESTs	6.2
	408418	AW963897	Hs.44743	KIAA1435 protein	6.2
20	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	6.2
	427078	AI676062	Hs.111902	ESTs	6.2
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	6.2
	449907	AA004825	Hs.103281	ESTs	6.1
	458509	AA654650	Hs.282906	ESTs	6.1
25	437323	AA371145	Hs.194397	leptin receptor	6.1
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	6.1
	429302	AJ076674	Hs.198899	eukaryotic translation initiation factor	6.1
	412673	AL042957	Hs.31845	ESTs	6.0
	410150	AW382942	Hs.260024	ESTs	6.0
30	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	6.0
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	6.0
	408968	AI652236	Hs.49376	hypothetical protein FLJ20644	6.0
	409047	AW961434	Hs.31539	ESTs	6.0
	418601	AA279490	Hs.86368	calmeglin	6.0
35	425710	AF030880	Hs.159275	solute carrier family, member 4	6.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	6.0
	414905	H40873	Hs.175971	ESTs	6.0
	450295	AI766732	Hs.210628	ESTs	6.0
	412505	AA974491	Hs.21734	ESTs	6.0
40	428730	AA625947	Hs.25750	ESTs	6.0
	445413	AA151342	Hs.12677	CGI-147 protein	6.0
	451424	AI862026	Hs.302810	Novel human gene mapping to chromosome 20	5.9
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	5.9
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	5.9
45	431359	AW993522	Hs.292934	ESTs	5.9
	404632			NM_022490: Homo sapiens hypothetical prot	5.9
	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	5.9
	449118	R67477	Hs.23103	Bel1 (S. cerevisiae) homolog	5.9
	405523			C8001409*:gij7441226[pir]jS31212 collage	5.9
50	448807	AI571940	Hs.7549	ESTs	5.8
	404642			NM_021965*: Homo sapiens phosphoglucomuta	5.8
	452598	AI831594		ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	427212	AW283849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	435047	AA454985	Hs.54973	cadherin-like protein VR20	5.8
55	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	5.8
	419038	AW134924	Hs.190325	ESTs	5.7
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	5.7
	432432	AA541323	Hs.115831	ESTs	5.7
	435937	AA830893	Hs.119769	ESTs	5.7
60	414528	AA148950	Hs.188836	ESTs	5.7
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	5.7
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	5.7
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	5.7
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	5.7
	420184	AA188408	Hs.95665	hypothetical protein	5.7
65	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	5.7
	443260	AI041530	Hs.132107	ESTs	5.7
	443324	R44013	Hs.164225	ESTs	5.7
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	5.7
70	448172	N75276	Hs.135904	ESTs	5.7
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.6
	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	5.6
	452242	R50956	Hs.159993	glycosyltransferase	5.6
	410141	R07775	Hs.287657	Homo sapiens cDNA: FLJ21291 fis, clone C	5.6
75	418019	R68911	Hs.176275	ESTs	5.6
	450813	AI739625	Hs.203376	ESTs	5.6
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	5.6
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.6
	451684	AF216751	Hs.26813	COA14	5.6
80	427674	NM_003528	Hs.2178	H2B histone family, member Q	5.6
	407275	AI364186		gb:qw34h07.x1 NC1_CGAP_U:4 Homo sapiens	5.6
	417958	AA767382	Hs.193417	ESTs	5.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	5.6
	435176	AA744875	Hs.189413	ESTs	5.5

	428465	AW970976	Hs.293653	ESTs	5.5
	431316	AA502663	Hs.145037	ESTs	5.5
	434804	AA649530	Hs.348148	gbns44f05.s1 NCL CGAP_Alv1 Homo sapiens	5.5
5	411890	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	5.5
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.5
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	5.5
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	5.5
	416239	AL038450	Hs.48948	ESTs	5.4
10	421470	R27496	Hs.1378	annexin A3	5.4
	408177	AI241733	Hs.43871	ESTs	5.4
	424084	AI940575	Hs.20914	hypothetical protein FLJ23056	5.4
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	5.4
	448072	AI459306	Hs.24908	ESTs	5.4
15	420397	NM_007018	Hs.97437	centrosomal protein 1	5.4
	429250	H56585	Hs.198308	tryptophan rich basic protein	5.4
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	5.4
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.4
	418866	T65754		gbvyc11c07.s1 Stratagene lung (937210) H	5.4
20	428364	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	5.4
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	5.4
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	5.4
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	5.4
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.3
25	412677	AW029608	Hs.17384	ESTs	5.3
	430412	AW341754	Hs.189305	ESTs	5.3
	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	5.3
	421433	AI829192	Hs.22380	ESTs	5.3
	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	5.3
30	458571	AV653731	Hs.282829	ESTs, Moderately similar to PC4259 ferri	5.3
	441054	AA913591	Hs.126480	ESTs	5.3
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	5.3
	433409	AI278802	Hs.25661	ESTs	5.3
	441102	AA973905		Intermediate filament protein syncollin	5.3
35	453387	AI990741	Hs.252809	ESTs	5.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	5.3
	433923	AI823453	Hs.146625	ESTs	5.3
	426503	AA380153		gb:EST93093 Skin tumor 1 Homo sapiens cD	5.2
40	447574	AF162666	Hs.18895	tousled-like kinase 1	5.2
	421896	N62293	Hs.45107	ESTs	5.2
	410870	U81599	Hs.66731	homeo box B13	5.2
	420729	AW964897	Hs.290825	ESTs	5.2
	425066	M82882	Hs.154365	E74-like factor 1 (ets domain transcript	5.2
	429457	NM_004477	Hs.203772	F5HD region gene 1	5.2
45	447816	NM_007233	Hs.274329	TP53 target gene 1	5.2
	446553	AB021179	Hs.15299	HMBA-inducible	5.2
	453308	AW959731	Hs.323099	ESTs	5.2
	452576	AB023177	Hs.29900	KIAA0960 protein	5.2
	421437	AW821252	Hs.104336	hypothetical protein	5.2
50	422295	AF051151	Hs.114408	tbl-like receptor 5	5.2
	453942	AW190920	Hs.19928	hypothetical protein SP329	5.2
	400424	AJ276316	Hs.287374	zinc finger protein 304	5.2
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.2
	452588	AA889120	Hs.110637	homeo box A10	5.2
55	448944	AB014605	Hs.22599	atrophin-1 Interacting protein 1; activi	5.1
	413991	H44725	Hs.176090	ESTs	5.1
	444454	BE018316	Hs.11183	sorting nexin 2	5.1
	446795	AI797713	Hs.156471	ESTs	5.1
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	5.1
60	432340	AA534222		gb:nj21d02.s1 NCL CGAP_AA1 Homo sapiens	5.1
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenit	5.1
	453293	AA382267	Hs.10653	ESTs	5.1
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	5.1
	409643	AW450866	Hs.257359	ESTs	5.1
65	427723	AI355260	Hs.279789	histone deacetylase 3	5.1
	438157	AW137011	Hs.49576	ESTs	5.1
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	5.1
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	5.1
	418051	AW192535	Hs.19479	ESTs	5.1
70	419926	AW900992	Hs.93796	DKFZP586D2223 protein	5.1
	425843	BE313280	Hs.159627	death associated protein 3	5.1
	440594	AW445167	Hs.126036	ESTs	5.1
	452449	AW068658	Hs.20943	ESTs	5.1
	429769	NM_004917	Hs.218366	kalikrein 4 (protease, enamel matrix, p	5.1
75	428898	AB033070	Hs.194408	KIAA1244 protein	5.1
	415339	NM_015156	Hs.78398	KIAA0071 protein	5.1
	450671	AI356957	Hs.43086	ESTs, Weakly similar to A46010 X-linked	5.1
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	5.0
80	433023	AW864793	Hs.87409	thrombospondin 1	5.0
	433862	D86960	Hs.3510	KIAA0205 gene product	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	418624	AI734080	Hs.104211	ESTs	5.0
	430291	AV660345	Hs.238126	CGI-49 protein	5.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	5.0

	429922	Z97630	Hs.226117	H1 histone family, member 0	5.0
	420218	AW958037	Hs.286	ribosomal protein L4	5.0
	425242	D13635	Hs.155287	KIAA0010 gene product	5.0
5	427176	AW381569	Hs.40334	ESTs	5.0
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	5.0
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	5.0
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	5.0
	450244	AA007534	Hs.125062	ESTs	5.0
10	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	5.0
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	5.0
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	5.0
	445866	H20899	Hs.13399	Homo sapiens clone 25032 mRNA sequence	4.9
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	4.9
15	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	4.9
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	4.9
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	4.9
	401451			NM_004496*Homo sapiens hepatocyte nucle	4.9
	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	4.9
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	4.9
20	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.9
	420608	BE548277	Hs.103104	ESTs	4.9
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	4.9
	424332	AA338919	Hs.101615	ESTs	4.9
25	430523	AW451385	Hs.161954	ESTs	4.9
	449300	AI656959	Hs.346514	ESTs	4.9
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	4.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	4.9
	438321	AA576635	Hs.6153	CGI-48 protein	4.9
30	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.8
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.8
	425174	D87450	Hs.154978	KIAA0261 protein	4.8
	430458	AA479300	Hs.225706	ESTs, Weakly similar to I38022 hypotheti	4.8
	455497	AA112573	Hs.278695	Homo sapiens prostein mRNA, complete cds	4.8
35	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	4.8
	449539	W80363	Hs.58446	ESTs	4.8
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.8
	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	4.8
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	4.8
40	420210	AI557257	Hs.44811	ESTs	4.8
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	4.8
	428647	AA830050	Hs.124344	ESTs	4.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	4.8
	441879	AI521936	Hs.107149	novel protein similar to archaeal, yeast	4.8
45	408990	AL022395	Hs.49526	f-box and leucine-rich repeat protein 4	4.8
	416030	H15261	Hs.21948	ESTs	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	423749	U09848	Hs.132390	zinc finger protein 36 (KIX 18)	4.8
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.7
50	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.7
	443684	AI681307	Hs.55098	ESTs	4.7
	415621	AI648602	Hs.55468	ESTs	4.7
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.7
	424433	H04607	Hs.9218	ESTs	4.7
55	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	4.7
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	4.7
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	4.7
	434973	AW449285	Hs.313636	EST	4.7
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.7
60	431587	NM_016179	Hs.262960	transient receptor potential channel 4	4.7
	452260	AA453208		RAB9, member RAS oncogene family	4.7
	412846	AW961245	Hs.55896	Homo sapiens PAC clone RP5-978E18 from 7	4.7
	418836	AI655499	Hs.161712	ESTs	4.7
	401558			ENSP00000220478*SECRETOTRANIN III.	4.7
65	441647	AA534210	Hs.285280	Homo sapiens cDNA: FLJ22095 fis, clone H	4.7
	443881	R64512	Hs.237146	hypothetical protein FLJ12752	4.7
	417169	R13550	Hs.246773	ESTs	4.7
	423349	AF010258	Hs.127428	homeo box A9	4.7
	458611	AI268407	Hs.211458	DC-specific transmembrane protein	4.7
70	444951	AI783767	Hs.148635	ESTs, Moderately similar to ALU8_HUMAN I	4.6
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.6
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.6
	423242	AL039402	Hs.125783	DEME-6 protein	4.6
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	4.6
75	419005	T86358	Hs.193931	ESTs, Weakly similar to I54374 gene NF2	4.6
	403046			NM_005656*Homo sapiens transmembrane pr	4.6
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.6
	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	4.6
	426011	AW996096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	4.6
80	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	4.6
	446015	T30968	Hs.13531	hypothetical protein FLJ10971	4.6
	452994	AW962597	Hs.31305	KIAA1547 protein	4.6
	446091	AW022192	Hs.200197	ESTs	4.6
	432908	AI861896	Hs.304505	ESTs	4.6

	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	4.6
	431673	AW971302	Hs.293233	ESTs	4.6
	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	4.6
	452355	N54926	Hs.29202	G protein-coupled receptor 34	4.6
5	432093	H28383		gb 152603.1 Soares breast 3NbHBst Homo	4.6
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	4.6
	409019	AW385412	Hs.9615	myosin regulatory light chain 2, smooth	4.6
	413812	AW186687	Hs.44748	ESTs	4.6
	414343	AL036166	Hs.323378	coated vesicle membrane protein	4.6
10	434423	NM_006769	Hs.3844	LIM domain only 4	4.5
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	421724	AB037832	Hs.107287	KIAA1411 protein	4.5
	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	4.5
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	4.5
15	446720	AI439136	Hs.140546	ESTs	4.5
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.5
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	4.5
	423412	AF109300		prostate cancer associated protein 5	4.5
20	433507	AI817336	Hs.191791	ESTs	4.5
	428966	AF069214	Hs.194687	cholesterol 25-hydroxylase	4.5
	423782	AI472209	Hs.323117	ESTs	4.5
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.5
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.5
25	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	4.5
	428715	AW293716	Hs.53126	ESTs	4.5
	429857	AF089897	Hs.294030	topoisomerase-related function protein 4	4.5
	459561	AI547306		ESTs	4.5
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.5
30	414272	AI651603	Hs.46988	ESTs	4.5
	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	4.5
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	4.5
	450094	AI74947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.5
	459324	AW080953		gb xc28c12x1 NCL_CGAP_Co18 Homo sapiens	4.5
35	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	4.5
	401519			C15000476*:g 12737279 ref XP_012163.1	4.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.5
	427484	N32859	Hs.37288	nuclear receptor subfamily 1, group D, m	4.5
40	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.4
	418858	AW981605	Hs.21145	hypothetical protein RG083M05.2	4.4
	433517	AW022133	Hs.189838	ESTs	4.4
	429559	AI985345	Hs.26425	ESTs	4.4
	452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	4.4
45	409190	AU076536	Hs.50984	sarcoma amplified sequence	4.4
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.4
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	4.4
	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	4.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	4.4
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	4.4
50	434384	AA631910	Hs.162849	ESTs	4.4
	444564	AI167877	Hs.143716	ESTs	4.4
	447500	AI381900	Hs.159212	ESTs	4.4
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.4
	408380	AF123050	Hs.44532	diubiquitin	4.4
55	448766	AI473827	Hs.31793	ESTs	4.4
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	4.4
	432810	AA863400		ESTs	4.4
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisocu	4.4
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.4
60	434022	R18374	Hs.117956	ESTs	4.4
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	4.4
	417728	AW138437	Hs.24790	KIAA1573 protein	4.4
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-II	4.4
	425810	AI923627	Hs.31903	ESTs	4.4
65	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	4.3
	448550	AL161983	Hs.21415	Homo sapiens mRNA; cDNA DKFZp761K2024 (f	4.3
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	4.3
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.3
	452335	AW188944	Hs.51272	ESTs	4.3
70	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	4.3
	450316	W84446	Hs.226434	hypothetical protein MGC4643	4.3
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	4.3
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	4.3
	424534	D87682	Hs.150275	KIAA0241 protein	4.3
75	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	4.3
	435023	AI692552		gb wd73f12x1 NCL_CGAP_Lu24 Homo sapiens	4.3
	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	4.3
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.3
	421163	AA375974	Hs.32450	ESTs, Weakly similar to T23762 hypotheti	4.3
80	420405	AA743396	Hs.189023	ESTs	4.3
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.3
	423998	H29138	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	4.3
	439764	T26535	Hs.22744	hypothetical protein MGC13105	4.3
	446351	AW444551	Hs.35380	x 001 protein	4.3

	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	4.3
	414312	AA155694	Hs.191060	ESTs	4.3
	438379	N23018	Hs.171391	C-terminal binding protein 2	4.3
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	4.3
5	414680	AA743331		hemoglobin, alpha 2	4.3
	423104	AJ005273	Hs.123647	antigenic determinant of recA protein (m	4.3
	440840	AW629666		ESTs, Weakly similar to S64054 hypothei	4.3
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	4.3
10	434874	NS2448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	4.2
	431429	AF072813		reticulon 3	4.2
	413492	D87470	Hs.75400	KIAA0280 protein	4.2
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	4.2
	435846	AA700870	Hs.14304	ESTs	4.2
15	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN IIII	4.2
	450546	AA010200	Hs.175551	ESTs	4.2
	414222	AL135173	Hs.878	sorbitol dehydrogenase	4.2
	416445	AL043004	Hs.79337	KIAA0135 protein	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
20	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.2
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	4.2
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	4.2
	449685	AW296669	Hs.66095	ESTs	4.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
25	450377	AB033091	Hs.74313	KIAA1265 protein	4.2
	419647	AA348947	Hs.91816	hypothetical protein	4.2
	442049	AA310393	Hs.190044	ESTs	4.2
	430669	AW969657	Hs.291029	ESTs	4.2
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	4.1
30	443634	H73972	Hs.134460	ESTs	4.1
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	4.1
	422634	NM_016010	Hs.118821	CGI-62 protein	4.1
	445895	D29954	Hs.13421	KIAA0056 protein	4.1
	447669	AL049985	Hs.19180	Homo sapiens mRNA; cDNA DKFZp564E122 (fr	4.1
35	407198	H91679		gb:vv04a07.s1 Soares fetal liver spleen	4.1
	447752	M73700	Hs.105938	lactotransferrin	4.1
	402855			NM_001839*:Homo sapiens calponin 3, acid	4.1
	443161	AI038316		gb:ox48c08.x1 Soares_fetal_fetus_Nb2HF8_	4.1
40	415827	H17462	Hs.23079	ESTs	4.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	4.1
	418365	AW014345	Hs.161690	ESTs	4.1
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	4.1
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	4.1
	446657	AI335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	4.1
45	421141	AW117261	Hs.125914	ESTs	4.1
	430335	D80007	Hs.239499	KIAA0185 protein	4.1
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.1
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	4.1
50	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	4.1
	410592	R94088	Hs.43569	ESTs	4.1
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.1
	428634	AA811845	Hs.106290	Kelch motif containing protein	4.1
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	4.1
55	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	4.0
	443273	AI042063	Hs.132156	ESTs	4.0
	428055	AA420564	Hs.101760	ESTs	4.0
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	4.0
	451294	AI457338	Hs.29894	ESTs	4.0
60	430519	AF129534	Hs.49210	F-box only protein 4	4.0
	441766	R53790	Hs.23294	hypothetical protein FLJ14393	4.0
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.0
	446354	AW449650	Hs.346335	ESTs	4.0
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.0
65	409706	BE158773	Hs.213207	ESTs	4.0
	447082	T85314		thioredoxin-like	4.0
	418594	AI732083	Hs.187619	ESTs	4.0
	426501	AW043782	Hs.293616	ESTs	4.0
70	436797	AA731491	Hs.334477	hypothetical protein MGC14879	4.0
	416288	H51299		gb:yp07c06.s1 Soares breast 3NbHBst Homo	4.0
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	4.0
	425920	AL049977	Hs.162209	claudin 8	4.0
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural era	4.0
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.0
75	433209	AB040907	Hs.278436	KIAA1474 protein	4.0
	428801	AW277121	Hs.254881	ESTs	4.0
	419629	AB020695	Hs.91662	KIAA0888 protein	4.0
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	3.9
80	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	3.9
	400695			C11002514*gl 11280151 pir E82756 beta-	3.9
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	3.9
	419985	H66373	Hs.5856	ESTs, Highly similar to bA393J16.3 [H.s.a	3.9
	429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (f	3.9
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	3.9

	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	3.9
	413450	Z99716	Hs.75372	N-acetylglucosaminidase, alpha-	3.9
	427615	BE410107	Hs.179817	CGI-82 protein	3.9
5	450649	NM_001429	Hs.25272	E1A binding protein p300	3.9
	445798	NM_012421	Hs.13321	rearranged L-myc fusion sequence	3.9
	416198	H27332	Hs.99598	hypothetical protein MGC5338	3.9
	431147	A1767751	Hs.20300	ESTs	3.9
	439192	AW970536	Hs.105413	ESTs	3.9
10	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.9
	451900	AB023199	Hs.27207	KIAA0882 protein	3.9
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	3.9
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020.1 E2IG5	3.9
	442320	A1287817	Hs.129636	ESTs	3.9
15	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	3.9
	444636	T96667	Hs.17877	ESTs	3.9
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	3.9
	412576	AA447718	Hs.107057	ESTs	3.9
	423952	AW877787	Hs.136102	KIAA0853 protein	3.9
20	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.9
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	3.9
	447280	BE617907	Hs.97635	ESTs	3.9
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	3.8
	450580	N40087		ESTs	3.8
25	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.8
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	3.8
	407332	A1801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis, clone HE	3.8
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	3.8
	412652	A1801777	Hs.260024	ESTs	3.8
30	426226	AA769045		gb:aa80h07.s1 NCI_CGAP_GCB1 Homo sapiens	3.8
	437816	A1823445	Hs.280699	ESTs	3.8
	444534	AW271626	Hs.42294	ESTs	3.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	3.8
	408242	AA251594	Hs.43913	PIBF1 gene product	3.8
35	443484	A1091458	Hs.134559	ESTs	3.8
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	3.8
	428043	T92248	Hs.2240	uteroglobin	3.8
	407192	AA609200		gb:af12a02.s1 Soares_testis_NHT Homo sap	3.8
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.8
40	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	3.8
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	3.8
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.8
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	3.8
	408547	AA574291	Hs.57837	ESTs	3.8
45	427635	BE397888	Hs.179982	tumor protein p53-binding protein	3.8
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	3.8
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothe	3.8
	453698	AA037615	Hs.42746	ESTs	3.8
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	3.8
50	431197	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k	3.8
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.8
	438138	R98299	Hs.177502	ESTs	3.8
	447906	AL050062	Hs.19999	DKFZP566K023 protein	3.8
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	3.7
55	435655	AW105663	Hs.6947	HSPC069 protein	3.7
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	3.7
	439398	AA284267	Hs.221504	ESTs	3.7
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	3.7
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
60	418576	AW968159	Hs.289104	Epithelial calcium channel 2, CaT-like A	3.7
	436024	A1800041	Hs.190555	ESTs	3.7
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.7
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.7
	442861	AA243837	Hs.57787	ESTs	3.7
65	448207	A1475490	Hs.170577	ESTs	3.7
	450628	AW382884	Hs.204715	ESTs	3.7
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.7
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	3.7
	443031	AW134696	Hs.49418	ESTs	3.7
70	447608	AW205042	Hs.18955	Homo sapiens cDNA FLJ20667 fis, clone KA	3.7
	408312	AF263813	Hs.44198	intracellular membrane-associated calcu	3.7
	412777	A1335773	Hs.270123	ESTs	3.7
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	3.7
	424882	A1379461	Hs.153636	far upstream element (FUSE) binding prot	3.7
75	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	3.7
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.7
	452129	AW291379	Hs.212827	ESTs	3.7
	453927	AA082465	Hs.125031	choline/ethanolaminephosphotransferase	3.7
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.7
80	425988	BE045897	Hs.274454	ESTs, Weakly similar to I38022 hypothe	3.7
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.7
	445467	A1239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.7
	423855	AA331761	Hs.254859	ESTs	3.7
	403790			NM_001334*:Homo sapiens cathepsin O (CTS	3.7

	434470	AA634818	Hs.298138	ESTs	3.7
	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible	3.7
	420026	AI831190	Hs.166676	ESTs	3.7
5	421838	AW881089	Hs.108806	Homo sapiens mRNA; cDNA DKFZp566M0947 (f	3.7
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	3.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.6
	445941	AI267371	Hs.172636	ESTs	3.6
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochondrion)	3.6
10	412533	AA679863	Hs.69606	ESTs	3.6
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	3.6
	442710	AI015631	Hs.23210	ESTs	3.6
	448212	AI475858		gbtc87d07.x1 NCLCGAP_CLL1 Homo sapiens	3.6
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolog)	3.6
	453038	AW292415	Hs.20509	HBV pX associated protein-8	3.6
15	427661	AA410292	Hs.104761	ESTs	3.6
	420923	AF097021	Hs.273321	differentially expressed in hematopoietic	3.6
	414844	AA296874	Hs.77494	deoxyguanosine kinase	3.6
	441866	BE464341	Hs.21201	necln 3; DKFZP566B0846 protein	3.6
	406815	AA833930	Hs.288036	RNA isopentenylpyrophosphate transferase	3.6
20	423482	BE280172	Hs.129228	galactokinase 2	3.6
	424677	U09414	Hs.151689	zinc finger protein 137 (clone pHZ-30)	3.6
	430160	AW968210	Hs.293357	ESTs, Weakly similar to ALUC_HUMAN IIII	3.6
	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	3.6
	433887	AW204232	Hs.279522	ESTs	3.6
25	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	3.6
	411890	H92738	Hs.75811	N-acylsphingosine amidohydrolase (acid c	3.6
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6
	431724	AA514535	Hs.283704	ESTs	3.6
	435703	AW630133	Hs.83313	GK003 protein	3.6
30	445674	BE410347	Hs.13063	transcription factor CA150	3.6
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (3.6
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	3.6
	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	3.6
35	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	3.6
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	3.6
	439379	AA835002	Hs.125611	ESTs	3.6
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.6
40	434579	T55958		gb:yb35f05.r1 Stratagene fetal spleen (9	3.6
	451367	AA923729	Hs.26322	cell cycle related kinase	3.6
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	3.6
	431263	AW129203	Hs.322915	ESTs	3.6
	431952	Z70695	Hs.272240	Homo sapiens cDNA FLJ11086 fis, clone PL	3.6
45	439092	AA830149		gb:oc44f08.s1 NCLCGAP_GC81 Homo sapiens	3.6
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	3.5
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	3.5
	419440	AB020689	Hs.90419	KIAA0882 protein	3.5
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	3.5
50	419241	AA523939	Hs.165258	ESTs	3.5
	410762	AF226053	Hs.66170	HSKM-B protein	3.5
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	3.5
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	3.5
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.5
	420390	AA330047	Hs.191187	ESTs	3.5
55	416662	T25853	Hs.7538	ESTs	3.5
	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	3.5
	433285	AW975944	Hs.237396	ESTs	3.5
	421991	NM_014918	Hs.110488	KIAA0990 protein	3.5
60	413950	AA248096	Hs.32793	ESTs	3.5
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-link	3.5
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.5
	411149	N68715	Hs.269128	ESTs	3.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.5
65	418334	AA319233	Hs.5521	ESTs	3.5
	422583	AA410506	Hs.27973	KIAA0874 protein	3.5
	425717	X07282	Hs.171495	retinoic acid receptor, beta	3.5
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.5
	434569	AI311295	Hs.344478	KIAA0196 gene product	3.5
	419436	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	3.5
70	437296	AA350994	Hs.20281	KIAA1700	3.5
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.5
	439605	AF086431	Hs.22380	ESTs	3.5
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	3.5
75	432589	AL135725	Hs.131708	ESTs	3.5
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.5
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.5
	421129	BE439899	Hs.89271	ESTs	3.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	3.5
80	434839	AI743069	Hs.134736	ESTs	3.5
	435166	AI391470	Hs.158618	ESTs	3.5
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.5
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.5
	453311	AW104911	Hs.126707	hypothetical protein FLJ11457	3.5

	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	3.5
	413786	AW613780	Hs.13500	ESTs	3.5
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	3.5
5	439904	AW892676		gb:CM3-NN0004-280300-131-c12 NN0004 Homo	3.5
	449909	AA004681	Hs.59432	ESTs	3.5
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	3.5
10	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.5
	438527	AJ969251	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
	453916	AW974874	Hs.75212	ornithine decarboxylase 1	3.5
	430200	BE613337	Hs.234896	geminin	3.4
	437187	AL080208	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	3.4
15	423645	AJ215632	Hs.147487	ESTs	3.4
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.4
	434966	AA657494		gb:nt66f04.s1 NCI_CGAP_Pr3 Homo sapiens	3.4
	404571			NM_015902*:Homo sapiens progesteron induce	3.4
	418727	AA227609	Hs.94834	ESTs	3.4
20	436374	AA400709	Hs.96716	ESTs, Weakly similar to T17210 hypothel	3.4
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	3.4
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.4
	402031			ENSP00000251056*:Plasma membrane calcium	3.4
25	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	449603	AJ655662	Hs.197698	ESTs	3.4
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	3.4
	436805	AA731533	Hs.270751	ESTs	3.4
	437367	AA749316	Hs.271879	ESTs, Moderately similar to ALU1_HUMAN A	3.4
30	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.4
	430144	AJ732722	Hs.187694	ERGL protein; ERGLC-53-like protein	3.4
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.4
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (3.4
	439375	AA689526	Hs.344249	steroid dehydrogenase homolog	3.4
35	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	408267	AW380525	Hs.343564	tubulin-specific chaperone e	3.4
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.4
	422564	AJ148006	Hs.222120	ESTs	3.4
40	424842	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	3.4
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	3.4
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.4
	436137	AJ056769	Hs.133512	ESTs	3.4
	440348	AW015802	Hs.47023	ESTs	3.4
45	442910	AJ365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	3.4
	443242	BE243910	Hs.9082	nucleoporin p54	3.4
	445469	AW298370	Hs.153714	complement-c1q tumor necrosis factor-rel	3.4
	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.4
50	433037	NM_014158	Hs.279938	HSPC067 protein	3.4
	423044	AA320829	Hs.97266	protocadherin 18	3.4
	434128	W93170	Hs.284164	protein x 0004	3.4
	449845	AW971183	Hs.9683	OpaJ (Hsp40) homolog, subfamily C, membe	3.4
55	423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Etav/Sex-	3.4
	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	3.4
	438825	BE327427	Hs.79953	ESTs	3.4
	446874	AW968304	Hs.56156	ESTs	3.4
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.4
	419131	AA406293	Hs.41167	ESTs	3.4
60	423178	AJ033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	3.4
	433764	AW753676	Hs.39982	ESTs	3.4
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	3.4
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	3.3
	452815	AA418841		gb:zw01e11.s1 Soares_NhHMPu_S1 Homo sapi	3.3
65	421234	AA907153	Hs.190060	ESTs	3.3
	424075	AJ807320	Hs.227630	RE1-silencing transcription factor	3.3
	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	3.3
	420041	AB005142	Hs.94592	klotho	3.3
	426174	AA547959	Hs.115838	ESTs	3.3
70	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	3.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	3.3
	436664	AW197887	Hs.253353	ESTs	3.3
	441124	T97717	Hs.119563	ESTs	3.3
	444169	AV648170	Hs.58756	ESTs	3.3
75	421476	AW953805	Hs.21887	ESTs	3.3
	422165	AL041199	Hs.1481	histidine decarboxylase	3.3
	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	3.3
	450747	AJ064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	3.3
	401197			ENSP00000229263*:HSPC213.	3.3
80	433404	T32982	Hs.102720	ESTs	3.3
	422546	AB007869	Hs.301478	KIAA0500 protein	3.3
	443884	N20617	Hs.194397	leptin receptor	3.3
	414341	D80004	Hs.75909	KIAA0182 protein	3.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.3

	414407	AA147026	Hs.76704	ESTs	3.3
	420324	AF163474	Hs.96744	prostate androgen-regulated transcript 1	3.3
	423453	AW450737	Hs.128791	CGI-09 protein	3.3
5	444170	AW613879	Hs.102408	ESTs	3.3
	445474	AI240014	Hs.259558	ESTs	3.3
	450582	AI339732		G-rich RNA sequence binding factor 1	3.3
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.3
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	3.3
10	444324	AI301330	Hs.143838	ESTs	3.3
	427581	NM_014788	Hs.179703	KIAA0129 gene product	3.3
	429258	AA448765		gb:zx10e09.r1 Soares_tctal_fetus_Nb2HF8_	3.3
	400880			NM_000611*:Homo sapiens CD59 antigen p18	3.3
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.3
15	451968	H56196	Hs.26409	Homo sapiens mRNA; cDNA DKFZp547K204 (fr	3.3
	411190	AA306342	Hs.69171	protein kinase C-like 2	3.3
	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.3
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I78885 serine/th	3.3
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	3.3
20	428523	AW974540	Hs.98626	ESTs	3.3
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	3.3
	432363	AA534489		gb:mf76g11.s1 NCL_CGAP_Co3 Homo sapiens	3.3
	435102	AW899053	Hs.76917	F-box only protein 8	3.3
	438147	AW250553		H-2K binding factor-2	3.3
25	445808	AV655234		ESTs, Moderately similar to PC4259 ferri	3.3
	453058	AW612293	Hs.288684	Homo sapiens cDNA FLJ11750 fis, clone HE	3.3
	453286	AA034319	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	3.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hbr1)	3.3
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.3
30	411373	BE326276	Hs.8861	ESTs	3.3
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.3
	443674	AI081330	Hs.145008	ESTs	3.3
	427528	AI077143	Hs.179565	minichromosome maintenance deficient (S.	3.3
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.3
35	420969	AI636310	Hs.28310	ESTs	3.3
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.3
	409542	AA503020	Hs.38563	hypothetical protein FLJ22418	3.3
	410119	F07841	Hs.13926	ESTs	3.3
40	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	3.3
	423201	NM_000163	Hs.125180	growth hormone receptor	3.3
	442787	W93048	Hs.250723	hypothetical protein MGC2747	3.3
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.3
	423427	AL137612	Hs.285848	KIAA1454 protein	3.3
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	3.3
45	426775	AA384564		ESTs	3.3
	432378	AI493046	Hs.146133	ESTs	3.3
	438875	AA827640	Hs.189059	ESTs	3.3
	452959	AI933416	Hs.189674	ESTs	3.3
50	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2
	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	3.2
	433002	AF048730	Hs.279906	cyclin T1	3.2
	430929	AA489166	Hs.156933	ESTs	3.2
	437444	H46008	Hs.31518	ESTs	3.2
	446297	AI346930	Hs.149728	ESTs	3.2
55	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	3.2
	429377	AA813192	Hs.200596	KIAA0547 gene product	3.2
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.2
	420583	H77859	Hs.65450	reticulon 4	3.2
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	3.2
60	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	3.2
	418871	NM_001608	Hs.1209	acyl-Coenzyme A dehydrogenase, long chai	3.2
	421029	AW057782	Hs.293053	ESTs	3.2
	452997	N64777	Hs.44656	ESTs	3.2
	435035	BE568487	Hs.47668	x 006 protein	3.2
65	408412	AW193033	Hs.124436	ESTs	3.2
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	3.2
	421887	AW161450	Hs.109201	CGI-86 protein	3.2
	432409	AA805538	Hs.130732	KIAA1575 protein	3.2
	434378	AA631739	Hs.335440	EST	3.2
70	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	3.2
	420195	N44348	Hs.28243	Homo sapiens cDNA FLJ11177 fis, clone PL	3.2
	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone PL	3.2
	410296	AW630675	Hs.271946	ESTs	3.2
	413838	AV661185	Hs.75574	mitochondrial ribosomal protein L19	3.2
75	414342	AA742181	Hs.75912	KIAA0257 protein	3.2
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.2
	425475	W56339	Hs.107057	ESTs	3.2
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	3.2
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	3.2
80	452295	BE379936	Hs.28866	programmed cell death 10	3.2
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	3.2
	432960	AW150945	Hs.144758	ESTs	3.2
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.2
	427299	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.2

	421645	AA974127	Hs.129777	ESTs	3.2
	457489	AJ693815	Hs.127179	cryptic gene	3.2
	415691	AW963979	Hs.24723	ESTs	3.2
5	433852	AJ378329	Hs.126629	ESTs	3.2
	439735	AJ635386	Hs.142846	hypothetical protein	3.2
	428279	AA425310	Hs.155756	ESTs, Weakly similar to A47582 B-cell gr	3.2
	427715	BE245274	Hs.180428	KIAA1181 protein	3.2
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	3.2
10	415715	F30384	Hs.302204	ESTs	3.2
	426172	AA371307	Hs.125056	ESTs	3.2
	434825	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.2
	436246	AW450963	Hs.119991	ESTs	3.2
	436401	AJ087958	Hs.29088	ESTs	3.2
15	408784	AW971350	Hs.63386	ESTs	3.2
	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.2
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.2
	405558			Target Exon	3.2
	434747	AA837085	Hs.220585	ESTs	3.2
20	414591	AJ888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.2
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.2
	426171	AJ128606	Hs.6557	zinc finger protein 161	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	3.2
25	433050	AJ093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	3.2
	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	3.2
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	448568	AA149121	Hs.71947	ESTs	3.2
30	420131	F08286	Hs.95262	nuclear factor related to kappa B bindin	3.1
	429299	AJ620463	Hs.347408	hypothetical protein MGC13102	3.1
	407913	BE393767	Hs.41569	phosphatidic acid phosphatase type 2A	3.1
	415009	C75253	Hs.220950	ESTs	3.1
	406627	T64904	Hs.163780	ESTs	3.1
35	438666	AW014493	Hs.126727	ESTs	3.1
	419875	AA853410	Hs.93557	proenkephalin	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.1
40	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	3.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	3.1
	431416	AA532718	Hs.178604	ESTs	3.1
	422662	BE274778	Hs.119007	RAB4, member RAS oncogene family	3.1
	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	3.1
45	437083	AW082597	Hs.244862	ESTs	3.1
	430294	AJ538226	Hs.32976	guanine nucleotide binding protein 4	3.1
	417380	T06809	Hs.332086	ESTs	3.1
	419965	H16382	Hs.70258	ESTs	3.1
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	3.1
	446146	AJ287539	Hs.148078	ESTs	3.1
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.1
	418555	AJ417215	Hs.87159	hypothetical protein FLJ12577	3.1
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	3.1
55	423947	AW451954	Hs.135941	KIAA1048 protein	3.1
	451893	AW192083	Hs.290855	ESTs	3.1
	447726	AL137638	Hs.19368	matrilin 2	3.1
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypothel	3.1
	453439	AJ572438	Hs.32976	guanine nucleotide binding protein 4	3.1
60	443331	AJ052026	Hs.149995	ESTs	3.1
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.1
	414372	AA143654		gbzo65a02.r1 Stratagene pancreas (93720	3.1
	427421	AA402414	Hs.3059	coatamer protein complex, subunit beta	3.1
	429399	AA452244	Hs.16727	ESTs	3.1
65	430092	AJ821399	Hs.16514	ESTs	3.1
	433577	AW007080	Hs.284192	ESTs	3.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	3.1
	436894	H80696	Hs.233313	ESTs	3.1
	437756	AA767537	Hs.197096	ESTs	3.1
70	438979	AW976218	Hs.32565	ESTs	3.1
	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	3.1
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.1
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	3.1
	419030	T79957	Hs.188466	ESTs	3.1
75	438308	AJ343469	Hs.127685	KIAA1627 protein	3.1
	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	3.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	3.1
	428878	AA436884	Hs.48926	ESTs	3.1
	432205	AJ805583	Hs.125291	ESTs	3.1
80	440099	AL080058	Hs.6909	DKFZP564G202 protein	3.1
	428259	AA424793	Hs.24144	ESTs	3.1
	434614	AJ249502	Hs.29669	ESTs	3.1
	420380	AA640891	Hs.102406	ESTs	3.1
	433323	AA805132	Hs.159142	ESTs	3.1

	439544	W26354	Hs.28891	hypothetical protein FLJ11360; artemis p	3.1
	412088	AI689496	Hs.108932	ESTs	3.1
	434361	AF129755	Hs.88474	ESTs	3.1
	400664			NM_002425:Homo sapiens matrix metallopro	3.1
5	436354	AI879252	Hs.5151	RAN binding protein 7	3.1
	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	3.1
	410595	AW628223	Hs.64794	zinc finger protein 183 (RING finger, C3	3.1
	415245	N59650	Hs.27252	ESTs	3.1
	418647	AA226198		gb:nc26a07.s1 NCL_CGAP_Pr1 Homo sapiens	3.1
10	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.1
	453716	AA037675	Hs.152675	ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.0
	408705	AA312135	Hs.46967	HSPCO34 protein	3.0
	430280	AA361258	Hs.237868	interleukin 7 receptor	3.0
15	445919	T53519	Hs.334692	hypothetical protein MGC14141	3.0
	441790	AW294909	Hs.132208	ESTs	3.0
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.0
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.0
	422788	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.0
20	439703	AF086538	Hs.196245	ESTs	3.0
	444489	AI151010	Hs.157774	ESTs	3.0
	453878	AW964440	Hs.19025	DC32	3.0
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.0
25	433680	AI805366	Hs.199945	ESTs	3.0
	426363	M58524	Hs.2025	transforming growth factor, beta 3	3.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	3.0
	426044	AA502490	Hs.170290	ESTs	3.0
	431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	3.0
	445084	H38914	Hs.250848	hypothetical protein FLJ14761	3.0
30	452737	AK001680	Hs.30488	DKFZP434F091 protein	3.0
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	3.0
	435712	AA694607	Hs.176956	ESTs	3.0
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.0
	414993	AW819403	Hs.77724	KIAA0586 gene product	3.0
35	419459	AW291128	Hs.278422	DKFZP586G1122 protein	3.0
	421988	AW450481	Hs.161333	ESTs	3.0
	432833	N51075	Hs.110028	ESTs	3.0
	445210	H09323	Hs.27133	ESTs	3.0
	447620	AW290951	Hs.224965	ESTs	3.0
40	449375	R07114	Hs.271224	ESTs	3.0
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.0
	443987	AW294013	Hs.200942	ESTs	3.0
	441224	AIJ076954	Hs.7753	calumenin	3.0
45	448822	BE149845	Hs.289038	hypothetical protein MGC4126	3.0
	435688	H72286	Hs.128387	ESTs	3.0
	441899	AI090455	Hs.268371	hypothetical protein FLJ20274	3.0
	411704	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
	416954	AA171850	Hs.42251	ESTs	3.0
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	3.0
50	420077	AW512260	Hs.87767	ESTs	3.0
	443475	AI056470	Hs.132809	ESTs	3.0
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	3.0
	438436	AA807168	Hs.271552	ESTs	3.0
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.0
55	443280	AA299688	Hs.24183	ESTs	3.0
	448264	AI478933	Hs.188260	ESTs	3.0
	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	3.0
	453843	D25215	Hs.35804	hect domain and RLD 3	3.0
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	3.0
60	445943	AW898533	Hs.181574	ESTs	3.0
	432286	AW327432	Hs.255843	ESTs	3.0
	431707	R21326	Hs.257905	hypothetical protein FLJ10422	3.0
	432675	AI791855	Hs.105884	ESTs	3.0
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.0
65	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked mol	3.0
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.0
	423583	AL122055	Hs.129836	KIAA1028 protein	3.0
	418304	AA215702		gb:zr97g10.r1 NCL_CGAP_GCB1 Homo sapiens	3.0
70	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.0
	410011	AB020641	Hs.57856	PFTAIKE protein kinase 1	3.0
	411850	AK002033	Hs.72782	hypothetical protein FLJ11171	3.0
	438986	AF085888	Hs.269307	ESTs	3.0
	445921	AW015211	Hs.146181	ESTs	3.0
75	447124	AW976438	Hs.17428	RBP1-like protein	3.0
	452953	AI932884	Hs.271741	ESTs, Weakly similar to A46010 X-linked	3.0

TABLE 60B

Pray. Unique Eos probeset identifier number

CAT number: Gene cluster number
Accession: Genbank accession numbers

	Pkey	CAT Number	Accessions
5	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
	411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW851034
10	414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
	414680	147525_1	AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA544620 AA652769 AA242975 AA151074 T19890
	415989	156454_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
	416288	1585983_1	H51299 H44619 H46391 R86024 H51892 T72744
15	416882	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AJ333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24577 R40635 H05100 R40597
	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	417379	167238_1	AA196390 AA507837 AA196468
	418304	173658_2	AA215702 AA368008 AA215703 BE066555 BE006876
20	418647	177521_1	AA226198 AA226513 AA383773
	418866	179788_1	T65754 AA229857 AA229658
	419536	185688_1	AA603305 AA244095 AA244183
	419544	185760_2	AJ909154 AA526337 AA244193 AI909153
	423412	228001_1	AF109300 AI299378 AI202654
25	423800	232161_1	AA331156 AA331157 AA331155
	426226	262918_1	AA769045 AA372590 AW963633
	426413	266650_1	AA377823 AW954494 AI022688
	426503	268283_1	AA380153 AA380233 AW963529
	426775	271683_1	AA384564 AW966475 H02121 N41297 D63213 AA886888 AI922414 AW044240 AW196808 AI076736 AA599294 AI954433 AW117617 AI640323 H98134
30	426991	27415_1	AK001536 AA191092 AW510354 AI554256 AL353968 AA134266
	428342	290035_2	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI092404 AI085630 AA731340
	429163	300543_1	AA884766 AW974271 AA592975 AA447312
35	429220	301384_1	AW207206 AW341473 AA448195 AI951341
	429258	301917_1	AA448765 C04967 C03045 AA656293
	430935	325772_1	AW072916 AI184913 AA489195 AW466994 AW69044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
	430968	325269_1	AW972830 AA527647 AA489820 AA570362
40	431429	33313_1	AF072813 AF119297 AA362885 AF059524 NM_006054 AA157365 AW163623 AA056148 AA227062 AA418057 AA227076 AA078753 AA233594 D58629 AA232373 AA233577 T59596 BE618035 AA354497 AA359082 T32010 AA134519 BE299901 BE268096 BE396826 AA324268 AL120308 AA187561 AA311680
	432093	341283_1	H28383 AW972670 H28359 AA525808
	432125	341776_1	AW972667 AA526539 AI057032 AW167842
45	432189	342819_1	AA527941 AI810608 AI620190 AA635266
	432340	345248_1	AA534222 AA632632 TB1234
	432363	345469_1	AA534489 AW970240 AW970323
	432600	350959_1	AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
	432810	354375_1	AA863400 AJ991439 AW016017 AW014704 AI367512 H17550 AA744762 R46187 AW471324 AI126670 AA626033 AI276287 AI094253 AI286003 AI147163 AI911443 AW512612 AA972102 AA999975 AI684428 AI335035 D63102 AI524234 AI539156 AA565542
50	434579	38916_1	T55958 T57205 AF147346
	434966	396504_1	AA657494 AI582663 AI581639
	435023	398093_1	AI692552 AI393343 AI800510 AI377711 F24263 AA661876
	437866	44433_2	AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI47188
55	438147	45074_1	AW250553 L07876 Z36843 R30893 AI190097 AW965317
	439092	468554_1	AA830149 AW978407 M85983 AW503637
	439518	47334_1	W76326 AF086341 W72300
	439904	479942_1	AW892676 AA853877 D44747
60	440840	50357_2	AW629666 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI979207 AA921877
	441102	509604_1	AA973905 AI299888 AA917019 H63235 T90771
	442562	54500_2	BE379584 R34211 BE544768 AW973709 AI653056 AI653173 AI266043 AI656750 H74180 AI492830 AI376090 AI472184 D59940 AW170056 AI082443 AW021142 AI167921 AI348677 AI278577 AW130886 AA761517 AI698203 AA115535 AI264790 R34328 D59939 AW205074 AA554902 D62102 AI0007
65	443161	561305_1	AI038316 AI344631 AI261653
	445808	65133_1	AV655234 AW966332 AA340239
	447082	707248_1	T85314 AI360684 T85528 T91254
	448212	755099_1	AI475858 AW969013
70	449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486 N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816888 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095 AA164518 AA730973 W00417 W65303
	450582	83929_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
75	452260	9074_1	AA453208 NM_004251 U44103 AI671547 N57463 AW007521 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228 BE326331 AI934576 AI922378 AW276431 AI718466 N36566 AA904753 BE464245 AI338752 AI659875 AW272338 AI423136 AI089270 AI160904 AA664354 BE1
	452598	92338_2	AI831594 AW970667 AW027959 AI129800 AI927949 AI650270 AI625105 AW514661 AI708393 AL138076 BE180510 AI926721 AI399955 AA749139 AI862160 AW874011 AI242763 AA262795 AA039864 H73499 AI093249 BE245661 AI816834 N25206 AA828301 AI084565 AI302816 AA026905 AA77255
80	452815	93255_1	AA418841 AI452657 AI768876 AA028973 BE179873 C00215 AA418930
	453802	981589_1	AL134757 AW079131
	455100	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW881034

457728 393853_1 AW974811 AA651634 AA650072

5 TABLE 60C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400664	8118496	Plus	13558-13721,13942-14090,14554-14679
400695	7249150	Plus	160456-160567,164757-164873
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
402031	7656761	Plus	33080-33263,33939-34094,36103-36507
402802	3287156	Minus	53242-53432
402855	9662953	Minus	59763-59909
403046	3540153	Minus	55707-55859,56369-56511
403047	3540153	Minus	59793-59968
403790	8084957	Minus	87826-87947,89835-90002
404571	7249169	Minus	112450-112648
404632	9796668	Plus	45096-45229
404641	9796810	Minus	32247-32362
404642	9796810	Plus	102999-103145
405523	9454643	Plus	114550-114688,117407,119490-119599,123237-123395,131140-131217
405558	1621110	Plus	4502-4644,5983-6083

35 Table 61A lists about 440 genes up-regulated in prostate cancer compared to normal prostate and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal prostate tissue was greater than or equal to 2.0 and the ratio to normal adult tissues was greater than or equal to 2.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95th percentile amongst prostate tissues. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

40 TABLE 61A: ABOUT 440 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE AND NORMAL ADULT TISSUES

45 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of prostate tumor to normal adult body tissue
 R2: Ratio of prostate tumor to normal prostate tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2	42.2
421566	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop	3.2	26.5
420729	AW964897	Hs.290825	ESTs	3.7	15.8
401197			ENSP00000229263*HSPC213.	3.0	12.6
450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4	12.4
449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3	12.3
443271	BE568568	Hs.195704	ESTs	11.6	11.6
434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	2.1	11.2
431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4	9.4
417315	AI080042	Hs.180450	ribosomal protein S24	2.3	9.0
416182	NM_004354	Hs.79069	cyclin G2	8.4	8.4
421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	2.2	8.4
434217	AW014795	Hs.23349	ESTs	8.3	8.3
425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3	8.3
442501	AA315267	Hs.23128	ESTs	2.0	8.3
429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1	8.1
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	3.1	8.0
417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	34.0	7.9
420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5	7.5
419078	M93119	Hs.89584	insulinoma-associated 1	7.4	7.4
425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	9.4	7.3
425018	BE245277	Hs.154196	E4F transcription factor 1	7.2	7.2
452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0	7.0
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	4.0	6.6
409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3	6.3
411373	BE326276	Hs.8861	ESTs	3.2	6.3
423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.7	6.2
422583	AA410506	Hs.27973	KIAA0874 protein	2.3	6.2
438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	6.1	6.1
437147	AL049964	Hs.8358	hypothetical protein FLJ20356	2.6	6.0

	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 much 2 p	6.0	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.2	6.0
	449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9	5.9
5	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	3.3	5.9
	431548	AI834273	Hs.9711	novel protein	15.7	5.8
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.2	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.5	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.9	5.8
10	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7	5.7
	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.5	5.6
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6	5.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.5	5.5
	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.7	5.5
15	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4	5.4
	451684	AF216751	Hs.26813	CDA14	3.9	5.4
	421470	R27496	Hs.1378	annexin A3	5.3	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.8	5.3
20	437571	AA760894	Hs.153023	ESTs	5.2	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2	5.2
	444917	R68651	Hs.144997	ESTs	5.1	5.1
	417318	AW953937	Hs.240845	ESTs	4.6	5.1
	434170	AA626509	Hs.122329	ESTs	5.1	5.0
25	432897	AF155099	Hs.279780	NY-REN-18 antigen	3.3	5.0
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.8	5.0
	421823	N40850	Hs.28625	ESTs	5.0	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9	4.9
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	29.8	4.9
	425242	D13635	Hs.155287	KIAA0010 gene product	2.2	4.8
30	439024	R96696	Hs.35598	ESTs	5.4	4.8
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8	4.8
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6	4.7
35	451952	AL120173	Hs.301663	ESTs	4.7	4.7
	431676	AI685464	Hs.159993	gb:tt88f04.x1 NCL_CGAP_Pr28 Homo sapiens	9.1	4.7
	452242	R50956	Hs.159993	glycosyltransferase	4.7	4.7
	401519			C15000476:gl 12737279 ref XP_012163.1	4.6	4.6
40	414342	AA742181	Hs.75912	KIAA0257 protein	3.4	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	3.3	4.6
	429467	NM_004477	Hs.203772	FSDH region gene 1	2.1	4.6
	408380	AF123050	Hs.44532	diubiquitin	4.2	4.6
	425907	AA365752	Hs.155965	ESTs	2.2	4.6
	427078	AI676062	Hs.111902	ESTs	4.8	4.5
45	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	2.7	4.5
	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5	4.5
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	2.5	4.5
	443250	AI041530	Hs.132107	ESTs	8.1	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4	4.4
50	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4	4.4
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4	4.4
	428826	AL048842	Hs.194019	atractin	2.0	4.3
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3	4.3
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN [III	4.2	4.2
55	429900	AA460421	Hs.30875	ESTs	4.2	4.2
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.2	4.2
	409151	AA305105	Hs.50785	SEC22, vesicle trafficking protein (S. c	3.5	4.2
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	10.0	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.8	4.2
60	443622	AI911527	Hs.11805	ESTs	2.2	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1	4.1
	421129	BE439899	Hs.89271	ESTs	4.1	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	3.9	4.1
65	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	2.8	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.0	4.1
	433887	AW204232	Hs.279522	ESTs	4.1	4.1
	436556	AI364997	Hs.7572	ESTs	4.1	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1	4.1
70	443646	AI085198	Hs.164226	ESTs	4.1	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	2.2	4.0
	418432	M14156	Hs.85112	Insulin-like growth factor 1 (somatomedi	4.0	4.0
	433409	AI278802	Hs.25661	ESTs	4.0	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0	4.0
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9	3.9
75	444755	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	3.9	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	2.2	3.9
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.3	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	2.2	3.9
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	3.9	3.9
80	423337	NM_004655	Hs.127337	adin 2 (conductin, adl)	3.4	3.8
	452588	AA889120	Hs.110637	homeo box A10	6.5	3.8
	422681	NM_014700	Hs.119004	KIAA0665 gene product	3.8	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	2.3	3.8
	410330	AW023630	Hs.159425	ESTs	6.2	3.8

5	422975	AA347720	Hs.122669	KIAA0264 protein	2.2	3.8
	425978	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.7	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	4.1	3.8
10	418821	AA436002	Hs.183161	ESTs	2.8	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.1	3.8
	453160	A1263307	Hs.239884	H2B histone family, member L	9.2	3.8
	424906	A1566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7	3.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked mol	3.7	3.7
15	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7	3.7
	448807	A1571940	Hs.7549	ESTs	3.6	3.7
	439209	AF087993	Hs.91954	ESTs	2.1	3.6
	420077	AW512260	Hs.87767	ESTs	4.4	3.6
	451009	AA013140	Hs.115707	ESTs	4.1	3.6
20	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6	3.6
	452561	A1692181	Hs.49169	KIAA1634 protein	3.2	3.6
	447033	A1357412	Hs.157601	ESTs	7.7	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6	3.6
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6	3.6
25	414680	AA743331		hemoglobin, alpha 2	3.5	3.5
	417380	T06809	Hs.332088	ESTs	3.5	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5	3.5
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoi	3.5	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	2.2	3.5
30	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5	3.5
	432101	A1918950	Hs.123642	EphA3	16.5	3.5
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.3	3.5
	435513	AW404075	Hs.42785	DC11 protein	2.2	3.5
	440643	M78878	Hs.7314	KIAA0614 protein	2.1	3.5
35	418293	A1224483	Hs.16063	hypothetical protein FLJ21877	6.7	3.4
	425900	AK000166	Hs.288809	hypothetical protein FLJ20159	2.1	3.4
	431689	AA305688	Hs.267695	UDP-Gal:beta-GlcNAc beta 1,3-galactosyltr	2.1	3.4
	440749	W22335	Hs.7392	hypothetical protein MGC3199	2.5	3.3
	408374	AW025430	Hs.155591	forkhead box F1	4.3	3.3
40	400277			Eos Control	2.4	3.3
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3	3.3
	443912	R37257	Hs.184780	ESTs	3.3	3.3
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	9.9	3.3
45	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3	3.3
	450094	A174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1184 (f	4.4	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.6	3.3
	451367	AA923729	Hs.26322	cell cycle related kinase	3.3	3.2
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	11.5	3.2
50	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	2.0	3.2
	421246	AW582962	Hs.102897	CGI-47 protein	3.2	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2	3.2
	402802			NM_001397:Homo sapiens endothelin conver	4.3	3.2
	419168	A1336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	2.7	3.2
55	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2	3.2
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.8	3.2
	444489	A1151010	Hs.157774	ESTs	3.2	3.2
	453124	A1139058	Hs.125790	leucine-rich repeat-containing 2	3.2	3.2
60	453078	AF053551	Hs.31584	melanin 2	2.1	3.1
	439444	A1277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	10.6	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	2.8	3.1
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCL CGAP_Alv1 Homo sapiens	2.1	3.1
	445840	A1277811	Hs.146291	ESTs	3.1	3.1
65	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	2.2	3.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1	3.1
	430519	AF129534	Hs.49210	F-box only protein 4	3.1	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	16.2	3.1
70	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1	3.1
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	9.0	3.1
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	20.9	3.1
	420154	A1093155	Hs.95420	JM27 protein	27.4	3.1
	453293	AA382267	Hs.10653	ESTs	3.7	3.1
75	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	2.4	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	2.9	3.0
	433285	AW975944	Hs.237396	ESTs	7.7	3.0
	450671	A1356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0	3.0
80	445921	AW016211	Hs.146181	ESTs	4.3	3.0
	416882	A1633044		tryptophanyl tRNA synthetase 2 (mitochon	3.5	3.0
	414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	2.5	3.0
	450580	N40087		ESTs	3.0	3.0
	447726	AL137638	Hs.19368	matrilin 2	3.9	2.9
	447816	NM_007233	Hs.274329	TP53 target gene 1	7.2	2.9
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-l	5.1	2.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	2.6	2.9

	420297	AJ628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9	2.9
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	2.9	2.9
	437812	AJ582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisou	2.9	2.9
	445808	AV555234		ESTs, Moderately similar to PC4259 fam	2.9	2.9
5	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	4.7	2.9
	442320	AI287817	Hs.129636	ESTs	3.7	2.9
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.4	2.9
	433050	AK093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	2.9	2.9
	451796	AL133019	Hs.27038	Homo sapiens mRNA; cDNA DKFZp434G2127 (f	2.9	2.9
10	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.0	2.9
	459029	AA131376	Hs.343809	fibroblast growth factor 12B	2.9	2.9
	441676	BE564206	Hs.49889	ESTs	4.4	2.9
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	2.1	2.9
	453628	AW243307	Hs.83937	hypothetical protein	2.9	2.9
15	412324	AW978439	Hs.69504	ESTs	2.0	2.8
	408063	BE086548	Hs.42346	calcineurin-binding protein calcscrln-1	5.0	2.8
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4	2.8
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.8	2.8
	433865	N29862	Hs.44104	ESTs	2.8	2.8
20	423201	NM_000163	Hs.125180	growth hormone receptor	6.3	2.8
	450832	AW970602	Hs.105421	ESTs	2.1	2.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8	2.8
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	2.8	2.8
25	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	2.8	2.8
	444668	AA654650	Hs.282906	ESTs	2.2	2.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	3.2	2.8
	432689	AB018320		Arg/Abi-interacting protein ArgBP2	2.1	2.8
	423482	BE280172	Hs.129228	galactokinase 2	2.4	2.8
30	448206	BE622585	Hs.3731	ESTs, Moderately similar to I38022 hypot	2.8	2.8
	450546	AA010200	Hs.175551	ESTs	2.2	2.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.6	2.7
	458332	AI000341	Hs.220491	ESTs	4.9	2.7
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	2.7	2.7
35	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	2.1	2.7
	412576	AA447718	Hs.107057	ESTs	2.7	2.7
	413336	AI569936	Hs.296178	hypothetical protein FLJ22637	2.7	2.7
	433577	AW007080	Hs.284192	ESTs	2.7	2.7
	439093	AA534163	Hs.5476	Homo sapiens, clone IMAGE:3530123, mRNA,	2.7	2.7
40	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.7	2.7
	447401	BE618582	Hs.97661	ESTs	2.7	2.7
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	2.7	2.7
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	2.2	2.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.2	2.7
45	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	9.0	2.7
	409205	AI952884	Hs.14832	ESTs, Moderately similar to unnamed prot	2.4	2.7
	422805	AA436989	Hs.121017	H2A histone family, member A	13.6	2.7
	446238	T95143	Hs.14511	SCO (cytochrome oxidase deficient, yeast	2.1	2.7
	447313	U92981	Hs.18081	Homo sapiens clone DT1P186 mRNA, CAG rep	8.1	2.7
50	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.2	2.6
	410592	R94088	Hs.43569	ESTs	2.6	2.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	2.6	2.6
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.6	2.6
	433419	AI830342	Hs.211272	ESTs	2.9	2.6
55	447509	AF107454	Hs.107537	chromosome 7 open reading frame 2	2.0	2.6
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	2.4	2.6
	407252	AA659037	Hs.163780	ESTs	2.6	2.6
	420061	AW024937	Hs.29410	ESTs	2.4	2.6
	424432	AB037821	Hs.146858	protocadherin 10	7.9	2.6
60	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	2.7	2.6
	414312	AA155694	Hs.191080	ESTs	2.6	2.6
	417135	AA422067	Hs.50547	ESTs	2.6	2.6
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	2.6	2.6
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.0	2.6
65	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	2.2	2.6
	406627	T64904	Hs.163780	ESTs	8.7	2.6
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	2.4	2.6
	425815	R94023	Hs.94560	ESTs, Moderately similar to I38022 hypot	2.6	2.6
	433805	AA706910	Hs.112742	ESTs	2.6	2.6
	431474	AL133990	Hs.190642	ESTs	9.3	2.5
70	436204	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	2.2	2.5
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	3.3	2.5
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	2.3	2.5
	437531	AI400752	Hs.112259	T cell receptor gamma locus	2.6	2.5
75	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	3.4	2.5
	403047			NM_005656*-Homo sapiens transmembrane pr	21.1	2.5
	416198	H27332	Hs.99598	hypothetical protein MGC5338	2.5	2.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.5	2.5
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.5	2.5
	436401	AI087958	Hs.29088	ESTs	2.5	2.5
80	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5	2.5
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	3.0	2.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	11.9	2.5
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	2.5	2.5

5	446791	AI632278	Hs.195922	ESTs	2.5	2.5
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.5	2.5
	419791	AI579909	Hs.105104	ESTs	2.7	2.5
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase	3.0	2.5
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.1	2.5
10	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	2.5	2.5
	447702	AI420256	Hs.161271	ESTs	2.1	2.4
	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRN	2.4	2.4
	421413	AI826128	Hs.57637	ESTs, Weakly similar to A49364 59 protel	2.4	2.4
	429128	AA446869	Hs.119316	ESTs	2.0	2.4
15	429258	AA448765		gb:zx10e09.r1 Soares_tctat_fetus_Nb2HF8_	2.4	2.4
	435102	AW899053	Hs.76917	F-box only protein 8	2.4	2.4
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	3.1	2.4
	407021	U52077		gb:Human mariner1 transposase gene, comp	7.3	2.4
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.1	2.4
20	408267	AW380525	Hs.343564	tubulin-specific chaperone e	4.3	2.4
	447713	AI420733	Hs.207083	ESTs	2.4	2.4
	456848	AL121087	Hs.296406	KIAA0685 gene product	2.2	2.4
	437617	AI026701	Hs.5716	KIAA0310 gene product	2.6	2.4
	432378	AI493046	Hs.146133	ESTs	5.2	2.4
25	443180	R15875	Hs.258576	claudin 12	10.1	2.4
	445929	AI089660	Hs.323401	dpy-30-like protein	2.2	2.4
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	2.3	2.4
	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	2.5	2.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	27.5	2.4
30	421709	AA159394	Hs.107056	CED-6 protein	2.3	2.4
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.7	2.4
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.4	2.4
	451071	AW138807	Hs.204939	ESTs, Highly similar to A54677 homeotic	2.4	2.4
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.1	2.3
35	433037	NM_014158	Hs.279938	HSPC067 protein	2.4	2.3
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	4.1	2.3
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	2.3	2.3
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	2.1	2.3
	450693	AW450461	Hs.203965	ESTs	2.3	2.3
40	452387	AI680772	Hs.306094	trinucleotide repeat containing 12	2.3	2.3
	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	4.1	2.3
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.0	2.3
	419438	AA406400	Hs.12482	glycerophosphate O-acyltransferase	2.7	2.3
	443194	AI954968	Hs.279009	matrix Gla protein	2.1	2.3
45	414869	AA157291	Hs.21479	ubiquitin 1	2.5	2.3
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	2.3	2.3
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.3	2.3
	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	2.3	2.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hibr1)	4.1	2.3
50	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.9	2.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	2.2	2.3
	431147	AI767751	Hs.20300	ESTs	5.8	2.3
	442677	AI557914		peroxisomal acyl-CoA thioesterase	2.5	2.3
	446091	AW022192	Hs.200197	ESTs	4.0	2.3
55	431563	AI027643	Hs.120912	ESTs	2.2	2.3
	439478	AFD49460	Hs.6574	deformed epidermal autoregulatory factor	2.1	2.3
	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	3.5	2.3
	405685			C2002829:gi4507689[ref][NP_003298.1] tra	2.3	2.3
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	2.3	2.3
60	450378	AW249181	Hs.19954	ESTs, Weakly similar to T19873 hypotheti	2.3	2.3
	429303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	2.3	2.3
	417248	AA329449	Hs.247302	twisted gastrulation	2.3	2.2
	429277	AW452016	Hs.127863	ESTs, Weakly similar to SFR4_HUMAN SPLIC	2.6	2.2
	431555	AI815470	Hs.260024	Cdc42 effector protein 3	4.5	2.2
65	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.9	2.2
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	3.4	2.2
	431542	H63010	Hs.5740	ESTs	7.0	2.2
	401558			ENSP00000220478*:SECRETORANIN III.	2.2	2.2
	418281	U09560	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	2.2	2.2
70	422295	AF051151	Hs.114408	toll-like receptor 5	2.2	2.2
	432453	AI885537	Hs.27172	ESTs, Moderately similar to PC4259 ferri	2.2	2.2
	447499	AW262580	Hs.147674	protocadherin beta 16	2.2	2.2
	452994	AW962597	Hs.31305	KIAA1547 protein	4.0	2.2
	450325	AI935962	Hs.26289	ESTs	11.9	2.2
75	422390	AW450893	Hs.121830	ESTs, Weakly similar to T42682 hypotheti	2.1	2.2
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6	2.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	11.8	2.2
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.2	2.2
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	13.6	2.2
80	410252	AW821182	Hs.61418	microtubular-associated protein 1	4.2	2.2
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	4.8	2.2
	422576	BE548555	Hs.118554	CGI-83 protein	2.1	2.2
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	11.0	2.2
	410733	D84284	Hs.66052	CD38 antigen (p45)	3.1	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.1	2.2
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.2	2.2
	408833	AW612232	Hs.254835	ESTs	3.0	2.2

	422424	AI186431	Hs.296638	prostate differentiation factor	4.4	2.2
	433444	AW975324	Hs.129816	ESTs	11.7	2.2
	446354	AW449650	Hs.346335	ESTs	2.6	2.2
	438869	AF075009		gb:Homo sapiens full length insert cDNA	5.9	2.2
5	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	12.8	2.2
	424036	AA770688		H2A histone family, member L	3.8	2.2
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.8	2.2
	404641			NM_021965*:Homo sapiens phosphoglucomuta	2.2	2.2
	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	2.2	2.2
10	406068			C2002008:gi7303957 gb AAAF59000.1 (AE00	3.1	2.1
	415162	AF035718	Hs.78061	transcription factor Z1	2.1	2.1
	423349	AF010258	Hs.127428	homeo box A9	5.9	2.1
	424534	D87682	Hs.150275	KIAA0241 protein	2.3	2.1
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5	2.1
15	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	2.5	2.1
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	2.1	2.1
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	2.1	2.1
	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	2.1	2.1
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.1	2.1
20	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	2.1	2.1
	452959	AI933416	Hs.189674	ESTs	2.1	2.1
	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	2.8	2.1
	408291	AB023191	Hs.44131	KIAA0974 protein	2.1	2.1
25	418727	AA227609	Hs.94834	ESTs	2.1	2.1
	440491	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	2.1	2.1
	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3	2.1
	432695	D63480	Hs.278634	KIAA0146 protein	2.3	2.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.2	2.1
30	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	2.5	2.1
	434569	AI311295	Hs.344478	KIAA0196 gene product	2.1	2.1
	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	2.1	2.1
	438520	AA706319	Hs.98416	ESTs	2.7	2.1
	414269	AA298489	Hs.303171	olfactory receptor, family 51, subfamily	17.3	2.1
35	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.5	2.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	7.4	2.1
	450861	AI523898	Hs.17617	ESTs	2.4	2.1
	419193	D29643	Hs.34789	dolichyl-diphosphooligosaccharide-protei	2.1	2.1
	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.2	2.1
40	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	6.4	2.1
	407182	AA312551	Hs.230157	ESTs	2.1	2.1
	421689	N87820	Hs.106826	KIAA1696 protein	2.1	2.1
	432833	N51075	Hs.110028	ESTs	2.1	2.1
	425170	AU077315	Hs.154970	transcription factor CP2	2.6	2.0
45	436278	BE396290	Hs.5097	synaptogyrin 2	2.8	2.0
	438719	AA357129	Hs.239625	Integral membrane protein 2B	2.3	2.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6	2.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.0	2.0
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.6	2.0
50	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.0	2.0
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	2.0	2.0
	413627	BE182082	Hs.246973	ESTs	3.3	2.0
	414133	AW022188	Hs.41187	ESTs	2.3	2.0
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	14.7	2.0
55	450244	AA007534	Hs.125062	ESTs	3.1	2.0
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	2.6	2.0
	409219	AA393383	Hs.133331	ESTs	2.1	2.0
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.0	2.0
	421969	AF052217	Hs.110099	core-binding factor, runt domain, alpha	2.0	2.0
60	434128	W93170	Hs.284164	protein x 0004	2.7	2.0
	434503	T96231	Hs.17762	ESTs	2.0	2.0
	443292	AK000213	Hs.9196	hypothetical protein	2.0	2.0
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.0	2.0
	448172	N75276	Hs.135904	ESTs	6.0	2.0
65	452039	AI922988	Hs.172510	ESTs	2.0	2.0
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	6.2	2.0
	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	10.1	2.0
	441406	Z45957	Hs.7837	phosphoprotein regulated by mitogenic pa	2.3	2.0
	451369	AA017321	Hs.269691	ESTs	2.1	2.0
70	434011	AW953437	Hs.5486	clone FLB5214	2.1	2.0
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	5.4	2.0
	433388	AI432672	Hs.288539	hypothetical protein FLJ22191	2.7	2.0
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	5.5	2.0
	446783	AW138343	Hs.141867	ESTs	4.4	2.0
75	437323	AA371145	Hs.194397	leptin receptor	2.5	2.0
	410076	T05387	Hs.7991	ESTs	2.9	2.0
	421501	M29971	Hs.1384	O-6-methylguanine-DNA methyltransferase	2.1	2.0
80	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	2.5	2.0

TABLE 618

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	414680	147525_1	AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288
	416882	162718_1	AA708749 AA644620 AA652769 AA242975 AA151074 T19890 AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784 AI951970 AW044233 N20018 AW863548 T90114 AI139947 AA809643 AA846232 AA581966 AA789002
10	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749854 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	419544	185760_2	AI909154 AA526337 AA244193 AI909153
	419733	187589_1	AW362955 H59488 AI040666 W60959 W94209 H27231 T84625 H75715 W04957 W63676 AA659693 AA514302 W63789 BE046412 T91396
	424036	23460_1	AI951970 AW044233 N20018 AW863548 T90114 AI139947 AA809643 AA846232 AA581966 AA789002 AA770688 H15373 AW161070 BE304523 BE378517 AA989300 AA904029 BE254211 AA449148 AI268420 AI300495 AI215637 AI300494 AI268551 AA928971 AA179427 AA947684 BE393792 H98018 AI885781 AI188567 AI290658 C15404
15	426413	266650_1	AA377823 AW954494 AI022688
	429258	301917_1	AA448765 C04967 C03045 AA658293
	431676	336411_1	AI685464 AW971336 AA513587 AA525142
	432689	35275_1	AB018320 H56457 AA247916 N83488 N87920 AA095653 T19858 AL134279 AA094167 AI673378 AI000340 R47500 W16595 AW152297 AI625937 AA020207 AI814851 AA902666 AI039729 AW975053 BE302243 AI240793 AA193203 N5581
20	438869	46651_1	AF075009 R63109 R63068
	439518	47334_1	W76326 AF086341 W72300
	442677	548626_1	AI557814 W81031 AW473764 AI814081 W81068 AW182826 AW173296 AI376594 AI220500 BE257195 BE246486 R55637 C20788 AI014407 AI248353 AW028015
25	445808	65133_1	AV655234 AW966332 AA340239
	449625	8113_1	NM_014253 AF100772 BE088769 AI022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T613 N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816891 AW816882 AW816888 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
30	453802	981589_1	AL134757 AW079131

TABLE 61C

35	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nt_position:	Indicates nucleotide positions of predicted exons.

40	Pkey	Ref	Strand	Nt_position
	401197	9719705	Plus	176341-176452
	401519	6649315	Plus	157315-157950
	401558	7139678	Plus	103510-104090
45	402802	3287156	Minus	53242-53432
	403047	3540153	Minus	59793-59968
	404641	9796810	Minus	32247-32362
	405685	4508129	Minus	37956-38097
50	406068	9114084	Plus	382-543

Table 62A lists about 600 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95th percentile amongst normal prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 62A: ABOUT 600 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE TISSUES

TABLE 62A: ABOUT 600 GENES OF PROSTATE TUMORS

60

Pkey:

Unique Eos probeset identifier number

ExAccn:

Exemplar Accession number, Genbank accession number

UnigeneID:

Unigene number

Unigene Title:

Unigene gene title

R1:

Ratio of prostate tumor to normal prostate tissue

65

Pkey	ExAccn	UnigeneID	Unigene Title	R1	
70	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.5
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	16.0
	420729	AW964897	Hs.290825	ESTs	15.8
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	14.7
75	416188	BE157280	Hs.79070	v-myc avian myelocytomatosis viral oncog	13.6
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	13.1
	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	12.6
	401197			ENSP00000229263~HSPC213.	12.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	12.6
80	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4
	449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3
	443271	BE568568	Hs.195704	ESTs	11.6
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	11.2
	423396	AI382555	Hs.127950	bromodomain-containing 1	11.2

	406038	Y14443		zinc finger protein 200	11.1
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	10.6
	419553	N34145	Hs.10177	ESTs, Moderately similar to ZN91_HUMAN Z	10.4
5	418036	Z37976	Hs.83337	latent transforming growth factor beta b	10.3
	410023	AB017169	Hs.57929	stII (Drosophila) homolog 3	10.1
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	9.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	9.9
	437866	AA156781		metallothionein 1E (functional)	9.5
10	440274	R24595	Hs.7122	scrapie responsive protein 1	9.4
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4
	405141	Y14443		zinc finger protein 200	9.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	9.2
	417315	AI080042	Hs.180450	ribosomal protein S24	9.0
15	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.0
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	8.9
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	8.9
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	8.8
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	8.6
20	425174	D87450	Hs.154978	KIAA0261 protein	8.6
	445701	AF055581	Hs.13131	lymphocyte adaptor protein	8.5
	416182	NM_004354	Hs.79069	cyclin G2	8.4
	445230	U97018	Hs.12451	echinoderm microtubule-associated protei	8.4
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	8.4
25	434217	AW014795	Hs.23349	ESTs	8.3
	417363	AW129357	Hs.329700	ESTs	8.3
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3
	442501	AA315267	Hs.23128	ESTs	8.3
	429503	AA394183	Hs.26873	ESTs	8.2
30	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1
	443837	AI984625	Hs.9884	spindle pole body protein	8.0
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	8.0
	444880	AW118683	Hs.154150	ESTs	7.9
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	7.9
35	436962	AW377314	Hs.5364	DKFZP564I052 protein	7.9
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	7.6
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	7.4
	419078	M93119	Hs.89584	Insulinoma-associated 1	7.4
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	7.3
	451900	AB023199	Hs.27207	KIAA0982 protein	7.3
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	7.3
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-fin	7.3
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	7.2
45	425018	BE245277	Hs.154196	E4F transcription factor 1	7.2
	447737	AK000643	Hs.19404	DKFZP564L0862 protein	7.2
	424897	D63216	Hs.153684	frizzled-related protein	7.1
	433867	AK000596	Hs.3618	hippocatalin-like 1	7.1
	427308	D26067	Hs.174905	KIAA0033 protein	7.1
50	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	7.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0
	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	6.9
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	6.9
	448076	AJ133123	Hs.20196	adenylate cyclase 9	6.9
55	426759	AI590401	Hs.21213	ESTs	6.8
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	6.8
	417302	BE245812	Hs.8941	ESTs	6.8
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	6.7
	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	6.7
60	452859	AI300555	Hs.288158	hypothetical protein FLJ23591	6.7
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	6.7
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	6.7
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.6
	426108	AA622037	Hs.166468	programmed cell death 5	6.6
65	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.6
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	6.5
	443020	AI350058	Hs.106129	ESTs	6.5
	415752	BE314524	Hs.78776	putative transmembrane protein	6.4
	412482	AI499930	Hs.334885	mitochondrial GTP binding protein	6.4
70	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	6.4
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.4
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	6.3
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	6.3
75	411373	BE326276	Hs.8861	ESTs	6.3
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.2
	422583	AA410506	Hs.27973	KIAA0874 protein	6.2
	418196	AI745649	Hs.26549	KIAA1708 protein	6.1
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transi	6.1
80	437147	AL049964	Hs.8358	hypothetical protein FLJ20366	6.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.0
	408242	AA251594	Hs.43913	PIBF1 gene product	5.9
	447965	AW292577	Hs.94445	ESTs	5.9

	449118	R67477	Hs.23103	Bcl1 (S. cerevisiae) homolog	5.9
	427472	AA522539	Hs.131250	transposon-derived Buser3 transposase-I	5.9
	431548	AI834273	Hs.9711	novel protein	5.8
5	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	5.8
	414734	AA151712	Hs.82572	ESTs	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	5.8
	419047	AW952771	Hs.90043	ESTs	5.8
10	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	5.8
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.8
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7
	431055	AL157645	Hs.48793	sialyltransferase 6 (N-acetylglucosaminid	5.7
	434540	NM_016045	Hs.3945	CGI-107 protein	5.7
15	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	5.7
	407938	AA905097	Hs.85050	phospholamban	5.7
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.6
	414812	X72755	Hs.77367	monokine induced by gamma interferon	5.6
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6
20	406672	M26041	Hs.198253	major histocompatibility complex, class	5.5
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.5
	453942	AW190920	Hs.19928	hypothetical protein SP329	5.5
	416619	AF013168	Hs.79393	tuberous sclerosis 1	5.5
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	5.5
25	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	5.4
	416384	AU076903	Hs.79283	selectin P ligand	5.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	5.4
30	458079	AI798870	Hs.54277	DNA segment on chromosome X (unique) 992	5.4
	451684	AF216751	Hs.26813	CDA14	5.4
	418758	AW959311	Hs.172012	hypothetical protein DKFZp434J037	5.4
	445757	AW449065	Hs.13264	KIAA0856 protein	5.4
	449907	AA004825	Hs.103281	ESTs	5.4
35	419159	AW974945	Hs.268049	hypothetical protein	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
	411486	N85785	Hs.181165	eukaryotic translation elongation factor	5.3
	429568	AI088691	Hs.208414	Homo sapiens mRNA: cDNA DKFZp564D0472 (f	5.3
40	403851			C5002154::gi 7299015 gb AAAF54217.1 (AE0	5.3
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	5.3
	417426	NM_002291	Hs.82124	laminin, beta 1	5.3
	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	5.3
45	422746	NM_004484	Hs.119651	glypican 3	5.2
	437571	AA760894	Hs.153023	ESTs	5.2
	407902	AL117474	Hs.41181	Homo sapiens mRNA: cDNA DKFZp727C191 (fr	5.2
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2
50	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	5.2
	453204	R10799	Hs.191990	ESTs	5.2
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	5.1
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	5.1
	444917	R68651	Hs.144997	ESTs	5.1
55	414212	AA138569	Hs.10848	KIAA0187 gene product	5.1
	451593	AF151879	Hs.25706	CGI-121 protein	5.1
	417318	AW953937	Hs.240845	ESTs	5.1
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	5.1
	433600	R42833	Hs.22232	ESTs	5.0
60	434170	AA626509	Hs.122329	ESTs	5.0
	424090	X99699	Hs.139262	XIAP associated factor-1	5.0
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.0
	435706	W31254	Hs.7045	GL004 protein	5.0
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	5.0
65	432897	AF155099	Hs.279780	NY-REN-18 antigen	5.0
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	5.0
	410762	AF226053	Hs.66170	HSKM-B protein	5.0
	421823	N40850	Hs.28625	ESTs	5.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.9
70	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.9
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	4.9
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	4.9
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	4.9
75	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.9
	437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	4.9
	411352	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa	4.8
	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDN	4.8
	425242	D13635	Hs.155287	KIAA0010 gene product	4.8
80	445800	AA126419	Hs.32944	Inositol polyphosphate 4-phosphatase, ty	4.8
	439024	R96696	Hs.35598	ESTs	4.8
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	4.7
	412953	Z45794	Hs.238809	ESTs	4.7

	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	4.7
	421863	AJ952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	4.7
5	451952	AL120173	Hs.301663	ESTs	4.7
	416155	AJ807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.7
	451831	NM_001674	Hs.460	activating transcription factor 3	4.7
	414522	AW518944	Hs.76325	step II splicing factor SLU7	4.7
	427176	AW381569	Hs.40334	ESTs	4.7
10	441390	AJ692560	Hs.131175	ESTs	4.7
	447382	AW027790	Hs.182261	ESTs	4.7
	431676	AJ685464		gb:tt88f04.x1 NCL_CGAP_Pr28 Homo sapiens	4.7
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	4.7
	452242	R50956	Hs.159993	glycosyltransferase	4.7
15	401519			C150004767.gij12737279[ref]XP_012163.1]	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	4.6
	429467	NM_004477	Hs.203772	FSHD region gene 1	4.6
	414341	D80004	Hs.75909	KIAA0182 protein	4.6
20	408380	AF123050	Hs.44532	diubiquitin	4.6
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.6
	425907	AA365752	Hs.155965	ESTs	4.6
	419111	AA234172	Hs.137418	ESTs	4.6
	425840	AW978731	Hs.301824	hypothetical protein PRO1331	4.6
25	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.5
	427078	AJ676062	Hs.111902	ESTs	4.5
	419326	W94915	Hs.42419	ESTs	4.5
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.5
	408705	AA312135	Hs.46967	HSPCO34 protein	4.5
30	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.5
	449673	AA002064	Hs.18920	ESTs	4.5
	438440	AA807228	Hs.225161	ESTs	4.5
	427210	BE396283	Hs.173987	eukaryotic translation initiation factor	4.5
35	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	4.5
	456974	M12529	Hs.169401	apolipoprotein E	4.4
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.4
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.4
	436420	AA443966	Hs.31596	ESTs	4.4
40	443250	AJ041530	Hs.132107	ESTs	4.4
	411962	AA099050		gb:ztk85d12.r1 Soares_pregnanLuterus_NbH	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4
45	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II	4.4
	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	4.4
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	4.4
	428328	AA426080	Hs.98489	ESTs, Weakly similar to I38022 hypotheti	4.4
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4
50	436446	AW016809	Hs.119021	ESTs	4.3
	450704	H85157	Hs.40696	ESTs	4.3
	438666	AW014493	Hs.126727	ESTs	4.3
	417308	H60720	Hs.81892	KIAA0101 gene product	4.3
	428826	AL048842	Hs.194019	atractin	4.3
55	444212	AW503976	Hs.10649	basement membrane-induced gene	4.3
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3
	447858	AW080339	Hs.80426	ESTs	4.3
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	4.3
	426827	AW067805	Hs.172665	methyltetrahydrofolate dehydrogenase	4.3
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	4.3
60	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.3
	417986	AA481003	Hs.97128	ESTs	4.3
	438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	4.3
	408088	AW157022	Hs.343551	hypothetical protein FLJ22584	4.3
	410853	H04588	Hs.30469	ESTs	4.3
65	414002	NM_008732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.2
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-link	4.2
	408554	AA836381	Hs.315111	nuclear receptor co-repressor HDAC3 comp	4.2
	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	4.2
	418701	AAB14948	Hs.95343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2
70	419083	AJ79560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.2
	429900	AA460421	Hs.30875	ESTs	4.2
	437672	AW748265	Hs.5741	flavohemoprotein b57	4.2
	439518	W76326		gb:zdf60d04.r1 Soares_fetal_heart_NbHH19W	4.2
	450661	AW952160	Hs.146550	ESTs	4.2
75	443907	AJ076484	Hs.9963	TYRO protein tyrosine kinase binding pro	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	4.2
	456804	AJ421645	Hs.139851	caveolin 2	4.2
	414291	AJ289619	Hs.13040	G protein-coupled receptor 86	4.2
80	420544	AA577577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	4.2
	448430	AJ500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	4.2
	429570	BE242256	Hs.2441	KIAA0022 gene product	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	4.2
	443622	AJ911527	Hs.11805	ESTs	4.1

	436576	AI458213	Hs.77542	ESTs	4.1
	443958	BE241880	Hs.10029	cathepsin C	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1
	411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA	4.1
5	421129	BE439899	Hs.89271	ESTs	4.1
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.1
	430383	AI861854	Hs.210778	hypothetical protein FLJ10989	4.1
	431475	AI567669	Hs.40342	putative nuclear protein	4.1
10	446468	AI765890	Hs.16341	MAWD binding protein	4.1
	448564	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.1
	404390			Target Exon	4.1
	408815	AW957974	Hs.25485	hypothetical protein FLJ22341	4.1
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	4.1
15	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.1
	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	4.1
	432242	AW02715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.1
	433887	AW204232	Hs.279522	ESTs	4.1
	436556	AI364997	Hs.7572	ESTs	4.1
20	430157	BE348706	Hs.278543	ESTs	4.1
	451259	NM_006052	Hs.26146	Down syndrome critical region gene 3	4.1
	458776	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1
	443646	AI085198	Hs.164226	ESTs	4.1
25	451491	AI972094	Hs.286221	Homo sapiens cDNA FLJ13741 fis, clone PL	4.1
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothe	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	4.0
	413275	W94748	Hs.48821	ESTs	4.0
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0
30	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	4.0
	433409	AI278802	Hs.25661	ESTs	4.0
	452186	AA120761	Hs.28307	WW domain binding protein 4 (formin bind	4.0
	417187	AB011151	Hs.334659	hypothetical protein MGC14139	4.0
	421921	H83363	Hs.6820	translocase of inner mitochondrial membr	4.0
35	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0
	415710	J04543	Hs.78637	annexin A7	4.0
	457794	AA689292	Hs.246850	ESTs	4.0
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	4.0
40	424401	H67220	Hs.169681	death effector domain-containing	4.0
	435905	AW997484	Hs.5003	KIAA0456 protein	4.0
	442731	AI868167	Hs.131044	ESTs	3.9
	418650	BE386750	Hs.86978	prolyl endopeptidase	3.9
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9
	439394	AA149250	Hs.56105	ESTs	3.9
45	442287	AW952703	Hs.8182	synaptic nuclei expressed gene 1b	3.9
	436758	AW977167	Hs.155272	ESTs	3.9
	451030	H40697	Hs.181426	ESTs, Moderately similar to YSHUT threon	3.9
	405934			Target Exon	3.9
50	438231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.9
	444755	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	3.9
	447276	AL049795	Hs.17987	hypothetical protein MGC1203	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	3.9
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.9
55	412978	AI431708	Hs.820	homeo box C6	3.9
	414962	AF273304	Hs.235376	XPMC2 protein	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	3.9
	449590	AA694070	Hs.268835	ESTs	3.9
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoacidipate aminotra	3.9
60	450899	T77447	Hs.177864	ESTs	3.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.8
	452588	AA889120	Hs.110637	homeo box A10	3.8
	422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8
	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	3.8
65	450506	NM_004460		fibroblast activation protein, alpha	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypothe	3.8
	410330	AW023630	Hs.159425	ESTs	3.8
	444143	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	3.8
70	415156	X84908	Hs.78060	phosphorylase kinase, beta	3.8
	422975	AA347720	Hs.122669	KIAA0264 protein	3.8
	403100			C2001027~gij7296271[gib]AAF51562.1 (AE0	3.8
	422449	AF168418	Hs.116784	thyroid hormone receptor interactor 4	3.8
	424163	NM_007071	Hs.142245	HERV-H LTR-associating 3	3.8
	424806	AA382523	Hs.105689	MSTP031 protein	3.8
75	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8
	432363	AA534489		gbnf76g11.s1 NCI_CGAP_Co3 Homo sapiens	3.8
	443441	AW291196	Hs.92195	ESTs	3.8
	432529	AI989507	Hs.162245	ESTs	3.8
	432908	AI861896	Hs.304506	ESTs	3.8
80	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	3.8
	424855	AW204725	Hs.25560	ESTs	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.8
	421828	AW891955	Hs.279789	histone deacetylase 3	3.8

	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	3.8
	418821	AA436002	Hs.183161	ESTs	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.8
5	453160	AI263307	Hs.239884	H2B histone family, member L	3.8
	416072	AL110370	Hs.79000	growth associated protein 43	3.7
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked mol	3.7
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.7
10	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7
	417348	AJ940507	Hs.318526	hypothetical protein FLJ12661	3.7
	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	3.7
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	3.7
	448807	AI571940	Hs.7549	ESTs	3.7
15	413403	AA129105	Hs.198425	ESTs, Moderately similar to S65657 alpha	3.7
	418323	NM_002118	Hs.1162	major histocompatibility complex, class	3.7
	449125	AJ671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	3.7
	408089	H59799	Hs.42644	thioredoxin-like	3.7
	428242	H55709	Hs.2250	leukemia Inhibitory factor (cholinergic	3.7
20	439209	AF087993	Hs.91954	ESTs	3.6
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	3.6
	431735	AW977724	Hs.75968	thymosin, beta 4, X chromosome	3.6
	456619	AV647917	Hs.107153	Inhibitor of growth family, member 1-lik	3.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
25	411213	AA676939	Hs.69285	neuropilin 1	3.6
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.6
	415339	NM_015156	Hs.78398	KIAA0071 protein	3.6
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.6
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	3.6
30	452260	AA453208		RAB9, member RAS oncogene family	3.6
	439506	AI361238	Hs.41136	ESTs	3.6
	420077	AW512260	Hs.87767	ESTs	3.6
	451009	AA013140	Hs.115707	ESTs	3.6
	436473	AI193122	Hs.132275	ESTs	3.6
35	413198	AW157712	Hs.47534	ESTs, Weakly similar to I38022 hypotheti	3.6
	443067	AI077389	Hs.269818	ESTs, Weakly similar to Z195_HUMAN ZINC	3.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fls, clone PL	3.6
	452561	AI692181	Hs.49169	KIAA1634 protein	3.6
	433269	AI343543	Hs.126890	ESTs	3.6
40	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.6
	447033	AI357412	Hs.157601	ESTs	3.6
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6
	442991	BE261238	Hs.8886	hypothetical protein FLJ20424	3.6
45	434974	AA778711	Hs.4310	eukaryotic translation initiation factor	3.5
	443399	AI452659	Hs.61153	proteasome (prosome, macropain) 26S subu	3.5
	401807			C7001350.gij6578126jgblAAF17706.1(AFO496	3.5
	413979	BE218090	Hs.279453	ESTs	3.5
	414680	AA743331		hemoglobin, alpha 2	3.5
50	417380	T06809	Hs.332086	ESTs	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	3.5
	445183	AB007877	Hs.12385	KIAA0417 gene product	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	3.5
55	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	446416	AV658299	Hs.163959	ESTs	3.5
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	3.5
	456719	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	3.5
60	432101	AI918950	Hs.123642	EphA3	3.5
	453565	BE298808	Hs.33363	DKFZP434N093 protein	3.5
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	3.5
	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	3.5
	450066	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.5
65	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.5
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.5
	415528	R17236		gb:yg12c04.r1 Soares infant brain 1N1B H	3.5
	435513	AW404075	Hs.42785	DC11 protein	3.5
	440643	M78878	Hs.7314	KIAA0614 protein	3.5
70	409068	AW236991	Hs.102495	ESTs, Moderately similar to I38022 hypot	3.5
	439132	H72803	Hs.38363	ESTs	3.5
	451173	AI765082	Hs.48317	ESTs	3.5
	422673	N59027		gb:yyv59d11.r1 Soares fetal liver spleen	3.4
	401597	AA172106		Rag C protein	3.4
	401744			Target Exon	3.4
75	432723	D29677	Hs.3085	KIAA0054 gene product; Helicase	3.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybl s	3.4
	450628	AW382884	Hs.204715	ESTs	3.4
	432125	AW972667		Homo sapiens cDNA FLJ12300 fls, clone MA	3.4
80	435411	AW444619	Hs.138211	ESTs	3.4
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.4
	437158	AW090198		KIAA1150 protein	3.4
	416375	H95567	Hs.124700	ESTs	3.4
	419441	AW023731	Hs.274368	MSTP032 protein	3.4

5	432741	AI732358	Hs.185118	ESTs, Moderately similar to A37413 calbi	3.4
	439192	AW970536	Hs.105413	ESTs	3.4
	440474	AI207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	3.4
	428466	AF151063	Hs.184456	hypothetical protein	3.4
	447397	BE247676	Hs.18442	E-1 enzyme	3.4
10	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	3.4
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	3.4
	424779	AL046851	Hs.153053	CD37 antigen	3.4
	415015	NM_002109	Hs.77798	histidyl-HRNA synthetase	3.4
	425900	AK000166	Hs.288809	hypothetical protein FLJ20159	3.4
15	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3.4
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	3.4
	414671	AA832479	Hs.72080	ESTs	3.4
	431689	AA305688	Hs.267695	UDP-GalbetaGlcNAc beta 1,3-galactosyltr	3.4
	444480	AI150730	Hs.265640	ESTs, Moderately similar to A47582 B-cel	3.3
20	403389			C3001393*gil3327090jdbjBAA31613.1 (AB	3.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	3.3
	408374	AW025430	Hs.155591	forkhead box F1	3.3
	410494	M36564	Hs.64016	protein S (alpha)	3.3
	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	3.3
25	433505	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	3.3
	400277			Eos Control	3.3
	411031	W37943	Hs.34892	KIAA1323 protein	3.3
	417295	AW993524	Hs.43148	ESTs	3.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	3.3
30	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3
	443912	R37257	Hs.184780	ESTs	3.3
	445270	AI762154	Hs.54982	Homo sapiens cDNA FLJ14014 fis, clone HE	3.3
	425836	AW955696	Hs.90960	ESTs	3.3
35	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	3.3
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALLUS_HUMAN A	3.3
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	3.3
	436499	AJ276678	Hs.283102	HEF like Protein	3.3
	448164	R81680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3
40	426848	H72531	Hs.36190	ESTs	3.3
	439553	AW021103	Hs.6631	hypothetical protein FLJ20373	3.3
	450094	AI174947	Hs.295789	Homo sapiens mRNA: cDNA DKFZp564D1164 (f	3.3
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.3
45	430280	AA361258	Hs.237868	interleukin 7 receptor	3.3
	408968	AI652236	Hs.49376	hypothetical protein FLJ20644	3.3
	453548	AL079983	Hs.116774	integrin, alpha 1	3.2
	451367	AA923729	Hs.26322	cell cycle related kinase	3.2
	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fis, clone K	3.2
50	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	3.2
	400658			ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
	410366	AI267589	Hs.302689	hypothetical protein	3.2
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	3.2
55	421246	AW582952	Hs.102897	CGI-47 protein	3.2
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2
	439047	AW979177		gb:EST391287 MAGE resequences, MAGP Homo	3.2
	444451	AV650179	Hs.282431	ESTs	3.2
60	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
	406973	M34996	Hs.198253	major histocompatibility complex, class	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
	431304	BE157283		gb:RC4-HT0373-130200-011-a03 HT0373 Homo	3.2
	406247			Target Exon	3.2
65	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	3.2
	412639	AW961284	Hs.296235	ESTs	3.2
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.2
	433561	BE540937	Hs.20104	hypothetical protein FLJ00052	3.2
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2
70	438461	AW075485	Hs.286049	phosphoserine aminotransferase	3.2
	455473	AW984768		gb:RC1-HN0015-120400-021-c07 HN0015 Homo	3.2
	441683	BE564214	Hs.102946	ESTs	3.2
	417386	AL037228	Hs.82043	D123 gene product	3.2
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	3.2
75	442355	AA456539	Hs.8262	lysosomal-associated membrane protein 2	3.2
	422473	U94780	Hs.117242	meningioma expressed antigen 6 (coiled-c	3.2
	407816	AW500857	Hs.40137	anaphase-promoting complex 1; meiotic ch	3.2
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2
80	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.2
	435129	AI381659	Hs.267086	ESTs	3.2
	424894	H83520	Hs.153678	reproduction 8	3.2
	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	3.2
	410185	BE294068	Hs.737	immediate early protein	3.2
	451149	AL047586	Hs.10283	RNA binding motif protein 8B	3.2
	410531	AW752953		gb:QV0-CT0224-261099-035-g02 CT0224 Homo	3.2
	411954	AA652523	Hs.269496	ESTs, Weakly similar to I38022 hypotheti	3.2

	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	3.2
	444489	AI151010	Hs.157774	ESTs	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2
5	452413	AW082633	Hs.212715	ESTs	3.1
	409390	AI927212	Hs.3734	ESTs	3.1
	453078	AF053551	Hs.31584	metaxin 2	3.1
	453024	AW846787		gb:QV3-CT0194-181099-004-e01 CT0194 Homo	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	3.1
10	441124	T97717	Hs.119563	ESTs	3.1
	416128	AA173632		CDC14 (cell division cycle 14, S. cerevi	3.1
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	3.1
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	3.1
15	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.1
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	3.1
	427399	NM_014883	Hs.177664	KIAA0914 gene product	3.1
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCL_CGAP_Alv1 Homo sapiens	3.1
	442906	AW296888	Hs.170939	ESTs	3.1
20	445840	AI277811	Hs.146291	ESTs	3.1
	446084	AL137658	Hs.13768	Homo sapiens mRNA; cDNA DKFZp434I1216 (f	3.1
	435293	AI040777	Hs.117170	ESTs	3.1
	400750			Target Exon	3.1
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	3.1
25	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.1
	409558	BE253407	Hs.72363	Homo sapiens mRNA for FLJ00116 protein,	3.1
	400194			NM_003763:Homo sapiens syntaxin 16 (STX1	3.1
	400479			Target Exon	3.1
	402896			ENSP00000252117:Myelin transcription fac	3.1
30	403423			Target Exon	3.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1
	410886	AW809324		gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1
	420121	AW968271	Hs.191534	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
35	430519	AF129534	Hs.49210	F-box only protein 4	3.1
	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypotheti	3.1
	422481	AL050163	Hs.117339	DNAX-activation protein 10	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	3.1
40	409549	AB029015	Hs.54886	phospholipase C, epsilon 2	3.1
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1
	431286	AW263476	Hs.44268	myelin gene expression factor 2	3.1
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	3.1
	408051	AI623351	Hs.172148	ESTs	3.1
	420090	AA220238	Hs.94986	ribonuclease P (38kD)	3.1
45	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.1
	414279	AW021691		GCN5 (general control of amino-acid synt	3.1
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	3.1
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	3.1
	420154	AI093155	Hs.95420	JM27 protein	3.1
50	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	3.1
	453293	AA382267	Hs.10653	ESTs	3.1
	434398	AA121098	Hs.3838	serum-inducible kinase	3.0
	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	3.0
	441527	W19504	Hs.7884	solute carrier family 21 (organic anion	3.0
55	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	3.0
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	3.0
	411315	AW836547		gb:PM3-LT0032-030100-006-e08 LT0032 Homo	3.0
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.0
	441401	AI824338	Hs.126891	ESTs	3.0
60	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0
	429600	X78565	Hs.289114	hexabrachion (tenascin C, cytobactin)	3.0
	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	3.0
65	421786	AI188653	Hs.21351	ESTs	3.0
	433285	AW975944	Hs.237396	ESTs	3.0
	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA10	3.0
	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	3.0
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	3.0
70	445345	AW003850	Hs.12532	chromosome 1 open reading frame 21	3.0
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
	434953	BE049102	Hs.179982	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.0
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	3.0
75	428130	AW444985	Hs.77603	ESTs	3.0
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	3.0
	445784	AI253155	Hs.146065	ESTs	3.0
	446677	AI800311	Hs.156291	ESTs	3.0
80	426448	R06054		gb:ye89g07.r1 Soares fetal liver spleen	3.0
	445921	AW015211	Hs.146181	ESTs	3.0
	406673	M34996	Hs.198253	major histocompatibility complex, class	3.0
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2. 2	3.0
	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.0
	435907	AW304025	Hs.258397	ESTs	3.0

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451102	AA015683	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	3.0
416882	AI633044		tryptophanyl (RNA synthetase 2 (mitochondrion	3.0
414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	3.0
450580	N40087		ESTs	3.0

5

TABLE 62B

10 Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410531	1207200_1	AW752953 H88044 BE156092
410886	1225822_1	AW809324 BE144977 BE144956
411315	1238570_1	AW836547 AW836513 AW836587
411962	126744_1	AA099050 AA099526 T47733
414279	143227_1	AW021691 AI537404 R45431 AI333439 AI741845 AI574468 R44190 R52535 R52617 AI220925 AI979148 AI744688 AW242437 AA618148
		AI983837 AA399623 AI676204 AI420077 N24944 D51042 AA282788 AA137264 AW236107 AW769
		AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA866905 AI141054 AW194991 AA252147 AA319500 AI184288
		AA708749 AA644620 AA652769 AA242975 AA151074 T19890
		R17236 R52580 F11642
		AA173632 AI174858 AA581361 AI700024 AA173988 BE165417 AI366964
		AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477
		AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
		N59027 AA314894 N53937 R08100
		R06054 AA378789 AW956453
		AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
		AW972830 AA527647 AA489820 AA570362
		BE157283 BE157287 AA502438
		AI685464 AW971336 AA513587 AA525142
		AW972667 AA526539 AI057032 AW167842
		AA534489 AW970240 AW970323
		AW090198 AW173544 AW439860 AW007307 AI762577 W86516 AA160485 AA974203 AI589521 AW451857 AW450602 AI702529 AA630766
		AI801808 AW611634 AI393606 AW235356 AW000736 AW468599 AI582546 AA962057 AA523012 AW51
		AA156781 AW238339 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992
		AA637481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA04
		AW979177 AA846994 AA829672
		W76326 AF086341 W72300
		NM_004460 U09278 U76833 AW630055 AW471133 C02434 W45237 AW793518 BE070112 AI587479 AI624429 AW190535 AI446661 AI478772
		AW022667 AA528235 AA599775 AW613820 AI435793 AW594230 AI051768 AI200109 AI680296
		N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
		AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
		AA453208 NM_004251 U44103 AI671547 N57463 AW007521 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228
		BE326331 AI934576 AI922378 AW276431 AI718466 N36566 AA904753 BE464245 AI338752 AI
		AW846787 AW903370 AW903378 AW752032 AW839052 AW839051 AW839054 AW839058 AW903374 AW839045 AW903373 AW903352
		AW839043 AW839049 AW903372 AW846755 AW846767 AW903368 AW846766 BE146826 AW839056 AW846802 AW
		AW984788 AW984816 AW984811 AW984807 AW984819 AW984790 AW984782 AW984784 AW984780 AW984814 AW984795 AW984793
		AW984789 AW984823 AW984802 AW984800 AW984799 AW984825 AW984792 AW984821 AW984820 AW
		Z43784 R13382 AW572911 AA449369 H17037 R19603 AI632565 AW004030 BE502530 Z25032 AA805324 AA449241 AI651825 AI264863
		AW196918 AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI867447 AW2

55 TABLE 62C

60 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NI_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NI_position
400479	8439786	Minus	115385-116348
400658	8118459	Minus	73525-73644
400750	8119067	Plus	198991-199168,199316-199548
401197	9719705	Plus	176341-178452
401519	6649315	Plus	157315-157950
401597	3293210	Plus	65838-66031
401744	2576349	Plus	14595-14751
401807	7331536	Plus	152325-152912
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402802	3287156	Minus	53242-53432
402895	9967547	Plus	85537-85671,86379-86469
403100	8954402	Minus	13683-13874
403389	9438331	Minus	163415-163634
403423	7105492	Plus	69340-69815
403851	7708872	Plus	22733-23007
404390	8887030	Minus	39624-40072
405141	8980911	Plus	99861-100054
405934	6758795	Plus	159913-160605
406038	8389537	Plus	37764-37877
406247	7417725	Minus	46234-46461

Table 63A lists about 366 genes significantly down-regulated in prostate cancer compared to normal prostate. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal prostate to "average" prostate cancer tissues was greater than or equal to 2.5. The "average" normal prostate level was set to the 75th percentile of normal prostate tissues. The "average" prostate cancer level was set to the 75th percentile amongst tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst all the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 63A: ABOUT 366 GENES SIGNIFICANTLY DOWN-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of normal prostate tissue to prostate tumor tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
425932	M81650	Hs.1968	semenogelin I	89.4
407245	X90568	Hs.172004	titin	35.4
425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	32.2
426752	X69490	Hs.172004	titin	29.5
400440	X83957	Hs.83870	nebulin	20.7
412519	AA195241	Hs.73980	troponin T1, skeletal, slow	13.9
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	12.0
420813	X51501	Hs.99949	prolactin-induced protein	11.8
415337	Z44881	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	10.2
407013	U35637		gb:Human nebulin mRNA, partial cds	9.1
433331	A1738815	Hs.117323	ESTs	8.9
432117	AL036195	Hs.2909	protamine 1	8.3
453863	X02544	Hs.572	orosomucoid 1	8.2
431847	A1791314		gb:aa46g12.y5 Stratagene lung carcinoma	7.4
408855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	7.1
448059	AI459021	Hs.170425	ESTs	6.8
403612			Target Exon	6.4
405001	U58196		Interleukin enhancer binding factor 1	6.2
441490	N46901	Hs.266720	ESTs	6.2
435805	AW470260	Hs.48495	ESTs	6.0
401917	AL050149		RAN binding protein 3	5.9
455649	BE065051		gb:RC1-BT0313-110500-017-c04 BT0313 Homo	5.7
450218	R02018	Hs.168640	apoptosis, progressive (mouse) homolog	5.6
404606			Target Exon	5.6
432326	AI280308	Hs.274361	amiloride-sensitive cation channel 2, ne	5.5
459708	AA776881	Hs.168812	Homo sapiens cDNA FLJ14132 fis, clone MA	5.5
440808	AK001339	Hs.7432	hypothetical protein FLJ10477	5.5
458339	AW976853	Hs.172843	ESTs	5.2
454278	AF217525	Hs.49002	Down syndrome cell adhesion molecule	5.2
417032	AA192469	Hs.271838	ESTs	5.2
434352	AF129505	Hs.86492	small muscle protein, X-linked	5.1
439175	AF086021	Hs.271113	ESTs	5.0
439749	AL389942	Hs.157752	Homo sapiens mRNA full length insert cDN	4.9
417364	N73749	Hs.222475	ESTs	4.9
400831			C11000936[g]3746443[gb]AAC63969.1[AF0	4.8
416935	AA190712		gb:zp87f09.r1 Stratagene HeLa cell s3 93	4.8
442082	R41823	Hs.7413	ESTs	4.8
452625	AA724771	Hs.61425	ESTs	4.7
440965	AI523646	Hs.169859	ESTs	4.7
456815	NM_013348	Hs.144011	potassium inwardly-rectifying channel, su	4.7
430611	AA837120	Hs.156481	ESTs	4.6
415981	R35694		gb:yg67b04.r1 Soares infant brain 1N1B H	4.6
441040	AW449782	Hs.178803	ESTs	4.6
442764	AI762254	Hs.131122	ESTs	4.6
411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	4.6
433081	Z85986	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	4.6
401896			Target Exon	4.5
445323	AW207282	Hs.213049	ESTs	4.5
458895	AI535663	Hs.39379	ESTs	4.5
417729	Z43798	Hs.6777	ESTs	4.5
431627	AW609720	Hs.265540	HSPC042 protein	4.5
420721	AA927802	Hs.159471	ZAP3 protein	4.4
449519	W04244	Hs.49829	ESTs	4.4
442089	AI801500	Hs.128457	ESTs	4.4
436781	AI914535	Hs.221377	ESTs	4.4
402797			Target Exon	4.4
404267			NM_004348*-Homo sapiens runt-related tra	4.3
442931	AI024376	Hs.150473	ESTs	4.3
418626	AW299508	Hs.135230	ESTs	4.3
423772	AA306637		EAP30 subunit of ELL complex	4.3
457136	AA428240	Hs.126083	ESTs	4.3
436404	AW968556	Hs.137240	Homo sapiens mRNA for partial 3'UTR, seq	4.3
458840	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	4.3
403649			Target Exon	4.2
435866	AA704538	Hs.119740	ESTs	4.2
423871	AA331906		gb:EST35805 Embryo, 8 week 1 Homo sapien	4.2

	436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.2
	400164			Eos Control	4.1
	435519	AI218950	Hs.125461	hypothetical protein FLJ11539	4.1
	425094	AI955956	Hs.21417	ESTs	4.1
5	415928	R46799	Hs.23966	ESTs	4.1
	415746	AA167670	Hs.21413	solute carrier family 12, (potassium-chl	4.1
	426663	AI028767	Hs.262603	ESTs	4.1
	453752	AL120800		gb:DKFZp762E152_r1 762 (synonym: hmal2)	4.1
10	404260			Target Exon	4.0
	453412	AJ003290		gb:AJ003290 Selected chromosome 21 cDNA	4.0
	401411			ENSP00000247172*HYPOTHETICAL 126.2 kDa	4.0
	415925	H09474	Hs.202341	Homo sapiens cDNA: FLJ23573 fis, clone L	4.0
	402817	H24185		hypothetical protein	4.0
	449233	BE048401	Hs.196511	ESTs	3.9
15	435457	AA682421	Hs.59125	ESTs	3.9
	444105	AW189097	Hs.166597	ESTs	3.9
	430610	AI821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.9
	411320	AW836646		gb:PM3-LT0032-090100-008-e05 LT0032 Homo	3.8
	409679	BE250521		ras homolog gene family, member A	3.8
20	415386	Z43087		gb:HSC13A121 normalized infant brain cDN	3.8
	446175	AL036568	Hs.291	glutamyl aminopeptidase (aminopeptidase	3.8
	459707	AA631362	Hs.120866	gb:nip86b01.s1 NCL_CGAP_Thy1 Homo sapiens	3.8
	406917	X65964		gb:H.sapiens nestin gene.	3.8
	455887	BE154173		gb:PM1-HT0340-201299-004-f12 HT0340 Homo	3.8
25	443313	AI796730	Hs.55513	ESTs	3.8
	452351	AA025647		gb:ze85d01.r1 Soares_fetal_heart_NbHH19W	3.8
	400499			C10001858:gil678124[ref]NP_032759.1] ne	3.7
	411829	AW865749		gb:QV3-SN0021-100500-185-c03 SN0021 Homo	3.7
	408229	AW176091		gb:QV0-BT0107-250899-007-b08 BT0107 Homo	3.7
30	427318	AF186081	Hs.175783	zinc transporter	3.7
	417620	R02530	Hs.191198	ESTs	3.7
	404660			C9000841*:gil12654691[gb]AAH01185.1]AAH0	3.7
	409144	AW341187	Hs.279714	ESTs	3.7
35	436524	AA922236	Hs.221037	ESTs	3.7
	459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	3.7
	418833	AW974899	Hs.292776	ESTs	3.7
	424887	AA348112	Hs.259461	ESTs	3.7
	404984			Target Exon	3.7
	454549	AW806910		gb:QV4-ST0023-160400-172-04 ST0023 Homo	3.7
40	426736	AA431615	Hs.130722	ESTs	3.7
	434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962, mRNA, comp	3.6
	438040	AI222422	Hs.121846	ESTs	3.6
	443618	T82009	Hs.300700	hypothetical protein FLJ20727	3.6
	442097	AW015799	Hs.128474	ESTs	3.6
45	435186	AL119470	Hs.145631	ESTs	3.6
	429853	AB020625	Hs.225949	butyrophilin-like 3	3.6
	456521	AW373450	Hs.286212	hypothetical protein FLJ11729	3.6
	453282	AK000043	Hs.32922	hypothetical protein FLJ20036	3.6
	400749			NM_003105*:Homo sapiens sortilin-related	3.6
50	450295	AI766732	Hs.210628	ESTs	3.5
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	3.5
	434378	AA631739	Hs.335440	EST	3.5
	421342	AA504749		gb:aa63f08.r1 NCL_CGAP_GCB1 Homo sapiens	3.5
55	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.5
	429043	AI824977	Hs.145319	ESTs	3.5
	438211	T08401	Hs.290856	ESTs, Moderately similar to ALU4_HUMAN A	3.5
	405258			Target Exon	3.4
	440207	AI371978	Hs.128326	ESTs	3.4
60	445045	AI652676	Hs.147256	ESTs	3.4
	406177			Target Exon	3.4
	438535	L09078		gb:Homo sapiens mRNA fragment	3.4
	405735			ENSP00000252164*:KIAA1578 protein (Fragm	3.4
	445797	AI253414		gb:aq14f04.x1 Stanley Frontal NS pool 2	3.4
65	444286	AI625304	Hs.190312	ESTs	3.4
	442027	AI652926	Hs.128395	ESTs	3.4
	447889	AW469180	Hs.346398	ESTs	3.4
	405152			Target Exon	3.4
	402460			C1001261*:gil2695979[emb]CAA70854.1] (Y0	3.4
70	448516	AW898595		gb:RC1-NN0073-260400-011-g09 NN0073 Homo	3.4
	450588	AA010319	Hs.60389	ESTs	3.4
	447600	AI420990		ESTs	3.4
	406085			Target Exon	3.3
	417959	AW977642	Hs.291742	ESTs	3.3
	418672	L44284	Hs.12915	ESTs	3.3
75	446593	W79572	Hs.13277	hypothetical protein FLJ22054	3.3
	446516	AW996592	Hs.257557	ESTs, Weakly similar to I38022 hypotheti	3.3
	415896	H08311	Hs.14822	ESTs, Weakly similar to I78885 serine/th	3.3
	410140	AL134435	Hs.247837	neurexin 3	3.3
	456539	AI733837	Hs.145661	ESTs	3.3
80	422399	AW410380	Hs.116056	mesenchymal stem cell protein DSC43	3.3
	413381	BE090690		gb:RC1-BT0720-280300-011-g02 BT0720 Homo	3.3
	429422	AK001494	Hs.202596	Homo sapiens cDNA FLJ10632 fis, clone NT	3.3
	428561	AW973652	Hs.283105	ESTs	3.2

5	445608	AIB30851	Hs.200014	ESTs, Weakly similar to ACIDIC PROLINE-R	3.2
	449017	AW002425	Hs.224142	ESTs	3.2
	415908	H08623	Hs.22833	ESTs	3.2
	457733	AW974812	Hs.291971	ESTs	3.2
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	3.2
10	428134	AA421773	Hs.161008	ESTs	3.2
	434407	AW815333		gb:QV0-ST0215-060100-083-g01 ST0215 Homo	3.2
	429973	AI423317	Hs.164680	ESTs	3.2
	418092	R45154	Hs.338439	ESTs	3.2
	411356	H45377		gb:ym99h03.r1 Soares adult brain N2b5HB5	3.1
15	443366	AI053501	Hs.278869	ESTs, Moderately similar to 2109260A B c	3.1
	422069	AJ010063	Hs.343603	titin-cap (telotholin)	3.1
	420778	AW970512		gb:EST382593 MAGE resequences, MAGK Homo	3.1
	403451			Target Exon	3.1
	451686	AA059246	Hs.110293	ESTs	3.1
20	423837	AW937063	Hs.275150	gb:PM3-DT0037-231299-001-g11 DT0037 Homo	3.1
	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3)	3.1
	450049	AI681234	Hs.258509	EST	3.1
	428656	AB037798	Hs.188790	KIAA1377 protein	3.1
	401278			Target Exon	3.1
25	418087	AA961613	Hs.127838	ESTs	3.1
	421813	BE048255		gb:tz49b05.y1 NCI_CGAP_Bm52 Homo sapien	3.1
	402490			Target Exon	3.1
	448001	AW293237	Hs.202037	ESTs	3.1
	445316	AI219833	Hs.166767	ESTs	3.1
30	405150			Target Exon	3.1
	413784	BE165819	Hs.207684	ESTs	3.1
	425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
	433224	AB040919	Hs.210958	KIAA1486 protein	3.1
	421894	AI418464	Hs.190836	ESTs	3.1
35	419386	AA236867		ESTs, Weakly similar to I38022 hypoteti	3.1
	402422			Target Exon	3.1
	435849	BE305242	Hs.16098	claudin 2	3.1
	405422			ENSP00000216658*-HYPOTHETICAL 133.5 kDa	3.0
	420543	AA278221	Hs.173344	ESTs	3.0
40	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.0
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	3.0
	406600			Target Exon	3.0
	408025	AI692784	Hs.41767	PTD002 protein	3.0
	426349	AI308855	Hs.301497	arglynyltransferase 1	3.0
45	444576	AI400974	Hs.182045	ESTs	3.0
	430661	AC005551	Hs.130714	Homo sapiens HSPC323 mRNA, partial cds	3.0
	441335	BE222470	Hs.150825	ESTs, Weakly similar to antigen NY-CO-33	3.0
	459647	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 1	3.0
	435713	AA699313	Hs.114071	ESTs	3.0
50	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_U14 Homo sapiens	3.0
	456103	Z39430	Hs.72350	ESTs	3.0
	435200	AA670310	Hs.145903	ESTs	3.0
	449245	AI636539	Hs.224296	ESTs	3.0
	428132	AA421765		gb:zu24g02.s1 Soares_NhHMPu_S1 Homo sapi	3.0
55	443454	AI057494	Hs.133421	ESTs	2.9
	423732	AF058058	Hs.132183	solute carrier family 16 (monocarboxylic	2.9
	411944	AW877139		gb:QV2-PT0010-160400-133-g01 PT0010 Homo	2.9
	432718	AA563943	Hs.244371	ESTs	2.9
	435534	AA830927	Hs.117306	ESTs	2.9
60	430348	AA476915	Hs.189225	ESTs, Weakly similar to I38022 hypoteti	2.9
	410289	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp7611071 (fr	2.9
	453126	AA032155	Hs.61622	ESTs	2.9
	459421	AA233154	Hs.12532	chromosome 1 open reading frame 21	2.9
	441543	AI733014	Hs.269715	ESTs	2.9
65	442252	AI733395	Hs.129124	ESTs	2.9
	419254	AI469453	Hs.222760	ESTs	2.9
	443727	Z25389	Hs.18459	ESTs	2.9
	419896	Z99362		gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA	2.9
	453898	AW003512	Hs.232770	arachidonate lipooxygenase 3	2.9
70	415098	D59687		gb:HUM056E10B Clontech human fetal brain	2.9
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	2.9
	406398			Target Exon	2.9
	433942	AW272166	Hs.123465	ESTs	2.9
	400461			Target Exon	2.9
75	442640	AI205646	Hs.147220	ESTs	2.9
	438814	AA826278	Hs.249596	ESTs	2.9
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	2.9
	422482	AI439905	Hs.344476	gb:z57g08.x1 NCI_CGAP_Lym12 Homo sapien	2.8
	407142	AA412535		gb:z199b10.s1 Soares_testis_NHT Homo sap	2.8
80	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527 hypoteti	2.8
	442907	AI023763	Hs.79707	ESTs	2.8
	456075	N73442		gb:yz31h09.r1 Soares_multiple_sclerosis_	2.8
	438690	AA815031	Hs.123598	ESTs	2.8
	452570	AW861293	Hs.336940	Homo sapiens cDNA: FLJ20861 fis, clone A	2.8
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.8
	447556	AI885187	Hs.210710	ESTs, Moderately similar to ALLU6_HUMAN A	2.8
	451632	BE005934	Hs.310625	EST	2.8

	426481	AW963941		gb:EST376014 MAGE resequences, MAGH Homo	2.8
	401656			Target Exon	2.8
	407269	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.8
5	435754	AA700752	Hs.117341	ESTs	2.8
	433565	AA599763	Hs.112520	ESTs	2.8
	451004	AA044967		gb:zF53d09.r1 Soares retina N2b4HR Homo	2.8
	425223	AA352825	Hs.146065	gb:EST60880 Activated T-cells XX Homo sa	2.8
	405770			NM_002362:Homo sapiens melanoma antigen,	2.8
10	456227	T84239	Hs.189788	ESTs	2.8
	454445	AW749432		gb:RC3-BT0386-301299-011-a09 BT0386 Homo	2.8
	419494	W01060	Hs.34382	ESTs	2.8
	427639	AW444530	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	2.8
	428079	AA421020	Hs.208919	ESTs	2.7
15	406337			C14000021:gil7242973[dbj]BAA92547.1[AB	2.7
	401884			Target Exon	2.7
	406881	D16154		gb:Human gene for cytochrome P-450c11, e	2.7
	428986	AA442884	Hs.201201	ESTs	2.7
	450044	R66444	Hs.51891	ESTs	2.7
20	403630			C3001708*gil4758026[ref]NP_004360.1[co	2.7
	445514	A1241280	Hs.148906	ESTs	2.7
	446362	AW612481	Hs.104105	ESTs	2.7
	432492	AW275110	Hs.271106	ESTs	2.7
	430889	U22491	Hs.248117	G protein-coupled receptor 7	2.7
25	434316	AW411330	Hs.118796	annexin A6	2.7
	413155	BE067952		gb:CM0-BT0365-061299-122-g09 BT0365 Homo	2.7
	433329	AF015041	Hs.199291	numb (Drosophila) homolog-like	2.7
	446523	NM_003063	Hs.334629	sarcolipin	2.7
	449923	BE258051		gb:601111034F1 NIH_MGC_16 Homo sapiens c	2.7
30	453826	AL138129		gb:DKFZp547F152_r1 547 (synonym: hbrf1)	2.7
	405678			CX001454:gil8393794[ref]NP_058881.1[myo	2.7
	432789	D26361	Hs.3104	KIAA0042 gene product	2.7
	455791	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.7
	449109	AW270992	Hs.120949	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
35	436255	F01143	Hs.284284	zinc finger 1111	2.7
	415984	R19046	Hs.5010	gb:yg21f11.1.1 Soares infant brain 1N1B H	2.7
	402844			C1000118*gil9851913[ref]NP_062832.1[pr	2.7
	456666	AA452512	Hs.76719	U6 snRNA-associated Sm-like protein	2.7
	414620	AA150120	Hs.244621	ribosomal protein S14	2.7
40	404979			Target Exon	2.7
	412318	AW936911	Hs.326729	hypothetical protein MGC11082	2.7
	424361	AK001551	Hs.145944	Homo sapiens cDNA FLJ10689 fis, clone NT	2.7
	412542	AW961516	Hs.95097	ESTs	2.7
	441975	AW173248	Hs.344285	EST	2.7
45	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	2.7
	457861	AW450205	Hs.305890	BCL2-like 1	2.7
	439204	AF087987	Hs.42696	EST	2.7
	415642	U19878	Hs.336224	transmembrane protein with EGF-like and	2.7
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.7
50	443359	AI792583	Hs.135354	ESTs	2.7
	447336	AW139383	Hs.245437	ESTs	2.7
	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	2.7
	422185	AL117530	Hs.112822	DKFZP434B172 protein	2.7
	436030	R02287	Hs.121052	ESTs	2.7
55	449589	AW752437	Hs.135258	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.6
	436092	AI345995	Hs.127383	ESTs	2.6
	415054	AI733907		gb:zo86h09.y5 Stratagene ovarian cancer	2.6
	412908	AA121913	Hs.293896	pregnancy-associated plasma protein-E	2.6
	409583	AW440117	Hs.256879	ESTs	2.6
60	410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.6
	435383	R61083		wee1 (S. pombe) homolog	2.6
	426629	AI203933	Hs.97142	ESTs	2.6
	415831	H15145	Hs.30509	ESTs	2.6
	412281	AI810054	Hs.141119	ESTs	2.6
65	434898	AW500458	Hs.29956	KIAA0460 protein	2.6
	422229	AF134414	Hs.113271	ABO blood group (transferase A, alpha 1-	2.6
	447518	T80061		gb:yd22f08.s1 Soares fetal liver spleen	2.6
	458546	AI215667	Hs.175044	ESTs	2.6
	438648	AA813125	Hs.146335	ESTs	2.6
70	450399	AW511049	Hs.202007	ESTs	2.6
	420833	R47948	Hs.188732	ESTs	2.6
	453903	AW299606	Hs.232777	ESTs	2.6
	443650	AI698330	Hs.151444	ESTs	2.6
	427419	NM_000200	Hs.177888	histatin 3	2.6
75	423741	AA330362		gb:EST34074 Embryo, 12 week II Homo sapi	2.6
	451577	N69101	Hs.40730	ESTs	2.6
	441358	AW173212	Hs.129041	ESTs	2.6
	402706			Target Exon	2.6
	436054	AI076262	Hs.119813	ESTs	2.6
80	402749			Target Exon	2.6
	442472	AW806859		gb:MR0-ST0020-081199-004-c03 ST0020 Homo	2.6
	445762	AI734002	Hs.264590	ESTs, Moderately similar to ALU5_HUMAN A	2.6
	441420	AA932872		gb:zo57d07.s1 NCL_CGAP_Lu5 Homo sapiens	2.6
	405564			Target Exon	2.6

	406003		Target Exon	2.6	
	459584	AJ910884	Hs.346429	ESTs	2.6
	441597	AW135032	Hs.203625	ESTs	2.6
5	411280	N50617	Hs.80506	small nuclear ribonucleoprotein polypept	2.6
	420509	M83554	Hs.1314	tumor necrosis factor receptor superfami	2.6
	445060	AA830811	Hs.282908	ESTs	2.6
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.6
	428717	T78001	Hs.133546	hypothetical protein FLJ21120	2.6
10	401716			C16000902:gi403440 gb AAA73168.1 (M817	2.6
	416628	W03955		gb:za62d04.r1 Soares fetal liver spleen	2.6
	443864	N37059	Hs.36250	ESTs, Weakly similar to I38022 hypothesi	2.6
	440702	AA904178	Hs.148233	ESTs	2.6
	456310	AA225522		gb:nc25c06.r1 NCL_CGAP_Pr1 Homo sapiens	2.6
15	451255	AA020857	Hs.90744	ESTs	2.6
	455737	BE072246		gb:QV4-BT0536-271299-059-b12 BT0536 Homo	2.6
	445326	AJ220072	Hs.344672	ESTs	2.6
	408432	AW195262		gb:cn67b05.x1 NCL_CGAP_CML1 Homo sapiens	2.6
	445874	BE326671	Hs.170058	ESTs	2.6
	441063	AA913819	Hs.188025	ESTs	2.6
20	455505	AW970640	Hs.309071	ESTs	2.6
	453491	AL040177		gb:DKFZp434F0213_r1 434 (synonym: htes3)	2.6
	455048	AW852749		gb:PM1-CT0247-080100-008-h09 CT0247 Homo	2.6
	456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	2.6
25	444130	AI125263	Hs.170410	ESTs	2.5
	422210	BE269319	Hs.171937	steroid dehydrogenase-like	2.5
	424241	AW995948	Hs.182339	Homo sapiens pyruvate dehydrogenase kina	2.5
	451606	AA018791	Hs.7945	AIE-75 binding protein protein	2.5
	400427	AB044934	Hs.287388	histamine H4 receptor	2.5
30	410443	BE062906	Hs.28338	KIAA1546 protein	2.5
	455210	AW866599		gb:QV4-SN0024-210400-181-b10 SN0024 Homo	2.5
	429909	AW977090	Hs.184860	CGI-203 protein	2.5
	441191	AI693930	Hs.148816	ESTs	2.5
	413489	BE144228		gb:MR0-HT0165-140200-009-d04 HT0165 Homo	2.5
35	448215	N34740	Hs.6658	ESTs	2.5
	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	2.5
	447610	AW296286	Hs.255534	ESTs	2.5
	450724	R55428		gb:yf79b05.r1 Soares breast 2NbHBst Homo	2.5
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	2.5
40	414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	2.5
	447730	AI421251	Hs.114085	Homo sapiens mRNA for KIAA1755 protein,	2.5
	434152	AI792665	Hs.291190	ESTs	2.5
	412671	AW977734	Hs.37931	gb:EST389963 MAGE resequences, MAGO Homo	2.5
	456401	W28146		gb:43111 Human retina cDNA randomly prim	2.5
45	404678			Target Exon	2.5
	408520	AA225063	Hs.161614	ESTs	2.5
	411332	AW837212		gb:QV2-LT0038-140300-081-c01 LT0038 Homo	2.5
	448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	2.5
	429906	AL080137	Hs.193743	ESTs	2.5
50	433712	AF090887	Hs.306562	Homo sapiens clone HQ0085	2.5
	438353	BE539951	Hs.306996	Homo sapiens, clone IMAGE:3447073, mRNA,	2.5
	446224	AW450551	Hs.13308	ESTs	2.5

TABLE 63B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

60	Pkey	CAT Number	Accession
	408229	1048462_1	AW175091 H24234
	408432	1058667_1	AW195262 R27868 AW811262
	409679	114787_1	BE250521 AA076837 BE249870 AA984291 AW502442 AW501551 AI221491 AA194239 D63046 AA193426 AA773243 AA193293
65	410483	1204995_1	BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW760178 BE163491 BE073763 BE073671
	411320	1238624_1	AW836646 AW836580 AW836610 AW836636 AW836603 AW836632
	411332	1239102_1	AW837212 AW837408 AW837265 AW837380 AW837213 AW837411 AW837418
	411356	1240273_1	H45377 H21137 AW838640
	411426	1245515_1	BE141714 AW845993 AW845989
70	411829	1260309_1	AW865749 BE179419 BE179492
	411944	1266482_1	AW877139 AW877135 AW877018 AW991835 AW877128 AW877108 AW877017 AW877107
	413155	1351148_1	BE067952 BE067945 BE067942 BE067943 BE067949 BE067954 BE067944 BE067953 BE067956 BE067946
	413381	1365950_1	BE090690 BE090688 BE090681 BE090693 BE090675
	413489	1373392_1	BE144228 BE144291
75	415054	151827_1	AI733907 AA159708 AI732614
	415098	1522174_1	D59687 D59694 D59656 D59589
	415131	1523680_1	D61119 D81508 D81734
	415386	1535560_1	Z43087 F07410 H15506 H54108 R95033 H98000
	415981	1564242_1	R35694 H12035 R53312
80	416628	1604848_1	W03955 H82332 H69247 H72486
	416935	163179_1	AA190712 AA190665 AA252564
	419386	184356_1	AA236867 AA237068 AA354236 AW957759 H08961
	419896	1888662_1	Z99362 Z99363
	420778	196389_1	AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481

5	421342	201427_1	AA504749 AA287498
	421813	207654_1	BE048255 AA313083 AA298419
	422731	220507_1	AL138411 AL138412 AA315860
	423741	231582_1	AA330362 AW962525 H87798
	423772	23188_1	AA306637 NM_007241 AF156102 BE388339 BE614027 AW935016 AA315261 AW376418 AW304951 AI859820 AA367436 AW516957 BE614519
			AI453152 AI453149 AI453139 AW168378 AI139491 AI538368 AW468227 AI680027 AW090513 AA662830 F30995 AI351985 AI424349 AW009599
			CO2215 AI6525
10	423871	232749_1	AA331906 AA332484
	426481	267878_1	AW963941 AW963944 AA379825 AA379564
	428132	287430_1	AA421765 AA456076 AI290275 AA455579
	431847	338402_1	AI791314 AI791434 AA516511
	434407	385744_1	AW815333 AW815409 AA632563
	435383	405360_1	R61083 R13743 AA679174 AA679193 Z42903
	436190	41555_1	AK001059 AA633055
15	438535	45946_1	L09078 L03145 L09094 L09098 L03165 L09102
	441420	516748_1	AA932872 W28068 W28643 T96110
	442472	543371_1	AW806859 AW806852 AF049582
	445797	650943_1	AI253414 AI366014 R34822
	447518	724787_1	T80061 AI382804
20	447600	728288_1	AI420990 AI399725 AI401757
	448516	766241_1	AW898595 AW898588 AW898590 AW898663 AW898592 AI525093
	449923	81926_1	BE258051 R45758 AA004732 BE255126
	450724	844585_1	R55428 AI820704 AI732283 R54983
	451004	85453_1	AA044967 H85327 AA013079 AA058776 BE242713 AA019987
25	452351	91233_1	AA025647 R45716 AW753786
	453412	966264_1	AJ003290 AJ003288 AW276947
	453491	969172_1	AL040177
	453752	979899_1	AL120800 BE378580
30	453826	982669_1	AL138129 AL138179 BE064231
	454445	1204468_1	AW749432 AW749434 R47332
	454549	1223789_1	AW806910 AW866461 AW866396 AW866373 AW866611 AW866616
	455048	1250599_1	AW852749 AW852755 AW852620
	455210	1260650_1	AW866599 AW866294 AW866468 AW866467
35	455649	1348708_1	BE065051 BE155165 BE064764 BE155231 BE064648 BE064671 BE064636
	455737	1353892_1	BE072246 BE072229 BE072225 BE072210 BE072221 BE072256 BE072211 BE072242
	455791	1365954_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698 BE090686
	455887	1380835_1	BE154173 BE154098 BE154096
	456075	1476756_1	N73442 R98100 BE410380
40	456310	177089_1	AA225522 AA225465 AI820979 AW973985 AI791935 AA558735
	456401	1844649_2	W28146 W28187

TABLE 63C

45	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nt_position:	Indicates nucleotide positions of predicted exons.

50	Pkey	Ref	Strand	Nt_position
	400461	9929654	Plus	32727-32846,32929-33051
	400499	9796071	Minus	148495-148806
	400749	7331445	Minus	9162-9293
55	400831	8576271	Minus	56502-57407
	401278	9799936	Plus	98428-98573
	401411	7799787	Minus	144144-144329
	401656	9100664	Minus	1-382
	401716	6715703	Plus	174722-174911
60	401884	8140731	Minus	89182-90053
	401896	8569194	Plus	115129-115294
	401917	9502466	Plus	25054-25229
	402422	9796344	Minus	32843-33008
	402460	9796884	Minus	108901-109254,110246-110581,113613-113960
65	402490	9797648	Plus	149982-150929
	402706	8894426	Minus	148640-148805
	402749	9212740	Minus	68787-68882,76602-76768
	402797	3421043	Minus	15758-15930
	402817	6822166	Minus	48611-49012
70	402844	9369286	Plus	54958-55313
	403451	9838240	Plus	77382-78300
	403612	8469060	Minus	94723-94859
	403630	8569999	Minus	13909-14466,15251-15760,16898-17431,41742-42440
	403649	8705159	Minus	27141-27247
75	404260	9366879	Plus	51396-51513
	404267	9581792	Minus	12209-12313,18241-18397
	404606	9212936	Minus	22310-23269
	404660	9797068	Plus	168215-168916
	404678	9797204	Plus	115196-115448
80	404979	4160139	Minus	87762-88217
	404984	6939882	Plus	87221-87505
	405001	6015406	Minus	104646-104819
	405150	9929758	Plus	126475-126773

	405152	9965561	Minus	137662-137969
	405258	7329310	Plus	129930-130076
	405422	7243869	Minus	101938-102079, 102261-102443, 102896-103202
5	405564	2114222	Minus	16766-17344
	405678	4079670	Plus	151821-152027
	405735	9931101	Minus	29854-29976
	405770	2735037	Plus	61057-62075
	406003	8247800	Plus	42079-42516
10	406085	9123888	Plus	18665-18843
	406177	7279760	Minus	18930-19148
	406337	9213455	Plus	90117-90337
	406398	9256276	Minus	118691-118959
	406600	8248616	Minus	36296-36610

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Table 64A lists about 703 genes up-regulated in BPH compared to normal adult tissues. These were selected from 59680 probesets on the Affymatrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

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TABLE 64A: ABOUT 703 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO NORMAL ADULT TISSUES

	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
25	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of BPH tissue to normal adult body tissue			
	Pkey	ExAccn	Unigene ID	Unigene Title	R1
30	420154	AI093155	Hs.95420	JM27 protein	49.6
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	47.2
	419526	AI821895	Hs.193481	ESTs	43.6
	432441	AW292425	Hs.163484	ESTs	42.7
	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypoteti	30.2
35	407202	N58172	Hs.109370	ESTs	26.1
	432101	AI918950	Hs.123642	EphA3	25.8
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	25.5
	425075	AA506324	Hs.1852	acid phosphatase, prostate	24.6
40	414569	AF109298	Hs.118258	prostate cancer associated protein 1	24.4
	410929	H47233	Hs.30643	ESTs	21.1
	400287	S39329	Hs.181350	kallikrein 2, prostatic	20.3
	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	19.8
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	18.6
	415989	AI267700		ESTs	17.8
45	428336	AA503115	Hs.183752	microseminoprotein, beta-	17.3
	450693	AW450461	Hs.203965	ESTs	16.7
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	16.7
	407168	R45175	Hs.117183	ESTs	15.5
50	408369	R38438	Hs.182575	solute carrier family 15 (H777 transport	15.5
	454119	BE549773	Hs.40510	uncoupling protein 4	14.5
	428819	AL135623	Hs.193914	KIAA0575 gene product	14.5
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	14.4
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	14.3
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	14.2
55	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypoteti	14.2
	433444	AW975324	Hs.129816	ESTs	13.8
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	13.5
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	12.9
60	401424			NM_001172:Homo sapiens arginase, type II	12.7
	432435	BE218886	Hs.282070	ESTs	12.5
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	12.3
	446100	AW987109	Hs.13804	hypothetical protein dJ462023.2	12.0
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.9
65	407275	AI364186		gb:qw34h07.x1 NCL_CGAP_U4 Homo sapiens	11.8
	452340	NM_002202	Hs.506	ISL1 transcription factor, LIM/homeodoma	11.7
	432473	AI202703	Hs.152414	ESTs	11.3
	410330	AW023830	Hs.159425	ESTs	11.2
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	11.2
70	452792	AB037765	Hs.30652	KIAA1344 protein	11.2
	418848	AI820961	Hs.193465	ESTs	10.9
	400292	AA250737	Hs.72472	BMP-R1B	10.9
	433647	AA603367	Hs.222294	ESTs	10.8
	453160	AI263307	Hs.239884	H2B histone family, member L	10.8
75	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	10.6
	431474	AL133990	Hs.190642	CEGP1 protein	10.3
	429220	AW207206		ESTs	10.3
	428134	AA421773	Hs.161008	ESTs	10.2
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	10.1
80	456497	AW987956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	9.8
	434792	AA649253	Hs.132458	ESTs	9.7
	433466	AA508353	Hs.105314	relaxin 1 (H1)	9.5
	439176	AI464444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	9.5
	428398	AI249368	Hs.98558	ESTs	9.4

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	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	9.3
	407709	AA456135	Hs.23023	ESTs	9.3
	415293	R49462	Hs.106541	ESTs	9.1
	429918	AW873986	Hs.119383	ESTs	9.1
5	440260	AI972867	Hs.7130	copine IV	9.1
	453096	AW294631	Hs.11325	ESTs	9.1
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	8.9
	456516	BE172704	Hs.222746	KIAA1610 protein	8.8
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.8
10	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
	453006	AI362575	Hs.303171	ESTs	8.7
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	8.7
	420424	AB033036	Hs.97594	KIAA1210 protein	8.7
	450642	R39773	Hs.7130	copine IV	8.7
15	434036	AI659131	Hs.197733	hypothetical protein MGC2849	8.7
	428927	AA441837	Hs.90250	ESTs	8.6
	418629	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	8.5
	420345	AW295230	Hs.25231	ESTs	8.5
	446336	AW815036	Hs.151251	ESTs	8.4
20	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	8.4
	428728	NM_016625	Hs.191381	hypothetical protein	8.3
	417169	R13550	Hs.246773	ESTs	8.2
	453387	AI990741	Hs.252809	ESTs	8.2
	434666	AF151103	Hs.112259	T cell receptor gamma locus	8.1
25	417958	AA767382	Hs.193417	ESTs	8.0
	433433	AI692623	Hs.121513	Homo sapiens clone Z'3-1 placenta expres	7.9
	444609	AW571659	Hs.278081	ESTs	7.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.8
	433923	AI823453	Hs.146625	ESTs	7.7
30	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	7.7
	441690	R81733	Hs.33106	ESTs	7.6
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.6
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	7.5
35	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	7.5
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
	413597	AW302885	Hs.117183	ESTs	7.4
	404592			NM_022739*:Homo sapiens E3 ubiquitin lig	7.3
	409557	BE182896	Hs.211193	ESTs	7.3
40	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
	438231	AW594539	Hs.155689	ESTs	7.1
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	7.1
	449300	AI656959	Hs.346514	ESTs	7.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	7.1
45	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	7.1
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	430187	AI799809	Hs.158989	ESTs	7.0
	434217	AW014795	Hs.23349	ESTs	6.9
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	6.9
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	6.9
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	6.8
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	6.8
	426384	AI472078	Hs.303662	ESTs	6.8
	458509	AA654650	Hs.282906	ESTs	6.8
55	449821	AI671141	Hs.211122	ESTs	6.8
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	6.7
	443250	AI041530	Hs.132107	ESTs	6.7
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	6.6
60	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	6.6
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	6.5
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
	424433	H04607	Hs.9218	ESTs	6.5
65	450164	AI239923	Hs.63931	ESTs	6.5
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	6.5
	450497	H64159	Hs.15328	ESTs	6.5
	425312	AA354940	Hs.145958	ESTs	6.4
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
70	440911	AA909536	Hs.143562	ESTs	6.4
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.3
	432600	AI821085		gb:ms95a12.y5 NCL_CGAP_Pr3 Homo sapiens	6.3
	435375	AI733610	Hs.187832	ESTs	6.3
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	6.3
75	431359	AW993522	Hs.292934	ESTs	6.2
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	6.1
	403867			Target Exon	6.1
	424846	AU077324	Hs.1832	neuropeptide Y	6.1
80	439569	AW602166	Hs.222399	CEGP1 protein	6.1
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
	448004	AW451477	Hs.257456	ESTs	6.1
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	6.0
	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	6.0
	415621	AI548602	Hs.55468	ESTs	6.0

	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	6.0
	442481	N99828		gbza32c04.r1 Soares fetal liver spleen	6.0
	432527	AW975028	Hs.102754	ESTs	5.9
	447156	AW274731	Hs.157920	ESTs	5.9
5	404003			Target Exon	5.9
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	5.9
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.9
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	5.9
10	438138	R98299	Hs.177502	ESTs	5.9
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.8
	434973	AW449285	Hs.313636	EST	5.8
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	5.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	5.8
15	434485	AI623511	Hs.118567	ESTs	5.8
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	5.7
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	5.7
	453200	AA033832	Hs.212433	ESTs	5.7
	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
20	432956	AA650114	Hs.325198	ESTs	5.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	5.7
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukemia	5.7
	425810	AI923627	Hs.31903	ESTs	5.6
	414312	AA155694	Hs.191060	ESTs	5.6
25	404571			NM_015902*:Homo sapiens progesteron induce	5.6
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
	439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	5.6
	427078	AI676062	Hs.111902	ESTs	5.6
	422805	AA436989	Hs.121017	H2A histone family, member A	5.6
30	417511	AL049176	Hs.82223	chordin-like	5.6
	449625	NM_014253		odc (odd Oz/ten-m, Drosophila) homolog 1	5.6
	433927	AI557019	Hs.116467	small nuclear protein PRAC	5.5
	441676	BE564206	Hs.49889	ESTs	5.5
	421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
35	432682	AI376400	Hs.159588	ESTs	5.5
	435021	AA922192	Hs.54709	ESTs	5.5
	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	5.5
	426581	AB040956	Hs.135890	KIAA1523 protein	5.5
	439079	AF085937	Hs.38348	ESTs	5.5
40	443635	AI080230	Hs.134214	ESTs	5.5
	400080			Eos Control	5.5
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	5.5
	436578	AI091435	Hs.134859	ESTs	5.5
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
45	450325	AI935962	Hs.26289	ESTs	5.4
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	5.4
	435072	AW592176	Hs.116932	ESTs	5.4
	428647	AA830050	Hs.124344	ESTs	5.4
50	441111	AI806867	Hs.126594	ESTs	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
	450244	AA007534	Hs.125062	ESTs	5.3
	400294	N95798	Hs.278695	Homo sapiens prostein mRNA, complete cds	5.3
	415539	AI733881	Hs.72472	BMP-R1B	5.3
55	437267	AW511443	Hs.258110	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
	446715	AI337735	Hs.173919	ESTs, Moderately similar to ZN91_HUMAN Z	5.3
	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypothetical	5.3
60	426503	AA380153		gb:EST93093 Skin tumor 1 Homo sapiens cD	5.3
	423101	M83941	Hs.123642	EphA3	5.3
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	5.3
	450813	AI739625	Hs.203376	ESTs	5.3
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	5.2
65	415890	H08226	Hs.268712	ESTs	5.2
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	441054	AA913591	Hs.126480	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
70	448072	AI459308	Hs.24908	ESTs	5.2
	419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	5.2
	421040	AA715026	Hs.135280	ESTs	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	415263	AA948033	Hs.130853	ESTs	5.2
75	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	445238	AA883971	Hs.187506	ESTs	5.1
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.1
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.1
80	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
	440995	T57773	Hs.10263	ESTs	5.0
	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	5.0

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	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.0
	418334	AA319233	Hs.5521	ESTs	5.0
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	5.0
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	5.0
5	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	5.0
	403696			C4001100*gi15852342[gb]AAD54015.1) (AF0	5.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	5.0
	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
10	430261	AA305127	Hs.237225	hypothetical protein HT023	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	443180	R15875	Hs.258576	claudin 12	4.9
	414422	AA147224	Hs.249195	Homeo box A13	4.9
15	418866	T65754		gb:yc11c07.s1 Striatogene lung (937210) H	4.9
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.9
	428715	AW293716	Hs.53126	ESTs	4.9
	435937	AA830893	Hs.119769	ESTs	4.8
	435136	R27299	Hs.10172	ESTs	4.8
20	438132	AA907076	Hs.122060	ESTs	4.8
	447058	AI939456	Hs.160870	ESTs	4.8
	419187	AA234852	Hs.44693	ESTs	4.8
	433523	H29882		ESTs	4.8
	420871	AA702972	Hs.65300	ESTs	4.8
25	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	453843	D25215	Hs.35804	hect domain and RLD 3	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	4.7
	452843	AI796769	Hs.208320	ESTs	4.7
30	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	4.7
	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	440354	AA889386	Hs.125468	ESTs	4.7
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.7
35	443361	AI792628	Hs.133273	ESTs	4.6
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	4.6
	420026	AI831190	Hs.166576	ESTs	4.6
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.6
40	415788	AW628686	Hs.78851	KIAA0217 protein	4.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	434408	AI031771	Hs.132586	ESTs	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
	447805	AW627932	Hs.302421	gemin4	4.6
45	438875	AA827640	Hs.189059	ESTs	4.6
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	445242	BE158478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.6
	428218	AA424266	Hs.123642	EphA3	4.6
	452277	AL049013	Hs.28783	KIAA1223 protein	4.6
50	418836	AI655499	Hs.161712	ESTs	4.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	430701	AI760833	Hs.293971	ESTs	4.5
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
55	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	420133	AA426117	Hs.155543	ESTs	4.5
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	447816	NM_007233	Hs.274329	TP53 target gene 1	4.5
60	431060	AF039307	Hs.249171	homeo box A11	4.5
	445372	N36417	Hs.144928	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.4
	418019	R68911	Hs.176275	ESTs	4.4
65	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	412643	AW971239	Hs.136433	ESTs	4.4
70	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.4
	445210	H09323	Hs.27133	ESTs	4.4
	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	4.4
	420608	BE548277	Hs.103104	ESTs	4.4
	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
75	444030	AW021254	Hs.135055	ESTs	4.4
	435655	AW105663	Hs.6947	HSPC069 protein	4.4
	400533			ENSP00000209376*-PRED65 protein (Fragmen	4.4
	435285	AW272603	Hs.266134	ESTs	4.4
80	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	4.3
	432950	AW150945	Hs.144758	ESTs	4.3
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	4.3
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	4.3

	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	454159	AW968065	Hs.44143	polybromo 1	4.3
	435176	AA744875	Hs.189413	ESTs	4.3
5	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	4.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.3
	420111	AA255652		gb:zs21h11.r1 NCL CGAP_GCB1 Homo sapiens	4.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	4.3
	459045	N69101	Hs.40730	ESTs	4.3
10	405348			C7001664:g[i]12698051[jdb][BAB21849.1] (AB	4.3
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.3
	449603	AI655662	Hs.197698	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	423782	AI472209	Hs.323117	ESTs	4.3
15	432887	AI926047	Hs.162859	ESTs	4.3
	420905	AA521307	Hs.186651	ESTs	4.2
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
20	444246	H93281	Hs.10710	hypothetical protein FLJ20417	4.2
	450597	AI701635	Hs.207077	ESTs	4.2
	434022	R18374	Hs.117956	ESTs	4.2
	427761	AA412205	Hs.140996	ESTs	4.2
	433209	AB040907	Hs.278436	KIAA1474 protein	4.2
25	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	4.2
	449655	AI021987	Hs.59970	ESTs	4.2
	440774	AI420611	Hs.153934	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	440594	AW445167	Hs.126036	ESTs	4.2
30	458912	AI911066		ESTs	4.2
	410790	AW803357		gb:1L2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	435743	T66861	Hs.12962	ESTs	4.1
35	442786	H50733	Hs.256261	ESTs, Moderately similar to ALLU8_HUMAN A	4.1
	436714	AA728964	Hs.293399	ESTs	4.1
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.1
	408177	AI241733	Hs.43871	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
40	430523	AW451385	Hs.161954	ESTs	4.1
	445206	AI350199	Hs.269990	ESTs	4.1
	452335	AW188944	Hs.61272	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	449907	AA004825	Hs.103281	ESTs	4.1
45	430487	D87742	Hs.241552	KIAA0268 protein	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	4.1
	423242	AL039402	Hs.125783	DEME-6 protein	4.1
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	4.1
50	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	446416	AV658299	Hs.163959	ESTs	4.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	4.1
	427203	AW629517	Hs.244855	ESTs	4.0
55	440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	4.0
	442338	AI761976	Hs.156080	ESTs	4.0
	446307	T50083	Hs.22247	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	415861	Z43123	Hs.144513	ESTs	4.0
60	418259	AA215404		ESTs	4.0
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
	432229	AW290976	Hs.143587	ESTs	4.0
	418310	AA814100	Hs.86693	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
65	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	448131	AI675054	Hs.200481	ESTs	4.0
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	4.0
	418243	W51873	Hs.171857	Homo sapiens testis protein mRNA, partial	4.0
70	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	4.0
	434844	AF157116	Hs.22350	hypothetical protein LOC56757	4.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	4.0
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.0
	446354	AW449650	Hs.346335	ESTs	4.0
75	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
	457498	AI732230	Hs.191737	ESTs	3.9
80	433234	AB040928	Hs.65366	KIAA1495 protein	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	448568	AA149121	Hs.71947	ESTs	3.9
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.9
	424940	AA985308	Hs.283902	ESTs	3.9

	16288	H51299	gb:yp07c06.s1 Soares breast 3NbHBst Homo	3.9
	420301	AA767526	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	ESTs	3.9
	435878	R08330	ESTs	3.9
5	446862	AV660697	ESTs	3.9
	447530	AW192063	ESTs, Moderately similar to JC5238 galac	3.9
	452619	AW298597	Homo sapiens, clone IMAGE:4298026, mRNA,	3.9
	401403		Target Exon	3.9
	448779	BE042877	ESTs	3.9
10	420533	AI809510	ESTs	3.9
	411084	T18987	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	KIAA0888 protein	3.9
	423453	AW450737	CGI-09 protein	3.9
	434833	AF156548	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.9
15	455646	BE064420	gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	411479	AW848047	gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
	419038	AW134924	ESTs	3.9
	421129	BE439899	ESTs	3.9
	424332	AA338919	ESTs	3.9
20	441766	R53790	hypothetical protein FLJ14393	3.9
	447033	AI357412	ESTs	3.9
	439306	BE220199	WD40 protein C1a01	3.8
	410352	AW969725	KIAA0373 gene product	3.8
25	407961	AW672939	origin recognition complex, subunit 2 (y	3.8
	410252	AW821182	microfibrillar-associated protein 1	3.8
	439560	BE565647	hypothetical protein FLJ12820	3.8
	440450	AI333129	ESTs	3.8
	458611	AI268407	DC-specific transmembrane protein	3.8
	419589	AW973708	Homo sapiens cDNA FLJ13446 fis, clone PL	3.8
30	431576	M76665	hydroxysteroid (11-beta) dehydrogenase 1	3.8
	447280	BE617907	ESTs	3.8
	438379	N23018	C-terminal binding protein 2	3.8
	416009	Z43062	gb:HSC12E041 normalized infant brain cDN	3.8
	416534	H69043	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
35	423044	AA320829	protocadherin 18	3.8
	424701	NM_005923	mitogen-activated protein kinase kinase	3.8
	433507	AI817336	ESTs	3.8
	437718	AI927288	ESTs	3.8
	419831	AW448930	ESTs	3.8
40	424830	AW270580	ESTs, Weakly similar to putative p150 [H	3.8
	426981	AL044675	KIAA0530 protein	3.8
	431447	AA505138	ESTs	3.8
	435932	W03928	ESTs	3.8
	442447	AA999723	ESTs	3.8
45	403242		Target Exon	3.8
	433908	AW298141	ESTs	3.8
	452323	W44356	ESTs, Weakly similar to T33468 hypothe	3.7
	412095	AI624707	Homo sapiens cDNA: FLJ21592 fis, clone C	3.7
	418759	AA227879	ESTs	3.7
50	422299	AK000181	hypothetical protein FLJ20174	3.7
	452462	BE173515	gb:RC2-HT0560-210200-012-03 HT0560 Homo	3.7
	423096	AA732684	progestin induced protein	3.7
	454037	AW998716	gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
55	428055	AA420564	ESTs	3.7
	447785	AL041765	ESTs	3.7
	451746	MB6178	ESTs	3.7
	453293	AA382267	ESTs	3.7
	436671	AW137159	ESTs	3.7
	407437	AF220264	gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
60	408418	AW963897	KIAA1435 protein	3.7
	420092	AA814043	ESTs	3.7
	446947	AF148747	polycythemia rubra vera 1; cell surface	3.7
	441865	AA384726	hypothetical protein FLJ23316	3.7
65	419875	AA853410	proenkephalin	3.7
	431231	AA653552	ESTs	3.7
	418348	AI537167	hypothetical protein FLJ23560	3.7
	419261	X07876	wingless-type MMTV integration site fami	3.7
	422899	D16471	Human mRNA, Xq terminal portion	3.7
70	429163	AA884766	gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.7
	439075	AF085933	ESTs	3.7
	440947	AA910403	ESTs	3.7
	404561		trichorhinophalangeal syndrome I gene (T	3.6
	430096	U91935	Retina-derived POU-domain factor-1	3.6
75	430320	BE245290	uncharacterized hypothalamus protein HCD	3.6
	444794	AI419991	ESTs	3.6
	426991	AK001536	Homo sapiens cDNA FLJ10674 fis, clone NT	3.6
	431316	AA502663	ESTs	3.6
	414178	AW957372	ESTs, Weakly similar to I38022 hypothe	3.6
80	450630	AA010429	ESTs	3.6
	411067	AI681006	ESTs	3.6
	436326	BE085236	aldo-keto reductase family 1, member B1	3.6
	410268	AA316181	six transmembrane epithelial antigen of	3.6
	423590	AW952412	ESTs, Weakly similar to A40348 Elav/Sex-	3.6

	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	416239	AL038450	Hs.48948	ESTs	3.6
5	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.6
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	3.6
	423349	AF010258	Hs.127428	homeo box A9	3.6
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
10	433563	AI732637	Hs.277901	ESTs	3.6
	425465	L18964	Hs.1904	protein kinase C, iota	3.5
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.5
	401132			C12000517:gij4758712[ref]NP_004659.1 a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42536	ESTs	3.5
15	449343	AI151418		protein phosphatase 3 (formerly 2B), cat	3.5
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	3.5
	419563	AA526235	Hs.193152	Homo sapiens cDNA FLJ11983 fis, clone HE	3.5
	419994	AA282881	Hs.190057	ESTs	3.5
20	427304	AA761526	Hs.163853	ESTs	3.5
	434763	AA648618		gb:ns07a11.r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	447497	AW167254	Hs.205722	ESTs	3.5
	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.5
25	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	3.5
	438680	AA906121	Hs.173421	ESTs	3.5
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypotheti	3.5
	443273	AI042063	Hs.132156	ESTs	3.5
	403510			Target Exon	3.5
30	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5
	435981	H74319	Hs.188620	ESTs	3.5
	449845	AW971183	Hs.9583	DnaJ (Hsp40) homolog, subfamily C, membe	3.5
	436024	AI800041	Hs.190555	ESTs	3.5
35	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	458332	AI000341	Hs.220491	ESTs	3.5
	435688	H72286	Hs.128387	ESTs	3.4
	435047	AA454985	Hs.54973	cadherin-like protein VR20	3.4
40	432605	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.4
	409047	AW961434	Hs.31539	ESTs	3.4
	404848			ENSP00000240769*:BG15303.1 (similar to C	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
45	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	3.4
	436340	R42245	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.205768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
50	449517	AW500106	Hs.23543	serine/threonine protein kinase MASK	3.4
	450257	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453582	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	444324	AI301330	Hs.143838	ESTs	3.4
55	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	419964	AA811657	Hs.220913	ESTs	3.4
	424026	AI798295	Hs.137576	ribosomal protein L34 pseudogene 1	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	453942	AW190920	Hs.19928	hypothetical protein SP329	3.4
60	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.4
	408784	AW971350	Hs.63386	ESTs	3.4
	420184	AA188408	Hs.95665	hypothetical protein	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	3.4
65	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	3.4
	427674	NM_003528	Hs.2178	H2B histone family, member Q	3.4
	412505	AA974491	Hs.21734	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
70	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.3
	436345	AA873008	Hs.121572	ESTs	3.3
	423023	N50128	Hs.173400	ESTs	3.3
75	427615	BE410107	Hs.179817	CGI-82 protein	3.3
	429588	AI080271	Hs.134533	ESTs	3.3
	400362	AF068294	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	3.3
80	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
	433554	AW957666	Hs.8108	disabled (Drosophila) homolog 1	3.3
	414818	BE541217	Hs.23606	ESTs	3.3

	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	436854	AA749167	Hs.173911	ESTs	3.3
	430865	AI073424	Hs.5232	HSPC125 protein	3.3
	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
5	423645	AI215632	Hs.147487	ESTs	3.3
	429227	AI961456	Hs.21275	hypothetical protein FLJ11011	3.3
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	3.3
	418051	AW192535	Hs.19479	ESTs	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
10	437714	AA766346	Hs.293242	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
15	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.3
	423412	AF109300		prostate cancer associated protein 5	3.3
	438962	AW377314	Hs.5364	DKFZP564I052 protein	3.3
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	3.3
	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
20	433213	AW665130	Hs.137190	ESTs	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.2
	428043	T92248	Hs.2240	uteroglobin	3.2
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	3.2
25	423595	R82826	Hs.220702	ESTs	3.2
	407021	U52077		gb:Human mariner1 transposase gene, comp	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
30	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh06c06.r1 Soares_fetal_liver_spleen_	3.2
	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.2
	425657	T89839	Hs.119471	ESTs	3.2
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.2
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.2
35	451025	AW028689	Hs.301985	ESTs	3.2
	401416			C14000338*:g 7459502 pir S74665 outer	3.2
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.2
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.2
	436995	AI160015	Hs.118112	ESTs	3.2
40	428736	AK001331	Hs.192662	hypothetical protein FLJ10469	3.2
	420120	AL049610	Hs.95243	transcription elongation factor A (Slit)-	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
	429037	X81895	Hs.194765	H.sapiens GEND-5624 mRNA, 3' UTR	3.2
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
45	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	437866	AA156781		metallothionein 1E (functional)	3.2
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.2
50	410870	U81599	Hs.66731	homeo box B13	3.2
	438899	AF085833	Hs.135624	ESTs	3.2
	415862	R51034	Hs.144513	ESTs	3.2
	420969	AI636310	Hs.28310	ESTs	3.2
	415467	R60891	Hs.260274	ESTs	3.2
55	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	417380	T06809	Hs.332086	ESTs	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
	419088	AI538323	Hs.52620	Integrin, beta 8	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
60	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.2
	452862	AW378065	Hs.8687	ESTs	3.2
	405548			Target Exon	3.1
	439584	AA838114	Hs.221612	ESTs	3.1
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.1
65	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.1
70	416836	D54745	Hs.80247	cholecystokinin	3.1
	432589	AL135725	Hs.131708	ESTs	3.1
	420512	AA262886	Hs.143817	ESTs	3.1
	417205	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.1
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypotheti	3.1
75	423855	AA331761	Hs.254859	ESTs	3.1
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
80	421823	N40850	Hs.28625	ESTs	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	445784	AI253155	Hs.146065	ESTs	3.1
	434384	AA631910	Hs.162849	ESTs	3.1
	416140	AB918035	Hs.301198	roundabout (axon guidance receptor, Dros	3.1

5	407426	AF129533	gbtHomo sapiens F-box protein Fb13b (FBL	3.1
	416423	H54375	ESTs	3.1
	418037	AI990212	ESTs	3.1
	419197	N48921	KIAA1615 protein	3.1
	420179	N74530	ESTs	3.1
	433610	AA806822	ESTs	3.1
	436295	N73895	gbza62d06.s1 Soares fetal liver spleen	3.1
	444800	AW119071	ESTs	3.1
10	418858	AW961605	hypothetical protein RG083M05.2	3.1
	446469	BE094848	homogenisate 1,2-dioxygenase (homogeni	3.1
	431992	NM_002742	protein kinase C, mu	3.1
	405510		ENSP00000233779*:Hypothetical 68.0 kDa p	3.1
	407349	AA825449	Hs.83332	3.1
15	410869	AW808361	Homo sapiens cDNA: FLJ22437 tis, clone H	3.1
	425354	U62027	gb:MR1-ST0111-111099-003-R04 ST0111 Homo	3.1
	425480	AB023198	complement component 3a receptor 1	3.1
	441492	AI149998	KIAA0981 protein	3.1
	447078	AW885727	ESTs	3.1
20	459324	AW080953	ESTs	3.1
	433852	AI378329	gbxc28c12.x1 NCL_CGAP_Co18 Homo sapiens	3.1
	448658	H71739	ESTs	3.0
	452242	R50956	ESTs, Moderately similar to A53959 throm	3.0
	424690	BE538356	glycosyltransferase	3.0
	405264		eukaryotic translation initiation factor	3.0
25	407253	AA411175	NM_030813*:Homo sapiens suppressor of po	3.0
	452234	AW084176	ESTs, Moderately similar to S65657 alpha	3.0
	434497	AI821803	ESTs, Weakly similar to I38022 hypotheti	3.0
	420355	AW968263	ESTs	3.0
30	403481		ESTs	3.0
	412988	BE046680	Target Exon	3.0
	452679	Z42387	gb:hn42h03.x1 NCL_CGAP_RDF2 Homo sapiens	3.0
	416642	T96118	transmembrane, prostate androgen induced	3.0
	418948	AI217097	ESTs	3.0
35	426174	AA547959	gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	430459	BE178539	ESTs	3.0
	439182	AF086030	ESTs	3.0
	446258	AI283476	hypothetical protein DKFZp762O076	3.0
40	448688	AA158659	ESTs	3.0
	453455	AA063553	hypothetical protein FLJ14744	3.0
	414441	AA234759	ESTs, Weakly similar to JC1087 RNA helic	3.0
	427302	AA400540	ESTs	3.0
	437048	AA743240	Homo sapiens cDNA FLJ11554 tis, clone HE	3.0
	450963	AI864668	ESTs	3.0
45	432336	NM_002759	ESTs	3.0
	459535	AV654907	protein kinase, interferon-inducible dou	3.0
	448734	BE614070	gb:AV654907 GLC Homo sapiens cDNA clone	3.0
	451468	AW503398	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.0
	407829	AA045084	ESTs, Moderately similar to I38022 hypot	3.0
50	420407	AA814732	hypothetical protein FLJ13197	3.0
	426743	AA383833	lipopolysaccharide-specific response 5-II	3.0
	442326	H92962	ESTs	3.0
	449913	AA004696	hypothetical protein MGC14817	3.0
	454096	AW062757	ESTs	3.0
55	437323	AA371145	gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
	407137	T97307	leptin receptor	3.0
	450580	N40087	gb:ye53h06.s1 Soares fetal liver spleen	3.0
	429084	AJ001443	ESTs	3.0
	418365	AW014345	splicing factor 3b, subunit 3, 130kD	3.0
60	423784	AK000039	ESTs	3.0
	435677	AA694142	Homo sapiens cDNA FLJ14913 tis, clone PL	3.0
	414951	AW794931	ESTs, Weakly similar to TSGA RAT TESTIS	3.0
	418819	AA228776	hypothetical protein FLJ14600	3.0
	428634	AA811845	ESTs	3.0
65	431869	AA521136	Kelch motif containing protein	3.0
	435008	AF150262	ESTs	3.0
	448880	AW205507	ESTs	3.0
	451391	AA017410	ESTs, Highly similar to I38587 retroviru	3.0
70	452959	AI933416	ESTs	3.0

TABLE 64B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410790	1221131_1	AW803357 AW803423 AW812233 R06814
410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934
		AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739
		AW808704 AW808558 AW808714 AW808420 AW8
411436	1245660_1	AW848433 AW846159 AW846377 AW846528

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			AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069
	411479	1247077_1	AW848905 AW848214
	412988	1342150_1	BE046680 BE046738 BE044958
5	413081	1348563_1	BE064415 BE064430 BE064448
	413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
	415989	156454_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355085
	416009	1566379_1	Z43062 R13213 H14422
	416288	1585983_1	H51299 H44619 H46391 R86024 H51892 T72744
10	416882	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AJ748815 AJ763294 AI333114 AI277384 AJ088297 AJ468477
			AI824624 AW189606 AI631751 Z40749 AJ984673 AI671316 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597
	418259	173388_1	AA215404 AI990909 BE464132 AW271459 N74332 AI262061
	418866	179788_1	T65754 AA229857 AA229658
	418948	180808_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043
	419536	185688_1	AA603305 AA244095 AA244183
15	420111	190755_1	AA255652 AA280911 AW967920 AA262684
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
	423412	228001_1	AF109300 AI299378 AI202654
	424200	236595_1	AA337221 AA336756 AW966196
	426413	266650_1	AA377823 AW954494 AI022688
20	426503	268283_1	AA380153 AA380233 AW963529
	426991	27415_1	AK001536 AA191092 AW510354 AI554256 AL353968 AA134266
	428002	285602_1	AA18703 AA18711 BE071915 BE071920 BE071912
	428342	290035_2	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438
			AI092404 AI085630 AA731340
25	429163	300543_1	AA884766 AW974271 AA592975 AA447312
	429220	301384_1	AW207206 AW341473 AA448195 AI951341
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
	432600	350959_1	AI621085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
	432765	353907_1	AJ003429 AJ003367 AA564825
30	433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
	434763	392847_1	AA648618 AW974389 H51771
	436295	41733_1	N73895 AJ001872
	436326	41795_2	BE085236 BE085317 X04236 AA577934 AA578392 AA502836 AA595852 AA578258 AW270791 AA507151 AA559152 T57040 BE503281
			AW593405 AI825755 AI350499 AI655710 AI972281 AI654949 BE073961 BE073962 BE041399 AW750214 AA228488 BE074016 AI908706
35	437866	44433_2	AW270601 AW873282
			AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992
			AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733
			AA812489 AW874142 AI47188
40	439092	468554_1	AA830149 AW978407 M85983 AW503637
	439306	47088_1	BE220199 W01813 AF086118 N70760 BE221405
	440840	50357_2	AW629666 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI797207
			AA921877
	440947	505904_1	AA910403 AI815593 W58361 AW162520 AI816550
	442481	543588_1	N99828 BE079873 AI110738 AF074645
45	445432	63943_1	AV653771 BE089370
	448044	747196_1	AA58682 H24240 R14537 R18426 AW867082
	449343	80517_2	AI151418 W60401 AW631238 AI346936 AA862855 W60310 N72501 H90060 BE150445 AW380821 AI540906 C04881 W03542 AA641764 H97053
			AW889353 AA521308 AA001203 W92828 AI207798 AA746655 R78710 W24617 AA024605 C01747 AW173095 W61229 W92685 AA742467
			H00789 R76925 AW1828
50	449570	81018_1	AA001793 AA001871
	449625	8113_1	N1L014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760
			N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486
	450317	831956_1	AI692689 R14223 R18395
55	450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816888 AW816889 AW816940
			AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095
			AA164518 AA730973 W00417 W65303
	450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
	452462	918580_1	BE173515 BE173560 AI902860
60	453682	977454_1	T79703 T96307 AL079725
	454037	996287_1	AW996716 AW022148 N68020
	454096	1007449_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	454457	1207274_1	AW753456 AW753036 AW854868 AW854862
65	454860	1237732_1	AW835767 AW835537 BE160187
	454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
	455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW886079 BE176576 BE176615 BE176555 BE176489 BE176610 BE176362
	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
70	457374	328758_1	AA493662 AW897396 BE154814
	458912	823104_1	AJ911066 AI933734 AJ680888 AJ003599

TABLE 64C

75	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
80	Nl_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nl_position
------	-----	--------	-------------

5	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401403	7710966	Plus	146180-146294
	401416	7452889	Minus	121456-121626
	401424	8176894	Plus	24223-24428
	403242	7637817	Minus	11297-12511
	403481	9965004	Plus	93496-93633
10	403510	7652047	Plus	61866-62027
	403667	6850483	Minus	1344-1442,1545-1697
	403696	3135242	Minus	143467-143634
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
15	404571	7249169	Minus	112450-112648
	404592	9943965	Minus	39067-39225
	404848	8248647	Minus	23955-24034,25143-25264
	405264	7329374	Plus	28556-28684
	405348	2914717	Minus	43310-43462
20	405510	7630909	Minus	101028-101174
	405548	1532158	Plus	11552-11686

25 Table 65A lists about 347 genes up-regulated in BPH compared to prostate cancer tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" prostate cancer tissue level was set to the 85th percentile amongst malignant prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

30 TABLE 65A: ABOUT 347 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER TISSUES

35	Pkey:	Unique Eos probeset identifier number		
	ExAccon:	Exemplar Accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
40	R1:	Ratio of BPH tissue to prostate tumor tissue		
	Pkey	ExAccon	Unigene ID	Unigene Title
	428134	AA421773	Hs.161008	ESTs
	446336	AW815036	Hs.151251	ESTs
45	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K
	400533			ENSP00000209376-PRED65 protein (Fragmen
	418310	AA814100	Hs.86693	ESTs
	404592			NM_022739:Homo sapiens E3 ubiquitin lig
50	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo
	400080			Eos Control
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c
55	438231	AW594539	Hs.155689	ESTs
	418387	R18085		gb:yg16b12.r1 Soares infant brain 1N1B H
	442481	N99828		gb:za32c04.r1 Soares fetal liver spleen
	449249	T62285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe
	404967			Target Exon
60	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222
	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens
	400440	X83957	Hs.83870	nebulin
65	454171	AW854832		gb:QV2-CT0261-201099-011-R05 CT0261 Homo
	400086			Eos Control
	440911	AA909536	Hs.143562	ESTs
	425312	AA354940	Hs.145958	ESTs
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence
70	419015	T79262	Hs.14463	ESTs
	453789	AA628517	Hs.118502	ESTs
	424940	AA985308	Hs.283902	ESTs
	403667			Target Exon
	429014	AI800518	Hs.118158	ESTs
75	417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitte
	419999	AI760942	Hs.191754	ESTs
	405348			C7001664:gi12698061[db]BAB21849.1 (AB
	404003			Target Exon
	453200	AA033832	Hs.212433	ESTs
	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi
	432319	AW510770	Hs.128388	ESTs
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi
	443361	AI792628	Hs.133273	ESTs
80	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo
	439079	AF085937	Hs.38348	ESTs
	422081	AW136820	Hs.196011	ESTs
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked
	423529	T87318	Hs.120411	ESTs

	436578	AI091435	Hs.134859	ESTs	5.5
	450920	AA011626	Hs.133324	ESTs	5.5
	435072	AW592176	Hs.116932	ESTs	5.4
	414403	AW969551	Hs.76064	ribosomal protein L27a	5.4
5	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	414818	BE541217	Hs.23606	ESTs	5.3
10	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheli	5.3
	454968	AW849046		gblL3-CT0214-150300-065-H06 CT0214 Homo	5.2
	415890	H08225	Hs.268712	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
15	435375	AI733610	Hs.187832	ESTs	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	5.2
	405321			Target Exon	5.1
20	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
	438206	AA780385	Hs.187885	ESTs	5.1
	445238	AA883971	Hs.187506	ESTs	5.1
	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
25	457374	AA493662		gb:nh05d12.s1 NCL_CGAP_Thy1 Homo sapiens	5.0
	440354	AA889386	Hs.125468	ESTs	5.0
	440388	AI693520	Hs.223000	ESTs	4.9
	421188	AA284658	Hs.261493	ESTs	4.9
	403481			Target Exon	4.8
30	438132	AA907076	Hs.122060	ESTs	4.8
	403333			NM_002518*:Homo sapiens neuronal PAS dom	4.8
	450317	AI692689		gb:wd86g05.x1 NCL_CGAP_Lu24 Homo sapiens	4.8
	433597	AA708205	Hs.100343	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
35	452843	AI796769	Hs.208320	ESTs	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
	442123	AI697790	Hs.159961	EST	4.7
	438727	AW978756	Hs.206879	ESTs	4.7
40	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	442160	AI337127	Hs.156325	ESTs	4.6
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.6
	434589	AF147363		gb:Homo sapiens full length insert cDNA	4.6
	404995			ENSP00000251890*:Monocytic leukemia zinc	4.6
45	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.5
	405549			C7001976*:gll4758712[ref]NP_004659.1] al	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	443998	AI620661	Hs.296276	ESTs	4.5
	455801	BE140643		gb:RCO-HT0015-310599-016 HT0015 Homo sap	4.5
50	444800	AW119071	Hs.153287	ESTs	4.5
	403371			Target Exon	4.5
	438431	AW207860	Hs.293116	ESTs	4.5
	421926	AA300591		gb:EST13437 Testis tumor Homo sapiens cD	4.5
55	439752	T78968	Hs.14411	ESTs	4.5
	414441	AA234759	Hs.132950	ESTs	4.5
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	4.4
	454585	BE069128		gb:QV3-BT0379-310100-071-g06 BT0379 Homo	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
60	418059	AA211586		gb:zn56d05.s1 Stratagene muscle 937209 H	4.4
	451469	NM_014809	Hs.26441	KIAA0319 gene product	4.4
	433072	AI928037	Hs.158832	ESTs	4.4
	443318	AI051603	Hs.133141	ESTs	4.4
	424686	AA345504		gb:EST51529 Gall bladder II Homo sapiens	4.3
65	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	415467	R60891	Hs.260274	ESTs	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	415417	F12038	Hs.140970	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.3
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	4.3
70	441620	R59595	Hs.26675	ESTs	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	448108	AW300021	Hs.170685	ESTs	4.2
	435345	AA873008	Hs.121572	ESTs	4.2
75	409500	U08098	Hs.54576	sulfotransferase, estrogen-prefering	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	403305	NM_006825		transmembrane protein (63kD), endoplasmic	4.2
	436338	W92147	Hs.118394	ESTs	4.2
	427521	AW973352	Hs.290685	ESTs	4.2
80	430124	AW204994	Hs.253450	ESTs	4.2
	410790	AW803357		gblL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	416385	H54253	Hs.205241	ESTs, Weakly similar to S65657 alpha-1C-	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1

	445206	AI350199	Hs.269990	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
	453713	R20640	Hs.79133	cadherin 8, type 2	4.1
5	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	442338	AI761976	Hs.156080	ESTs	4.0
	455388	AW936234		gb:QV0-DT0020-090200-106-g05 DT0020 Homo	4.0
10	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	421312	AA824827	Hs.291670	ESTs	4.0
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	4.0
	448862	AJ001531	Hs.22404	protease, serine, 12 (neurolypsin, mole	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
15	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	3.9
	454024	AA993527	Hs.293507	hypothetical protein FLJ23403	3.9
	453387	AI990741	Hs.252809	ESTs	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
20	454806	AW872430	Hs.273743	ESTs	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JCS238 galac	3.9
25	407834	AW084991	Hs.26100	ESTs	3.9
	400398	AF137396	Hs.283879	ubiquitin 3	3.9
	421353	AW292857	Hs.255130	ESTs	3.9
	401459			C14000482:gi 9790241 ref NP_062628.1 S	3.9
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.9
30	444911	U06117	Hs.250	xanthene dehydrogenase	3.9
	436350	AA713661	Hs.121091	ESTs	3.9
	447930	R44574	Hs.107510	ESTs	3.9
	410559	AW754192		gb:RC2-CT0321-131299-012-a04 CT0321 Homo	3.8
	452320	AA042873	Hs.160412	ESTs	3.8
35	402145			Target Exon	3.8
	458438	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN IIII	3.8
	440450	AI333129	Hs.156147	ESTs	3.8
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
40	434381	AA631834		gb:np77h05.s1 NCL_CGAP_P12 Homo sapiens	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	433523	H29882		ESTs	3.8
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
45	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
	442447	AA999723	Hs.129607	ESTs	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	403242			Target Exon	3.8
50	455490	AW953477		gb:EST365547 MAGE resequences, MAGB Homo	3.8
	449264	AI637649	Hs.196105	ESTs	3.8
	443635	AI080230	Hs.134214	ESTs	3.7
	428200	AI039624	Hs.98388	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-403 HT0560 Homo	3.7
55	418759	AA227879	Hs.187621	ESTs	3.7
	450497	H64159	Hs.15328	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
	416321	H94331	Hs.34024	ESTs	3.7
60	448135	AI470874	Hs.343799	ESTs	3.7
	405510			ENSP00000233779:Hypothetical 68.0 kDa p	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	451859	H44491	Hs.252938	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	455135	AW857989		gb:PM2-CT0328-281299-003-e04 CT0328 Homo	3.7
65	409189	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	3.7
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.7
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	3.7
	434306	AW081757	Hs.44241	Homo sapiens cDNA: FLJ21447 fis, clone C	3.7
	456354	X58411	Hs.1219	alcohol dehydrogenase 4 (class II), pl p	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
70	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	411421	BE272110	Hs.21177	ESTs	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
75	440947	AA910403		ESTs	3.7
	417565	AI203405	Hs.47831	ESTs	3.6
	430095	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	404561			trichorhinophalangeal syndrome I gene (T	3.6
80	429073	AA446167	Hs.47385	ESTs	3.6
	419002	T78625	Hs.268594	ESTs	3.6
	450630	AA010429	Hs.191939	ESTs	3.6
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-43882	3.6

	439481	AF086294	Hs.125844	ESTs	3.6
	419622	AA452054	Hs.119338	ESTs	3.6
	449821	AI671141	Hs.211122	ESTs	3.6
	451193	N29850	Hs.44098	ESTs	3.6
5	412701	AW984757		gb:RC1-HN0015-040400-011-g10 HN0015 Homo	3.6
	419611	AB031479	Hs.91600	SEEK1 protein	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	427235	AI126298	Hs.192232	ESTs	3.6
10	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fls. clone HE	3.5
	401132			C12000517*gi4758712[ref NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	405264			NM_030813*:Homo sapiens suppressor of po	3.5
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.5
	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
15	434763	AA648618		gb:ns07a11.r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	416379	N38857	Hs.203933	ESTs	3.5
	407557	Z83803		gb:H.sapiens mRNA for axonemal dynein he	3.5
	437956	AA773283	Hs.203559	hypothetical protein FLJ12701	3.5
	403510			Target Exon	3.5
20	451722	H86374	Hs.40861	ESTs	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	427125	AA683362	Hs.97612	ESTs	3.5
	424287	AL133105	Hs.144633	hypothetical protein DKFZp434F2322	3.4
	434497	AI821803	Hs.136580	ESTs	3.4
25	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	404848			ENSP00000240769*:BG15303.1 (similar to C	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
30	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
35	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	410551	R36730	Hs.21816	ESTs	3.4
	423357	AI285124	Hs.157505	ESTs	3.4
	450582	AI339732		G-rich RNA sequence binding factor 1	3.4
40	437662	AA765387	Hs.145095	ESTs	3.4
	442388	AW663442	Hs.129485	ESTs	3.4
	445004	AI204616	Hs.148701	ESTs	3.4
	450597	AI701635	Hs.207077	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
45	450003	AA777809	Hs.191995	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	428923	BE047698	Hs.188785	ESTs	3.4
	407344	AI038025	Hs.271418	gb:cx29f07.x1 Soares_total_fetus_Nb2HF8_	3.3
50	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	437115	AA744703	Hs.129030	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
55	453328	AW282635	Hs.346145	ESTs	3.3
	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	449256	AA059050	Hs.59847	ESTs	3.3
	432550	AW297206	Hs.164018	ESTs	3.3
	423101	M83941	Hs.123642	EphA3	3.3
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	3.3
60	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	402703			Target Exon	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
65	452011	AW628911	Hs.211429	ESTs	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.2
	420355	AW968263	Hs.123126	ESTs	3.2
	418898	T66847	Hs.194040	ESTs, Weakly similar to I38022 hypotheti	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
70	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	408304	AW810279		gb:MR4-ST0125-151299-029-a09 ST0125 Homo	3.2
	402454			C1002501*gi129092[sp P23270]OLF7_RAT O	3.2
	411552	AW851255		gb:IL3-CT0220-160200-066-H02 CT0220 Homo	3.2
	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	3.2
75	435786	H09175	Hs.26085	ESTs	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	432625	AI243586	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
80	447183	AI554733	Hs.173182	ESTs	3.2
	426629	AI203933	Hs.97142	ESTs	3.2
	447892	AI435848	Hs.172978	ESTs	3.2
	457136	AA428240	Hs.126083	ESTs	3.2
	443585	AW466983	Hs.283949	enamelin	3.1

5	451399	AL042110	Hs.326728	ESTs	3.1
	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	458251	AL040927	Hs.210422	ESTs	3.1
	439950	AW937417	Hs.293561	ESTs	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
10	403805			Target Exon	3.1
	422666	AA677981	Hs.119023	SMC2 (structural maintenance of chromoso	3.1
	408799	AA059412	Hs.47986	hypothetical protein MGC10940	3.1
	429350	A1754634	Hs.131987	ESTs	3.1
	430454	AW469011	Hs.105635	ESTs	3.1
15	441817	AW969706	Hs.293332	ESTs	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	415901	H08396	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.1
	445758	R60715	Hs.25804	ESTs	3.1
	403291			Target Exon	3.1
20	436295	N73895		gb:za62d08.s1 Soares fetal liver spleen	3.1
	455772	W28799		gb:52g11 Human retina cDNA randomly prim	3.1
	418037	A1990212	Hs.86447	ESTs	3.1
	438142	T90309	Hs.269651	ESTs	3.1
	416423	H54375	Hs.268921	ESTs	3.1
25	448765	R15337	Hs.21958	Homo sapiens mRNA: cDNA DKFZp547D086 (tr	3.1
	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	3.1
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.1
	420721	AA927802	Hs.159471	ZAP3 protein	3.1
	436013	AA703419	Hs.287749	Homo sapiens cDNA: FLJ23593 fis, clone L	3.1
30	441492	A149998	Hs.146346	ESTs	3.1
	410869	AW808361		gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	3.1
	435628	W88732	Hs.36107	ESTs	3.0
	444326	AJ939357	Hs.270710	ESTs	3.0
35	413774	AA131782	Hs.182314	ESTs	3.0
	434352	AF129505	Hs.86492	small muscle protein, X-linked	3.0
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	3.0
	416422	H60457		ESTs, Moderately similar to ZN91_HUMAN Z	3.0
	416642	T96118	Hs.226313	ESTs	3.0
40	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
	418948	A1217097		gb:gd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	433796	AA810867	Hs.186997	ESTs	3.0
	427813	D29833	Hs.2207	salivary proline-rich protein	3.0
	405733			NM_021140*:Homo sapiens ubiquitously tra	3.0
45	426743	AA383833	Hs.245022	ESTs	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Sle20-lik	3.0
	410929	H47233	Hs.30643	ESTs	3.0
50	458187	D56919	Hs.265848	myomegalin	3.0
	429430	A1381837	Hs.155335	ESTs	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0

55 TABLE 65B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

60	Pkey	CAT Number	Accession
	408304	1050848_1	AWB10279 BE146684 BE146693 BE146694 BE146679 AWB10472 AWB10208 AWB10356 AWB10193 AW178838 AW178837 AW178857 AWB10515 AWB10330 AWB10514 AWB10441 AWB10358 AW178852 AWB10359 AWB10322 AWB10327 AWB10211 AW178835 AWB10635 AWB10288 AWB10263 AWB10325 AWB10443 AWB AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 NB4829 AA084752 AA076512 AA085119 AA085208 AA085045 AW754192 W00554 AWB57797 AW754203 AW754197 AW754193 AWB03357 AWB03423 AWB12233 R06814 AWB08361 AWB08404 AWB08386 AWB08594 AWB08654 AWB08813 AWB08551 AWB08676 AWB08350 AWB08406 AWB08694 AWB08934 AWB08829 AWB08385 AWB08422 AWB08401 AWB08409 AWB08760 AWB08863 AWB08521 AWB08539 AWB08609 AWB08472 AWB08739 AWB08704 AWB08558 AWB08714 AWB08420 AWB AWB48433 AWB46159 AWB46377 AWB46528 AWB50246 AWB50251 AWB50302 AWB51255 AWB51432 AWB50955 AWB984757 AWB984797 AWB984734 AWB984745 BE046680 BE046738 BE044958 BE064415 BE064430 BE064448 BE145899 BE145848 BE145849 BE145853 BE145927 BE145925 Z43062 R13213 H14422 H60457 H68709 H73528 H54335 R87154 AA211586 F35799 AA211641 F29720 AW937387 AW937408 R18085 AA219028 R17712 Z44345 A1217097 AWB86090 W38035 W38792 AA232835 AW936043
65	409189	110687_1	
	410559	1208283_1	
	410790	1221131_1	
	410869	1225123_1	
70			
	411436	1245660_1	
	411518	1248692_1	
	411552	1249255_1	
75	412701	1322288_1	
	412988	1342150_1	
	413081	1348563_1	
	413525	1374635_1	
	416009	1566379_1	
80	416422	1593811_1	
	418059	171879_1	
	418387	174731_1	
	418948	180808_1	

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5	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
	421926	209246_1	AA300591 AW963893 AA300493
	424200	236595_1	AA337221 AA336756 AW966196
	424686	242486_1	AA345504 AA345251 AW963243
	424994	245786_1	AW954525 AI372685 AA349501 AI372687 H10564
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
	432765	353907_1	AJ003429 AJ003367 AA564825
10	433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AJ686466 AJ336390 AW864390 AW864320
	434381	385155_1	AA631834 AA633425 AA632455 AI792312 AI792311
	434589	38929_1	AF147363 T47219 T47218
	434763	392847_1	AA648618 AW974389 H51771
	436295	41733_1	N73895 AJ001872
15	440947	505904_1	AA910403 AI815593 W58361 AW162520 AJ816550
	442481	543588_1	N98828 BE079873 AI110738 AF074645
	445432	63943_1	AV653771 BE089370
	449570	81018_1	AA001793 AA001871
	450317	831956_1	AI692689 R14223 R18395
20	450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
	452462	918580_1	BE173515 BE173560 AI902860
	453682	977454_1	T79703 T96307 AL079725
25	454096	1007449_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	454457	1207274_1	AW753456 AW753036 AW854868 AW854862
	454585	1225852_1	BE069128 BE069023 AW809375
	454665	1228599_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
30	454860	1237732_1	AW835767 AW835537 BE160187
	454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
	455067	1252050_1	AW854538 AW854418 AW854412
	455135	1254729_1	AW857989 AW858016 AW861677 AW861689 AW861691 AW858056
	455276	1272541_1	BE176479 BE176878 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
35	455388	1287904_1	AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
	455490	1297826_1	AW953477 Z41970 F12435 T73989 T09387
	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
	455747	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
40	455772	1363114_1	W28799 BE086078
	455801	1370508_1	BE140643 BE140645 BE140644 BE140657 BE140660 BE140659 BE140661
	456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225080 AA225101
	457374	328758_1	AA493662 AW897396 BE154814

45

TABLE 65C

50	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nt_position:	Indicates nucleotide positions of predicted exons.

55	Pkey	Ref	Strand	Nt_position
	400533	6981826	Minus	277132-277595
	400746	7328328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401459	9212270	Minus	182001-183323
	402145	8018280	Plus	113086-114800
60	402454	7534025	Minus	14826-15803
	402703	8705069	Minus	15335-15500
	403242	7637817	Minus	11297-12511
	403291	7230870	Plus	95177-95435
	403305	8099945	Plus	114632-114805
65	403333	8568833	Minus	124794-124941
	403371	9087278	Plus	106655-106050
	403433	9719611	Minus	72225-72437
	403481	9965004	Plus	93496-93633
	403510	7652047	Plus	61866-62027
70	403667	6850483	Minus	1344-1442,1545-1697
	403805	8140491	Minus	51483-51742,53429-53511
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
	404582	9943965	Minus	39067-39225
75	404848	8248647	Minus	23955-24034,25143-25264
	404967	7523744	Minus	89944-90729
	404995	6006247	Minus	154015-154123
	405264	7329374	Plus	28556-28684
	405321	3419846	Minus	44554-45210
80	405348	2914717	Minus	43310-43462
	405510	7630909	Minus	101028-101174
	405549	1552494	Plus	10878-11048
	405733	9884689	Plus	124832-125051

Table 66A lists about 370 genes up-regulated in BPH compared to prostate cancer and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer and normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" prostate cancer and normal adult tissue level was set to the 85th percentile amongst malignant prostate tissues and normal adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 66A: ABOUT 370 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER AND NORMAL ADULT TISSUES

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of BPH tissue to prostate tumor and normal body tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
410929	H47233	Hs.30643	ESTs	21.1
450693	AW450461	Hs.203965	ESTs	16.7
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	14.2
432473	AI202703	Hs.152414	ESTs	11.3
446336	AW815036	Hs.151251	ESTs	10.9
407275	AI364186		gb:qw34h07.x1 NCI_CGAP_UI4 Homo sapiens	10.7
428134	AA421773	Hs.161008	ESTs	10.2
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	9.8
433466	AA508353	Hs.105314	relaxin 1 (H1)	9.5
415293	R49462	Hs.108541	ESTs	9.1
458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
428927	AA441837	Hs.90250	ESTs	8.6
420345	AW295230	Hs.25231	ESTs	8.5
453387	AI990741	Hs.252809	ESTs	8.2
454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopola	7.5
431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	7.4
400080			Eos Control	7.4
431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
404592			NM_022739: Homo sapiens E3 ubiquitin lig	7.3
420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
438231	AW594539	Hs.155689	ESTs	7.3
410330	AW023630	Hs.159425	ESTs	7.2
449300	AI656959	Hs.346514	ESTs	7.1
449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
426384	AI472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	6.8
454171	AW854832		gb:QV2-CT0261-201099-011-005 CT0261 Homo	6.6
408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.6
421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
424433	H04607	Hs.9218	ESTs	6.5
442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	6.4
425312	AA354940	Hs.145958	ESTs	6.4
426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
440911	AA909536	Hs.143562	ESTs	6.4
400533			ENSP00000209376: PRED65 protein (Fragmen	6.2
418310	AA814100	Hs.86693	ESTs	6.2
403667			Target Exon	6.1
436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
404003			Target Exon	5.9
424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	5.9
438138	R98299	Hs.177502	ESTs	5.9
424940	AA985308	Hs.283902	ESTs	5.8
434485	AI623511	Hs.118567	ESTs	5.8
453200	AA033832	Hs.212433	ESTs	5.7
428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	5.6
443361	AI792628	Hs.133273	ESTs	5.6
421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
439079	AF085937	Hs.38348	ESTs	5.5
430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	5.5
436578	AI091435	Hs.134859	ESTs	5.5
424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
435072	AW592176	Hs.116932	ESTs	5.4
435375	AI733610	Hs.187832	ESTs	5.4
444609	AW571659	Hs.278081	ESTs	5.4
416602	NM_006159	Hs.79389	nel (chicken)-like 2	5.4
433087	AI720686	Hs.152520	ESTs	5.3
439092	AA830149		gb:cc44f08.s1 NCI_CGAP_GC81 Homo sapiens	5.3
437267	AW511443	Hs.258110	ESTs	5.3
441916	AA993571	Hs.129075	ESTs	5.3
452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypothe	5.3

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	423101	M83941	Hs.123642	EphA3	5.3
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	5.2
	415890	H08225	Hs.268712	ESTs	5.2
	454968	AWB49046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
5	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	5.2
10	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	416705	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.1
15	445238	AA883971	Hs.187506	ESTs	5.1
	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	440354	AA889386	Hs.125468	ESTs	5.0
20	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CLIA	5.0
	457374	AA493662		gb:nh05d12.s1 NCL_CGAP_Thy1 Homo sapiens	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	4.9
25	450497	H64159	Hs.15328	ESTs	4.8
	438132	AA907076	Hs.122060	ESTs	4.8
	414818	BE541217	Hs.23606	ESTs	4.8
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.8
	433523	H29882		ESTs	4.8
30	450317	AI692689		gb:wd86g05.x1 NCL_CGAP_Lu24 Homo sapiens	4.8
	443635	AI080230	Hs.134214	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.7
	452843	AI796769	Hs.208320	ESTs	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
35	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
40	405348			C7001664:gi12698061 kbj BAB21849.1 (AB	4.6
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	447058	AI939456	Hs.160870	ESTs	4.6
	428218	AA424266	Hs.123642	EphA3	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
45	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	4.5
	449821	AI671141	Hs.211122	ESTs	4.5
	420905	AA521307	Hs.186651	ESTs	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.4
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	420154	AI093155	Hs.95420	JM27 protein	4.4
55	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	452498	AK000011	Hs.29700	hypothetical protein FLJ20094	4.4
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	433597	AA708205	Hs.100343	ESTs	4.3
60	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	420111	AA255652		gb:zs21h11.r1 NCL_CGAP_GCB1 Homo sapiens	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.2
	433433	AI692623	Hs.121513	Homo sapiens clone Z'3-1 placenta expres	4.2
65	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	420355	AW968263	Hs.123126	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
70	458912	AI911066		ESTs	4.1
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
75	450597	AI701635	Hs.207077	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	445206	AI350199	Hs.269990	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
80	438875	AA827640	Hs.189059	ESTs	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	404967			Target Exon	4.0
	427203	AW629517	Hs.244855	ESTs	4.0

	442338	AI761976	Hs.156080	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypotheH	4.0
5	435136	R27299	Hs.10172	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441735	AW292779	Hs.8182	ESTs	4.0
10	448882	AJ001531	Hs.22404	protease, serine, 12 (neurotrypsin, moto	4.0
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
15	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	3.9
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	3.9
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	Hs.91662	KIAA0888 protein	3.9
20	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	414441	AA234759	Hs.132950	ESTs	3.9
	425810	AI923627	Hs.31903	ESTs	3.9
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	3.9
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
25	440450	AI333129	Hs.156147	ESTs	3.8
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	3.8
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
	416534	H69043	Hs.224981	Homo sapiens cDNA FLJ14368 fis, clone HE	3.8
30	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
35	442447	AA999723	Hs.129607	ESTs	3.8
	403242			Target Exon	3.8
	433908	AW298141	Hs.157975	ESTs	3.8
	454037	AW998716		gb:PM4-BN0067-250300-002-111 BN0067 Homo	3.7
40	432101	AI918950	Hs.123642	EphA3	3.7
	418759	AA227879	Hs.187621	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-403 HT0560 Homo	3.7
	448568	AA149121	Hs.71947	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
45	436345	AA873008	Hs.121572	ESTs	3.7
	446862	AV660697	Hs.282700	ESTs	3.7
	419875	AA853410	Hs.93557	proenkephalin	3.7
	421040	AA715026	Hs.135280	ESTs	3.7
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.7
50	450687	AA495800		gb:czw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	431474	AL133990	Hs.190642	CEGP1 protein	3.7
	448004	AW451477	Hs.257456	ESTs	3.7
	419261	X07876	Hs.89791	wingless-type MMTV Integration site fami	3.7
55	422899	O16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
	440947	AA910403		ESTs	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
60	403481			Target Exon	3.6
	404561			trichorhinophalangeal syndrome I gene (T	3.6
	417565	AI203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	449655	AI021987	Hs.59970	ESTs	3.6
65	450630	AA010429	Hs.191939	ESTs	3.6
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	420026	AI831190	Hs.166576	ESTs	3.6
70	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	3.5
	456373	BE247708	Hs.89751	membrane-spanning 4-domains, subfamily A	3.5
75	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13448 fis, clone PL	3.5
	401132			C120005177:gil4758712[ref]NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
	434763	AA848618		gb:ns07a11.r1 NCI_CGAP_Ew1 Homo sapiens	3.5
80	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	3.5
	403510			Target Exon	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5

	430865	AI073424	Hs.5232	HSPC125 protein	3.5
	444800	AW119071	Hs.153287	ESTs	3.5
	428647	AA830050	Hs.124344	ESTs	3.5
5	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.5
	429643	AA458889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	430124	AW204994	Hs.253450	ESTs	3.4
	430701	AI760833	Hs.293971	ESTs	3.4
10	436714	AA728964	Hs.293399	ESTs	3.4
	404848			ENSP00000240769:BG15303.1 (similar to C	3.4
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	3.4
15	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
20	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	405510			ENSP00000233779: Hypothetical 68.0 kDa p	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
25	419964	AA811657	Hs.220913	ESTs	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.4
	430829	AW451999	Hs.194024	ESTs	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
30	433628	AI821784	Hs.188578	ESTs	3.4
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.4
	427235	AI126288	Hs.192232	ESTs	3.4
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.4
35	428923	BE047698	Hs.188785	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
40	450003	AA777809	Hs.191995	ESTs	3.4
	448108	AW300021	Hs.170685	ESTs	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
45	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	432229	AW290876	Hs.143587	ESTs	3.3
	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-006 BT0532 Homo	3.3
50	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.3
	416662	T25853	Hs.7538	ESTs	3.3
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	3.3
55	428715	AW293716	Hs.53126	ESTs	3.3
	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	434497	AI821803	Hs.136580	ESTs	3.2
60	439306	BE220199		WD40 protein C1a01	3.2
	420608	BE548277	Hs.103104	ESTs	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
65	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	3.2
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.2
	402145			Target Exon	3.2
	448131	AI675054	Hs.200481	ESTs	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
70	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	447183	AI554733	Hs.173182	ESTs	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
	415467	R60891	Hs.260274	ESTs	3.2
75	434408	AI031771	Hs.132586	ESTs	3.2
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi p	3.2
	453789	AA628517	Hs.118502	ESTs	3.2
	412656	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
80	419088	AI538323	Hs.52620	integrin, beta 8	3.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
	448044	AI458682		gb:tk13e01.x1 NCL_CGAP_Lu24 Homo sapiens	3.2
	454565	AW812856		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	3.1

	405321		Target Exon	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th
	434512	AW139932	Hs.188941	ESTs
5	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-
	433444	AW975324	Hs.129816	ESTs
	410821	A1114811	Hs.92526	ESTs, Weakly similar to T00365 hypothet
	415861	Z43123	Hs.144513	ESTs
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174
10	432527	AW975028	Hs.102754	ESTs
	427773	AA412290	Hs.98124	ESTs
	441817	AW969706	Hs.293332	ESTs
	416812	H91010	Hs.44940	ESTs
	417958	AA767382	Hs.193417	ESTs
15	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL
	416423	H54375	Hs.268921	ESTs
	418037	A1990212	Hs.86447	ESTs
	419197	N48921	Hs.27441	KIAA1615 protein
	420179	N74530	Hs.21168	ESTs
20	436295	N73895		gb:za52006.s1 Soares fetal liver spleen
	405548			Target Exon
	423595	R82826	Hs.220702	ESTs
	412533	AA679863	Hs.69606	ESTs
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds
25	405264			NM_030813:Homo sapiens suppressor of po
	410869	AW808361		gb:MR1-ST0111-111099-003-04 ST0111 Homo
	425354	U62027	Hs.155935	complement component 3a receptor 1
	441492	A1149998	Hs.146346	ESTs
	447078	AW885727	Hs.9914	ESTs
30	435021	AA922192	Hs.54709	ESTs
	408832	AW085890	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC
	450580	N40087		ESTs
	432319	AW510770	Hs.128386	ESTs
	453713	R20640	Hs.79133	cadherin 8, type 2
35	445784	A1253155	Hs.146065	ESTs
	416642	T96118	Hs.226313	ESTs
	418948	A1217097		gb:xd43h07.x1 Soares_fetal_heart_NbHH19W
	433796	AA810867	Hs.186997	ESTs
	439182	AF086030	Hs.21621	hypothetical protein DKFZp762C0076
40	404995			ENSP00000251890*:Monocytic leukemia zinc
	444794	A1419991	Hs.145225	ESTs
	443634	H73972	Hs.134460	ESTs
	420133	AA426117	Hs.155543	ESTs
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197
45	426743	AA383833	Hs.245022	ESTs
	442326	H92962	Hs.124813	hypothetical protein MGC14817
	449913	AA004696	Hs.333016	ESTs
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo
	419622	AA452054	Hs.119338	ESTs
50	449745	A1668593		gb:y138a05.x5 Soares breast 3NbHBst Homo
	428412	AA428240	Hs.126083	ESTs
	428200	A1039624	Hs.98388	ESTs
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600
	431869	AA521136	Hs.190176	ESTs
55	451391	AA017410	Hs.40568	ESTs
	452959	A1933416	Hs.189674	ESTs

TABLE 66B

60	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
<hr/>			
65	Pkey _i	CAT Number	Accession
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
	410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
70	411436	1245660_1	AW846433 AW846159 AW846377 AW846528
	411479	1247077_1	AW846047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
	412988	1342150_1	BE046680 BE046738 BE044958
	413081	1348563_1	BE064415 BE064430 BE064448
75	413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
	416009	1566379_1	Z43062 R13213 H14422
	418948	180808_1	A1217097 AW860509 W38035 W38792 AA232835 AW936043
	420111	190755_1	AA255652 AA280911 AW967920 AA262684
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 A1580388 BE071923 R36280
80	424200	236595_1	AA337221 AA336756 AW966196
	424994	245786_1	AW954525 A1372685 AA349501 A1372687 H10564
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912

	428342	290035_2	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438
			AI092404 AI085630 AA731340
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
5	432765	353907_1	AJ003429 AJ003367 AA564825
	433523	368873_1	H28682 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
	434763	392847_1	AA648618 AW974389 H51771
	436295	41733_1	N73895 AJ001872
	439092	468554_1	AA830149 AW978407 M85983 AW503637
10	439306	47088_1	BE220199 W01813 AF086118 N70760 BE221405
	440947	505904_1	AA910403 AI815593 W58361 AW162520 AI816550
	442481	543588_1	N99828 BE079873 AI110738 AF074645
	445432	63943_1	AV653771 BE089370
	448044	747196_1	AI458682 H24240 R14537 R18426 AW867082
	449570	81018_1	AA001793 AA001871
15	449745	814534_1	AI688593 AI820774 R86205 H39971 H22177 H26241
	450317	831956_1	AI692689 R14223 R18395
	450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
			AW816892 AW816941 AW816578 AA029183 T83320 H66850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023805 AW022095
			AA164518 AA730973 W00417 W65303
20	450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
	452462	918580_1	BE173515 BE173560 AI902860
	453682	977454_1	T79703 T96307 AL079725
	454037	996287_1	AW998716 AW022148 N68020
25	454096	1007449_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	454457	1207274_1	AW753456 AW753036 AW854868 AW854862
	454665	1228599_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
	454860	1237732_1	AW835767 AW835537 BE160187
30	454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
	455067	1252050_1	AW854538 AW854418 AW854412
	455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
35	457374	328758_1	AA493662 AW897396 BE154814
	458912	823104_1	AI911066 AI933734 AI680888 AJ003599

TABLE 66C

40	Key:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
45	NI_positon:	Indicates nucleotide positions of predicted exons.

	Play	Ref	Strand	NI_positon
	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
50	401132	8705350	Minus	85679-85795
	402145	8018280	Plus	113088-114800
	403242	7637817	Minus	11297-12511
	403481	9965004	Plus	93496-93633
	403510	7652047	Plus	61866-62027
55	403667	6850483	Minus	1344-1442,1545-1697
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
	404592	9943965	Minus	39067-39225
	404848	8248647	Minus	23965-24034,25143-25264
60	404987	7523744	Minus	89944-90729
	404995	6006247	Minus	154015-154123
	405264	7329374	Plus	28556-28684
	405321	3419846	Minus	44654-45210
	405348	2914717	Minus	43310-43462
65	405510	7630909	Minus	101028-101174
	405548	1532158	Plus	11552-11686

70 TABLE 67A: 689 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

75 Table 67A lists about 689 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 689 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

80	Key:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigene number
	Unigene Title:	Unigene gene title
	R1:	Ratio of tumor to normal body tissue

	Pkey	ExAcon	UnigeneID	Unigene Title	R1
5	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	73.2
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	65.0
	432441	AW292425	Hs.163484	ESTs	56.0
	446057	AI420227	Hs.149358	Trp-p8 transient receptor potential cati	55.0
	400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	48.1
10	414569	AF109298	Hs.118258	prostate cancer associated protein 1	41.4
	432240	AI894767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	40.3
	419526	AI821895	Hs.193481	ESTs	35.9
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	35.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
15	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	33.9
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	32.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	32.6
	400292	AA250737	Hs.72472	BMP-R1B	28.8
	400287	S39329	Hs.181350	kallikrein 2, prostatic	28.8
20	425075	AA506324	Hs.1852	acid phosphatase, prostate	28.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.8
	415539	AI733881	Hs.72472	BMP-R1B	27.0
	428819	AL135623	Hs.193914	KIAA0575 gene product	25.7
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	25.5
25	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	24.8
	407168	R45175	Hs.117183	ESTs	24.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	23.6
	428336	AA503115	Hs.183752	microseminoprotein, beta-	23.5
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	23.4
30	403047			NM_005656*:Homo sapiens transmembrane pr	23.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	22.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	21.6
	407709	AA456135	Hs.23023	ESTs	21.5
	401424			NM_001172:Homo sapiens arginase, type II	20.6
35	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	19.7
	434666	AF151103	Hs.112259	T cell receptor gamma locus	18.5
	415989	AI267700		ESTs	17.9
	437052	AA881697	Hs.120591	ESTs	17.8
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	16.8
40	431548	AI834273	Hs.9711	novel protein	16.6
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	16.5
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	16.5
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	16.5
	413597	AW302885	Hs.117183	ESTs	16.1
45	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	15.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	15.3
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	15.3
	407122	H20276	Hs.31742	ESTs	15.1
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	14.1
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	13.9
	426501	AW043782	Hs.293616	ESTs	13.9
	428898	AB033070	Hs.194408	KIAA1244 protein	13.7
	418961	AW957646	Hs.23023	ESTs	13.3
	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	13.2
55	418848	AI820961	Hs.193465	ESTs	13.1
	428398	AI249368	Hs.98558	ESTs	13.0
	429220	AW207206		ESTs	12.7
	401451			NM_004496*:Homo sapiens hepatocyte nucle	12.4
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	12.4
60	419078	M93119	Hs.89584	Insulinoma-associated 1	12.3
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.9
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.4
	429918	AW873986	Hs.119383	ESTs	11.3
65	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	412446	AI768015		ESTs	11.1
	433404	T32982		ESTs	10.9
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	10.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	10.6
70	444151	AW972917	Hs.126749	alpha-methylacyl-CoA racemase	10.4
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	10.3
	418278	AI088489	Hs.83937	hypothetical protein	10.3
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	10.2
	433927	AI557019	Hs.116467	small nuclear protein PRAC	10.2
75	408000	L11690	Hs.198689	bulbous pemphigoid antigen 1 (230/240kD)	10.1
	449625	NM_014253		odc (odd Oz/ten-m, Drosophila) homolog 1	10.1
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	10.0
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothe	9.8
	437718	AI927288	Hs.196779	ESTs	9.8
80	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	9.7
	453160	AI263307		H2B histone family, member L	9.7
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	9.7
	450325	AI935962	Hs.91973	ESTs	9.6
	434170	AA626509	Hs.122329	ESTs	9.6
	428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	9.6

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	447033	AI357412	Hs.157601	ESTs	9.5
	401747			Homo sapiens keratin 17 (KRT17)	9.3
	434423	NM_006769	Hs.3844	LIM domain only 4	9.3
5	411887	AW182924	Hs.128790	ESTs	9.2
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	9.2
	415263	AA948033	Hs.130853	ESTs	9.2
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	9.2
	421896	N62293	Hs.45107	ESTs	9.1
10	432101	AI918950	Hs.123642	EphA3	9.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.0
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	8.9
	420218	AW958037		ribosomal protein L4	8.8
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.6
15	424692	AA429834	Hs.151791	KIAA0092 gene product	8.6
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	8.6
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	8.5
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	8.5
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	8.5
20	416182	NM_004354	Hs.79069	cyclin G2	8.5
	431542	H63010	Hs.5740	ESTs	8.4
	447397	BE247676	Hs.18442	E-1 enzyme	8.3
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypothe	8.1
	456660	AA909249	Hs.112262	solute carrier family 30 (zinc transport	8.1
25	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	8.1
	451684	AF216751	Hs.26813	CDA14	8.1
	437124	AA554458		KIAA0686 protein	8.0
	416239	AL038450	Hs.48948	ESTs	8.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.9
30	424800	AL035588	Hs.153203	MyoD family inhibitor	7.9
	428728	NM_016625	Hs.191381	hypothetical protein	7.9
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.8
	442049	AA310393	Hs.190044	ESTs	7.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.8
35	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	7.7
	443180	R15875	Hs.258576	claudin 12	7.5
	433285	AW975944	Hs.237396	ESTs	7.5
	410870	U81599	Hs.66731	homeo box B13	7.4
	418836	AI655499	Hs.161712	ESTs	7.4
40	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	7.3
	431992	NM_002742	Hs.2891	protein kinase C, mu	7.3
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	7.3
	432586	AA568548		ESTs	7.3
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	7.3
45	435047	AA454985	Hs.54973	cadherin-like protein VR20	7.3
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypothe	7.2
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.2
	426108	AA622037	Hs.166468	programmed cell death 5	7.1
	433323	AA805132	Hs.159142	ESTs	7.1
50	423349	AF010258	Hs.127428	homeo box A9	7.0
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	6.9
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	6.9
	438869	AF075009		gb:Homo sapiens full length insert cDNA	6.9
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	6.8
55	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.8
	418601	AA279490	Hs.86368	calmegin	6.8
	429769	NM_004917	Hs.218366	kalikrein 4 (protease, enamel matrix, p	6.8
	436962	AW377314	Hs.5364	DKFZP564I052 protein	6.8
	425465	L18964	Hs.1904	protein kinase C, iota	6.6
	450377	AB033091		KIAA1265 protein	6.6
60	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	6.6
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isof	6.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (6.5
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	6.5
65	440774	AI420811	Hs.153934	ESTs	6.5
	413992	W26276	Hs.136075	RNA, U2 small nuclear	6.4
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	6.4
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.4
70	451027	AW519204	Hs.40808	ESTs	6.4
	436063	AK000028		ribosomal protein S24	6.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	6.3
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.2
75	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	6.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	6.2
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (tr	6.1
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (tr	6.1
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	6.1
80	448045	AJ297436	Hs.20166	prostate stem cell antigen	6.0
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	6.0
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.0
	433517	AW022133	Hs.189838	ESTs	6.0
	424036	AA770688		H2A histone family, member L	5.9

	420092	AA814043	Hs.88045	ESTs	5.9
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.8
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	5.8
5	441866	BE464341	Hs.21201	nectin 3; DKFZP56680846 protein	5.8
	450244	AA007534	Hs.125062	ESTs	5.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.7
	451952	AL120173	Hs.301663	ESTs	5.7
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	5.7
10	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-4	5.7
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.7
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24395 hypothet	5.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	5.7
	415621	AJ648602	Hs.55468	ESTs	5.7
15	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.6
	433332	AJ367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.5
	455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	5.5
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	5.4
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.4
20	425211	M18667	Hs.1867	progastriclin (pepsinogen C)	5.4
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	5.4
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	5.4
	410762	AF226053	Hs.66170	HSKM-B protein	5.4
	440594	AW445167	Hs.126036	ESTs	5.4
25	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	5.3
	447805	AW627932	Hs.302421	gemin4	5.3
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	5.3
	453308	AW959731	Hs.323099	ESTs	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
30	418555	AJ417215	Hs.87159	hypothetical protein FLJ12577	5.2
	404632			NM_022490:Homo sapiens hypothetical prot	5.1
	450861	AJ523898	Hs.17617	ESTs	5.1
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.1
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.1
35	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.1
	410037	AB020725	Hs.58009	KIAA0918 protein	5.1
	410240	AL157424	Hs.61289	synaptotagmin 2	5.0
	403046			NM_005656:Homo sapiens transmembrane pr	5.0
	419647	AA348947	Hs.91816	hypothetical protein	5.0
40	450203	AF097994		L-kynurenine/alpha-aminoadipate aminotra	5.0
	450164	AJ239923	Hs.63931	ESTs	5.0
	417318	AW953937	Hs.240845	ESTs	4.9
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.9
	412350	AJ659306	Hs.73826	protein tyrosine phosphatase, non-recept	4.9
45	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	4.9
	433852	AJ378329	Hs.126629	ESTs	4.9
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.9
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.8
50	441021	AW578716	Hs.7644	H1 histone family, member 2	4.8
	453171	R76472	Hs.65646	ESTs	4.8
	416795	AJ497778	Hs.20509	HBV pX associated protein-8	4.8
	427815	BE410107	Hs.179817	CGI-82 protein, PSDR1	4.8
	419440	AB020689	Hs.90419	KIAA0882 protein	4.8
55	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.8
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	4.8
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	4.7
60	431724	AA514535	Hs.283704	ESTs	4.7
	423242	AL039402	Hs.125783	DEME-6 protein	4.7
	434485	AJ623511	Hs.118567	ESTs	4.7
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	4.6
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	4.6
65	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	4.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	4.6
	439735	AJ635386	Hs.142846	hypothetical protein	4.6
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	4.6
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	4.5
70	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	4.5
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	4.5
	426006	R49031	Hs.22627	ESTs	4.5
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	4.5
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JCS238 galactosy	4.5
75	409799	D11928	Hs.76845	phosphoserine phosphatase-like	4.5
	423583	AL122055	Hs.129836	KIAA1028 protein	4.4
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	4.4
	451468	AW503398	Hs.293653	ESTs, Moderately similar to I38022 hypot	4.4
80	429467	NM_004477	Hs.203772	F5HD region gene 1	4.4
	451752	AB032997		KIAA1171 protein	4.3
	430294	AJ538226	Hs.32976	guanine nucleotide binding protein 4	4.3
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.3
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.3

5	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.3
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.3
	427308	D26067	Hs.174905	KIAA0033 protein	4.3
	435706	W31254	Hs.7045	GL004 protein	4.2
	416854	H40164	Hs.80296	Purkinje cell protein 4	4.2
10	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	4.2
	410076	T05387	Hs.7991	ESTs	4.2
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.2
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.2
	442501	AA315267	Hs.23128	ESTs	4.2
15	436761	AI817776	Hs.236557	ESTs	4.2
	420380	AA640891	Hs.102406	ESTs	4.2
	436556	AI364997	Hs.7572	ESTs	4.2
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	4.2
	446416	AV658299	Hs.163959	ESTs	4.2
20	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	4.1
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.1
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	4.1
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.1
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.1
25	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	4.1
	408418	AW963897	Hs.44743	KIAA1435 protein	4.1
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.1
	432363	AA534489		gbnf76g11.s1 NCL CGAP_Co3 Homo sapiens	4.0
	447574	AF162666	Hs.18895	tousled-like kinase 1	4.0
30	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.0
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.0
	444108	R55784	Hs.140942	ESTs	4.0
	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.0
	417379	AA196390		gbzpp99b10.s1 Stratagene muscle 937209 H	4.0
35	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	4.0
	418821	AA436002	Hs.183161	ESTs	4.0
	438825	BE327427	Hs.79953	ESTs	4.0
	433233	AB040927	Hs.301804	KIAA1494 protein	4.0
40	415276	U88666	Hs.78353	SFRS protein kinase 2	4.0
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.0
	407819	R42185		ESTs	4.0
	450402	BE218027	Hs.89969	ESTs	4.0
	432527	AW975028	Hs.102754	ESTs	3.9
45	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	3.9
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	3.9
	432435	BE218886	Hs.282070	ESTs	3.9
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.9
	436420	AA443966	Hs.31595	ESTs	3.9
50	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	3.9
	411031	W37943	Hs.34892	KIAA1323 protein	3.9
	429259	AA420450	Hs.292911	Plakophilin	3.9
	407813	AL120247	Hs.40109	KIAA0872 protein	3.9
	417057	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.9
55	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	3.9
	417958	AA767382	Hs.193417	ESTs	3.9
	427176	AW381569	Hs.40334	ESTs	3.8
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	3.8
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.8
60	432675	AI791855		ESTs	3.8
	419713	AW958058	Hs.92381	nudix (nucleoside diphosphate linked mol	3.8
	427479	BE410092	Hs.178471	KIAA0798 gene product	3.8
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.8
	413950	AA249096	Hs.32793	ESTs	3.8
65	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.8
	419083	AA79560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	3.8
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	3.8
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	3.8
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	3.8
70	447620	AW290951		ESTs	3.8
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.8
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.8
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	3.8
	459284	AF155660	Hs.300496	mitochondrial solute carrier	3.7
75	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	3.7
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	3.7
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	3.7
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.7
80	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	3.7
	453469	AB014533	Hs.33010	KIAA0633 protein	3.7
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	3.7
	422072	AB018255	Hs.111138	KIAA0712 gene product	3.7
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
	420522	AW957137	Hs.98541	hypothetical protein	3.6
	408833	AW612232	Hs.254835	ESTs	3.6
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.6

5	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.6
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	3.6
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.6
	422424	AI185431	Hs.296638	prostate differentiation factor	3.6
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.6
10	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.6
	421687	AW161450	Hs.109201	CGI-86 protein	3.6
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.6
	412520	AA442324	Hs.795	H2A histone family, member O	3.6
	436476	AA326108	Hs.33829	bHLH protein DEC2	3.6
15	441224	AU076964	Hs.7753	calumenin	3.5
	404922			NM_003071:Homo sapiens SWI/SNF related,	3.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.5
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	3.5
	429686	AI871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.5
20	408001	AA046458	Hs.95296	ESTs	3.5
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.5
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.5
	428055	AA420564	Hs.101760	ESTs	3.5
	418827	BE327311	Hs.47166	HT021	3.5
25	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.5
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (nls	3.5
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.5
	409151	AA306105		SEC22, vesicle trafficking protein (S. c	3.5
	439671	AW162840	Hs.6641	kinesin family member 5C	3.4
30	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.4
	443884	N20617	Hs.194397	leptin receptor	3.4
	403752			NM_002753*:Homo sapiens mitogen-activate	3.4
35	427723	AI355260	Hs.279789	histone deacetylase 3	3.4
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	3.4
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.4
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.4
	433647	AA603367	Hs.222294	ESTs	3.4
40	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	427715	BE245274	Hs.180428	KIAA1181 protein	3.3
	437617	AI026701	Hs.5716	KIAA0310 gene product	3.3
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.3
45	414407	AA147026	Hs.76704	ESTs	3.3
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.3
	435655	AW105663	Hs.6947	HSPC069 protein	3.3
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.3
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	3.3
50	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.3
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3.3
	420568	F09247	Hs.247735	protocadherin alpha 10	3.3
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	3.3
55	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	3.3
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.3
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	3.3
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.3
	409960	BE261944		hexokinase 1	3.3
60	433891	AA613792		gb:nc97h03.s1 NCI_CGAP_P2 Homo sapiens	3.3
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.3
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3
	419972	AL041465	Hs.182982	golgin-67	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
65	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.3
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.3
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.3
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.3
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.3
70	414922	D00723		glycine cleavage system protein H (amino	3.3
	437898	W81260	Hs.43410	ESTs	3.2
	426126	AL118747	Hs.26691	ESTs	3.2
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPUC	3.2
	450649	NM_001429	Hs.25272	E1A binding protein p300	3.2
75	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.2
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.2
	401519			C15000476:gil12737279[refXP_012163.1]	3.2
	419517	AF052107	Hs.90797	Homo sapiens clone Z3620 mRNA sequence	3.2
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	3.2
80	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.2
	453288	AW583292	Hs.274412	similar to yeast Upr3, variant A	3.2
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.2
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.2
	439593	BE073597	Hs.124863	ESTs	3.2
	451945	BE504055	Hs.211420	ESTs	3.2
	434614	AI249502	Hs.29669	ESTs	3.2
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.2

	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	3.2
	408101	AW968504	Hs.123073	CDG2-related protein kinase 7	3.2
	425810	AI923627	Hs.31903	ESTs	3.2
5	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.2
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.2
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.1
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.1
	436087	BE300296	Hs.5054	CGI-133 protein	3.1
10	414222	AL135173		sorbitol dehydrogenase	3.1
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.1
	418559	AA225048	Hs.104207	ESTs	3.1
	408784	AW971350	Hs.63386	ESTs	3.1
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.1
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.1
15	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.1
	436489	AJ272269	Hs.121429	zinc-binding protein Rboc728	3.1
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	3.1
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.1
20	445943	AW898533	Hs.181574	ESTs	3.1
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.1
	432426	AW973152	Hs.31050	ESTs	3.1
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.1
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.1
25	423453	AW450737	Hs.128791	CGI-09 protein	3.1
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.1
	436278	BE396290	Hs.5097	synaptogyrin 2	3.1
	432908	AI861896		ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.1
30	438705	AI049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.1
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.1
	409757	NM_001898	Hs.123114	cystatin SN	3.1
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.1
35	434293	NM_004445	Hs.3795	EphB6	3.1
	410001	AB041036	Hs.57771	kallikrein 11	3.1
	434970	AW272262	Hs.225767	ESTs	3.1
	432800	BE391046	Hs.278962	AIM-1 protein	3.1
	423392	AA195037	Hs.169341	HTPAP protein	3.1
40	432205	AI806583	Hs.125291	ESTs	3.1
	448807	AI571940	Hs.7549	ESTs	3.1
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.0
	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
45	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.0
	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypothi	3.0
	429638	AI916662	Hs.211577	kinesin 1 (kinesin receptor)	3.0
	452908	AB001451	Hs.30865	neuronal Shc adaptor homolog	3.0
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.0
50	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.0
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.0
	418610	AW245893	Hs.223394	hypothetical protein MGC2742	3.0
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.0
	433556	W58321	Hs.111460	calcium/calmodulin-dependent protein kin	3.0
55	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.0
	449459	BE546846	Hs.195048	ESTs	3.0
	438523	H66220	Hs.278177	ESTs	3.0
	434263	N34895	Hs.44648	ESTs	3.0
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.0
60	408681	AW953853	Hs.292833	ESTs, Weakly similar to I38022 hypothi	3.0
	429866	BE081342	Hs.283037	HSPC039 protein	3.0
	412652	AI801777		ESTs	3.0
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	3.0
	450832	AW970602	Hs.105421	ESTs	3.0
65	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypothi	3.0
	436032	AA150797	Hs.109276	latexin protein	3.0
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.0
	421674	T10707	Hs.298355	hypothetical protein FLJ23138	2.9
	432302	AA345857	Hs.274307	KIAA1442 protein	2.9
70	415172	AF079529	Hs.78105	phosphodiesterase 8B	2.9
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	2.9
	413142	M81740	Hs.75212	ornithine decarboxylase 1	2.9
	437179	AA393508		serologically defined colon cancer antig	2.9
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	2.9
75	439609	AW971945	Hs.293236	ESTs	2.9
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	2.9
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	2.9
	408340	BE174629	Hs.321130	hypothetical protein MGC2771	2.9
	420061	AW024937	Hs.29410	ESTs	2.9
80	431663	NM_016569	Hs.267182	TBX3-iso protein	2.9
	417622	AW298163	Hs.82318	WAS protein family, member 3	2.9
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	2.9
	446791	AI632278	Hs.195922	ESTs	2.9
	433313	W20128	Hs.296039	ESTs	2.9

	428465	AW970976	Hs.293653	ESTs	2.9
	457489	AI693815	Hs.127179	cryptic gene	2.9
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.9
5	446880	AI811807	Hs.108846	Homo sapiens cDNA FLJ14934 fis, clone PL	2.9
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PCA259 feml	2.9
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.9
	413125	BE244589	Hs.75207	glyoxalase I	2.9
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	2.9
10	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	2.9
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.9
	437286	AA350994	Hs.20281	KIAA1700	2.9
	421254	AK001724	Hs.102950	coat protein gamma-coo	2.9
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	2.9
	423551	AA327598	Hs.89633	ESTs	2.9
15	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	2.9
	410193	AJ132592	Hs.59757	zinc finger protein 281	2.9
	435854	AJ278120	Hs.4596	putative ankyrin-repeat containing prote	2.9
	423396	AI382555	Hs.127950	bromodomain-containing 1	2.8
20	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	2.8
	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	2.8
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	2.8
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.8
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	2.8
25	418166	AI754416		Cdc42 effector protein 3	2.8
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.8
	413550	W03011	Hs.306881	MSTP043 protein	2.8
	426170	BE181065	Hs.167531	methylcrotonyl-Coenzyme A carboxylase 2	2.8
	444101	R19175	Hs.169793	ribosomal protein L32	2.8
30	425320	U29344	Hs.83180	fatty acid synthase	2.8
	431631	AA548906	Hs.122244	ESTs	2.8
	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	2.8
	431416	AA532718		ESTs	2.8
	447881	BE620886		GCN1 (general control of amino-acid synt	2.8
35	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	2.8
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	2.8
	439778	AL109729	Hs.99354	putative transmembrane protein	2.8
	425010	T16837	Hs.4241	ESTs	2.8
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.8
40	450546	AA010200	Hs.175551	ESTs	2.7
	431674	AA098901	Hs.301642	G-protein coupled receptor	2.7
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.7
	443181	AI039201	Hs.283316	ESTs	2.7
	448913	AA194422	Hs.22564	myosin VI	2.7
45	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	2.7
	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulfa	2.7
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	2.7
	411190	AA306342	Hs.69171	protein kinase C-like 2	2.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	2.7
50	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	2.7
	434747	AA837085		ESTs	2.7
	428171	AA489323	Hs.182825	ribosomal protein L35	2.7
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	2.7
55	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	2.7
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.7
	407748	AL079409	Hs.38176	KIAA0506 protein; SCN Circadian Oscillat	2.7
	445596	R89543	Hs.12942	vesicle trafficking protein	2.7
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.7
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	2.7
60	438157	AW137011	Hs.49576	ESTs	2.7
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	2.7
	409648	AW451449	Hs.57749	ESTs	2.7
	401866			Target Exon	2.7
	400301	X03635	Hs.1657	estrogen receptor 1	2.7
65	453390	AA862496	Hs.28482	ESTs	2.7
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.7
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.7
	405387			NM_022170*:Homo sapiens Williams-Beuren	2.7
70	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.7
	432388	X15218	Hs.2969	v-eld avian sarcoma viral oncogene homol	2.7
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	2.7
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	2.7
	445098	AL050272	Hs.12305	DKFZP566B183 protein	2.7
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.7
75	409650	T08490	Hs.288969	HSCARG protein	2.7
	452707	AI093823	Hs.45070	ESTs	2.7
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.7
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	2.7
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	2.7
80	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.7
	406627	T64904	Hs.163780	ESTs	2.7
	442315	AA173992	Hs.7856	ESTs, Moderately similar to ZN91_HUMAN Z	2.7
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.6
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.6

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	440695	AW088363	Hs.246240	ESTs	2.6
	416941	BE000150	Hs.48778	nitban protein	2.6
	422717	AI557623	Hs.119475	cold inducible RNA-binding protein	2.6
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	2.6
5	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.6
	401197			ENSP00000229263*:HSPC213.	2.6
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	2.6
	410297	AA148710		lumican	2.6
10	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.6
	437546	AW074836	Hs.173984	T-box 1	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.6
	408157	AA047685	Hs.62946	ESTs	2.6
15	420805	L10333	Hs.99947	reticulin 1	2.6
	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.6
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp566L2022 (f	2.6
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	2.6
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	2.6
20	425174	D87450	Hs.154978	KIAA0261 protein	2.6
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.6
	413435	X51405	Hs.75360	carboxypeptidase E	2.6
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	2.6
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.6
25	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 knueppel-	2.6
	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.6
	406670	W79632	Hs.256301	hypothetical protein MGC13170	2.6
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.6
	429922	Z97630	Hs.226117	H1 histone family, member 0	2.6
30	449518	BE395253	Hs.30861	ESTs	2.6
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.6
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.6
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.6
	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.6
35	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 poly	2.6
	434672	AW284020	Hs.117721	ESTs	2.6
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.6
	452576	AB023177	Hs.29900	KIAA0960 protein	2.6
40	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor t	2.6
	430375	AW371048	Hs.93758	H4 histone family, member H	2.6
	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.6
	424339	BE257148		endoglycan	2.6
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	2.6
45	451040	AA324743	Hs.40808	ESTs	2.6
	445636	AW105401		ribosomal protein L29	2.6
	419175	AW270037		KIAA0779 protein	2.6
	422000	M30599	Hs.110637	homeo box A10	2.6
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.6
50	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	2.5
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	2.5
	406789	AI041403		ribosomal protein L29	2.5
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.5
55	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.5
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.5
	436165	AI373544	Hs.331328	intermediate filament protein syncollin	2.5
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.5
	452827	AI571835	Hs.55468	ESTs	2.5
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.5
60	431108	AA991508	Hs.105317	ESTs	2.5
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.5
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	2.5
	439664	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	2.5
	438821	AA826425	Hs.192375	ESTs	2.5
65	421091	W22821		ribosomal protein L26	2.5
	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.5
	400263			Eos Control	2.5
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti	2.5
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.5
70	431615	AW295859	Hs.235860	ESTs	2.5
	433037	NM_014158	Hs.279938	HSPC087 protein	2.5
	408504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.5
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.5
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	2.5
	450628	AW382884	Hs.204715	ESTs	2.5
75	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.5
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.5
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.5
	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.5
	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.5
80	416737	AF154335	Hs.79691	LIM domain protein	2.5
	414869	AA157291	Hs.21479	ubiquitin 1	2.5
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.5
	403532			NM_024638:Homo sapiens hypothetical prot	2.5

5	418649	AI095485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.5
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypophelli	2.5
	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibitor	2.5
	414556	AW975063	Hs.343443	ribosomal protein L36	2.5
	446911	N27605	Hs.16492	OKFZP564G2022 protein	2.5
	435126	AI393666	Hs.42315	p10-binding protein	2.5
	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.5
	426788	U86615	Hs.172280	SWVSNF related, matrix associated, acti	2.5
10	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	2.5
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.5
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fls, clone NT	2.5
	443837	AI984625	Hs.9884	spindle pole body protein	2.5
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	2.5
15	435021	AA922192	Hs.73962	ESTs	2.5
	435750	AB029012	Hs.4990	KIAA1089 protein	2.5
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeast	2.5
	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.5
	425976	C75094	Hs.334514	NG22 protein	2.5
20	449458	AI805078	Hs.208261	ESTs	2.5
	428013	AF151020	Hs.181444	hypothetical protein	2.5
	424369	R87622	Hs.26714	KIAA1831 protein	2.5
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.5
	452779	AA418775	Hs.47234	ESTs	2.5
25	433586	T85301	Hs.194397	gbyd78d06.s1 Soares fetal liver spleen	2.5
	438682	AA354489	Hs.222103	EBP50-PDZ Interactor of 64 kD	2.5
	427515	T79526	Hs.179516	Integral type I protein	2.5
	418700	AI983808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	2.5

TABLE 67B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

35	Pkey	CAT Number	Accession
	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236
40	429220	15103_7	AW341473 AA448195 AW207206 AI951341 AA969259
	412446	63467_1	BC021735 AI669212 AL120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 BI035538 BF908052 BF908057 BF900026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721 AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815
45	433404	7392_1	BC022980 BF224081 BG149908 AW672842 BE670687 AI702161 AW341832 BE222503 N71836 AI026061 AW953116 AW083132 AI979261 AV725377 AI423298 AI640707 AW675518 AI032611 AI818044 AI299508 AI911386 AI270418 BE219257 BM141826 AA826491 Z25159 AA587421 N59447 Z39436 T32982 R54110 BF115783 F09044 BF808433
	449625	249224_1	BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360
50	453160	6028_5	BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H07775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R08336
	420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI585211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
55	437124	59408_1	AL050013 BG939500 AW969191 AA769925 AI377973 AI625545 AA811365 AA521114 N24705 AI379579 AA424899 AI684671 AA29715 AI453010 N35401 AA677452 AA504340 AI209149 AA838754 AI379062 AI084455 AI280147 AA644327 BF432508 H27873 N47364 N34880 AI147024 T86860 AI219716 AA960926 H25544 BI857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AI292318 AA829888 N95742 AI218758 H25588 N36282 AA024987 N36687 BI919187 N49471 AA889970 AW166152 AA468546 AI262504 AI452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AI016509 AW663972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108636 N49381 R49886 D61278 BI756612 AA508234 R49885 BF850422
60	432586	6633_1	BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548
	438869	52134_1	AF075009 R63109 R63068
	450377	12109_1	AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 AI679751 AI873695 BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AI857643 AI768486 AW512118 AA479302 AW770384 AW072470 AI041596 AI049699 AW592885 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699 AL050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 BI038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AAD43474 AI351615 AI969490 AI910763 R50866 AI699181 N73808 H08164
65	436063	5483_1	AK000028 AA494483 AI288674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593
70	428342	6712_1	AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 AI332765 AW500888 AW576558 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 HA5700 AA761333 AW265424 AA909524 AA635311 AA649040 AI392620 Z40708 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166
75	424036	6226_1	NM_033445 BC001193 AI885781 BF794032 AA476620 AA810906 AA810905 AI291244 AI885097 AI359708 AI335629 H97396 AI344589 AA300377 AA457568 AW771833 BE465621 AI364068 AI364452 AI548505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329095 BM045465 AL531028 BG437151 BE868021 AA179427
	450203	19009_1	AK056952 BG182168 BG220105 BG181569 BG188964 BG187388 BG220104 BG183714 BE645998 AI819354 AW974068 AI393635 AI580846 AI024796 AW020098 BI491127 AI393644 W74993 AW472959 BM478854 BI597437 H12165 BI458612 BE543192
80	451752	10408_5	AB032997 AI141678 AW978722 BE467119 AI761408 BF727385 AW237035 AI934521 BF436248 AI479668 Z40632 AA832081 AW295901 BF057835 BE465977 AI621269 BE465983 BF756369 N74056 AI817898 AA716567 AA934774 H62600 H09497 BF943762 BE395335 BE883333 AW970240 AA534489 AW970323
	432363	1234917_1	

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422890	61426_1	AK057805 AW162343 AI190479 AI093318 BE048820 AI198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964436 AW004030 AI632565 BE502530 B1792383 BF065628 AA449241 AI651825 AA805324 AI264863 AW196918 AA948267 AI953735 AI263703 BF056387 AW594171 AI867447 AA319159 AI903440 AW956110 AI366013 AI867923 BG911906 D81142 C15616 AL538697 Z25032 Z43784 R13382 AV746924 AA493369 AA318815 BF364265 H17038 H10064 F04161 T87230 R40898 AW204071 BI819428 AA683393 AA683376 Z43192 T74078 T05103 F12527 T7951 H10118 H17037 BF855407 R19603 AA196390 AA507837 AA196468 AK056626 AI800896 BF939022 BE644718 AI954754 BE218177 BE348567 AI962406 AW293122 AI968798 AI457321 BE327228 BG913531 AW939055 T30280 R54166 Z43366 BG819153 BF003119 BE646274 BF940881 R18246 R42185 AK027321 W63676 W63789 BE046412 BF114614 BE646183 BM126230 AW044233 AI951970 AW663548 AI139947 AA514302 AA846232 BM126251 AA789002 AA581966 AA809643 AW188870 BE706664 BE706539 BE153177 BF084925 AI133779 AW961788 AA659693 AA347970 AA295134 AA526037 AA449282 BG190454 H61476 T91396 N20018 T90114 H75644 BE710736 BF687723 H28581 AA249370 BF726698 BE841554 BI045099 T84625 AW129578 BG770826 AW973834 AI791932 AI791855 AI732640 AA558833 AA558997 AI821610 AI973051 AI400921 AI796154 AW241817 AW290951 NM_004892 AF047442 BE275338 BF724863 BI917206 BE276993 AL602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA456385 AA234796 AI002726 AA354813 BI092644 BG778400 BI280001 BG007325 AI267455 AA426574 AI160782 AI472186 AA255500 AA434006 BG435520 AI356111 H00525 AV749060 BG944007 BG292031 AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R65766 AW958448 BE090972 BF693195 AV738979 R65855 R80136 AA484677 BE644758 AI082238 BF940027 AI201079 AI436035 AW275966 AI085394 AI291655 AW070441 AI474134 AI268978 AI769279 AI567682 AA693941 BF477668 AW664149 AA283782 BF509538 AW296868 AI268977 AI168133 BM352065 AI262769 BF941976 AI056920 AA481861 BF763697 AI565888 BM352383 AA427768 AA385346 AI186968 AA931831 AA134972 BF217480 BF111012 AA908246 AA319849 AA318136 AI514271 BF364291 AL515057 AV702312 AA377395 AL544217 AI341000 AW193583 AI350789 AA888338 BF945380 AW879092 AI430839 T91066 N92326 AI004389 AA078832 AL572370 W04622 BE314003 AW960808 BM360872 AA319160 AA130778 AL514257 AW182329 AA613792 T05304 AW658385 BG107484 AA632009 AI432670 AI656660 AI650884 AI521919 AI264653 AW150793 AW611894 AI917098 BI091245 AI651454 BF434889 AI580286 AI880735 BE301995 AI392959 AW613965 BM023628 AW515374 AA460102 BM023318 BE328188 AI952820 AI581363 AA557165 AI656577 AL562079 AI700926 AI470561 BF063058 AW196387 AU132984 BI064046 AI970157 R02122 H55924 AI521721 AA808206 AA725223 AI766003 AW339821 AA805951 AI287969 AW664827 BC021085 AL527872 AL526296 AL557087 BI255090 AU143499 AI560356 BG823170 BE736988 AU141388 AL580262 BI764173 AU120299 AU141755 AU141988 AU142941 AU141330 AU141784 BI770885 BI911394 BE901426 BI918039 BG760842 BE883026 BI254740 BE732690 BG430761 BE792868 AW328267 AL135173 AA102674 BF726985 AL564735 BE155962 BE155979 BF741679 BF7776 H59234 H96665 AW117774 AW274435 L29008 NM_003104 U07361 BF002824 BI222949 AI458045 AW951537 BF196474 AI668049 AI042523 BE463928 AU160125 AU160580 AW069877 AW015214 AI948718 BE219706 AI953605 BE217755 AI991382 AI245005 BF431179 AI521843 BE048908 AI204449 AW275385 AA336950 BE501521 BF740566 AA311404 AA384639 BI772535 BG473076 BE891298 BE246928 BM012986 BE242693 BE901342 BG746358 BF374053 AL564430 AU143835 AI635707 BF195492 AI280559 BF741685 AA385257 BE247655 W94974 BE163702 AI025167 AI827118 N78641 AL581093 AU158964 AU158917 AI282516 AU146399 AA713947 AI285028 AA101228 AI338522 AA832316 AI284986 AA857926 BF372568 AU570172 AI753825 AA171568 AU159257 BM194320 W93390 AW132101 AA550898 BI259678 AA522554 N55172 AW013929 AI826274 AI871237 C75260 AA934846 AA555036 AA526579 AA526466 N80270 AI538347 AW615805 AU158875 AU158883 AU159396 AU016667 AU159238 AI282517 AA406317 AI285043 N53050 AA969446 N57718 H93323 W93374 AI873751 H56011 AI936174 AA937830 AW438877 AI800550 AW328268 AI244886 AA948424 AA700604 AA832317 AA011555 H97671 AA988711 AW150529 W07093 HA4325 AV657614 AA902238 AA644018 AA034050 T71053 N71444 AA831158 T40892 AA706106 AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM468657 AU128438 BE384458 AL353967 BI857117 BF686525 BI465223 BM460132 AU129877 BI222283 BG171592 BI043544 BG496295 BG750710 BI256542 BG108520 AU150719 AW510354 AI554256 AL353968 AA191092 BF132635 AF119847 AA437261 AA436987 AI132965 AF150424 AI861896 AA570057 AV738855 AI801777 BE677762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AA670058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF449023 AI289476 AW074381 BF972912 AI991780 AA899119 AI537472 Z39730 AI868953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981 AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AA134107 BM023515 AA977504 AI859222 AI348454 B69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 AI028416 AI074114 BG656536 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R55480 AI400988 R54266 R31422 AK055915 BE867252 AI523348 AA765350 BF446858 Z43575 R19529 AL133837 BG389444 AW382942 BE702956 AA081961 BE835247 BE835308 BE835295 AA376302 BE645790 AA375690 AA376592 AW954423 N85732 AA249770 AI754416 AA213816 BF592044 AA811729 AW514842 AI633486 AI096810 AW183016 AI635738 N27524 BE645916 AI247842 AW991230 AI754277 H16814 AI766892 BF108422 AI800361 T95129 F11313 R97946 R93889 AA375242 BF109388 AI860939 AI680060 AW953899 BF971486 AI972337 AW953841 AA372437 AI216746 H11384 R38484 AA249043 AA249732 AW969151 AA532718 AA504784 AI791194 AI821930 AI821485 F37127 AA654206 F27974 AK074291 AW293424 BE676135 AI832125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28618 BF924261 AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119 AW814195 BE879126 AI697926 BF594155 BE205787 BF063513 N35828 AI948557 AI433839 AI379679 BG056182 AI589094 N23123 AA588805 AW316581 AI080272 AI421980 AI483318 BF194830 N87590 AA495993 N32996 AA698844 H96845 H96592 N28741 BI035539 BF747723 BF171066 W01350 H05495 AI243785 Z39522 AA887432 AI350659 R46102 AA602964 AA609200 AW976537 AI033582 AA837085 AA745261 AA648395 BC013939 BI494690 BI491211 AI928393 AA843540 BG938644 AU185628 BI495842 AW173255 BM052709 AI743999 AI690144 AI922209 AI740907 AW340368 AA928759 AI118737 BF513970 AA707807 BF435295 AI339463 AI373842 AI433809 BE222392 AA602308 AA428261 AI460355 AW662760 AI888087 AI342098 AA722418 W78151 N64382 BE221848 AW025801 AA452120 AI150479 AI016166 AA779515 AA651791 BM474307 BI911169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BM461961 BG681168 BI602483 BE889592 AW954311 BM062986 BI962893 AI989299 Z42328 BF029604 T35668 BG402602 AU185770 AU023271 AA147719 AI434079 AI569000 AI276488 AA992453 AA342821 AA648303 AI349364 AI051008 AA926941 AA350894 AW071451 N22249 AI784138 AA083847 N22258 AA440825 AA661570 AA376687 AA659125 AI356299 R70463 AI383586 AA827189 BI494872 AW021094 BI494871 AA905500 AA460923 BI492041 AW028965 BI624611 BG271780 AI497723 H88882 D59858 N89979 AA658425 N81154 D62341 AI274437 N66697 H96993 AI370663 AA728850 H05232 R59374 H12223 AI935759 AI362553 D60006 N29572 AI916833 N75273 AA148710 BI597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA452342 AW965441 W19723 R32966 BE883841 R61003 AI910374 AI866522 R55325 AI468927 R34681 H96211 Z39807 BF954386 NM_015720 AF219137 AL534420 AL524055 AL537346 AL538442 BG765888 AL530054 AL525377 BG474596 BG473144 BE251553 BG706099 AL536039 BG703131 BE255805 BF055256 F12128 AL566773 BI826886 BF761480 AI204971 BG818818 BI199246 AL534816 BF529941 AA324163 AL523285 BG914330 H07952 AL534815 BE769903 AI867802 BM310135 AL533702 BE254484 BF528852 BE867462 BE740130 AL134164 AL567115 AL533701 AL524054 AL515904 AL523284 AL568203 AL534419 BF981162 BE257148 AL561833
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445636	8561_5	BF339388 AI345516 BG391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310 AA090672
419175	35068_1	AB018322 BC012480 BI524873 AW665554 AI934469 AI479916 BF096179 BF096162 BF096132 AA744972 AI951988 AI858339 BE076331 AA886998 AI570585 AI916688 AI678811 AI693109 AI308135 AA669046 AA961064 AI018062 H80618 BE221942 R52609 AI915164 AA365626 Z44671 BI052776 BF882486 BG286184 AI589558 AA831663 AA534979 AI275392 AI273455 R52553 AA829920 H80652 AA360728 F10618 AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572 AA994211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 AI203159 N49403 F02090 AI187299 AI609644 Z40516 AW952314
441128	20932_1	BC014072 BE328850 AI356567 AI148171 AI022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AI473237 BF033706 N90525 AW973623 AI359627 BG674574 BE903322
406789	0_0	AI041403 Z49148
421091	24941_2	AK057700 BC015899 BE867108 AL526926 AL527436 BG913023 AI884867 BE858461 AI885227 AI935218 BE645596 AI922406 AA778161 BF345973 AW195853 AI687121 AI336147 AI091364 AI769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812396 AI356396 AA932022 BE222881 AW016109 BM352667 BF528099 BG818616 AI935916 AA912295 BG910887 AL568301 AI567278 BI522445 BI754384 BG819375 BF835950 AA323718 AA860955 AI089847 AL520776 AL526045 AL538507 AL567798 AL536876 AL574332 BF834531 BF340116 BF835954 AL573997 AL581252 BF957667 AL580170 AW952324 AL569382 AW148695 AL559234 BG034270 BI913839 AL581327 AL565842 H43568 BF945188 AL559686 AL539326 T15481 AW895092 AL582684 BI519896
400263	18977_1	Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG988348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084

TABLE 67C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816, 119119-119244, 119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859, 56369-56511
404922	7341893	Plus	13248-13428
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401519	6649315	Plus	157315-157950
401785	7249190	Minus	165776-165995, 166189-166314, 166408-16656
401866	8018106	Plus	73128-73623
405387	6587915	Minus	3769-3833, 5708-5895
401197	9719705	Plus	176341-176452
403532	8076842	Minus	81750-81901

TABLE 68A: 995 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 68A lists about 995 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 995 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 85th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	85.6
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	68.6
448057	AJ420227	Hs.149358	Trp-p8 transient receptor potential cati	65.6
400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	61.9
432441	AW292425	Hs.163484	ESTs	60.4
419526	AJ821895	Hs.193481	ESTs	45.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	45.7
424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	45.2
432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fs, clone PL	44.9
400298	AA032279	Hs.61635	stx transmembrane epithelial antigen of	40.9
453370	AJ470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	39.6

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	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	37.7
	400299	X07730	Hs.171995	kalikrein 3, (prostate specific antigen	34.9
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.7
	400292	AA250737	Hs.72472	BMP-R1B	31.4
5	425075	AA506324	Hs.1852	acid phosphatase, prostate	31.4
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	31.4
	428819	AL135623	Hs.193914	KIAA0575 gene product	31.2
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolog	30.3
	407168	R45175	Hs.117183	ESTs	29.6
10	400287	S39329	Hs.181350	kalikrein 2, prostatic	29.6
	415539	AI733881	Hs.72472	BMP-R1B	28.8
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	28.1
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	27.5
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	27.4
15	403047			NM_005656*:Homo sapiens transmembrane pr	25.7
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	25.0
	428336	AA503115	Hs.183752	microseminoprotein, beta-	24.9
	401424			NM_001172:Homo sapiens arginase, type II	24.7
	407709	AA456135	Hs.23023	ESTs	24.6
20	407122	H20276	Hs.31742	ESTs	23.2
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	23.1
	415989	AI267700		ESTs	22.7
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	22.6
	437052	AA861697	Hs.120591	ESTs	22.5
25	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	21.2
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	20.8
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	20.5
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	20.5
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	19.8
30	431548	AI834273	Hs.9711	novel protein	19.4
	434666	AF151103	Hs.112259	T cell receptor gamma locus	19.3
	426501	AW043782	Hs.293516	ESTs	18.9
	413597	AW302885	Hs.117183	ESTs	18.7
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	18.0
35	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	17.9
	429220	AW207206		ESTs	17.6
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	17.3
	418961	AW967646	Hs.23023	ESTs	17.3
	428898	AB033070	Hs.194408	KIAA1244 protein	16.8
40	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	16.3
	428398	AI249368	Hs.98558	ESTs	15.8
	419078	M93119	Hs.89584	insulinoma-associated 1	15.4
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	15.2
	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	14.9
45	401451			NM_004496*:Homo sapiens hepatocyte nucle	14.9
	447033	AI357412	Hs.157601	ESTs	14.7
	452594	AI076405	Hs.29981	solute carrier family 26 (sulfate transp	14.6
	448519	AW176665	Hs.278695	Homo sapiens protein mRNA, complete cds	14.5
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	14.4
50	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	14.3
	418848	AI820981	Hs.193465	ESTs	14.2
	429918	AW873986	Hs.119383	ESTs	14.1
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	14.1
	418278	AI088489	Hs.83937	hypothetical protein	13.9
55	408000	L11690	Hs.198689	bulbos pemphigoid antigen 1 (230/240kD)	13.3
	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	13.3
	432101	AI918950	Hs.123642	EphA3	13.1
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	12.7
	412446	AI768015		ESTs	12.6
60	437718	AI927288	Hs.196779	ESTs	12.6
	433404	T32982		ESTs	12.6
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	12.5
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	12.5
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	12.4
65	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	12.4
	428046	AW812795	Hs.337534	ESTs, Moderately similar to 138022 hypot	12.2
	453160	AI263307		H2B histone family, member L	12.1
	433927	AI557019	Hs.116457	small nuclear protein PRAC	12.1
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	11.9
70	424800	AL035588	Hs.153203	MyoD family inhibitor	11.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	11.7
	424692	AA429834	Hs.151791	KIAA0092 gene product	11.3
	415263	AA948033	Hs.130853	ESTs	11.3
	416182	NM_004354	Hs.79069	cyclin G2	11.3
75	420218	AW958037		ribosomal protein L4	11.2
	411887	AW182924	Hs.128790	ESTs	11.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.2
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	11.1
	450325	AI935962	Hs.91973	ESTs	11.1
80	439444	AI277652	Hs.54578	ESTs, Weakly similar to 138022 hypotheti	11.0
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.0
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	11.0
	428600	AW863261	Hs.138860	hypothetical protein DKFP434K1421	11.0

	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	11.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	10.7
	434423	NM_005769	Hs.3844	LIM domain only 4	10.6
5	434170	AA626509	Hs.122329	ESTs	10.6
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.5
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	10.4
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	10.4
	421896	N62293	Hs.45107	ESTs	10.3
	401747			Homo sapiens keratin 17 (KRT17)	10.1
10	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	10.1
	431542	H63010	Hs.5740	ESTs	10.0
	447397	BE247676	Hs.18442	E-1 enzyme	10.0
	433285	AW975944	Hs.237396	ESTs	10.0
15	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	9.9
	410889	X91682	Hs.66744	twist (Drosophila) homolog (acrocephalos	9.8
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	9.6
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	9.6
	442049	AA310393	Hs.190044	ESTs	9.6
20	443180	R15875	Hs.258576	claudin 12	9.5
	406964	M21305		FGENES predicted novel secreted protein	9.5
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	9.5
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	9.5
	448045	AJ297436	Hs.20166	prostate stem cell antigen	9.5
25	451694	AF216751	Hs.26813	CDA14	9.5
	440594	AW445167	Hs.126036	ESTs	9.4
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	9.3
	418601	AA279490	Hs.86368	calmegin	9.3
	433332	AJ367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.2
30	437124	AA554458		KIAA0668 protein	9.2
	428728	NM_016625	Hs.191381	hypothetical protein	9.2
	438869	AF075009		gb:Homo sapiens full length insert cDNA	9.1
	431992	NM_002742	Hs.2891	protein kinase C, mu	8.9
	413992	W26276	Hs.138075	RNA, U2 small nuclear	8.9
35	428342	AJ739168		Homo sapiens cDNA FLJ13458 fis, clone PL	8.9
	418836	AJ655499	Hs.161712	ESTs	8.8
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	8.8
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	8.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	8.7
40	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isoto	8.7
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	8.7
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	8.7
	450203	AF097994		L-tyrosine/alpha-amino acid/peptide aminotra	8.7
	425465	L18964	Hs.1904	protein kinase C, iota	8.5
45	416239	AL038450	Hs.48948	ESTs	8.5
	439962	AW377314	Hs.5364	DKFZP564I052 protein	8.4
	450164	AJ239923	Hs.63931	ESTs	8.4
	452744	AJ267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	8.4
	440774	AJ420611	Hs.153934	ESTs	8.3
50	444922	AJ921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	8.3
	410870	U81599	Hs.66731	homeo box B13	8.3
	435047	AA454985	Hs.54973	cadherin-like protein VR20	8.2
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	8.2
	451027	AW519204	Hs.40808	ESTs	8.2
55	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	8.2
	423349	AF010258	Hs.127428	homeo box A9	8.1
	421928	AF013758	Hs.109643	polyadenylation binding protein-interactin	8.1
	432586	AA568548		ESTs	8.0
	426108	AA622037	Hs.166468	programmed cell death 5	8.0
60	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	8.0
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	7.9
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	7.9
	450377	AB033091		KIAA1265 protein	7.8
	429769	NM_004917	Hs.218366	kalikrein 4 (protease, enamel matrix, p	7.7
65	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	7.7
	433323	AA805132	Hs.159142	ESTs	7.7
	451952	AL120173	Hs.301663	ESTs	7.7
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	7.7
	421470	R27496	Hs.1378	annexin A3	7.7
70	420092	AA814043	Hs.88045	ESTs	7.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (7.6
	440749	W22335	Hs.7392	hypothetical protein MGC3199	7.6
	441866	BE464341	Hs.21201	nacln 3; DKFZP566B0846 protein	7.6
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	7.5
75	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop	7.4
	451418	BE387780	Hs.26369	hypothetical protein FLJ20287	7.4
	433517	AW022133	Hs.189838	ESTs	7.4
	415621	AJ648602	Hs.55468	ESTs	7.4
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	7.3
80	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	7.3
	450244	AA007534	Hs.125062	ESTs	7.2
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	7.2
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	7.2
	434485	AJ623511	Hs.118567	ESTs	7.2

5	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.1
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	7.1
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	7.0
	408418	AW963897	Hs.44743	KIAA1435 protein	7.0
	436063	AK000028		ribosomal protein S24	7.0
10	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.9
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	6.9
	428465	AW970976	Hs.293653	ESTs	6.9
	436476	AA326108	Hs.33829	bHLH protein DEC2	6.8
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	6.8
15	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.7
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.7
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	6.6
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	6.6
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	6.6
20	410227	AB009284	Hs.61152	exostosins (multiple)-like 2	6.6
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.5
	410037	AB020725	Hs.58009	KIAA0918 protein	6.5
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.4
	409648	AW451449	Hs.57749	ESTs	6.4
25	448148	NM_016578	Hs.20509	HBV pX associated protein-8	6.4
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	6.4
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.3
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	6.3
	404632			NM_022490:Homo sapiens hypothetical prot	6.3
30	412935	BE267045	Hs.75064	tubulin-specific chaperone c	6.3
	453308	AW959731	Hs.323099	ESTs	6.3
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.3
	410762	AF226053	Hs.66170	HSKM-B protein	6.3
	436032	AA150797	Hs.109276	latexin protein	6.3
35	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	6.3
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	6.2
	425071	NM_013989	Hs.154424	deiodinase, liothyronine, type II	6.2
	424036	AA770688		H2A histone family, member L	6.2
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	6.2
40	450861	AI523898	Hs.17617	ESTs	6.1
	418821	AA436002	Hs.183161	ESTs	6.1
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	6.1
	432527	AW975028	Hs.102754	ESTs	6.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	6.1
45	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	6.1
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	6.1
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	6.0
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	6.0
	419647	AA348947	Hs.91816	hypothetical protein	6.0
50	455497	AA112573	Hs.278695	Homo sapiens prostein mRNA, complete cds	6.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.9
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.9
	446416	AV658299	Hs.163959	ESTs	5.9
	407819	R42185		ESTs	5.9
55	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.9
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	5.9
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.9
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	5.8
	410240	AL157424	Hs.61289	synaptotagmin 2	5.8
60	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	5.8
	416795	AA497778	Hs.20509	HBV pX associated protein-8	5.7
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	5.7
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	5.7
65	433852	AI378329	Hs.126629	ESTs	5.7
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	5.6
	419440	AB020689	Hs.90419	KIAA0882 protein	5.6
	435706	W31254	Hs.7045	GL004 protein	5.6
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.6
70	442409	BE208843	Hs.129544	hypothetical protein MGC15438	5.6
	453171	R76472	Hs.65646	ESTs	5.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	5.6
	429638	AI916662	Hs.211577	kinectin 1 (kinesin receptor)	5.5
75	403046			NM_005656:Homo sapiens transmembrane pr	5.5
	447805	AW527932	Hs.302421	gemin4	5.5
	443162	T49951	Hs.9029	DKFZP434G032 protein	5.4
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	5.4
80	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	5.4
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	5.4
	427308	D26067	Hs.174905	KIAA0033 protein	5.4
	409151	AA306105		SEC22, vesicle trafficking protein (S. c	5.4
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	5.3
	423242	AL039402	Hs.125783	DEME-6 protein	5.3
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	5.3

	415276	U88666	Hs.78353	SFRS protein kinase 2	5.3
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.3
	432435	BE218886	Hs.282070	ESTs	5.3
5	417318	AW953937	Hs.240845	ESTs	5.3
	429457	NM_004477	Hs.203772	FSHD region gene 1	5.3
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	5.3
	410076	T05387	Hs.7991	ESTs	5.3
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	5.2
10	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	5.2
	436420	AA443966	Hs.31595	ESTs	5.2
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	5.1
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	5.1
	427176	AW381569	Hs.40334	ESTs	5.1
15	450832	AW970602	Hs.105421	ESTs	5.1
	448807	AI571940	Hs.7549	ESTs	5.1
	420568	F09247	Hs.247735	protocadherin alpha 10	5.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	5.0
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	5.0
20	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
	452576	AB023177	Hs.25900	KIAA0960 protein	5.0
	431724	AA514535	Hs.283704	ESTs	5.0
	409757	NM_001898	Hs.123114	cystatin SN	5.0
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.0
25	407103	AA424881	Hs.256301	hypothetical protein MGC13170	5.0
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	5.0
	400301	X03635	Hs.1657	estrogen receptor 1	5.0
	426006	R49031	Hs.22627	ESTs	5.0
30	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
	446880	AB11807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	4.9
	444108	R55784	Hs.140942	ESTs	4.9
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.9
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.9
	416854	H40164	Hs.80296	Purkinje cell protein 4	4.9
35	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.9
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	4.9
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	4.9
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.9
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.9
40	442501	AA315267	Hs.23128	ESTs	4.8
	439735	AI635386	Hs.142846	hypothetical protein	4.8
	451752	AB032997		KIAA1171 protein	4.8
	423583	AL122055	Hs.129836	KIAA1028 protein	4.8
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	4.8
45	432363	AA534489		gb:nt776g11.1 NCI_CGAP_Co3 Homo sapiens	4.8
	433313	W20128	Hs.296039	ESTs	4.8
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.8
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.8
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	4.7
50	447574	AF162666	Hs.18895	tosus-like kinase 1	4.7
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.7
	420522	AW957137	Hs.98541	hypothetical protein	4.7
	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	4.7
	411031	W37943	Hs.34892	KIAA1323 protein	4.7
55	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	4.7
	441224	AU076964	Hs.7753	calumenin	4.7
	407813	AL120247	Hs.40109	KIAA0872 protein	4.7
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	4.7
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.7
60	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	4.7
	414922	D00723		glycine cleavage system protein H (amino	4.7
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.7
	438825	BE327427	Hs.79953	ESTs	4.7
	425174	D87450	Hs.154978	KIAA0261 protein	4.7
65	420380	AA640891	Hs.102406	ESTs	4.7
	410193	AJ132592	Hs.59757	zinc finger protein 281	4.7
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.6
	436761	AB17776	Hs.236557	ESTs	4.6
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.6
70	404922			NM_003071:Homo sapiens SWI/SNF related,	4.6
	436556	AI364997	Hs.7572	ESTs	4.6
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	4.6
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.6
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	4.5
75	407894	AJ278313	Hs.41143	phospholipase-specific phospholipase	4.5
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.5
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	4.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.5
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.5
80	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	4.5
	453390	AA862496	Hs.28482	ESTs	4.5
	417061	AI875944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.5
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.5
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	4.5

	408001	AA046458	Hs.95296	ESTs	4.4
	413950	AA249096	Hs.32793	ESTs	4.4
	416555	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	4.4
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	4.4
5	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	4.4
	433233	AB040927	Hs.301804	KIAA1494 protein	4.4
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.4
	417958	AA767382	Hs.193417	ESTs	4.4
10	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	4.4
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.4
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	4.4
	425810	A1923627	Hs.31903	ESTs	4.4
	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	4.3
15	452747	BE153855	Hs.61460	lg superfamily receptor LNIR	4.3
	429259	AA420450	Hs.292911	Plakophilin	4.3
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	4.3
	437957	BE277414	Hs.5947	mel transforming oncogene (derived from	4.3
	459284	AF155660	Hs.300496	mitochondrial solute carrier	4.3
20	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	4.3
	423453	AW450737	Hs.128791	CGI-09 protein	4.3
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.3
	448826	A1580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	4.3
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	4.3
25	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	4.3
	450402	BE218027	Hs.89969	ESTs	4.3
	428055	AA420564	Hs.101760	ESTs	4.3
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	4.2
	432675	AJ791855		ESTs	4.2
30	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	4.2
	445707	AJ248720	Hs.114390	ESTs	4.2
	410297	AA148710		tumican	4.2
	416737	AF154335	Hs.79691	LIM domain protein	4.2
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.2
35	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	4.2
	447620	AW290951		ESTs	4.2
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	4.2
	432886	BE169028	Hs.279704	chromatin accessibility complex 1	4.2
	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	4.2
40	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	4.2
	423337	NM_004655	Hs.127337	axin 2 (conductin, axl)	4.2
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.2
	427723	A1355260	Hs.279789	histone deacetylase 3	4.2
	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	4.2
45	416140	A1918035	Hs.301198	roundabout (axon guidance receptor, Dros	4.2
	428231	U17989	Hs.183105	nuclear autoantigen	4.2
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	4.1
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	4.1
	432621	A1298501	Hs.21192	ESTs, Weakly similar to T46428 hypotheti	4.1
50	408063	BE086548	Hs.42346	calcineurin-binding protein calcarsin-1	4.1
	407192	AA609200		gb:caf12a02.s1 Soares_testis_NHT Homo sap	4.1
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	4.1
	427479	BE410092	Hs.178471	KIAA0798 gene product	4.1
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	4.1
55	422072	AB018255	Hs.111138	KIAA0712 gene product	4.1
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	4.1
	449459	BE546846	Hs.195048	ESTs	4.1
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	4.1
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
60	412520	AA442324	Hs.795	H2A histone family, member O	4.0
	448663	BE614599		hypothetical protein MGC14797	4.0
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	4.0
	433647	AA603367	Hs.222294	ESTs	4.0
65	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	4.0
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	4.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	4.0
	422634	NM_016010	Hs.118821	CGI-62 protein	4.0
	453469	AB014533	Hs.33010	KIAA0633 protein	4.0
	418827	BE327311	Hs.47166	HT021	4.0
70	446791	AK632278	Hs.195922	ESTs	4.0
	443884	N20617	Hs.194397	leptin receptor	4.0
	416857	AA188775	Hs.292453	ESTs	4.0
	401519			C150004766.gli12737279[ref]XP_012163.1]	4.0
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	4.0
75	431689	AA305688	Hs.267695	UDP-GalbetaGlcNAc beta 1,3-galactosyltr	3.9
	408784	AW971350	Hs.63386	ESTs	3.9
	435655	AW105663	Hs.6947	HSPC069 protein	3.9
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.9
	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	3.9
80	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.9
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.9
	414869	AA157291	Hs.21479	ubiquitin 1	3.9
	429163	AA884766		gb:zmm20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.9

	444190	A1878918	Hs.10526	cysteine and glycine-rich protein 2	3.9
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.9
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.9
5	435021	AA922192	Hs.73962	ESTs	3.9
	412834	R77123	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.9
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	3.9
	408833	AW612232	Hs.254835	ESTs	3.9
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.9
10	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.8
	433345	A1681545	Hs.152982	hypothetical protein FLJ13117	3.8
	421887	AW161450	Hs.109201	CGI-88 protein	3.8
	434614	A1249502	Hs.29669	ESTs	3.8
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.8
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.8
15	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.8
	435114	AA775483	Hs.288938	mitochondrial ribosomal protein L9	3.8
	439024	R96696	Hs.35598	ESTs	3.8
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.8
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.8
20	439671	AW162840	Hs.6641	kinesin family member 5C	3.8
	418113	A1272141	Hs.83484	SRY (sex determining region Y)-box 4	3.8
	422424	A186431	Hs.296638	prostate differentiation factor	3.8
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.8
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.8
25	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.8
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.8
	440695	AW088363	Hs.246240	ESTs	3.8
	429686	A1871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.8
30	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	3.8
	411190	AA306342	Hs.69171	protein kinase C-like 2	3.8
	426126	AL118747	Hs.26691	ESTs	3.8
	434263	N34895	Hs.44648	ESTs	3.8
	414407	AA147026	Hs.76704	ESTs	3.7
	432426	AW973152	Hs.31050	ESTs	3.7
35	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	3.7
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.7
	444101	R19175	Hs.169793	ribosomal protein L32	3.7
	432908	A1861896		ESTs	3.7
40	432800	BE391046	Hs.278962	AIM-1 protein	3.7
	429966	BE081342	Hs.283037	HSPC039 protein	3.7
	419972	AL041465	Hs.182982	golgin-67	3.7
	410001	AB041036	Hs.57771	kallikrein 11	3.7
	432205	A1806583	Hs.125291	ESTs	3.7
45	401197			ENSP00000229263*:HSPC213.	3.7
	420061	AW024937	Hs.29410	ESTs	3.7
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.7
	433577	AW007080	Hs.284192	ESTs	3.7
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.7
50	420805	L10333	Hs.99947	reticulin 1	3.7
	401866			Target Exon	3.7
	457183	H91882	Hs.118569	Dvl-binding protein IDAX (inhibition of	3.7
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.7
	405387			NM_022170*:Homo sapiens Williams-Beuren	3.7
55	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.7
	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	3.7
	438157	AW137011	Hs.49576	ESTs	3.7
	451945	BE504055	Hs.211420	ESTs	3.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.6
60	454229	AW957744	Hs.278469	lactrinal proline rich protein	3.6
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.6
	421637	BE383488	Hs.105547	neural proliferation, differentiation an	3.6
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.6
	440494	BE516768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.6
65	407748	AL079409	Hs.38176	KIAA0806 protein; SCN Circadian Oscillat	3.6
	453049	BE537217	Hs.30343	ESTs	3.6
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPUC	3.6
	408096	BE250162	Hs.83765	dihydrofolate reductase	3.6
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
70	450649	NM_001429	Hs.25272	E1A binding protein p300	3.6
	436489	AJ272269	Hs.121429	zinc-binding protein Rboc728	3.6
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequanca	3.6
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.6
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	3.6
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.6
75	427715	BE245274	Hs.180428	KIAA1181 protein	3.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	3.6
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.6
	403752			NM_002753*:Homo sapiens mitogen-activate	3.6
80	418559	AA225048	Hs.104207	ESTs	3.6
	438523	H66220	Hs.278177	ESTs	3.6
	438705	A1049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.6
	443960	A1093577	Hs.255416	hypothetical protein FLJ21986	3.5
	412513	AA322599	Hs.51563	ESTs, Weakly similar to AF151840 1 CGI-8	3.5

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	428685	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.5
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.5
	446494	AA463276	Hs.268906	VW Domain-Containing Gene	3.5
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.5
5	433891	AA613792		gbno97h03.s1 NCI_CGAP_Pr2 Homo sapiens	3.5
	427315	AA178949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.5
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.5
	434672	AW294020	Hs.117721	ESTs	3.5
10	453288	AW583292	Hs.274412	similar to yeast Upt3, variant A	3.5
	434970	AW272262	Hs.225767	ESTs	3.5
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.5
	437617	AK026701	Hs.5716	KIAA0310 gene product	3.5
	445943	AW898533	Hs.181574	ESTs	3.5
15	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.5
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.5
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.5
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.5
20	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	3.5
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.5
	436087	BE300296	Hs.5054	CGI-133 protein	3.5
	437898	W81260	Hs.43410	ESTs	3.5
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.5
25	439609	AW971945	Hs.293236	ESTs	3.5
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	3.5
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.5
	409960	BE261944		hexokinase 1	3.5
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.5
30	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.5
	442323	AW016669	Hs.29190	ESTs	3.5
	452707	AI093823	Hs.45070	ESTs	3.5
	421437	AW821252	Hs.104336	hypothetical protein	3.4
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.4
35	450628	AW382884	Hs.204715	ESTs	3.4
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.4
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	3.4
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.4
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.4
40	429922	Z97630	Hs.226117	H1 histone family, member 0	3.4
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.4
	434293	NM_004445	Hs.3796	EphB6	3.4
	414222	AL135173		sorbitol dehydrogenase	3.4
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	3.4
45	438279	AA805166	Hs.154762	HIV-1 rev binding protein 2	3.4
	411078	AI222020	Hs.182364	CocoaCrisp	3.4
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.4
	432302	AA345857	Hs.274307	KIAA1442 protein	3.4
	407944	R34008	Hs.239727	desmocollin 2	3.4
50	431674	AA098901	Hs.301642	G-protein coupled receptor	3.4
	408291	AB023191	Hs.44131	KIAA0974 protein	3.4
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.4
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.4
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.4
55	452295	BE379936	Hs.28866	programmed cell death 10	3.4
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.4
	439593	BE073597	Hs.124863	ESTs	3.4
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.4
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.3
60	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.3
	417315	AI080042	Hs.180450	ribosomal protein S24	3.3
	423392	AA195037	Hs.169341	HTPAP protein	3.3
	412652	AI801777		ESTs	3.3
	416172	AF079529	Hs.78106	phosphodiesterase 8B	3.3
65	418372	AA311833	Hs.84318	replication protein A1 (70kD)	3.3
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	3.3
	425010	T16837	Hs.4241	ESTs	3.3
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.3
	443181	AI039201	Hs.283316	ESTs	3.3
70	442064	AI422867	Hs.88594	ESTs	3.3
	431663	NM_016569	Hs.267182	TBX3-Iso protein	3.3
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	3.3
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	3.3
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfat	3.3
75	408681	AW853853	Hs.292833	ESTs, Weakly similar to 138022 hypotheti	3.3
	436278	BE365290	Hs.5097	synaptogyrin 2	3.3
	424560	AA158727	Hs.150555	protein predicted by clone 23733	3.3
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.3
	418166	AI754416		Cdc42 effector protein 3	3.2
80	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.2
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	434747	AA837085		ESTs	3.2
	413125	BE244589	Hs.75207	glyoxalase I	3.2

5	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.2
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase	3.2
	422522	AI023428	Hs.34549	ESTs, Highly similar to S945411 clone 4	3.2
	423396	AI382555	Hs.127950	bromodomain-containing 1	3.2
	401785			NM_002275: Homo sapiens keratin 15 (KRT1	3.2
10	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	3.2
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypothe	3.2
	422173	BE385828	Hs.250619	phorbol-like protein MDS019	3.2
	452099	BE612992	Hs.27931	hypothetical protein FLJ10507 similar to	3.2
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	3.2
15	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.2
	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.2
	406214			NM_016371: Homo sapiens hydroxysteroid (1	3.2
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.2
	438714	AA814859	Hs.160074	ESTs	3.2
20	433213	AW665130	Hs.137190	ESTs	3.2
	412170	D16532	Hs.73729	very low density lipoprotein receptor	3.2
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	3.2
	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.2
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	3.2
25	437179	AA393508		serologically defined colon cancer anti	3.2
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALL5_HUMAN A	3.2
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	3.2
	450546	AA010200	Hs.175551	ESTs	3.2
	409995	AW960597	Hs.129206	ESTs	3.2
30	408739	W01556	Hs.44685	ESTs, Moderately similar to I38022 hypot	3.2
	438821	AA826425	Hs.192375	ESTs	3.2
	403532			NM_024638: Homo sapiens hypothetical prot	3.2
	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulfa	3.1
	414341	D80004	Hs.75909	KIAA0182 protein	3.1
35	423044	AA320829	Hs.97266	protocadherin 18	3.1
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.1
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	3.1
	423551	AA327598	Hs.89633	ESTs	3.1
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	3.1
40	413550	W03011	Hs.306881	MSTP043 protein	3.1
	431933	AI187057	Hs.132554	ESTs	3.1
	439778	AL109729	Hs.99364	putative transmembrane protein	3.1
	448044	AI458682		gbtk13e01.x1 NCL CGAP_Lu24 Homo sapiens	3.1
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.1
45	421254	AK001724	Hs.102950	coat protein gamma-cop	3.1
	424339	BE257148		endoglycan	3.1
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	3.1
	425320	U29344	Hs.83190	fatty acid synthase	3.1
	426170	BE161085	Hs.187531	methylcrotonoyl-Coenzyme A carboxylase 2	3.1
50	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.1
	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	3.1
	417622	AW298163	Hs.82318	WAS protein family, member 3	3.1
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.1
	433038	AA574091	Hs.105964	ESTs	3.1
55	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	3.1
	436299	AK000767	Hs.51111	hypothetical protein FLJ20729	3.1
	408380	AF123050	Hs.44532	diubiquitin	3.1
	407910	AA650274	Hs.41295	fibronectin leucine rich transmembrane p	3.1
	445098	AL050272	Hs.12305	DKFZP566B183 protein	3.1
60	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	3.1
	437296	AA350994	Hs.20281	KIAA1700	3.1
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	3.1
	448913	AA194422	Hs.22564	myosin VI	3.1
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	3.0
65	408157	AA047685	Hs.62946	ESTs	3.0
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	3.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.0
	437546	AW074836	Hs.173984	T-box 1	3.0
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	3.0
70	423932	T95633	Hs.189703	ESTs	3.0
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	3.0
	453293	AA382267	Hs.10653	ESTs	3.0
	428171	AA489323	Hs.182825	ribosomal protein L35	3.0
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	3.0
75	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.0
	406627	T64904	Hs.163780	ESTs	3.0
	418259	AA215404		ESTs	3.0
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	3.0
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	3.0
80	431416	AA532718		ESTs	3.0
	431631	AA548906	Hs.122244	ESTs	3.0
	409251	R10723	Hs.20573	ESTs	3.0
	434974	AA778711		eukaryotic translation initiation factor	3.0
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypothe	3.0
	450937	R49131	Hs.26267	ATP-dependant interferon response protel	3.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.0
	433037	NM_014158	Hs.279938	HSPC067 protein	3.0

	411598	BE336654	Hs.70937	H3 histone family, member A	3.0
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	3.0
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	3.0
	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	3.0
5	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transi	3.0
	434392	AW983709	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	3.0
	432810	AA863400	Hs.23054	ESTs	3.0
10	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.0
	445586	R89543	Hs.12942	vesicle trafficking protein	3.0
	406670	W79632	Hs.256301	hypothetical protein MGC13170	3.0
	452779	AA418775	Hs.47234	ESTs	3.0
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	3.0
15	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	2.9
	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.9
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	2.9
	425920	AL049977	Hs.162209	claudin 8	2.9
	409927	T69981		gb:yc19d03.r1 Stratagene lung (937210) H	2.9
20	447881	BE620886		GCN1 (general control of amino-acid synt	2.9
	439584	AA838114	Hs.221612	ESTs	2.9
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.9
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.9
	422576	BE548555	Hs.118554	CGI-83 protein	2.9
25	438510	AL060220	Hs.6285	DKFZP586P0123 protein	2.9
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.9
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.9
	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.9
30	429351	AK001490	Hs.200016	hypothetical protein FLJ10628	2.9
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.9
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.9
	416439	AA180363	Hs.118769	ESTs	2.9
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
35	446911	N27605	Hs.16492	DKFZP564G2022 protein	2.9
	428801	AW277121	Hs.254881	ESTs	2.9
	430462	AI584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mRNA,	2.9
	420552	AK000492	Hs.98806	hypothetical protein	2.9
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.9
40	418222	AI675881	Hs.86538	ESTs	2.9
	433009	AA761668		gb:ncz24c08.s1 NCLCGAP_GCB1 Homo sapiens	2.9
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	2.9
	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.9
	448718	AA220235	Hs.153959	hypothetical protein MGC15436	2.9
45	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.9
	419849	BE041436	Hs.93379	eukaryotic translation initiation factor	2.9
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	2.9
	430375	AW371048	Hs.93758	H4 histone family, member H	2.9
	409650	T08490	Hs.288969	HSCARG protein	2.9
50	413588	AA971014	Hs.75432	IMP (inosine monophosphate) dehydrogenas	2.9
	412719	AW016610		ESTs	2.9
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.9
	439621	AI200281	Hs.123910	ESTs, Highly similar to B34087 hypotheti	2.9
	437050	AA766420		ESTs	2.9
55	414256	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr	2.9
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.9
	416941	BE000150	Hs.48778	riban protein	2.9
	421594	RA5689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.9
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.9
60	436823	AW749865		ESTs, Weakly similar to I38022 hypotheti	2.8
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.8
	426751	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586i2022 (f	2.8
	413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	2.8
	457733	AW974812		ESTs	2.8
65	400860			Target Exon	2.8
	436165	AI373544	Hs.331328	Intermediate filament protein syncoilin	2.8
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	2.8
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.8
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.8
	453912	AL121031		SWI/SNF related, matrix associated, acti	2.8
70	435703	AW630133	Hs.83313	GK003 protein	2.8
	431108	AA991508	Hs.105317	ESTs	2.8
	451040	AA324743	Hs.40808	ESTs	2.8
	443837	AI984625	Hs.9884	spindle pole body protein	2.8
75	418196	AI745849	Hs.26549	KIAA1708 protein	2.8
	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.8
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.8
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.8
80	433586	T85301	Hs.194397	gb:yd78d05.s1 Soares fetal liver spleen	2.8
	424720	M69907	Hs.152292	SWI/SNF related, matrix associated, acti	2.8
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.8
	422717	AI557623	Hs.119475	cold inducible RNA-binding protein	2.8
	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor t	2.8
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	2.8

	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.8
	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.8
	423318	AW467064	Hs.5740	ESTs	2.8
5	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.8
	452827	AI571835	Hs.55468	ESTs	2.8
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypotheti	2.8
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	2.8
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	2.8
10	419286	AA236006	Hs.128764	ESTs	2.8
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	2.8
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	2.8
	428054	AI948688	Hs.266619	ESTs	2.8
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.8
	440080	AW051597		ESTs	2.8
15	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.8
	447896	AA36124	Hs.294069	Homo sapiens cDNA FLJ13384 fts, clone PL	2.8
	431525	AA506656	Hs.6185	KIAA1557 protein	2.8
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fts, clone C	2.8
20	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.8
	449052	AW029507	Hs.161102	ESTs	2.8
	418663	AK001100	Hs.41690	desmocollin 3	2.8
	442013	AA506476	Hs.10500	Human DNA sequence from clone RP11-353C1	2.8
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.8
	453038	AW292415	Hs.20509	HBV pX associated protein-8	2.8
25	419175	AW270037		KIAA0779 protein	2.8
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.8
	421091	W22821		ribosomal protein L26	2.8
	413435	X51405	Hs.75360	carboxypeptidase E	2.8
30	432651	AW973744	Hs.293100	ESTs	2.8
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.8
	454148	AW732837	Hs.42390	nasopharyngeal carcinoma susceptibility	2.8
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	2.8
	425491	AA883316	Hs.255221	ESTs	2.8
35	414556	AW975063	Hs.343443	ribosomal protein L36	2.8
	435126	AI393666	Hs.42315	p10-binding protein	2.8
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.7
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.7
	440340	AW895503	Hs.125276	ESTs	2.7
40	410339	AI916499	Hs.298258	ESTs	2.7
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.7
	406789	AI041403		ribosomal protein L29	2.7
	424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	2.7
	449518	BE395253	Hs.30861	ESTs	2.7
45	410099	AA081630		KIAA0036 gene product	2.7
	422000	M30599	Hs.110637	homeo box A10	2.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	2.7
	415443	T07353	Hs.7948	ESTs	2.7
	432745	AI821926		gbn178105.x5 NCL CGAP_Pr3 Homo sapiens	2.7
50	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.7
	424369	R87622	Hs.26714	KIAA1831 protein	2.7
	417831	H16423	Hs.82685	CD47 antigen (Rb-related antigen, integr	2.7
	424723	BE408813	Hs.152337	protein arginine N-methyltransferase 3(h	2.7
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti	2.7
55	400263			Eos Control	2.7
	435750	AB029012	Hs.4990	KIAA1089 protein	2.7
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.7
	421709	AA159394	Hs.107056	CED-6 protein	2.7
	421077	AK000061	Hs.101590	hypothetical protein	2.7
60	418359	AL042210	Hs.16493	hypothetical protein DKFZp762N2316; KIAA	2.7
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.7
	411605	AW006831		ESTs	2.7
	437133	AB018319	Hs.5460	KIAA0776 protein	2.7
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.7
65	432125	AW972687	Hs.183006	Homo sapiens cDNA FLJ12300 fts, clone MA	2.7
	427657	AV652249	Hs.180107	polymerase (DNA directed), beta	2.7
	445636	AW105401		ribosomal protein L29	2.7
	443801	AW206942	Hs.253594	Intron of trichorhinophalangeal syndro	2.7
	420223	N27807		ribosomal protein L4	2.7
	427515	T79526	Hs.179516	Integral type I protein	2.7
70	447673	AI823987	Hs.182285	ESTs	2.7
	411960	R77776	Hs.18103	ESTs	2.7
	433212	BE218049	Hs.121820	ESTs	2.7
	448244	BE613416	Hs.336425	Homo sapiens, clone MGC:17286, mRNA, com	2.7
75	441551	AA318224	Hs.296141	ESTs	2.7
	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pompe disease,	2.7
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.7
	434851	AA806164	Hs.116502	ESTs	2.7
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.7
80	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.7
	432450	AI990739	Hs.158184	ORF	2.7
	426174	AA547959	Hs.115838	ESTs	2.7
	445919	TS3519	Hs.334692	hypothetical protein MGC14141	2.7
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.7

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	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.7
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.7
	431615	AW295859	Hs.235860	ESTs	2.7
5	418649	AJ096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.7
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.7
	438682	AA354489	Hs.222103	EBP50-PDZ interactor of 64 kD	2.7
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	2.7
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
10	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	2.7
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	2.7
	435176	AA744875	Hs.189413	ESTs	2.7
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	2.7
	428013	AF151020	Hs.181444	hypothetical protein	2.7
	441094	U33819	Hs.7647	MYC-associated zinc finger protein (puri	2.7
15	451356	AA748418	Hs.164577	ESTs	2.7
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.7
	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	2.7
	423476	AL035633		Human DNA sequence from clone RP5-1046G1	2.7
	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	2.7
20	404913			NM_024408*:Homo sapiens Nclch (Drosophil	2.7
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.6
	441054	AA913591		ESTs	2.6
	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.6
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	2.6
25	433301	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone H	2.6
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.6
	443666	AI458179	Hs.41528	ESTs, Weakly similar to neuronal thread	2.6
	427378	BE515037	Hs.177556	melanoma antigen, family D, 1	2.6
	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.6
30	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.6
	421605	BE440108	Hs.106127	RNA polymerase I 16 kDa subunit	2.6
	426797	AW936258	Hs.342849	ADP-ribosylation factor-like 5	2.6
	410935	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	2.6
	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibito	2.6
35	430341	NM_006348	Hs.239631	golgi transport complex 1 (90 kDa subuni	2.6
	424956	AW198103	Hs.18724	ESTs, Weakly similar to granule cell mar	2.6
	452748	AB011128	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,	2.6
	408212	AA297567	Hs.43728	hypothetical protein	2.6
	407893	BE408359	Hs.43621	Homo sapiens, Similar to hypothetical pr	2.6
40	425976	C75094	Hs.334514	NG22 protein	2.6
	448424	AW009892	Hs.31924	ESTs	2.6
	420164	AW339037	Hs.24908	ESTs	2.6
	443444	AW952619	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ	2.6
	412774	AA120865	Hs.23136	ESTs	2.6
45	445922	AJ337316	Hs.147998	ESTs	2.6
	429925	NM_000786		cytochrome P450, 51 (lanosterol 14-alpha	2.6
	419222	AD001528	Hs.89718	spermine synthase	2.6
	417327	NM_004922	Hs.81964	SEC24 (S. cerevisiae) related gene famil	2.6
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.6
50	408743	AL110246	Hs.47367	KIAA1785 protein	2.6
	434011	AW953437	Hs.5486	clone FLB5214	2.6
	434976	AI963821		ESTs	2.6
	417454	NM_000202	Hs.172458	Iduronate 2-sulfatase (Hunter syndrome)	2.6
55	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6
	441049	W88920	Hs.29341	hypothetical protein FLJ22376	2.6
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	2.6
	425017	AL119305	Hs.26409	ESTs	2.6
	440333	AI378424	Hs.288761	hypothetical protein FLJ21749	2.6
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.6
60	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	2.6
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	2.6
	444550	BE250716	Hs.87614	ESTs	2.6
	446258	AI283478	Hs.263478	ESTs	2.6
	440191	AI890417		tubulin, beta 5	2.6
65	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.6
	412133	U83460	Hs.73614	solute carrier family 31 (copper transpo	2.6
	426841	AI052358	Hs.193726	ESTs	2.6
	435937	AA830893	Hs.119769	ESTs	2.6
	425960	AW410646	Hs.164649	hypothetical protein DKFZp434H247	2.6
70	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	2.6
	456236	AF045229	Hs.82280	regulator of G-protein signaling 10	2.6
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.6
	416751	T48130	Hs.6897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f	2.6
	458946	AA009716	Hs.42311	ESTs	2.6
75	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.6
	449458	AI805078	Hs.208261	ESTs	2.6
	432409	AA806538	Hs.130732	KIAA1575 protein	2.6
	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen	2.6
	442336	AW340958	Hs.7572	ESTs	2.6
80	445622	AF106697	Hs.12971	thioredoxin reductase beta	2.6
	440409	AW294316		ESTs	2.6
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.6
	425863	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	2.6

5	436972	AA284579	Hs.25640	claudin 3	2.6
	426809	BE313114	Hs.29706	ESTs	2.6
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.6
	457638	AI792670	Hs.144406	ESTs	2.6
	442821	BE391829	Hs.8752	transmembrane protein 4	2.5
	435522	N54214	Hs.9774	synovial sarcoma translocation gene on c	2.5
	406764	AA429825	Hs.343443	ribosomal protein L36	2.5
	422032	AA476966	Hs.110857	polymerase (RNA) III (DNA directed) poly	2.5
10	409125	R17258	Hs.343567	axonal transport of synaptic vesicles	2.5
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	2.5
	446091	AW022192		ESTs	2.5
	419848	AA251242	Hs.103238	ESTs	2.5
	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	2.5
15	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	2.5
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.5
	447087	AW403870	Hs.301872	hypothetical protein MGC4840	2.5
	456050	R79445	Hs.76230	ribosomal protein S10	2.5
	426178	AA371409	Hs.105664	hypothetical protein FLJ22294	2.5
20	414528	AA148950	Hs.188836	ESTs	2.5
	426494	AL119528	Hs.170098	KIAA0372 gene product	2.5
	407656	AW747986	Hs.37443	Homo sapiens mRNA; cDNA DKFZp434B2119 (f	2.5
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	2.5
	449139	BE268315	Hs.23111	phenylalanine-tRNA synthetase-like	2.5
25	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
	417386	AL037228	Hs.82043	D123 gene product	2.5
	409420	Z16008	Hs.54451	laminin, gamma 2 (niclin (100kD), kalini	2.5
	408796	AA688292	Hs.170345	ESTs	2.5
	407627	AI418020	Hs.62620	chromosome 6 open reading frame 1	2.5
30	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide syntha	2.5
	415862	R51034	Hs.144513	ESTs	2.5
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	2.5
	436657	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	2.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypothe	2.5
35	449500	AW956345	Hs.12926	ESTs	2.5
	457090	AL080243	Hs.180920	ribosomal protein S9	2.6
	445389	NM_016831	Hs.12592	period (Drosophila) homolog 3	2.5
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	2.5
	452906	BE207039	Hs.306123	MAGEF1 protein	2.5
40	450341	N90956	Hs.17230	hypothetical protein FLJ22087	2.5
	419430	AI878942	Hs.90336	ATPase, H transporting, lysosomal (vacuo	2.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.5
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypothe	2.5
	431843	AA516420		ESTs, Weakly similar to I38022 hypothe	2.5
45	424795	AW102850	Hs.153177	ribosomal protein S28	2.5
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.5
	450704	H85157	Hs.40696	ESTs	2.5
	400262			Eos Control	2.5
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	2.5
50	418039	R06859	Hs.193172	ESTs, Weakly similar to I38022 hypothe	2.5
	429491	NM_012111	Hs.204041	chromosome 14 open reading frame 3	2.5
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.5
	413781	J05272	Hs.850	IMP (inosine monophosphate) dehydrogenas	2.5
	437450	AL390154	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	2.5
55	424005	AB033041	Hs.137507	vang (van gogh, Drosophila)-like 2	2.5
	429332	AF030403	Hs.199263	Ste-20 related kinase	2.5
	438572	BE267017	Hs.6315	acetylserotonin O-methyltransferase-like	2.5
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.5
	431188	W06656	Hs.169755	ESTs	2.5
60	408803	AF248953	Hs.24049	golgi autoantigen, golgin subfamily a, 2	2.5
	414482	S57498	Hs.76252	endothelin receptor type A	2.5
	437762	T78028	Hs.154679	synaptotagmin I	2.5
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	2.6
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.5
65	451585	AK001171	Hs.326422	hypothetical protein MGC4549	2.5
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.5
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	2.5
	446054	AB014537	Hs.13604	KIAA0637 gene product	2.5
	452556	H78517	Hs.33905	ESTs	2.5
70	421026	AL047332	Hs.101087	GCN5 (general control of amino-acid synt	2.5
	407687	AK002011	Hs.37558	hypothetical protein FLJ11149	2.5
	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	2.5

TABLE 68B

75	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
80	Pkey	CAT Number	Accession	
	415989	10194_1	BC013389 BC017398 AJ023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909580 BF095153 BG285837 AI720344 BF541715 AA355088 AA172236	
	429220	15103_7	AW341473 AA448195 AW207206 AI951341 AA969259	

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449625	249224_1	BI918168 AW779760 N48674 AJ375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45528 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360 BC021735 AI669212 AL120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 BI035538 BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721 AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815 BC022980 BF224081 BG149508 AW672842 BE670687 AI702161 AW341832 BE222503 N71836 AI026061 AW953116 AW083132 AI979261 AV725377 AI423298 BI640707 AW675518 AI032611 AI818044 AI299508 AI911386 AI270418 BE219257 BM141826 AA826491 Z25159 AA587421 N59447 Z39436 T32982 R54110 BF115783 F09044 BF808433 BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R08338 AW958037 R42567 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727 AL050013 BG939500 AW969191 AA769925 AI377973 AI625545 AA811365 AA521114 N24705 AI379579 AA424899 AI684671 AA829715 AI453010 N35401 AA677452 AA504340 AI209149 AA883574 AI379062 AI084455 AI280147 AA644327 BF432508 N27873 N47364 N34880 AI147024 T86860 AI219716 AA960926 H25544 BI857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AI292318 AA829886 N95742 AI218758 H25588 N36282 AA024987 N36687 BI919187 N49471 AA889970 AW166152 AA468546 AI262504 AI452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 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		AU150404 AI680674 AW969901
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		AA886998 AI570585 AI916688 BI678811 AI693109 AI308135 AA669046 AA961064 AI018062 H08618 BE221942 R52609 AI15164 AA355626
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5 421091 24941_2

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25 445636 8561_5

30 411605 10026_3

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429925 33135_145 434976 121716_1
440191 MH790_2

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70 400262 18977_1

75 445636 8561_5

80 445636 8561_5

TABLE 68C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634
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 BG256892 H10532 N46614 R52610 AW977696 BM460488 W56819 B1042183 BG977498 BE767451 BF870009 BG477472 R61137 R14274 R20259
 R09686 B1838226 BF034269 AA429173 BE741829 AW867495 A123683 AW006831 BE831162 AW452753 AV742717 W86152 BF115102 A1633815
 BF921562 AA094230 BE092587 W86151 AA526153 A1672156 BF914496 R12579 BF852352 AA699780 T57386 BF903222 R09933 AA678298
 BF339388 A1345516 BG391657 BE708967 BG026034 BE261703 H56716 H55572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310
 AA090672
 N27807 AA256634 BE276324
 AF263308 BF951698 T66089 F11783 F11794 H29379 R19493 H18042 AL133995 AW134660 A1299437 AA057405 AA917450 A1002692 T09282
 R43839 H29290 T65008 N78357
 A1221207 A1659856 AA913591 A1220302
 NM_000786 U23942 B1601050 BG771947 BG773455 B1561558 B1460206 BG714348 BM126447 AU129411 AU129401 AL119303 AV724389
 AU099323 AU127089 BG701614 B1015364 D55653 AV702235 BE090408 AU151526 AW149661 BG054754 W42624 W52098 AV709923 W79867
 W74235 AV709052 A1217688 AA399409 BE182318 BM128040 A1693998 AW615411 AW070426 A124550 AW778736 AA477781 AW263013
 A4599619 AA860513 BF809548 AA643635 AA864975 H42020 AW901189 AA904786 BF432722 B1916393 BF956085 A1565178 AL554305 AL573240 AL572917
 U47727 BG773392 N58531 AA226450 BG679564 AA292178 W56883 BE813131 C03646 BG287974 A3366261 H47580 R48858 T91611 H42019
 B1869421 BG502073 BG425943 W37290 W31363 BE004451 BF208311 B1048717 N78122 AA26597 A1525334
 A1963821 AA657925 AA935436 AW975068
 BC000222 AL136871 NM_032261 BC009497 BM481705 BG470749 BG826905 BG285127 B1253235 BE397026 BG704967 AW961225 BM352817
 B1227161 BG820180 AA454463 AA255885 N31549 AA326504 BC019924 BG257230 B1092368 B1869896 BG251883 BF034444 BG286577
 BE260391 AA599912 BF686779 A1755222 AA452272 AW241170 AU155655 F28259 T16319 AA362506 N64153 BM016416 BM458963 BG739972
 AV729565 BE268285 BE867433 BM011110 BG285856 A1922439 BE270975 AL119339 BF956085 A1565178 AL554305 AL573240 AL572917
 A129627 AL546640 BE392285 A1092843 A1371057 BE302410 A1608753 AW674261 A1750057 A1052649 N47822 AL516249 A1589903 BG258439
 A123662 A126014 AA778101 AA243218 AW498837 AA748311 A1754395 T15728 AA775369 AA858195 W73625 AA216784 AW513778 AW243958
 A1061112 A1783806 A1589622 AA070466 BF229936 N58159 H80288 N32598 H80293 H80279 AL581253 AW571884 A1361698 AW073321
 AA876464 H95640 T34421 AA331419 N99897 H80274 B1262120 AA205826 AA070716 AA653206 AA653483 BG389811 W20432 AA670295
 AA653197 D51888 AA382527 BG056668 AW118162 AW073071 BE293868 BF792321 BF792258 BG107176 T56604 BM193556 H03238 AA618045
 AA908004 B1085686 AA564566 A1221630 D52045 C14510 AA029390 W60153 H98743 A1682641 H28485 AA723093 A1081730 AA641309
 AA687083 B1224818 AW204722 A1309186 A1215122 A1200785 BE467373 BM352502 A1304400 A193071 A1742483 AW003408 A1002001 A156740
 AW665173 A1215120 A1147599 A1803429 A1076110 A1754349 AW205103 A1262491 A1808243 A1281007 A1051273 A1004801 AW768918 A103289
 A1474637 A1264446 A1699509 BE704420 AA989278 AA918256 AA830856 AA989425 AA911929 AA262598 BE740563 BE727592 BE781003
 BG030940 BE256750 W23528 AL517059 H95714 W00970 H74304 W32684 H38210 BE617658 AW593584 AA580593 H49863 N68544 AA181762
 D20132 T55734 T60892 R76858 AA022848 AW770291 R50934 AA205918 R97811 H40328 R86252 AA936029 A1813809 AA933607 AA129695
 AA548261 AA714393 AA775006 AA653439 AA983808 AA743251 AA401150 AA581651 AA555005 AA554408 D51494 C13991 D51478 D52007
 AA489663 D52138 D51696 D55942 D52740 A1000118 AL516304 AL534259 N54940 AL579194 A1669399 A1342925 BE939201 AA633000 B1222963
 A1619676 AW190306 BF035010 AW087897 A1864969 T57243 R48211 AA113880 R26594 C14457 C14444 B1195459 BE896346 BE270780
 AL568073 BG389833 BE891549 B1223147 AW381001 AA448464 AW799744 AA412194 AA948107 AA927157 AA983841 BF752571 BE731304
 A1380443 A1240179 AA977516 AA884643 AW079380 AW294316 A1913755 A1864320 A1685770 H25135 A1972654 A1538592
 A1174783 R12271 R83569
 A1274757 A1559500 AW022192
 AW970134 AA516420 AA543007 BG057526 B1001430 A1498371 D60181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818
 C15161 D60184 D60556
 Z11692 X51466 NM_001961 M19997 B1224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 B1868669 BG337216 AW629935
 BM016525 A1560409 A1562866 A1909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 B1261304 BG770095
 B1033486 B1517580 BG876486 B1011828 A1313235 BG831724 BF869862 BG998348 B1011834 BF888337 BF898627 BF092380 AW803215 F01241
 BF805719 BG876487 AW498536 BF868866 BG998849 AA248724 BG829202 BG756456 BG032392 B1859287 BM016990 BG332369 BE933685
 BE166758 BM452445 A1937808 AW026128 N23684 AW006041 A1337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671
 BM007368 BF669385 BE772007 B1199487 BF761700 B1261519 BF944452 BF898506 A1038390 BM044934 AW381142 BG743618 BE769206
 BE893973 B1015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964
 BF089940 B1000274 BG255503 BG674499 BG774174 B1015084

Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816,119119-119244,119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859,56369-56511
404922	7341893	Plus	13248-13428
401519	6649315	Plus	157315-157950
401197	9719705	Plus	176341-176452
401866	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833,5708-5895
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401785	7249190	Minus	165776-165996,166189-166314,166408-16656
406214	7342036	Plus	86320-86523
403532	8076842	Minus	81750-81901
400860	9757499	Minus	151830-152104,152649-152744
404913	7341740	Plus	97717-97976

Table 69A lists about 200 genes that are upregulated in human umbilical vein endothelial cells (HUVEC) compared to normal body tissues. These genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 70A lists about 148 genes that are downregulated using the mean of vessels (veins and arteries) compared to the mean of HUVEC. These genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting relative level of mRNA expression.

TABLE 69A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of the mean of HUVEC AI's to the mean of the normal body tissue AI's

Pkey	ExAccn	UnigenelD	Unigene Title	R1
424806	AA382523	Hs.105689	MSTP031 protein	1.51
418036	Z37976	Hs.83337	latent transforming growth factor beta b	1.94
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothetical	1.60
442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.73
417944	AU077198	Hs.82985	collagen, type V, alpha 2	1.48
410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	1.91
452516	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.59
425139	AW630488	Hs.25338	protease, serine, 23	1.63
402463			NM_014624:Homo sapiens S100 calcium-bind	1.50
423798	AF047033	Hs.132804	solute carrier family 4, sodium bicarbon	1.31
412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.53
419948	AB041035	Hs.93847	NM_016931:Homo sapiens NADPH oxidase 4 (2.06
447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	2.10
446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	1.67
441457	AW996651	Hs.43838	ESTs	1.30
408296	AL117452	Hs.44155	DKFZP586G1517 protein	1.61
418994	AA286520	Hs.89546	selectin E (endothelial adhesion molecu	1.87
413795	AL040178	Hs.142003	ESTs	1.64
441689	AI123705	Hs.289068	ESTs	1.44
412567	AI750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	1.75
424432	AB037821	Hs.146858	protocadherin 10	1.65
432673	AB028859	Hs.278605	DnaJ (Hsp40) homolog, subfamily B, membe	1.31
418683	U90908	Hs.87241	hypothetical protein from clones 23549 a	1.42
453085	AW954243		KIAA0251 protein	1.47
438887	R68857	Hs.265499	ESTs	1.49
436729	BE621807		transmembrane 4 superfamily member 1	1.91
400494			ENSP00000238970:CIG30 (Fragment).	1.34
442506	BE566411		ESTs	1.54
425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	1.55
414476	AA301867	Hs.76224	EGF-containing fibrin-like extracellular	2.65
452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	1.62
422389	AF240635	Hs.115897	protocadherin 12	1.38
417124	BE122762	Hs.25338	ESTs	2.13
433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	1.31
419883	W55956	Hs.94030	Homo sapiens mRNA: cDNA DKFZp586E1624 (f	1.54
414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.51
450534	AI570189	Hs.25132	KIAA0470 gene product	1.43
449618	AI078459	Hs.15978	KIAA1272 protein	1.42
446098	AW072215	Hs.208470	ESTs	1.53
413281	AA861271	Hs.222024	transcription factor BMAL2	1.40
448674	W31178	Hs.154140	ovary-specific acidic protein	1.47
407051	X97748		gb:H.sapiens PTX3 gene promotor region.	1.33

	434846	AW295389	Hs.119768	ESTs	1.29
	408570	AL046406	Hs.103483	KIAA1798 protein	1.47
	436772	AW975688		metallothionein 1E (functional)	1.81
	453789	AA628517	Hs.118502	ESTs	1.41
5	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	1.35
	441020	W79283	Hs.35962	ESTs	1.62
	401234			mitogen-activated protein kinase 8 inter	1.48
	420174	AI824144	Hs.199749	ESTs	1.75
	445684	AK001696	Hs.13109	Ran binding protein 11	1.49
10	418693	AI750878	Hs.87409	thrombospondin 1	1.89
	426535	AU077012	Hs.289582	ESTs, Weakly similar to ubiquitous TPR m	1.77
	412330	NM_006100	Hs.788	A kinase (PRKA) anchor protein (gravin)	2.02
	412646	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	1.64
	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	1.26
15	433376	AI249361	Hs.74122	caspace 4, apoptosis-related cysteine pr	1.49
	422099	AA156022	Hs.111518	hypothetical protein	1.56
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HE	1.54
	445119	AF035121	Hs.12337	kinase insert domain receptor (a type II	1.40
	438142	T90309	Hs.269651	ESTs	1.45
20	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	1.44
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	1.42
	453459	BE047032	Hs.257789	ESTs	1.61
	442711	AF151073	Hs.8645	hypothetical protein	1.42
	426428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	1.32
25	400288	X08256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.67
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	2.47
	407252	AA559037	Hs.163780	(AB075832) KIAA1952 protein [Homo sapien	1.76
	418825	AA228881	Hs.22394	hypothetical protein FLJ10893	1.40
	417805	U38545	Hs.82587	phospholipase D1, phosphatidylcholine-spe	1.35
30	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	1.55
	415714	NM_002290	Hs.78672	laminin, alpha 4	1.90
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	1.71
	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	1.88
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	1.75
35	452298	AI039243	Hs.278585	NM_024756; Homo sapiens hypothetical pro	1.86
	434596	T59538		gbv65g12s1 Stratagene ovary (937217)	1.52
	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	1.61
	433374	AI821409	Hs.304471	EST	1.45
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.14
40	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	1.50
	435705	AA782114	Hs.28043	ESTs	1.53
	456999	AA319798	Hs.298581	eukaryotic translation elongation factor	1.52
	453983	H94997	Hs.16450	ESTs	1.94
	406506			Target Exon	1.97
45	424503	NM_002205	Hs.149809	integrin, alpha 5 (fibronectin receptor,	2.32
	452924	AW580939	Hs.97199	complement component C1q receptor	2.36
	426696	AW363332	Hs.171844	NM_006505 Homo sapiens poliovirus recept	1.41
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	1.70
50	450152	AI138635	Hs.22968	intron of VEGFR	1.60
	437269	AA334384	Hs.149420	ESTs	1.59
	445279	R41900	Hs.22245	ESTs	1.52
	409509	AL036923	Hs.322710	ESTs	1.61
	410240	AL157424	Hs.61289	synaptotagmin 2	1.96
55	424711	NM_005795	Hs.152175	calcitonin receptor-like	1.81
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	1.91
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	1.85
	410057	R66634	Hs.268107	multimerin	1.67
	446727	AB011095	Hs.16032	KIAA0523 protein	1.51
60	412564	X83703		cardiac ankyrin repeat protein	1.71
	414786	AI246482	Hs.243010	Homo sapiens ras homolog gene family, me	1.91
	410276	AI554545	Hs.71832	angiopoietin-2	1.76
	406627	T64904	Hs.163780	ESTs	1.69
	405025			Bone morphogenetic protein 6	2.33
65	422648	D86983	Hs.118893	Melanoma associated gene	1.78
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	1.79
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfam	2.02
	432004	BE018302	Hs.2894	placental growth factor, vascular endoth	1.93
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	1.65
70	429276	AF056085	Hs.198612	G protein-coupled receptor 51	1.48
	407704	BE315072	Hs.78768	malignant cell expression-enhanced gene/	2.01
	448694	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2	1.83
	434398	AA121098	Hs.3838	serum-inducible kinase	1.65
	416851	AW963951	Hs.85618	ESTs	1.69
75	412420	AL036668	Hs.73853	bone morphogenetic protein 2	1.71
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	1.86
	450689	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	1.65
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	1.83
80	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	1.77
	428206	AB020643	Hs.183006	KIAA0836 protein	2.00
	412755	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	1.61
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.94
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	

5	425234	AW152225	Hs.165909	ESTs, Weakly similar to I380222 hypotheti	1.74
	444409	AJ792140	Hs.49265	ESTs	1.88
	421340	F07783	Hs.1359	decay accelerating factor for complement	1.74
	445701	AF055581	Hs.13131	lymphocyte adaptor protein	2.18
	444009	AJ380792	Hs.135104	ESTs	1.90
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfam	2.16
	416940	N75620	Hs.43157	ESTs	2.03
	418922	AW956580	Hs.42699	ESTs	2.09
10	431548	AJ834273	Hs.9711	novel protein	1.81
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.14
	434558	AW264102	Hs.39168	ESTs	1.83
	438183	BE263252	Hs.6101	hypothetical protein MGC3178	2.05
	428438	NM_001955	Hs.2271	endothelin 1	2.46
15	453365	AA035211	Hs.17404	SOX7 SRY (sex determining region Y)-box	2.20
	418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	2.26
	439410	AA632012	Hs.188746	ESTs	1.93
	453467	AJ535997	Hs.30089	ESTs	2.39
	420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	1.84
20	417933	X02308	Hs.82962	thymidylate synthetase	1.70
	436420	AA443966	Hs.31595	ESTs	1.97
	414430	AJ346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.93
	412140	AA219691	Hs.73625	RAB8 interacting, kinesin-like (rabkines	1.80
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.03
25	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	1.58
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	1.81
	413745	AW247252	Hs.75514	nucleoside phosphorylase	1.99
	405121			mitogen-activated protein kinase 8 inter	2.99
30	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.76
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	2.13
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	2.71
	421937	AJ878857	Hs.109708	hematological and neurological expressed	1.65
	408669	AJ493591	Hs.78146	platelet/endothelial cell adhesion molec	2.39
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.77
35	418203	X54942	Hs.83758	CDC28 protein kinase 2	1.67
	408243	Y00787	Hs.624	interleukin 8	2.09
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.42
	407891	AA486620	Hs.41135	endomucin-2	2.34
	407891	AA486620	Hs.41135	endomucin-2	2.34
40	436032	AA150797	Hs.109276	latadin protein	2.24
	439382	BE247684	Hs.103070	ESTs	2.07
	419172	AW338625	Hs.22120	ESTs; similar to TRANSMEMBRANE 4 SUPERF	2.00
	442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	2.33
	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	2.11
45	432128	AA127221	Hs.296502	ESTs	2.27
	417426	NM_002291	Hs.82124	laminin, beta 1	2.11
	434217	AW014795	Hs.23349	ESTs	2.03
	439265	AL134430	Hs.6906	Homo sapiens cDNA: FLJ23197 fs, clone R	2.08
	442923	AW248322	Hs.95835	ESTs, Weakly similar to unnamed protein	1.57
50	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	1.60
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	2.37
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	2.55
	442544	AB018259	Hs.118140	KIAA0716 gene product	2.09
	449722	BE280074	Hs.23960	cyclin B1	1.76
55	413794	AF234532	Hs.61638	myosin X	2.01
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	2.15
	406964	M21305		gb:Human alpha satellite and satellite 3	3.08
	448231	AJ701916	Hs.202509	ESTs	2.27
	408989	AW361666	Hs.49500	KIAA0746 protein	1.43
60	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	2.67
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	2.18
	418185	AW958272	Hs.347326	intercellular adhesion molecule 2	2.60
	417308	H60720	Hs.81892	KIAA0101 gene product	1.86
	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	2.92
65	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.92
	400666			NM_002425:Homo sapiens matrix metallopro	2.59
	431728	NM_007351	Hs.268107	multimerin	2.72
	440086	NM_005402	Hs.288757	v-rel simian leukemia viral oncogene hom	2.25
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	1.76
70	451979	F06972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX),	3.37
	416138	C18356	Hs.295944	tissue factor pathway inhibitor 2	3.11
	414577	AJ056548	Hs.72116	hypothetical protein FLJ20992 similar to	3.11
	444330	AJ597655	Hs.49265	ESTs	3.08
	422424	AJ186431	Hs.296638	prostate differentiation factor	2.96
75	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	4.84
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (Interstitial	11.91

TABLE 69B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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453085	10017_1	BC017336 BG716430 BG501286 BI458528 AI582223 N98532 AI338138 AI273442 AW102617 AA831177 AA745642 AA412583 AA355375 BG547492 AW954243 BI766546 BG057641 AI192435 AI338935 AI312651 AI708679 AI191125 AI206832 AA676899 AI078010 AI888718 AA452830 BF445542 N69930 AA715017 BF446713 BE046852 AW771909 AA907729 AI143749 AI761290 AA890233 BF925759 AI783713 AI767267 AA814538 W56778 AA918481 BG743526 BE645242 AI025328 AI298436 AI290445 H27710 AI475034 BG740023 AI090348 AI340003 BI602481 W38495 AI183314 AI927418 BG397181 AA878310 W19369 W56507 C05751 AW380760 AW380770 AW380790 BF930729 H28425 AA037326 AA375805 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI270939 AI927769 BE439795 AI963432 AA292956 AW192593 AI865838 AI696905 AI242384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349188 AA043217 BE219784 AI798114 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA577735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF959847 BG055071 AW675302 C003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 BF05782 AI589264 D57558 AI458237 AI432033 AA989862 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AI568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377595 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722205 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843697 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545285 AL540643 AU118627 AI4501379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AI556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI651761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906686 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392485 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308638 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 NM_002640 L03777 BG227962 AI925897 W60100 BG980023 AA853496 AA360401 AW956168 W61361 AI074846 AA373798 BG193973 BG499418 BF816267 AI675932 BG611734 BG777123 AW449485 BF912016 BE566411 BM068728 AW976385 AI121194 AI767324 BM054718 AW366882 AA156151 Z25109 C05177 AW975688 AA731063 N57084 AF147374 T59538 T59589 T59598 T59542 X83703 NM_014391 BC018667 AU139209 BE924924 BE924899 BE924977 BE924985 BE924947 BF229055 BE924917 BE924938 BE812621 BE924937 AA969184 BE924898 BF229066 BF229054 BF081177 BE924934 BF229040 BE925037 BE925011 BG943776 AA488072 AA486364 Z36249 AW455806 AW582753 BF081131 BE924910 BF229058 BF081172 BE924956 AW378093 BF081132 BF081168 BE812736 BE812738 BF081165 C04160 C04483 BF229048 AW975183 AA973583 AI365103 AI699495 AI301787
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TABLE 69C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402463	9796896	Minus	8818-8952
400494	9714719	Plus	169845-170272
401234	9929642	Plus	120173-120337
406506	7711374	Minus	6843-8077
405025	7107727	Plus	105267-105343,106184-106294,106387-10653
405121	8102330	Minus	35816-36004,36587-36684
400666	8118496	Plus	17982-18115,20297-20456

TABLE 70A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of the mean of the vessel A's to the mean of the HUVEC A's

Pkey	ExAccn	UnigenelD	Unigene Title	R1
428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	0.99
439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.06
412636	NM_004415		desmoplakin (DPI, DPIP)	1.25
426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.36
414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	1.50
417878	U90816	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	1.55
414572	AU077174	Hs.288181	cathepsin H	1.64
415314	N88802	Hs.5422	glycoprotein M6B	1.70
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	1.75
406973	M34996	Hs.198253	major histocompatibility complex, class	1.88
456974	M12529	Hs.169401	apolipoprotein E	1.90
430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	1.91
406828	AA419202	Hs.84298	CD74 antigen (invariant polypeptide of m	1.97
422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	1.99

	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	2.02
	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	2.03
	413391	A1223328	Hs.75335	glycine amidinotransferase (L-arginine)	2.12
5	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	2.15
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.17
	437536	X91221	Hs.144465	ESTs	2.21
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	2.26
	446945	A193115	Hs.16611	tumor protein D52-like 1	2.27
10	422639	A1929377	Hs.173724	creatine kinase, brain	2.29
	427451	A1690916	Hs.178137	transducer of ERBB2, 1	2.31
	454042	H22570		hypothetical protein FLJ20093	2.37
	418283	S79895	Hs.83942	cathepsin K (pseudosclerosis)	2.38
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	2.39
15	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	2.41
	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	2.43
	427393	AB029018	Hs.177635	KIAA1095 protein	2.47
	414217	A1309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.49
	414063	H26904	Hs.75736	epitopoprotein D	2.50
20	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	2.51
	414803	X03100	Hs.914	Human mRNA for S8 class II histocompati	2.51
	410532	T53088	Hs.155376	hemoglobin, beta	2.56
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (2.58
	437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	2.58
25	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	427980	AA418305	Hs.303205	EST	2.59
	442695	AC002425	Hs.8603	p8 protein (candidate of metastasis 1)	2.62
30	425751	T19239	Hs.1940	crystallin, alpha B	2.63
	414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid c	2.63
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	2.66
	453464	AJ884911	Hs.32989	receptor (calcitonin) activity modifying	2.67
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.67
35	452685	A1634651	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	2.67
	425869	AA524547	Hs.160318	FXD domain-containing ion transport reg	2.73
	406643	N77976	Hs.347939	hemoglobin, alpha 2	2.73
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	2.74
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	2.80
40	444195	AB002351	Hs.10587	KIAA0353 protein	2.81
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.86
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	2.92
	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	2.93
	440820	AL031846		plakophilin 4	2.94
45	429123	AB011099	Hs.196647	KIAA0527 protein	2.97
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.01
	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	3.01
	425822	AW360847	Hs.16578	ESTs	3.01
	420195	N44348	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.04
50	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	3.04
	407869	A1827976	Hs.24391	hypothetical protein FLJ13612	3.08
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3.07
	410036	R57171	Hs.57975	caldesmon 2 (cardiac muscle)	3.10
	412047	AA934589	Hs.49696	ESTs	3.12
55	414840	R27319	Hs.23823	hairy/enhancer-of-split related with YRP	3.14
	424651	AW93206		ESTs	3.17
	443932	AW888222	Hs.9973	tensin	3.18
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.20
	434025	AF114264	Hs.216381	Homo sapiens clone H1409 unknown mRNA	3.20
60	421834	BE543205	Hs.288771	DKFZP586A0522 protein	3.20
	423961	D13666	Hs.136348	periostin(OSF-2cs)	3.24
	447384	A1377221	Hs.40528	ESTs	3.24
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-like	3.25
	447023	AA358764	Hs.17109	integral membrane protein 2A	3.25
65	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	3.25
	406972	M32053		gb:Human H19 RNA gene, complete cds.	3.26
	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	3.27
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	3.28
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	3.29
70	443523	AA345519	Hs.9641	complement component 1, q subcomponent,	3.33
	410614	A1091195	Hs.65029	growth arrest-specific 1	3.35
	451529	A817901	Hs.208641	ESTs	3.35
	430310	U60115	Hs.239069	four and a half LIM domains 1	3.37
	424897	D63216	Hs.153684	frizzled-related protein	3.37
75	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	3.38
	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	3.41
	421913	A1934365	Hs.109439	osteoglycin (osteoinductive factor, mime	3.43
	451331	AK002039	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.44
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	3.46
80	407938	AA905097	Hs.85050	phospholamban	3.48
	418005	A1186220	Hs.83164	collagen, type XV, alpha 1	3.51
	452877	A1250789	Hs.32478	ESTs	3.52
	419577	L36531	Hs.91296	integrin, alpha 8	3.52
	404277			NM_019111: Homo sapiens major histocompa	3.54

5	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	3.58
	421853	AL117472	Hs.108924	SH3-domain protein 5 (ponsin)	3.64
	447111	AI017574	Hs.17409	cysteine-rich protein 1 (intestinal)	3.68
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.70
	418371	M13560	Hs.84298	CD74 antigen (Invariant polypeptide of m	3.71
10	440274	R24595	Hs.7122	scrapie responsive protein 1	3.73
	427818	AW511222	Hs.193765	ESTs	3.73
	433465	AV657778	Hs.3314	selenoprotein P, plasma, 1	3.75
	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	3.77
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	3.80
15	424205	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	3.83
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	3.86
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	3.89
	434868	R50032	Hs.159263	collagen, type VI, alpha 2	3.90
	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	3.95
20	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	3.95
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	3.97
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	4.01
	449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	4.03
	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	4.07
25	430572	U33114	Hs.245188	tissue inhibitor of metalloproteinase 3	4.09
	421823	N40850	Hs.28625	ESTs	4.17
	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	4.25
	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	4.26
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	4.29
30	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.34
	419939	AJ076772	Hs.1279	complement component 1, r subcomponent	4.37
	415165	AW887604	Hs.78065	complement component 7	4.37
	414176	BE140638	Hs.75794	endothelial differentiation, lysophospha	4.41
	452114	N22687	Hs.8236	ESTs	4.43
35	406850	AI624300	Hs.172928	collagen, type I, alpha 1	4.43
	428411	AW291464	Hs.10338	ESTs	4.48
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	4.51
	406849	AA454809	Hs.172928	collagen, type I, alpha 1	4.54
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	4.57
40	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxin)	4.57
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.68
	421814	L12350	Hs.108623	thrombospondin 2	4.73
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	4.76
	414290	AI568801	Hs.71721	ESTs	4.98
45	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	5.13
	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium	5.14
	416784	AA334592	Hs.79914	tumican	5.20
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	5.50
	408221	AA912183	Hs.47447	ESTs	5.65
50	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	5.87
	416585	X54162	Hs.79386	telomodin 1 (smooth muscle)	6.47
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	6.65
	426408	AJ742501	Hs.169756	complement component 1, s subcomponent	7.94
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	9.90
	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hev9)	9.91

TABLE 70B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
60	412636	1438_1
65		M77830 NM_004415 AF139065 BG681115 BG740377 B1712964 BG000656 AA128470 BM438324 H27408 BE831630 BE167165 AW370827
70		AW370813 J05211 BG688865 BG740734 BG680618 BG739778 B1765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592
75		BE182164 BF149266 BE940187 B1060445 B1060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316
80		B1039774 BE713818 BE713548 AW170253 BE160433 B1039775 AW886475 BM462504 BE931734 BF149284 AA340777 BF381183 BG621737
		AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 B58704 AA852212 AW366566 B1090358 BF087707 BE819046
		BE819005 AA377127 BE073467 BE819069 BE819048 B1036306 BG990973 B1040954 BF919911 AU140155 A1951766 A1434518 AW804674
		BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 B1039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510
		AW265328 BG436319 BE182168 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276
		BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421
		BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE174632 BE184948 BG985845
		AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705968 AW848723
		AW376699 AW376817 AW376697 BG005097 BF751115 BE695084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211
		AW997139 BE865474 BE185187 BE156821 BE715089 BE713297 BE713298 BE719915 AW799309 BF872345 BF086676 BF094833 BF094748 BF094583
		BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583
		AW377699 AW607238 BE082519 AW377700 BF349467 A190590 A1554403 A1392926 AU158477 B1467252 AU159919 A1760816 BF082516
		A139101 AA451923 A1340326 A1590975 B1791553 A1700963 A142882 AA039975 AA946936 AA644381 BM314884 AA702424 A1417612
		AW190555 A1220573 A1304772 A170345 A1627383 AA552300 A1911702 AW166807 A1346078 W95070 AA149191 AA026864 A1830049 AW780435
		A1078449 A1819984 A1858282 B1468588 A1860584 A1025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 A1927207
		A1205263 BF082491 AW021347 A1568096 A1627383 AA552300 A1911702 AW166807 A1346078 W95070 AA149191 AA026864 A1830049 AW780435
		H44405 A1910434 BF082513 A1494069 A170027 A1635878 A128330 BG681425 BE706078 R20904 EG680059 BG676647 BF764409 AA026654
		AV745530 B1762796 BG287391 AW798780 BE708045 BE226470 AW799118 BF087996 BE002273 AW879451 A1571075 BE067786 AV721320
		A1022862 N29754 C03378 N84767 AA131077 H30146 BE714290 A1686669 A1568892 A1915596 AW105614 A1887258 A1538577 BE926474
		BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763
		BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 A1905927 BF992780 AW853812 BG954443 B1770853 BG679406

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454042 30254_1
440820 3091_1
424651 46029_5

BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 B1089483 BE006273 BE872225 AW391912 BE925515 BG677012
 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 B1040941 A337270 AW384371 AW847442
 B1058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 A1284090
 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 B1013292 BE001925 AW365158 AW365154 AW606653
 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 A498487
 AJ420458 A1018523 AA708686 BF949633 AL119553 BF945960 A1081305 AA041432 A1921013 A1684910 A1654847 AW874199 A1206120
 AW241428 R43035 T66767 AW103715 W28478 BF953052 H45926 BF807568 AW903943 BE170143 B1040435 BF931989 B1600000 AV722350
 W27787 H45331 B1549761 R53955 B1549855 BG991583 B1491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199
 A431587 BE858679 AW292267 A1421678 AA041195 BE466753 A1243913 A1358894 AW137298 A1365468 N64350 AA779107 AW025969 R49056
 AA347011 R55722 AW771106 F04969 Z38381 F01659 H17395 B1493714 A1880103 AW771447 A1202561 AA788851 A1494436 BF856114 H22570
 AW964381 BG007409 BM314056 AA465642 T30561 T33111 Z42834 C04542 BF948152 BF944325 BF858895 AA935284 A1267360 N64249
 W67500 F07962 AA322394 B1489987 BE644965 BM313782 AA910364 A1809246 AA836750 BF115228 AA829730 N27413 BM141766 A1742325
 AA455261 AA938708 A1420241 A1130039 BF222341 BF941301 AA771807 Z41034 BF447457 BF447426 AW515347 T03874 F02360 F02302
 N34898 A1678586 AA807824 AA948556 AW204638 BM142045 BF446775 AV648364 A1801368 AA971739 A1017351 AA760722 A1460007 A1458383
 A1694152 AA226536 BE467282 N47808 BE348825 BE830581 BE830583 N53009 N59351 N41056 W67501 AA016246 H43293 F21282 R59121
 R56280
 BG435302 BM083687 AA904035 AA488889 W76175 AA761874 H28767 AA910081 AA837086 A1521825 BG986378 A1478562 AA743152 AA746092
 H88863 BG986375 AA635644 A1493206 AA669979 BE245127 BG986430 BG986529 BF665873 BG030157 BG622575 AA766495

TABLE 70C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
404277	1834458	Minus	91665-91946

TABLE 71A: 774 GENES UP-REGULATED IN EWING SARCOMA COMPARED TO NORMAL ADULT TISSUES

Table 1A lists 774 genes up-regulated in Ewing Sarcoma compared to normal adult tissues. These were selected from 35371 probesets on the Affymetrix/Eos Hu30 GeneChip array such that the ratio of "average" Ewing Sarcoma to "average" normal adult tissues was greater than or equal to 2.1. The "average" Ewing Sarcoma level was set to the 75th percentile amongst numerous Ewing sarcomas. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAcn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: 75th percentile of ewing sarcoma to 85th percentile of body map

Pkey	ExAcn	UnigeneID	Unigene Title	R1
104659	AW969769	Hs.105201	ESTs	70.3
101447	M21305		gb:Human alpha satellite end satellite 3	64.7
105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	50.5
115881	NM_005756	Hs.184942	G protein-coupled receptor 64	48.8
121792	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	46.7
101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	46.6
110278	AF061573	Hs.19492	protocadherin 8	46.1
126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	41.4
116752	AL008583	Hs.91622	neuronal pentraxin receptor	40.9
119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	39.6
104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	36.9
110728	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	35.5
121362	AF050147	Hs.97932	chondromodulin I precursor	34.7
131291	NM_004350	Hs.170019	runx-related transcription factor 3	33.0
101063	D54745	Hs.80247	cholecystokinin	31.7
121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidylseri	28.7
122651	AW975398	Hs.293836	ESTs	28.0
100299	D49493	Hs.2171	growth differentiation factor 10	26.5
129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.2
123619	AA602964		gb:nc97c02.s1 NCL CGAP_P12 Homo sapiens	26.1
124006	A1147155	Hs.279727	ESTs; homologue of PEM-3 (Clona savigny)	23.1
116301	AW969706	Hs.293332	ESTs	22.6
121231	AA814948	Hs.96343	ESTs, Weakly similar to ALLC_HUMAN III	22.3
106533	AL134708	Hs.145998	ESTs	22.3
109166	AA218691	Hs.73625	RAB6 Interacting, kinesin-like (rabkinases	21.3
131313	R96290	Hs.75874	ribosomal protein L44	20.8
116790	AW161357		microtubule-associated protein tau	18.7
105316	A1671245	Hs.24835	hypothetical protein FLJ14594	18.2
102123	NM_001809	Hs.1594	centromere protein A (17kD)	17.8
126218	AL049801	Hs.13649	Novel human gene mapping to chromosome 13	17.8
119791	AA554907	Hs.58291	ESTs	16.7
113003	AW292315	Hs.7215	ESTs	16.3
102836	U94320	Hs.158330	neuropeptide Y receptor Y5	16.3
126799	AW753865	Hs.74376	olfactomedin related ER localized protei	16.3
105298	BE387790	Hs.26369	hypothetical protein FLJ20287	15.5
107160	AA314490	Hs.27669	KIAA1563 protein	14.8
115313	AA808001	Hs.184411	albumin	14.6
123308	C14187	Hs.103538	ESTs	14.2

	126077	M78772	Hs.210836	ESTs	14.0
	100698	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	13.9
	106821	NM_006594	Hs.28298	adaptor-related protein complex 4, beta	13.9
	110288	H40665	Hs.31554	ESTs	13.8
5	106498	AI221919		hypothetical protein FLJ10582	13.8
	112134	R41823	Hs.7413	ESTs;catyntenin-2	13.7
	115265	AA334274	Hs.18368	DKFZP564B0769 protein	13.4
	126639	AW582962	Hs.102897	CGI-47 protein	13.2
	125698	AF078847	Hs.191356	general transcription factor IIH, polype	12.8
10	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	12.3
	119456	AA248897	Hs.48784	ESTs	12.2
	135155	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	12.1
	105614	AA648459	Hs.335951	hypothetical protein AF301222	12.0
	131941	BE252983	Hs.35086	ubiquitin specific protease 1	12.0
15	132968	AF234532	Hs.61638	myosin X	11.7
	132725	NM_006276	Hs.184167	splicing factor, arginine/serine-rich 7	11.7
	111353	W20090	Hs.6616	ESTs	11.4
	123289	AA495904	Hs.103316	ESTs	11.3
	104958	AI249502	Hs.29669	ESTs	11.1
20	123532	AA608733		gb:ae58f06.s1 Stratagene lung carcinoma	11.0
	104173	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	10.7
	125556	AB033064	Hs.236463	KIAA1238 protein	10.7
	127240	AJ005683	Hs.86998	nuclear factor of activated T-cells 5, l	10.6
	123049	BE047680	Hs.211869	clckopf (Xenopus laevis) homolog 2	10.6
25	132315	AF091086	Hs.44563	hypothetical protein	10.5
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-link	10.5
	128609	NM_003616	Hs.102456	survival of motor neuron protein Interac	10.4
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	10.4
	110730	N67655	Hs.26411	ESTs	10.3
30	119186	AI979147	Hs.101265	hypothetical protein FLJ22583	10.3
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAPI_HUMAN DEATH	10.3
	121916	AW117207	Hs.98523	ESTs	10.2
	131402	Y08890	Hs.113503	karyopherin (importin) beta 3	10.1
	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	10.0
35	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	10.0
	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	10.0
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	9.9
	103446	X98834	Hs.79971	sal (Drosophila)-like 2	9.7
	105091	AA148859	Hs.179909	hypothetical protein FLJ22995	9.6
40	106146	W07288	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	9.5
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	9.5
	115414	AA662240	Hs.283099	AF15q14 protein	9.4
	117829	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN I	9.4
	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	9.3
45	121910	AI204600	Hs.96978	hypothetical protein MGC10764	9.2
	130625	AF176012	Hs.260720	J domain containing protein 1	9.2
	129755	R42216	Hs.7759	Homo sapiens clone 24538 mRNA sequence	9.1
	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	9.0
	111109	AI940675	Hs.20914	hypothetical protein FLJ23056	9.0
50	120217	AA862257	Hs.66035	ESTs	9.0
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-link	8.9
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	8.8
	126262	AI085153	Hs.143764	ESTs, Weakly similar to unknown (H.sapie	8.8
55	113903	AI368034	Hs.36679	ESTs, Weakly similar to A46010 X-linked	8.7
	105253	AW997484	Hs.5003	KIAA0456 protein	8.6
	102581	AJ077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	8.6
	105172	AA187554	Hs.300496	mitochondrial solute carrier	8.6
	100380	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	8.6
	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.5
60	102725	AB026187	Hs.159156	protocadherin 11	8.5
	130298	AI347487	Hs.132781	class I cytokine receptor	8.4
	132294	AB023191	Hs.44131	KIAA0974 protein	8.2
	118644	AA443241		ribosomal protein L44	8.2
	106575	AW970602	Hs.105421	ESTs	8.2
65	133142	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	8.1
	119499	AI918906	Hs.55080	ESTs	8.1
	100248	NM_015156	Hs.78398	KIAA0071 protein	8.1
	114837	BE244930	Hs.166895	ESTs	8.0
	107098	AI823593	Hs.27688	ESTs	8.0
70	123960	AW082862	Hs.287733	hypothetical protein FLJ23189	7.9
	105280	AA894638	Hs.14600	ESTs	7.9
	115147	AA745781	Hs.38399	hypothetical protein MGC2454	7.9
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	7.9
	133063	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.8
75	106730	AW377314	Hs.5364	DKFZP564I052 protein	7.8
	126426	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	7.8
	107254	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	7.8
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	7.8
	119082	AF252937	Hs.91546	cytochrome P450 retinoid metabolizing pr	7.7
80	125400	AL110151	Hs.128797	DKFZP566D0824 protein	7.7
	129413	AW377610	Hs.11123	DKFZP564G092 protein	7.7
	116766	AI608657	Hs.95097	ESTs	7.7
	129075	BE250162	Hs.83765	dihydrofolate reductase	7.6

5	105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypothe	7.6
	132438	AW363887	Hs.82916	chaperonin containing TCP1, subunit 6A (7.6
	118036	AI471862	Hs.196008	Homo sapiens cDNA FLJ111723 fls, clone HE	7.6
	131170	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	7.5
	104548	R39398	Hs.91559	ESTs	7.5
10	131495	AA812434		SMC2 (structural maintenance of chromoso	7.5
	132543	BE568452	Hs.344037	protein regulator of cytokinesis 1	7.4
	124040	U23752	Hs.32964	SRY (sex determining region Y)-box 11	7.4
	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous ri	7.3
	132559	AF119848	Hs.270863	hypothetical protein PRO1580	7.3
15	101050	AJ077324	Hs.1832	neuropeptide Y	7.2
	111823	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	7.2
	116401	AW893940	Hs.59698	ESTs	7.1
	105127	AA045648	Hs.301957	nrdix (nucleoside diphosphate linked moi	7.1
	128478	AA708205	Hs.100343	ESTs	7.1
20	110456	H52348	Hs.36636	ESTs	7.1
	118846	AW295958	Hs.50895	homeo box C4	7.1
	120934	AA226198		gb:nc26a07.s1 NCL_CGAP_Pr1 Homo sapiens	7.1
	128132	AA225632		gb:nc08a07.r1 NCL_CGAP_Pr1 Homo sapiens	7.0
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	7.0
25	106157	W37943	Hs.34892	KIAA1323 protein	6.9
	117852	AW877787	Hs.136102	KIAA0853 protein	6.9
	106213	N45018	Hs.8769	hypothetical protein DKFZp761J17121	6.9
	118013	AJ674126	Hs.94031	ESTs	6.9
	120147	AJ917116		hemoglobin, beta	6.8
30	118267	N34905	Hs.44653	Homo sapiens cDNA: FLJ22669 fls, clone H	6.8
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624	6.8
	120325	AA195651		AP-2 beta transcription factor	6.8
	133276	AW978439	Hs.69504	ESTs	6.8
	127742	AW293496	Hs.180138	ESTs	6.7
35	127664	AA806164	Hs.116502	ESTs	6.7
	108778	AF133123	Hs.90847	general transcription factor IIIC, polyp	6.6
	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associate	6.6
	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Ro	6.6
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	6.6
40	115197	R18656		ESTs	6.5
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	6.5
	103346	X87613	Hs.5464	thyroid hormone receptor coactivating pr	6.4
	126967	AA205976		gb:zg48a10.r1 Stratagene hNT neuron (937	6.4
	118499	N67274	Hs.50141	EST	6.4
45	105301	AW352357	Hs.7457	MAGE1 protein	6.3
	113617	AI869372	Hs.17207	Homo sapiens cDNA FLJ11922 fls, clone HE	6.3
	127968	AA830201	Hs.124347	ESTs	6.3
	134719	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	6.3
	110748	AW581992	Hs.301434	KIAA1387 protein	6.3
50	115844	AJ373062	Hs.332938	hypothetical protein MGC5370	6.3
	121885	AA934883	Hs.98467	ESTs, Highly similar to AF257737 1 cilia	6.2
	102398	U42359		gb:Human N33 protein form 1 (N33) gene,	6.2
	130882	AA497044	Hs.20887	hypothetical protein FLJ10392	6.2
	132256	AJ078645	Hs.431	murine leukemia viral (bml-1) oncogene h	6.2
55	106383	AA447453	Hs.27860	Homo sapiens mRNA: cDNA DKFZp586M0723 (f	6.2
	135186	U73328	Hs.172648	distal-less homeobox 4	6.2
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	6.2
	109261	BE466639	Hs.81779	Homo sapiens cDNA FLJ13591 fls, clone PL	6.1
	114357	R41677	Hs.8107	Homo sapiens cDNA FLJ14839 fls, clone OV	6.1
60	128501	AL133572	Hs.199009	protein containing CXXC domain 2	6.1
	109747	AJ223001	Hs.22969	ESTs, Weakly similar to Z141_HUMAN ZINC	6.1
	128361	AW172570	Hs.14600	ESTs	6.1
	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	6.0
	104689	AA420450	Hs.292911	Plakophilin	6.0
65	113575	AW138168	Hs.15671	ESTs, Weakly similar to KBF3_HUMAN NUCLE	6.0
	121830	AW394055	Hs.98427	ESTs, Weakly similar to I38022 hypothe	5.9
	119298	NM_001241	Hs.155478	cyclin T2	5.9
	109841	H01052		gb:yj32h01.s1 Soares placenta Nb2HP Homo	5.9
	115622	AJ088691	Hs.208414	Homo sapiens mRNA: cDNA DKFZp564D0472 (f	5.8
70	122969	AW821252	Hs.104336	hypothetical protein	5.8
	109872	R65841	Hs.28653	ESTs	5.8
	114208	AL049468	Hs.7859	ESTs	5.8
	113494	T91451	Hs.86638	ESTs	5.8
	127684	AA668631	Hs.159971	KIAA0379 protein	5.8
75	128300	W94197	Hs.110165	ribosomal protein L26 homolog	5.8
	127489	AA650250	Hs.272076	ESTs	5.8
	133479	W01558	Hs.238797	ESTs, Moderately similar to I38022 hypot	5.8
	105909	AA195191		hypothetical protein FLJ20729	5.8
	101255	BE385864	Hs.149894	mitochondrial translational initiation f	5.8
80	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	5.7
	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	5.7
	125395	AJ468004	Hs.278958	hypothetical protein FLJ12929	5.7
	130723	BE247676	Hs.18442	E-1 enzyme	5.7
	107230	AJ034467	Hs.34650	ESTs	5.7
80	102745	AW753865	Hs.74376	oligodendrocyte related ER localized protal	5.6
	108699	AA121514	Hs.70832	ESTs	5.6
	128080	F12310		gb:HSC38D041 normalized infant brain cDN	5.6

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	117357	N24829		gb:yx98h12.s1 Soares melanocyte 2NbHM Ho	5.6
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transposo	5.6
	123494	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.5
	100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	5.5
5	126165	AI741816	Hs.125897	ESTs	5.5
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	5.5
	124370	AI243499	Hs.170652	ESTs	5.5
	106135	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.5
	106668	R49390	Hs.254129	KIAA1678	5.4
10	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.4
	109606	Z43371	Hs.7012	ESTs	5.4
	115816	BE042915	Hs.22572	Homo sapiens cDNA FLJ13575 fis, clone PL	5.4
	125186	AA610620	Hs.181165	major histocompatibility complex, class	5.4
	131185	BE280074	Hs.23950	cyclin B1	5.4
15	111227	T06701	Hs.12268	ESTs	5.4
	105516	AK001269	Hs.30738	hypothetical protein FLJ10407	5.4
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	5.3
	116008	T79153	Hs.48589	zinc finger protein 228	5.3
	106394	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	5.3
20	115121	AI634549	Hs.325422	ESTs	5.3
	125464	N71807		gb:yz29d09.r1 Soares_multiple_sclerosis_	5.3
	115596	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	5.3
	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	5.3
	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (5.3
25	110151	H18835	Hs.31608	hypothetical protein FLJ20041	5.2
	105539	AB040884	Hs.109694	KIAA1451 protein	5.2
	130567	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
	111077	N41367	Hs.173002	ESTs, Weakly similar to I38022 hypothe	5.2
	120830	AI568170	Hs.96886	ESTs	5.2
30	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (5.2
	103316	X83301	Hs.324728	SMA5	5.2
	116129	AF189011	Hs.49163	putative ribonuclease III	5.2
	131253	R71802	Hs.24853	ESTs	5.2
	116680	AW902848	Hs.273829	ESTs	5.2
35	123949	AA621665	Hs.208957	EST	5.2
	105511	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	5.2
	125847	AW161885	Hs.269745	ESTs	5.1
	108301	AA068728	Hs.184582	ribosomal protein L24	5.1
	110799	AI089660	Hs.323401	dpy-30-like protein	5.1
40	104899	AA054726	Hs.285574	ESTs	5.1
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein	5.1
	107869	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypothe	5.1
	121309	AA293834	Hs.97312	ESTs	5.1
	125321	T86652	Hs.178294	ESTs	5.1
45	102627	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	5.0
	104446	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	5.0
	126020	H79863	Hs.114243	ESTs	5.0
	116814	H50834	Hs.77899	gb:yp88a10.s1 Soares fetal liver spleen	5.0
	130622	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisocu	5.0
50	110818	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp588N2424 (f	4.9
	127765	AA971146	Hs.129074	ESTs, Moderately similar to MEG1 MOUSE M	4.9
	108768	AF181721	Hs.61345	RU2S	4.9
	120484	AA253170	Hs.96473	EST	4.9
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	4.9
55	129012	R81936		ribosomal protein L44	4.9
	124973	AI476066	Hs.102243	ESTs, Weakly similar to I78885 serine/th	4.9
	124648	AA249086	Hs.125034	hypothetical protein FLJ13340	4.9
	126904	AA948033	Hs.130853	ESTs	4.9
	131528	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.8
60	130637	AA356764	Hs.17109	integral membrane protein 2A	4.8
	126769	AA083456		gb:zn09g08.r1 Stratagene hNT neuron (937	4.8
	126086	H75681		gb:yr77g01.r1 Soares fetal liver spleen	4.8
	100169	AL037228	Hs.82043	D123 gene product	4.8
	130262	D63216	Hs.153684	frizzled-related protein	4.8
65	109260	AW878515	Hs.131915	KIAA0863 protein	4.8
	103120	BE410731	Hs.74050	follicular lymphoma variant translocation	4.8
	111099	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.8
	126142	H86261	Hs.40568	ESTs	4.8
	126802	AW805510	Hs.97056	hypothetical protein FLJ21634	4.7
70	105848	AW954064	Hs.24951	ESTs	4.7
	127987	AI022103	Hs.124511	ESTs	4.7
	129706	AAA43241		ribosomal protein L44	4.7
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.7
	126629	AL096739	Hs.107260	hypothetical protein DKFZp586H0623	4.7
75	111348	AA034922	Hs.9585	ESTs	4.7
	100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	4.7
	127542	AA703684	Hs.179833	ESTs, Moderately similar to ALU5_HUMAN A	4.7
	132452	AW973521	Hs.247324	mitochondrial ribosomal protein S14	4.7
	123778	AW352149	Hs.102314	ESTs	4.7
80	126521	AI475110	Hs.203933	ESTs	4.6
	110343	AW136703	Hs.17268	ESTs	4.6
	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta	4.6
	127207	AA377165	Hs.44833	ESTs	4.6

5	113974	AW989756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bind	4.6
	133098	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	4.6
	109920	H05840	Hs.111323	ESTs	4.6
	103487	AA743603	Hs.172108	nucleoporin 88kD	4.6
	125353	AB033043	Hs.149377	hypothetical protein DKFZp761L0424	4.6
10	100893	BE245294	Hs.180789	S164 protein	4.6
	135047	AL134187	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.6
	111148	AB020690	Hs.7782	paraneoplastic antigen MA2	4.6
	107681	BE379594	Hs.49138	ESTs, Moderately similar to ALU7_HUMAN A	4.6
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	4.5
15	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.5
	104912	AA813192	Hs.200596	KIAA0547 gene product	4.5
	110223	H19836	Hs.31697	ESTs	4.5
	113047	AJ571940	Hs.7549	ESTs	4.5
	101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.5
20	113002	BE243513	Hs.7212	hypothetical protein PP1044	4.5
	105304	AW134924	Hs.190325	ESTs	4.5
	112386	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fis, clone NT	4.5
	106489	AA452054	Hs.119338	ESTs	4.5
	122792	AW188551	Hs.99519	hypothetical protein FLJ14007	4.5
25	112651	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypotheti	4.5
	111346	AW970976	Hs.293653	ESTs	4.5
	123596	AA421130	Hs.112640	EST	4.5
	125447	AJ582222	Hs.128686	ESTs	4.5
	106178	AL049935	Hs.301763	KIAA0654 protein	4.4
30	102250	AJ243631	Hs.74122	caspase 4, apoptosis-related cysteine pr	4.4
	105868	AA378780	Hs.334842	tubulin alpha 1	4.4
	127496	AJ031650		ESTs	4.4
	127315	AF116822		gb:Homo sapiens clone FLB4217 mRNA seque	4.4
	101913	AJ004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	4.4
35	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.4
	129445	W52452	Hs.29797	ribosomal protein L10	4.4
	114721	D61939	Hs.103822	ESTs	4.4
	120922	AA481003	Hs.97128	ESTs	4.3
	115167	AA749209	Hs.43728	hypothetical protein	4.3
40	102407	AW602154	Hs.82143	E74-like factor 2 (ets domain transcript	4.3
	106111	AW875398	Hs.6451	PRO0659 protein	4.3
	123829	AF251237	Hs.112208	XAGE-1 protein	4.3
	103616	NM_002647	Hs.32971	phosphoinositide-3-kinase, class 3	4.3
	100269	NM_001949	Hs.1189	E2F transcription factor 3	4.3
45	112728	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.3
	135098	AW274526	Hs.277721	membrane component, chromosome 17, surfa	4.3
	106034	AW952005	Hs.14928	hypothetical protein FLJ12903	4.3
	133571	BE150307	Hs.177556	melanoma antigen, family D, 1	4.3
	106246	AL036917	Hs.288821	KIAA1638 protein	4.3
50	125724	AL360190	Hs.318501	Homo sapiens mRNA full length insert cDN	4.3
	132206	AA425204	Hs.334721	hypothetical protein FLJ13391	4.3
	130227	BE397151	Hs.153003	serine/threonine kinase 16	4.3
	129650	AF109298	Hs.118258	prostate cancer associated protein 1	4.3
	130382	NM_003450	Hs.155204	zinc finger protein 174	4.3
55	105073	AL157441	Hs.17834	downstream neighbor of SON	4.2
	105403	AJ473827	Hs.31793	ESTs	4.2
	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.2
	134126	NM_003747	Hs.131814	tankyrase, TRF1-interacting ankyrin-rela	4.2
	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	4.2
60	106012	AJ240665		ESTs	4.2
	116732	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.2
	130832	AW838006	Hs.20082	zinc finger protein 3 (A8-51)	4.2
	125960	AJ754693	Hs.145968	ESTs	4.2
	133916	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.2
65	106232	AB037828	Hs.15370	KIAA1407 protein	4.2
	129228	U40714	Hs.239307	tyrosyl-IRNA synthetase	4.2
	109929	AA773187	Hs.294027	ESTs	4.2
	123729	AL039779	Hs.278672	membrane component, chromosome 11, surfa	4.2
	101266	L36645	Hs.73964	EphA4	4.2
70	132389	AA310393	Hs.190044	ESTs	4.2
	124320	H95749	Hs.102342	EST	4.2
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.1
	116133	AW449597	Hs.313652	EST, Weakly similar to I38022 hypothetic	4.1
	129001	AA443323	Hs.107812	BPOZ protein	4.1
75	119271	AJ061118	Hs.65328	Fanconi anemia, complementation group F	4.1
	114767	AJ859865	Hs.154443	minichromosome maintenance deficient (S.	4.1
	126107	H75477	Hs.93361	ESTs	4.1
	115333	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	4.1
	100571	L14561	Hs.78546	ATPase, Ca ⁺⁺ transporting, plasma membra	4.1
80	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	4.1
	120150	BE005771	Hs.153746	hypothetical protein FLJ22490	4.1
	134470	X54942	Hs.83758	CDC28 protein kinase 2	4.1
	129948	AJ537162	Hs.263988	ESTs	4.1
	106882	AA149537	Hs.26994	hypothetical protein FLJ20477	4.1
	126199	AW088276	Hs.125829	ESTs	4.1
	112727	T91029	Hs.15069	ESTs	4.1
	118872	AJ039201	Hs.283316	ESTs	4.1

5	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	4.0
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic acid)	4.0
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retrovirus	4.0
	127153	AJ732303	Hs.186518	hypothetical protein MGC25599 similar to	4.0
	124105	H11484	Hs.79133	ESTs	4.0
10	100031			AFFX control - DapX-M	4.0
	106897	AF039023	Hs.167496	RAN binding protein 6	4.0
	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	4.0
	133928	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo)	4.0
	126965	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR)	4.0
15	103100	NM_005574	Hs.184585	LIM domain only 2 (rhotin-like 1)	4.0
	119005	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	4.0
	118751	N74210	Hs.50454	ESTs	4.0
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	4.0
	111387	AI244489	Hs.285724	ESTs	4.0
20	118676	N45312	Hs.46506	ESTs	4.0
	107348	AW937553	Hs.182426	ribosomal protein S2	4.0
	120528	AI923511	Hs.104413	ESTs	4.0
	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	4.0
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.0
25	115399	AF151534	Hs.92023	core histone macroH2A.2	4.0
	133615	M82843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	4.0
	118129	N57493		gbvyy54c08.s1 Soares_multiple_sclerosis_	4.0
	126522	W31912	Hs.21168	gbzcc76d03.s1 Pancreatic Islet Homo sapi	4.0
	131965	W79283	Hs.35962	ESTs	3.9
30	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	3.9
	126029	AA704253	Hs.169359	ESTs	3.9
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	3.9
	105808	AI133161	Hs.266131	CGI-101 protein	3.9
	134087	U51166	Hs.173824	thymine-DNA glycosylase	3.9
35	133195	AI434760	Hs.279949	KIAA1007 protein	3.9
	112996	BE276112	Hs.7165	zinc finger protein 259	3.9
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	3.9
	118967	AI668670	Hs.216756	ESTs	3.9
	127335	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.9
40	106636	AW958037	Hs.286	ribosomal protein L4	3.9
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	3.9
	102266	U29725	Hs.3080	mitogen-activated protein kinase 7	3.9
	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	3.9
	103080	AU077231	Hs.82932	cyclin D1 (PRAD1; parathyroid adenomas	3.9
45	131971	BE567100	Hs.154938	hypothetical protein MDS025	3.9
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	3.9
	128895	AW467000	Hs.106985	ESTs	3.9
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	3.9
	112921	R91095	Hs.4276	KIAA1701 protein	3.8
50	120820	AA347417	Hs.96869	EST	3.8
	106459	AA789081	Hs.4029	glioma-amplified sequence-41	3.8
	114253	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.8
	105476	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.8
	122682	AA984531	Hs.159293	ESTs	3.8
55	130580	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.8
	130174	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), cat	3.8
	115577	AA393167	Hs.41294	ESTs	3.8
	129785	H19006	Hs.184780	ESTs	3.8
	126127	N95428		gbzbb80d09.s1 Soares_senescent_fibroblas	3.8
60	109793	F13088	Hs.8040	heparan sulfate (glucosamine) 3-O-sulfot	3.8
	103175	X89089	Hs.79227	myomesin (M-protein) 2 (165kD)	3.8
	100154	H60720	Hs.81892	KIAA0101 gene product	3.8
	106140	AB006624	Hs.14912	KIAA0286 protein	3.8
	129052	BE275031	Hs.158210	hypothetical protein MGC2555	3.8
65	103319	X83492	Hs.82359	tumor necrosis factor receptor superfam	3.8
	106319	W22335	Hs.7392	hypothetical protein MGC3199	3.8
	102391	AA285874	Hs.77494	deoxyguanosine kinase	3.8
	127262	AA828125		gbxrd71a09.s1 NCI_CGAP_Ov2 Homo sapiens	3.7
	126872	AW450979		gb:UH-BI3-ala-a-12-0-ULs1 NCI_CGAP_Su	3.7
70	107315	AA316241	Hs.90691	nucleophosmin/nucleoplasm 3	3.7
	113119	T47910		gbvby18b11.s1 Stratagene fetal spleen (9	3.7
	126962	R12014	Hs.20976	ESTs	3.7
	116203	AW137166	Hs.87305	ESTs	3.7
	123377	AW969183	Hs.271297	ESTs	3.7
75	122798	AW366286	Hs.145696	splicing factor (CC1.3)	3.7
	107780	AA018927	Hs.269213	ESTs	3.7
	132733	AB020631	Hs.123654	PCF11p homolog	3.7
	120649	AA687322	Hs.192843	leucine zipper protein FKSG14	3.7
	131163	AA099524	Hs.23754	ESTs	3.7
80	126708	AW962593	Hs.135260	ESTs	3.7
	117417	AI241733	Hs.43871	ESTs	3.7
	106272	AW969731	Hs.323099	ESTs	3.7
	110834	AW273860	Hs.5759	ESTs	3.7
	123663	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	3.7
	124250	AA350256		EST, Weakly similar to 2109260A B cell g	3.7
	127038	AA233014	Hs.105965	ESTs	3.7
	107711	W96141	Hs.220687	ESTs	3.7

	130850	AB040822	Hs.20237	DKFZP566C134 protein	3.7
	119126	R45175	Hs.117183	ESTs	3.7
	125466	R08234	Hs.180461	ESTs	3.6
5	105150	AA631977	Hs.155995	KIAA0843 protein	3.6
	103163	AJ077018	Hs.3235	keratin 4	3.6
	104495	AW975687	Hs.292979	ESTs	3.6
	107599	AW664072	Hs.60136	ESTs	3.6
	113577	AJ300699	Hs.111334	PRO0470 protein	3.6
10	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.6
	109411	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	3.6
	127563	AB035898	Hs.150587	kinesin-like protein 2	3.6
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	3.6
	114118	F01598	Hs.175930	ESTs	3.6
15	103937	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	3.6
	125174	W51835	Hs.231082	EST	3.6
	104799	AA029703		gbzse95h08.s1 Soares_fetal_heart_NbHH19W	3.6
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	3.6
	135191	X16866	Hs.333497	cytochrome P450, subfamily IID (debrisoq	3.6
20	124367	AJ683183	Hs.99348	distal-less homeo box 5	3.6
	113560	T91015		ESTs	3.6
	119232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypotheti	3.6
	113988	W87536	Hs.36473	ESTs, Weakly similar to JC5238 galactosy	3.6
	115173	BE612940	Hs.88252	ESTs	3.6
25	126600	AA699949	Hs.191385	ESTs	3.6
	127256	AJ738610	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN A	3.6
	123419	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	3.6
	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.6
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.6
30	132339	D80030	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
	115691	AW190215	Hs.62348	hypothetical protein FLJ11753	3.6
	134853	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide ribonucle	3.6
	134075	NM_012201	Hs.78979	Golgi apparatus protein 1	3.6
	128468	T23625	Hs.150580	putative translation initiation factor	3.6
35	127229	AA316181	Hs.61635	stx transmembrane epithelial antigen of	3.6
	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	3.5
	133421	AF134160	Hs.7327	claudin 1	3.5
	135332	AW393883	Hs.98968	hypothetical protein FLJ23058	3.5
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	3.5
40	125562	AJ494372	Hs.98968	hypothetical protein FLJ23058	3.5
	126996	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.5
	125558	R59305		gb:cyh16c10.r1 Soares infant brain 1NIB H	3.5
	117265	AA451966		RAB9-like protein	3.5
	130215	BE301883	Hs.152707	glioblastoma amplified sequence	3.5
45	109482	AJ002238	Hs.11482	splicing factor, arginine/serine-rich 11	3.5
	133726	AJ803188	Hs.252716	oxysterol-binding protein-related protei	3.5
	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	3.5
	117613	AW029507	Hs.161102	ESTs	3.5
	100944	L07518		mucin 6, gastric	3.5
50	105226	R58958	Hs.26608	hypothetical protein MGC15880	3.5
	125032	T74884		gb:cy58d02.s1 Stratagene liver (937224)	3.5
	123720	AA609734	Hs.112755	EST	3.5
	128846	AA730767	Hs.285753	SCG10-like-protein	3.5
	116443	AW962196	Hs.339808	LBP protein 32	3.5
55	128770	AB015982	Hs.143460	protein kinase C, nu	3.5
	106918	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fs, clone HE	3.5
	131244	AJ638429	Hs.24763	RAN binding protein 1	3.5
	128765	AF073310	Hs.143648	insulin receptor substrate 2	3.5
	111223	AA852773	Hs.334838	KIAA1866 protein	3.5
60	104857	AJ920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	3.5
	105395	AJ580880	Hs.268149	putative methyltransferase	3.5
	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	3.5
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	3.5
	106357	AA504747	Hs.136102	KIAA0853 protein	3.5
65	103392	X94563		gb:H.sapiens dbt/acbp gene exon 1 & 2.	3.5
	101086	AA382524	Hs.250959	histatin 1	3.5
	133423	T84084	Hs.195008	Homo sapiens cDNA FLJ11723 fs, clone HE	3.5
	117714	N45226	Hs.46495	EST	3.5
	110986	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	3.5
70	114096	AF060219	Hs.27007	chromosome condensation 1-like	3.4
	117147	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	133347	BE257758	Hs.71475	acid cluster protein 33	3.4
	132456	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	3.4
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	3.4
75	109734	AJ927212	Hs.3734	ESTs	3.4
	132786	BE083422	Hs.56851	hypothetical protein MGC2668	3.4
	106685	AJ076617	Hs.16251	cleavage and polyadenylation specific fa	3.4
	105593	AA279341	Hs.174151	aldehyde oxidase 1	3.4
	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	3.4
80	108687	BE544475	Hs.54347	ESTs	3.4
	113115	AJ141426	Hs.8705	ESTs	3.4
	107234	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (tr	3.4
	123110	AA486256	Hs.193510	EST	3.4
	131019	W28614		chorionic somatomammotropin hormone 1 (p	3.4

	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	3.4
	111122	N63753	Hs.16492	DKFZP564G2022 protein	3.4
	103934	BE278111	Hs.134200	DKFZP564C186 protein	3.4
	128671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory su	3.4
5	123258	AA490829	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	3.4
	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	3.4
	120149	AA227609	Hs.94834	ESTs	3.4
	128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	3.4
	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	3.4
10	122365	AA813546	Hs.99034	GTP-binding protein Rho7	3.4
	134455	BE378152	Hs.83530	hypothetical protein	3.4
	115508	AB037756	Hs.45207	hypothetical protein KIAA1335	3.4
	134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	3.4
	106691	AA443164	Hs.23259	hypothetical protein FLJ13433	3.4
15	105169	BE245284	Hs.180789	S164 protein	3.4
	120120	BE547267	Hs.59791	hypothetical protein MGC13183	3.4
	126538	AA649257	Hs.86998	ESTs	3.4
	128531	H03721	Hs.63236	ribosomal protein S15a	3.3
20	106650	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (f	3.3
	108859	AL121500		ESTs	3.3
	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypotheti	3.3
	125693	H23989	Hs.169743	Homo sapiens clone 25121 neuronal olfact	3.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	3.3
	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.3
25	124691	R05835	Hs.110153	ESTs	3.3
	112511	AW970420		dynactin 2 (p50)	3.3
	132985	AL045579	Hs.62113	KIAA0717 protein	3.3
	125743	H17151	Hs.7416	gbym37a05.r1 Soares infant brain 1NIB H	3.3
	133363	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	3.3
30	107908	AF087999		ESTs	3.3
	105312	BE613348	Hs.211579	melanoma cell adhesion molecule	3.3
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	3.3
	132073	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	3.3
	107090	AW809208	Hs.183297	DKFZP566F2124 protein	3.3
35	105463	AA825974	Hs.32646	hypothetical protein FLJ21901	3.3
	109592	AI198059	Hs.26370	ESTs	3.3
	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	3.3
	103898	AA248884		gbk3517.seq.F Human fetal heart, Lambda	3.3
40	116439	AA251594	Hs.43913	PIBF1 gene product	3.3
	129535	AA397972	Hs.112603	chimerin (chimaerin) 1	3.3
	113283	T66813	Hs.12947	EST	3.3
	128992	H04150	Hs.107708	ESTs	3.3
	133160	N54968	Hs.66309	hypothetical protein MGC11061	3.3
45	134076	AF086215	Hs.78980	gb:Homo sapiens full length insert cDNA	3.3
	128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	3.3
	127728	AW404061		protein kinase C, beta 1	3.3
	126516	R95872	Hs.117572	chemokine binding protein 2	3.3
	127506	T61039	Hs.76067	ribosomal protein L10a	3.3
50	104769	AA025887	Hs.293943	hypothetical protein MGC11266	3.3
	126666	AA648886	Hs.151999	ESTs	3.3
	130453	U80735	Hs.173854	PAX transcription activation domain inte	3.3
	107131	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.3
	130422	AW160614	Hs.180034	cleavage stimulation factor, 3' pre-RNA,	3.3
55	121292	AA401807		gb:zv65f11.s1 Soares_tetal_fetus_Nb2HF8_	3.3
	123284	AA488988	Hs.293796	ESTs	3.3
	130734	AW137091	Hs.18624	KIAA1052 protein	3.3
	105400	AF198620	Hs.10283	RNA binding motif protein 8A	3.3
	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC0	3.3
60	114988	AA251089		gb:zs04f05.s1 NCL_CGAP_GCB1 Homo sapiens	3.3
	132867	AF226667	Hs.58553	CTP synthase II	3.3
	124169	BE079334	Hs.271630	ESTs	3.3
	114652	AI521936	Hs.107149	novel protein similar to archael, yeast	3.3
	113876	AI799751	Hs.5635	ESTs	3.3
65	111520	AI985369	Hs.301134	ESTs	3.3
	121748	BE536911	Hs.234545	hypothetical protein NUF2R	3.3
	106834	AL044182	Hs.28070	KIAA0753 gene product	3.3
	128869	AA768242	Hs.80618	hypothetical protein	3.3
	129619	AA209534	Hs.284243	tetraspan NET-6 protein	3.3
70	126770	AI292320	Hs.81381	heterogeneous nuclear ribonucleoprotein	3.3
	116734	AW900992	Hs.93796	DKFZP586D2223 protein	3.3
	100253	D38024	Hs.157425	double homeobox, 2	3.3
	130999	AA326683	Hs.21992	likely ortholog of mouse variant polyade	3.3
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.3
75	129284	AA318224	Hs.296141	ESTs	3.3
	119127	AA708035	Hs.12248	ESTs	3.3
	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	3.3
	132664	AI740461	Hs.54542	ESTs	3.3
	118397	BE139479	Hs.161492	ESTs	3.3
80	107003	AW138437	Hs.24790	KIAA1573 protein	3.3
	126735	M69113	Hs.226795	glutathione S-transferase pi	3.2
	130847	AI672483	Hs.20220	lipase protein	3.2
	101186	AA020956	Hs.179881	core-binding factor, beta subunit	3.2
	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	3.2

	121782	AW452957	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.2
	119863	AA081218	Hs.58608	Homo sapiens cDNA FLJ14206 fis, clone NT	3.2
	106103	BE620779	Hs.12094	mitochondrial ribosomal protein L30	3.2
5	123808	AA620552		gb:ae58g11.s1 Stratagene lung carcinoma	3.2
	133761	AF041430	Hs.75922	brain protein l3	3.2
	110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.2
	115239	BE251328	Hs.73291	hypothetical protein FLJ10881	3.2
	117457	N29682	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.2
10	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	3.2
	129673	D38552	Hs.1191	KIAA0073 protein	3.2
	105154	AA307279	Hs.35947	methyl-CpG binding domain protein 4	3.2
	126722	N66148	Hs.11125	HSPC033 protein	3.2
	109966	H09103	Hs.30897	EST	3.2
15	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	3.2
	109517	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.2
	105252	AB039670	Hs.9728	ALEX1 protein	3.2
	101754	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.2
	110384	H45282	Hs.268798	ESTs	3.2
20	134118	BE336680	Hs.182877	KIAA0116 protein	3.2
	134869	AL157518	Hs.90421	PRO2463 protein	3.2
	100780	BE561958	Hs.293441	immunoglobulin heavy constant mu	3.2
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	3.2
	129794	AF161399		hypothetical protein FLJ13433	3.2
25	129056	AI769958	Hs.108336	ESTs, Weakly similar to ALU6_HUMAN IIII	3.2
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.2
	103038	AA926960		CDC28 protein kinase 1	3.2
	130553	AF062649	Hs.252587	pituitary tumor-transforming 1	3.2
	125394	BE178502	Hs.173772	ESTs, Weakly similar to I78885 serine th	3.2
30	132305	AI806090	Hs.44344	hypothetical protein FLJ20534	3.2
	131136	AB033099	Hs.23413	KIAA1273 protein	3.2
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	3.2
	117639	AA377165	Hs.44833	ESTs	3.2
	127076	AI422951	Hs.146162	ESTs	3.2
35	126153	H85692	Hs.40730	ESTs	3.2
	132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypotheti	3.2
	104946	AW242407	Hs.73848	carcinoembryonic antigen-related cell ad	3.2
	122110	AI123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	3.2
40	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	3.2
	109442	AW296134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	3.2
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	3.2
	115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	3.2
	119651	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.2
	127211	AA305520	Hs.108812	hypothetical protein FLJ22004	3.2
45	134984	AI803516	Hs.272891	hippocampin-like protein 4	3.1
	105551	AW005822	Hs.25292	ribonuclease H1, large subunit	3.1
	119750	AI538880	Hs.94812	ESTs	3.1
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	3.1
50	104590	AW373062		nuclear receptor subfamily 1, group I, m	3.1
	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	3.1
	116429	AF191018	Hs.279923	putative nucleotide binding protein, est	3.1
	133915	AA815092	Hs.77554	Homo sapiens cDNA FLJ14967 fis, clone TH	3.1
	128721	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.1
55	128538	R44214	Hs.101189	ESTs	3.1
	129179	AW969025	Hs.109154	ESTs	3.1
	108793	AA129395	Hs.71139	ESTs	3.1
	108807	AI652236	Hs.49376	hypothetical protein FLJ20644	3.1
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	3.1
60	132571	AW674699	Hs.5169	suppressor of G2 allele of SKP1, S. cere	3.1
	134937	AI251449	Hs.171939	ESTs	3.1
	125756	BE174587	Hs.289721	growth arrest specific transcript 5	3.1
	112369	AW966243	Hs.4243	hypothetical protein FLJ12650	3.1
	127002	AL353940	Hs.24979	hypothetical protein DKFp761P1010	3.1
65	128179	AW293689	Hs.127116	ESTs	3.1
	117121	H95044	Hs.321386	EST	3.1
	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	3.1
	128403	AI908008	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	3.1
	127930	AA809672	Hs.123304	ESTs	3.1
70	114250	AI914699	Hs.13297	ESTs	3.1
	108828	AK001693	Hs.273344	DKFZP564O0463 protein	3.1
	105225	AA211777		gb:zn57d02.s1 Stratagene muscle 937209 H	3.1
	117997	N52090	Hs.47420	EST	3.1
	104558	R56678	Hs.88959	hypothetical protein MGC4816	3.1
75	124777	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
	106035	N35568	Hs.5245	hypothetical protein FLJ20643	3.1
	127521	AW297206	Hs.164018	ESTs	3.1
	120215	AF109219	Hs.108787	phosphatidylinositol glycan, class N	3.1
	119403	AL117554	Hs.119908	nucleolar protein NOP5/NOP58	3.1
80	105024	AA126311	Hs.9879	ESTs	3.1
	123485	AI308876	Hs.103849	hypothetical protein DKFZp761D112	3.1
	109416	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	3.1
	132490	NM_001290	Hs.4980	LIM domain binding 2	3.1
	115348	AA281562	Hs.766	ESTs	3.1
	117297	AW779829		gb:hn88a05.x1 NCL_CGAP_Jkd11 Homo sapien	3.1

5	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.1
	107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	3.1
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	3.1
	132425	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.1
	115188	AK000219	Hs.88367	hypothetical protein FLJ20212	3.1
	129707	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	3.1
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	3.0
	106472	AI207162	Hs.3815	stathmin-like-protein RB3	3.0
10	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.0
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	3.0
	105522	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	133650	D84294	Hs.118174	tetratricopeptide repeat domain 3	3.0
	134624	AF035119	Hs.8700	deleted in liver cancer 1	3.0
15	112435	NM_013255	Hs.288791	muskelin 1, Intracellular mediator conta	3.0
	134654	AK001741	Hs.8739	hypothetical protein FLJ10679	3.0
	106651	AA450421	Hs.30875	ESTs	3.0
	109597	AA989362	Hs.293780	ESTs	3.0
	132342	AW162758	Hs.341729	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.0
20	106057	BE614474	Hs.289074	F-box only protein 22	3.0
	106378	AA824298	Hs.21331	hypothetical protein FLJ10036	3.0
	126660	AA011597	Hs.177398	ESTs	3.0
	115467	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	3.0
	128504	AI879099	Hs.102397	G1OT-3 for gonadotropin inducible transc	3.0
25	125219	AI804331	Hs.99423	ATP-dependent RNA helicase	3.0
	126598	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypotheti	3.0
	133866	BE280478	Hs.182695	hypothetical protein MGC3243	3.0
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN A	3.0
	131586	AA460352	Hs.26966	KIAA1171 protein	3.0
30	100237	D30715		Human PAP (pancreatitis-associated prote	3.0
	105515	T24968	Hs.23038	HSPC071 protein	3.0
	123073	AA485061	Hs.105652	ESTs	3.0
	111375	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.0
	130724	AK001507	Hs.44143	Homo sapiens clone FLB6914 PRO1821 mRNA,	3.0
35	129928	AI338993	Hs.134535	ESTs	3.0
	118922	AW206193		hypothetical protein DKFZp761B2423	3.0
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	3.0
	125165	W45350		gb:zc81h08.s1 Pancreatic Islet Homo sepi	3.0
40	122219	AA436002	Hs.183161	ESTs	3.0
	132195	BE018717	Hs.42124	ESTs	3.0
	102298	AA382169	Hs.54483	N-myc (and STAT) Interactor	3.0
	103286	D38616	Hs.54941	phosphorylase kinase, alpha 2 (liver)	3.0
	130168	AK001389	Hs.15144	hypothetical protein DKFZp564O043	3.0
45	126997	AI377150	Hs.150914	ESTs	3.0
	128902	AA036637	Hs.107052	ESTs	3.0
	117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-II	3.0
	106711	BE390125	Hs.143187	hypothetical protein	3.0
50	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	3.0
	135029	H58818		hydroxysteroid (17-beta) dehydrogenase 7	3.0
	112003	AW978731	Hs.301824	hypothetical protein PRO1331	3.0
	106735	R77698	Hs.337778	ESTs	3.0
	126628	N49776	Hs.170994	hypothetical protein MGC10946	3.0
55	133350	AA499220	Hs.71573	hypothetical protein FLJ10074	3.0
	110312	BE256986	Hs.11896	hypothetical protein FLJ12089	3.0
	125659	T57693	Hs.87929	Homo sapiens cDNA FLJ13707 fis, clone PL	3.0
	129801	AB032964	Hs.115726	KIAA1138 protein	3.0
	123423	AA598484		gb:ae38f04.s1 Gessler Wilms tumor Homo s	3.0
60	128695	NM_003478	Hs.101299	cullin 5	3.0
	123470	AW303285		Human DNA sequence from clone RP11-110H4	3.0
	109252	BE440157	Hs.85944	ESTs	3.0
	101445	M21259		gb:Human Alu repeats in the region 5' to	3.0
	102126	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhib	3.0
65	116475	AA733050	Hs.334612	small nuclear ribonucleoprotein polypept	3.0
	106573	AA223447	Hs.12835	A kinase (PRKA) anchor protein 7	3.0
	103106	W27172	Hs.1857	phosphodiesterase 6G, cGMP-specific, rod	3.0
	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	3.0
	112246	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MA	3.0
70	126887	H20832		gbym48d03.s1 Soares Infant brain 1N1B H	3.0
	117960	AA310417	Hs.47044	ESTs	3.0
	133626	AW836130	Hs.75277	hypothetical protein FLJ13910	3.0
	113179	BE622021	Hs.152571	ESTs, Highly similar to IGF-II mRNA-bind	3.0
	109668	H09232	Hs.26484	HIRA-interacting protein 3	3.0
75	125770	AA143045	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma v	2.1

TABLE 71B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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5	123619	371681_1		131495	142008_1
	101445	1650_5		100944	25682_2
10	117265	10421_1		117297	647718_1
	108859	137143_1		125165	1852047_1
15	116790	19864_1			
20					
25	103038	15024_1			
30					
35					
40	126086	1606216_1		126098	1629789_1
	125464	168460_1		126127	1205826_1
	125558	1703083_1		126426	110687_1
45	118644	81501_1			
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55	127282	231725_1		127315	37938_1
	103898	187213_3		126769	119008_1
60	120147	386607_2		128080	1540039_1
	104590	44964_1			
65					
70	127496	340470_1		126872	142696_1
	126887	1572189_1		128132	177108_1
75	126967	169750_1		120325	166688_1
	112511	17406_2			
80					

	106012	96214_1	AI240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 AI095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292 R31981 H12498 H02668 AA035018 R75957 AI803329 R27528 R36203 AI809932 AI808765 R78948 AA411449 AA976929 AI378760 AI378620 T48870 R73906 R75632 H03612 AA909684 N50695 H02580 H12839 N58781 AA742532 AI360919 H03502 BE208298 R68588 AI350463 R31935 AW069127 AA411621 R25671 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933 AJ003322 AJ003324 AW404061 R09654 T67160 N50566 N53259 R81936 D78695 D78806 D78780 C17009 AA004405 AA122102 R70625 AA148932 H59583 H81146 H80378 H49863 H21182 H46534 H51478 H02702 H46515 H40200 H50046 H23647 H50439 H18383 H21846 H23849 H40182 R21924 H01290 H01283 H42464 W31947 W39660 AA048219 H03539 H01741 R22008 AA043911 AA156838 D78832 R36616 R66039 AI492481 AA088608 R69918 R36334 H80281 N58483 AI075154 AI086754 AA595787 H81051 H01187 AI057251 T96992 H59584 T47016 R31800 H13647 H01193 N74660 AA156601 H03455 R66040 R81937 R92416 H89486 R36617 R65795 AI088338 AI373324 H66992 R96235 AI494132 R16678 AA088178 AA705356 AA962143 AA148933 R09231 AI160937 R70525 T46980 AI200046 H02301 AA367587 R35968 T97106 D78703 N78072 D78668 D63268 R28197 AA085579 R63766 R92415 W00998 R80766 R67875 R27583 R09343 H13646 R27682 T89007 AI221919 Z19957 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 AI341345 AW298800 AA724961 AA931158 AI741227 AI806660 AI982628 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 AI492961 AI361526 F04002 AA452141 T23551 AI472655 AI193667 AI341984 N92658 T32870 R52664 N50428 AW089291 AI934175 AI423737 D60665 AA226198 AA226513 AA383773 R18656 AW968014 AA262288 AW968002 X93079 AJ002788 R51324 AI381600 D80031 AW500520 AW593740 F09382 AA810597 AA262174 AA810595 AA810596 AA443241 R23784 R67255 R00047 AI457612 R63254 R28645 R27616 H01310 R78329 R76046 R76055 AA369734 N57914 H94864 AI953638 R31669 AW769278 R82398 AA131925 R21776 R79031 AI129553 N70340 AI276116 AA709381 N63734 AI342605 AA327133 AI805980 AA005377 AW611716 T86946 AA369083 R67250 H00240 R32578 W86279 R80248 R23734 H00977 R21732 R78932 AA368675 R16780 R26523 H40161 W93671 R99823 R77956 H51601 R98785 R09738 H78317 H53537 H81056 T53780 H12600 R82345 AA653499 AW953717 R63207 R33888 H54071 H66993 T48748 AI702300 R30775 H68996 AI014957 AA369082 AF075351 AI110886 AI742050 AW954245 AI768458 C19062 AI393674 C18911 C18029 AA708613 AI168432 R67389 AI168453 H00188 R21233 H03055 R53822 AA367558 R75872 W04151 AI220869 AI090290 AA368730 R94434 H81153 H70950 AA367783 H81514 H53536 C16968 C17797 C17677 C17084 AA082581 C17044 D63217 C18791 D78839 D63290 D78838 N91085 H54070 R80360 H78318 H40199 R33887 R02529 H94918 R00900 T87029 AA131924 R99891 AA004267 D78764 D78757 H61600 C18615 H60972 R98784 W86323 R09737 C17492 D78811 R67494 D78775 AA368244 H12650 D79043 AW957062 R62759 C19002 H01715 W28614 W27435 AI983043 AA364395 AW572472 AW190386 AI129278 AI913081 AW473549 AA830713 AI982871 AI638647 AI828466 AW572486 N52583 N89587 AI075567 AI571047 AI867478 AI559459 AI685802 AA805256 AI458777 AA974369 AI866929 AI886032 AI823925 AI823566 AW198135 AI287510 AI565910 AA765775 AI866019 AI263697 AI358825 R42668 AA894603 AW105585 AI824555 AW339175 D20479 NM_014253 AF100772 BE088769 AI022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486 AW303285 AW117396 AA888929 BE174517 Z70704 AL042292 H54958 AA310063 AW499643 AW501380 AW501202 AW501293 AW501596 AW630166 AL041326 AA780690 L40517 U21556 AI093182 AW062487 AA883387 AA931302 BE252601 BE258381 AA827330 AL043930 AA356337 AW862830 AW393814 Z70703 AW389484 T62231 AW780049 AL043931 BE149744 AW963292 BE439669 BE091737 BE091657 AA484004 AI673095 AA699106 AW601545 AI538739 AI538730 AI521786 AW366369 AW021010 AA362576 AI289927 AA382592 AA608733 T74884 AA620552 U42359 N57493 H01052 AW206193 AW137594 AI953685 AI919143 AI424371 AW007698 AW025681 AI954289 R40438 AW070364 AI679653 AI679081 AI623213 AI652310 AI631411 AI556384 AI566734 AA149597 AI538172 AI040831 AI770021 AI914287 AA279311 W73001 AI493117 AI693374 AI802007 AI990645 N29752 R94559 AA806475 AA806828 R90998 R94558 AW300112 W24097 AW003016 N91920 T47910 AA029703 T91015 AF093097 AI869509 T27070 AA326718 AA024743 W23922 AA479593 AI765668 W23908 U92986 AA081632 N50578 AA065245 AW365046 AW365014 AA961091 AA150231 H53426 AA234651 N50522 T79343 T87399 N91858 H41179 AW009453 AA024744 T27068 AI346379 H88431 AA152289 R45373 AA477432 AI745607 AI807602 H41152 AA065244 AI242569 AI091032 AI251849 F03857 H88369 AI174488 AI002696 H53427 T87293 N91869 W35270 AA453723 AA453705 AW071829 AI393866 AW071807 W23592 AI342074 D31158 AA833756 AI991896 AA447791 AI864125 AW377239 AA295365 AI687970 R34076 F07607 AA521310 AW499865 R94584 R21283 AA350256 H68126 M21305 N24829 X94563 H58818 AA211777 AA401807 AA195191 AA190578 AI632307 AA195227 AA743633 AI823408 AI832203 AI653114 AA205307 AW021913 AI687980 AI674198 AI675563 AI417935 AA707350 AA135157 AI434721 AI151036 AI038305 R52643 AA780141 AW207645 D19691 AI474370 AA401739 N22905 N70378 D30715 AA251089 AA599484
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Table 72A shows the Seq ID No, Pkey, ExAccn, UnigenelD, and Unigena Title for all of the sequences in Table 73.

80	Pkey:	Unique Eos probates Identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigena number
	Unigena Title:	Unigena gene title

Seq ID No:	Seq ID number correlation for those sequences in Table 73				Seq ID No
Pkey	ExAcon	UnigeneID	Unigene Title		Seq ID No
5	103080	AU077231	Hs.82932	cyclin D1 (PRAD1; parathyroid adenomas	Seq ID No B1 & B2
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Clona savignyi	Seq ID No B3 & B4
	101104	AW862258	Hs.169256	neuropeptide Y receptor Y1	Seq ID No B5 & B6
	447761	AF061573	Hs.19492	protocadherin 8	Seq ID No B7 & B8
	428183	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	Seq ID No B9 & B10
10	439221	AA737106	Hs.32250	ESTs, Moderately similar to 178885 serin	Seq ID No B11 & B12
	121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidylseri	Seq ID No B13, B14, & B15
	104659	AW969769	Hs.105201	ESTs	Seq ID No B16
	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	Seq ID No B17 & B18
	129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	Seq ID No B19 & B20
15	100299	D49493	Hs.2171	growth differentiation factor 10	Seq ID No B21 & B22
	116301	AW969706	Hs.293332	ESTs	Seq ID No B23 & B24
	106533	AL134708	Hs.145998	ESTs	Seq ID No B25-B27
	131313	R96290	Hs.75874	ribosomal protein L44	Seq ID No B28 & B29
	105316	AI671245	Hs.24835	hypothetical protein FLJ14594	Seq ID No B30 & B31
20	113003	AW292315	Hs.7215	ESTs	Seq ID No B32
	102836	U94320	Hs.158330	neuropeptide Y receptor Y5	Seq ID No B33 & B34
	102745	AW753865	Hs.74376	olfactomedin related ER localized protel	Seq ID No B35-B40
	123308	C14187	Hs.157208	ESTs	Seq ID No B41 & B42
	120147	AI917116		hemoglobin, beta	Seq ID No B43
25	123049	BE047680	Hs.211869	clckopf (Xenopus laevis) homolog 2	Seq ID No B44 & B45
	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	Seq ID No B46 & B47
	105301	AW352357	Hs.7457	MAGE1 protein	Seq ID No B48 & B49
	128478	AA708205	Hs.100343	ESTs	Seq ID No B50-B53
	106111	AW875398	Hs.6451	PRO0659 protein	Seq ID No B54 & B55
30	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	Seq ID No B56 & B57
	120830	AI568170	Hs.96886	ESTs	Seq ID No B58 & B59
	127664	AA806164	Hs.116502	ESTs	Seq ID No B60
	102725	AB026187	Hs.159156	protocadherin 11	Seq ID No B61 & B62
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	Seq ID No B63 & B64
35	130637	AA356764	Hs.17109	integral membrane protein 2A	Seq ID No B65 & B66
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	Seq ID No B67 & B68
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	Seq ID No B69 & B70
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	Seq ID No B71 & B72
	125770	AA143045	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma v	Seq ID No B73 & B74
40	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	Seq ID No B75 & B76
	420462	AF050147	Hs.97932	chondromodulin precursor	Seq ID No B77 & B78
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	Seq ID No B79 & B80
	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	Seq ID No B81 & B82
	416836	D54745	Hs.80247	cholecystokinin	Seq ID No B83 & B84
50	Table 72B				
	Pkey:	Unique Eos probeset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
		Pkey	CAT Number	Accession	
55			NM_000025 X72861 X70811 M29932 X70812 S53291 AW015148 AW581776 AJ276134		
			R96290 H02411 C18327 AA367588 AA367557 H89632 C17954 AA568860 AF752983 AA699451 H04260 AH128118 AW193364 N94503		
			AA029995 T40538 AA368746 AI189909 BE047384 AA747591 R22855 AI032539 AI151343 AA148534 H63941 T49595 AA694405 H74226		
			AI200363 R79731 AA702947 AI400076 AI088494 C17938 AA599478 H02962 R77665 C17370 R65618 H73711 R58545 D79189 AW265710		
			R77684 T62101 AW953745 AW953739 D79107 AA029105 AW953738 AA456487 R67000 AA156623 AA368336 H63662		
60	116301	52669_2	AW969706 AA456258 AA491881 BE501639 D62113 AW969710 AI591236 AI379869 AW968997 AA040053 AI807206 AW5663917 AA454645		
			AA489238 BE241958 AA743491		
	103080	17092_1	AU077231 AA852219 M74092 X59798 M64349 NM_001758 AA226806 M73554 BE409154 AA160096 BE384352 AA160820 BE382880		
			BE261734 AA113821 BE407745 AA156380 BE390287 BE390020 AA100854 AA127152 AW794066 AW367101 AW367093 U47703 AI347077		
			W05266 AI824103 AI499061 AA642944 AI042558 AA906539 W60380 AI571777 AL135581 AA112340 N75459 AA592929 AI085348 AI278890		
65			AA126942 AI023701 AI873252 AA156319 AI190622 W60289 AI274886 R81309 AA100801 AA227161 AI568929 AA160603 AI074344 AI344561		
			AI150778 AA852218 AA158286 N20142 AA622148 AA864225 AA576367 AW182124 T89175 AI758455 AA780573 N71757 R81200 AI659596		
			AI674613 AA642544 AW503909 AA128851 W39350 N40420 AA113072 BE168116 AI620604 AI298125 BE075272 N40078 BE075109 BE080779		
			AI918938 BE168117 BE087369 AW995539 BE080949 BE080727 BE075271 BE075108 BE080955 BE089555 BE081115 AW750304 H56084		
			AI146884 BE075154 AW992247 AI186525 AI752230 AW263140 W03329 N26056 AA948080 AA113073 H99284 AA227101 AA631077		
70			AA148042 AI740837 BE082728 AA149570 W44495 BE089351 AA375044 N26775 H27771 AA064705 BE091204 R89337 N32676 N27141		
			BE164704 H98049 W67603 AA25549 W31090 AA807411 BE173280 BE000178 T09020 W23852 AA062709 BE167894 AA076515 R97329		
			BE541980 N42088 AA102307 AA113772 BE276181 H20622 W44436 W67604 W48412 AW771113 AI700678 AA502628 AA133137 BE274186		
			BE396090 BE613371 BE612645 W46650 W95203 W92651 AI087288 R76299 AW604781 N55320 AI912334 AA403248 AW169156 H24970		
			AW298822 AW080962 AI073747 W24123 AA577596 H21716 H27825 H26436 AI288304 AA148043 AA204678 BE047090 W48631 AA908347		
75			AA599485 AI276505 AI953979 AA563710 H25674 H51747 AA425369 AA516104 AI095335 T77237 AA151696 T92084 AI689037 AI624162		
			W49709 AW514883 AA100676 AI366087 AA069474 AA52589 AW771076 AA029402 AA994114 AI351505 AW770816 AI333594 AI289794		
			AI346589 AA487700 AI081104 AA613344 AI377520 AI284911 AI311390 AA622062 AI065890 AI660881 AI365117 AA403090 AI272818		
			AI073353 W46300 AA062689 AI755078 AI753397 AI633584 AI273471 AI339890 AA699584 AA983722 AI079968 AI752231 AA076431 AA113245		
			AI168564 AA918965 AI066484 AI123599 AI921518 W94586 AA535600 AA064665 AA705388 AA064623 AA962503 AI924926 AW131206		
80			AW275281 AI280632 T29597 AW48728 AW954336 W38317 W94768 AI084717 W46567 AI245645 AW302501 N72201 AW510563 AW079132		
			AA207064 AI143740 AW440672 AA632154 AI290286 AI350704 AI271377 AA025369 AI864756 T77451 H97348 AA852165 AI932951 N98526		
			AA487486 R92970 AA934071 AI080448 AA063257 C05788 N99099 R42969 AA887065 AA662686 AA533833 AA662304 H51748 BE539444		
			AI382164 AI814595 BE537043 AI168307 BE408935 AA453606 R89428 AA936527 AA936890 AW369618 AW264602 R18074 AI474189		
			AW372354 AI094358 R37210 AA948510 AA226909 BE175257 AI086652 BE408324 AW292848 AI768962 BE540703 BE409478 AA931692		

5	132520	45737_1	AA257992 AA317029 AA362097 D17042 H48100 AW838107 AW838106 AW838110 AW838231 AW610241 AW838442 AA045061 AW384991 BE000988 AA131806 BE180577 AW838269 AL039831 A1754380 C06051 AA131737 AW838239 A1767465 A1480134 AA610312 AW838190 AA379252 AW838282 AA484027 A1423413 A1685064 BE328307 A1241857 AW838281 AW838284 A1671267 A1814928 AA828367 A1476306 A1270180 AA622362 A1076497 A1635919 A1444994 A1194026 A1669159 A1928131 AA48853 A1350143 AW079289 AW467807 AA480442 AA522935 BE180570 AW380087 AW380109 A1081015 A1690818 A1589485 A1698510 AA642019 AA714366 A1580430 AA985527 A1740475 C21398 AA257993 A1302393 A1689018 AW770194 AW753750 A1079164 BE550338 AA559851 T16108 A1864822 A1932827 AA045095 AA045062 A1954225 AA768569 AA709308 AW958363
10	117602	10565_4	N35020
	102725	11582_1	AB026187 NM_014522 U79247 F13304 AA224524 F10902 R39431
	102745	13186_1	AW753865 F07644 F11280 F06355 F08136 U79299 F07459 F08750 F12419 F12842 F06488 F08585 F13403 F05921 F05512 F11683 F05416 F12841 F12810 F05418 F12850 F24551 F06276 H11803 H10237 H11542 H22894 R59563 H19351 H18722 F11237 F08507 H23123 R61595 F07796 F06201 F12289 F07107 T78113 F08734 F13344 F05760 F11784 F08780 F05835 R20588 F07739 F11497 R17410 H17414 R20440 T66090 R25292 T66236 T78766 T79908 R25286 R60071 C14761 AW905192 AA331914 AW985291 H09000 F05212 F08313 F05825 H06399 H15135 H11378 R66424 R61541 AA235405 A1205041 R59564 H23124 H18638 R37359 A1571275 R41780 T66174 T66159 R54102 W07657 H10794 R52337 R42890 H14354 R40952 T17391 H12068 R56797 R51000 R60011 R37617 R39434 H29286 T16403 H09129 R49114 H15161 H11729 R39160 H10468 H24454 H11432 R54433 H08768 H24042 H09511 H17281 H15292 R37849 A1991965 R52815 R42850 T17390 T16438 T17388 T16285 R48963 R50782 R44247 R46729 R55558 R40696 R43575 R44420 T17403 R37754 R46637 R51039 R40513 T23785 F10433 T16350 H10191 R43688 T23543 H08591 R44351 R37575 R49508 F04379 F04056 F05067 F02010 F09158 F10036 F08900 F02559 F09914 F09434 F05034 H17415 F02644 H10650 F10451 H14589 F10444 T16440 R44517 R46843 F03993 F10443 F02170 F09343 F10414 F04794 F11122 F04997 F03894 AW005932 F02767 F10941 F01777 R45260 F03386 R45261 T65009 F10990 F08942 F01673 H23253 F04533 F20082 F01669 F03689 H09568 R40763 H06400 R05958 N80570 A1082296 A198226 T23763 AA814486 AW015823 A1886272 H06514 AA515969 F10049 A1984267 A1886279 AA558516 F02071 A1783843 A1804884 F01468 AA730438 AF035301 R38389 R14440 R59468 R14437 T89036 R43560 H10821 R52850 R56722 R14559 T09299 H10467 R25829 F13546 R56796 R51151 D82657 T32952 T68257 H06569 F12430 T74326 H08489 R34430 R13083 H23364 R21134 T77098 AW957157 H24150 H11403 R52336 F12830 T77173 T7281 T77663 T74736 H10649 H12067 R20092 T74735 R54530 R17552 R59557 R54529 H1280 T75171 H14694 T74975 H15291 R18574 R54157 R13446 H15221 R35120 R35031 R21277 R19632 R35820 R50899 R13923 R36771 R26485 R33061 R20100 H24426 H09184 H15958 R19253 H15196 H09510 R36032 R19691 H14402 H14885 T17068
20			AF252297 N27888 F13415 R34552 R14377 AA323962 AW611514 AW614097 AW195487 A1026040 A1097663 AA012834 AW969885 AA988198 R49069 AW873673 R37774 F08840 AA484668 AW873664 AA170805 AA170825 AA585275 AA585280 AA012833
30	119082	34131_1	U94320 NM_006174 U66275
	102836	25380_1	AA143045 AW271802 A1017093 AA450183 W93694 A1885044 A1890068 AW264522 AW073559 A1355325 A1051302 A1567686 A1143554 A1457891 AW468784 A1567693 AW884460 A1424892 AA401298 AW244098 A122936 N24824 AA552932 AA873164 A1308810 A126968 H81852 N20798 AW263947 A1696267 AA449422 AW877967
	120147	386607_2	A1917116 AA633698 A1580389 Z39483
35	113003	420161_1	AW292315 A1090408 AW517041 A1928695 A1092060 AA716741 N98235 T23629
	104659	82594_1	AW969769 AA484137 A1291362 N64753 AL133784 AA007153 BE046923 D59990 C15166 D59991 D60194 AA648108 N76160 D61027 D60630 U29680 AF272890 AW078166 AA010748 R23839 H59572 R23383 A1625747 AA011176 AW665324 D02674 H59573 AA757931 H12502 R66851
	104691	41308_1	AA702310 AA748431 AA749352 C01127 A1003679 T99352
40	105301	27795_5	AW352357 AA852419 T80568 AA332510 AW149659 AA341609 AA809550 A183690 AA730875 T31719 AW965361 AA779709 T05461 AA564806 A142536 A1553857 D53384 D53747 D54101 D55112 AW071935 A1082447 A1290911 AW168872 AA199743 A1091646 A1246702 A1271662 AW117296 A1032138 A1741489 A1538705 AA233541 A1682685 AW136268 A1689641 AA599916 A174443 A1432175 A131328 AW136277 AA852418 AA243035 T03902 C15651 D52660 H08108 AA844525 A120648 A1282445 AW068986 AW497637 AA779042 AA298564
	105316	181763_1	BE262936
45	127664	394361_1	A1671245 D81062 A1085879 A1193252 A1870535 N23132 H97661 H18098 AA552173 AA233924 AA503379 H19618 D60732 F04762 H11343
	106111	4671_1	AW590283
50	128478	370722_2	AA808164 AA678564 AW978234 AW023951 AA651859 A1699785 AA913686 AW974569 A1681287
	105782	246361_1	AW875398 A1064861 NM_014138 AF090943 BE071887 BE547232 BE622599 A1345700 AA284315 AA147700 AW376340 BE220170 BE348475
	120830	244476_1	AA025037 AA057284 AA025038 T16193 AW130196 AW594516 A1989991 A1139091 AW675747 AA830435 A1924977 A1670778 A1051887
	128797	20410_1	AA912574 AW130213 A1828335 A1570587 A1332760 A1313115 AA804653 AA77920 AA147645 A1916912 AW768839 AA715098 AA292723 AA732421 T33122 A1631550 A1698686 A185386 R43829 AA421638 AA961400 C00503 AA604025 AA554026 AA553885 BE172244 R24040 AA708205 H15963 R20851 L13829 A1934608 A1950163 H92893 A1267243 N66614 H28983 R42031 H06198 A1468628 H92779 L13828 T34896
55	106533	305354_1	H09748 R61554 AA350215 R40551
	121619	284072_1	A1668170 AA731212 AW294848 AW466878 AA568908 A1281804 A1923633 AA347885 A1718854 AA714940
	123049	30801_1	NI_002975 AF020044 AB009244 BE620464 AA541683 AW000991 AW089850 AW664612 A1636676 A1627854 A1885823 A1864548 A1554122
60	129703	64196_1	A199682 A1570905 A1376008 A1871364 A1074230 A1383719 AA905016 AA977446 AA844732 T78922 AW244007 A1924747 A1958230 A1824575 A1699224 A1699490 AW379856 AW292314 A1016874 AW292037
65			AL134708 AW206610 AW665919 AW594227 A1917093 A1498361 AA635141 AA453786 D54178 D53224 A1804341 D53111 M78885 A1134707 AA453903 A1278054 A1334339 A1380496 AW236938 D60373 D60993 D81246
70			AA528339 A1017218 AA416911
	100299	2801_1	BE047680 AF177395 NM_014421 AB033208 AB035161 W55979 A1093106 A1863392 AA715452 AA300480 AW022313 AA648103 AA720544
	129977	2039_1	D61856 AA481794 AA737112 AW316551 AA714937 AW974378 A1370632 A1184289 A1333982 AA714945
75			BE388665 AA740614 A1394542 AA484451 AW070575 AA877654 A1360981 A1475799 BE349560 AL037351 N29437 A1246453 AW083444 AA844441 A1150871 A1440477 A1889061 AA682422 AA680053 AA740212 A1858728 AA490589 AW243692 A1249450 A1304448 AA534421 A1500317 A1273337 AW027729 A1979132 C08120 A1680916 AW651923 A1803174 A1559264 BE250500 AW675522 AA883284 T71033 A1346638 A1066764 A1197913 AA931979 AA427699 A1304730 A1285159 A1273325 A1038450 A1033760 N74972 AA136517 A1304448 A1262652 AA401348 AW514617 A1361795 AW514389 N30307 N93439 AA190775 BE349902 A1342114 A1186831 AA039628 H74242 A1914825 A1955761 A1343851 AA693856 T71096 A1498359 AA778995 AA084278 A1274678 A1022673 AW339621 AA704929 AW089735 AA041252 AA161337 A1185333 AW189397 A1160990 A1082392 A1935848 A1144404 A1141633 AA447987 AA464241 A1342103 AW026118 AA834025 AW664459 AA603777 AA630752 AA115450 N49944 AW166071 AW769795 AA991877 AA873609 AW083441 H99130 AA910538 AA486199 AW083358 AA151767 A1161193 N54945 AA180193 A1423477 A1188387 A1089747 N58900 A1038449 A1136852 AA565913 AA180502 H61741 AA701125 A1127678 AA278541 R76523 AA666187 H85083 F24755 R77729 AA135137 BE250395 R76239 AW794625 AW794404 H61957 AA308197 AW996031
80	123308	322009_1	AA345524 N52726 AA34360 AA179785 N57375 R16447 AA160645 W21481
	101104	26442_2	D49493 NM_004962 D49492 AA948479 AA93843 AA017558 AA922557 AA912897 A1185363 AA018254 N83253 AA297544 T19187 R53287
	130637	7040_1	AA069337 AA287489 N62906 AW023929 AA018253 AA017615 W25110 R52085 R52633 W16549 H88916 H89134 AA069338 NM_000399 AA018140 AF139463 J04076 AW390694 AW361758 A1079830 A1190587 AA731059 AA742743 A1635915 AA578209 A1262612 A1264201 AA446300 AA715016 AA446027 A1274101 AA593330 AA593338 AW015388 A1681724 A1347984 AL045275 AA970069 AA018188 AW014396 AW769445 A1588889 AW338296 A1801548 A1637702 A1888410 C14187 AA496211 D80456 AA484051 D80455 AA528446
			AW862258 L07615
			AA356764 NM_004867 AF038953 W16628 R50284 A1929589 R01594 AA010474 W37917 N64212 N78175 R57511 AA329322 W77834 AA169689 AA285240 AA356670 T93146 AA325779 AA357064 AA328151 AA306939 AA306801 N31250 AA306202 AA312530 BE242703 AA354371 N42258 AL021788 H50965 H38038 A1655965 A1566732 A1953952 AW972835 A1077300 A1948482 A1760966 AA648335 W72197 N32615 AA768073 AW338181 AW001742 A1819896 A1015666 N58011 AA677584 A1183750 AW105514 W37875 AW301679 AA775257

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410102 117657_1
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414761 14860_1

416836 16233_1

420462 19379_1

428183 287965_1
439221 46993_1

447761 7355_1

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AA736720 AA664587 AA648672 AA503406 AA508123 AA503140 H46638 N75812 AA730938 D60546 AA483039 AA507705 AA480448
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AW248508 AI278454 AI369343 AW291235 AI343946 AI347189 AA970152 AI279668 AI971894 AA654359 AI191039 AA084598 AA081641
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AA864892 AA173156 AI292066 T79837 W83995 AA506427 AA815135 AI376342 AA010144 AI310421 AI223350 AA970576 N33926 T89364
AI090913 N55098 AA101673 AA626665 AA251840 N58857 AI890053 H05930 AI474199 AI436166 AA628810 N64452 AI205538 AA055310
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T99430 AI051764 R45991
D54745 AI077189 NM_000729 R71188 H87563 R80701 AW956319 AA376289 R82442 H46452 R22481 R64323 AW043690 L00354 AW005571
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AF050147 NM_007015 AB006000 AB006999 BE218114 AI703147 AI985891 BE222034 BE549774 BE327618 AI651459 BE549987 AI657194
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AW136179 AA327834 BE327350 BE327366
AW969726 AA424028 AI266636 AI271571 AA423988 AI266534 AA702780 AA452037 AI424866 AA742931 AA483361
AA737106 N35765 N35779 AF088045 N30152 AW374028 AI478237 AA923562 AI382236 AA846668 AI627389 AI371709 H98083 H95983
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Table 73: Sequences

Seq ID NO: B1 DNA sequence
Nucleic Acid Accession #: NM_053056.1
Coding sequence: 210..1097

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10	AGGGAGCGCG	GGGAGAGAGA	AGCAGAGGCC	GAGCGCGGAC	CCAGCCAGGA	CCCACAGCCC	180
	TCCCCAGCTG	CCCAGGAAGA	GCCCCAGCCA	TGGAACACCA	GCTCCTGTGC	TGCGAAGTGG	240
	AAACCATCCG	CCGCGCGTAC	CCCGATGCCA	ACCTCCTCAA	CGACCGGGTG	CTGCGGGCCA	300
	TGCTGAAGGC	GGAGGAGACC	TGCGCGCCCT	CGGTGTCCTA	CTTCAAATGT	GTGAGGAAGG	360
	AGGTCTGCCC	GTCCATGCGG	AAGATCGTCG	CCACCTGSGT	GCTGGAGGTC	TGCGAGGAAC	420
15	AGAAGTGCGA	GGAGGAGGTC	TTCCCGCTGG	CCATGAACCTA	CCTGGACCCG	TTCTGTGCGC	480
	TGGAGCCCGT	GAAGAAAGAGC	CGCCTGCAGC	TGCTGGGGGC	CACCTGCATG	TTGTTGGCCT	540
	CTAAGATGAA	GGAGACCATC	CCCCTGACGG	CCGAGAAGCT	GTGCATCTAC	ACCGACAACCT	600
	CCATCCGGCC	CGAGGAGCTG	CTGCAAAATG	AGCTGCTCCT	GGTGAACAA	CTCAAGTGGA	660
	ACCTGGCCGC	AATGACCCCG	CACGATTTC	TTGAACACTT	CCTCTCCAAA	ATGCCAGAGG	720
20	CGGAGGAGAA	CAACAGATTC	ATCCGCAAAC	ACGCGCAGAC	CTTCGTTGCC	CTCTGTGCCA	780
	CAGATGTGAA	GTTCAATTCC	AATCGGCCCT	CCATGGTGGC	AGCGGGGAGC	GTGGTGGCCG	840
	CAGTGCAAGG	CCTGAACCTG	AGGAGCCCCA	ACAACCTCCT	GTCTACTAC	CGCTCACAC	900
	GCTTCCTCTC	CAGAGTGATC	AAGTGTGACC	CAGACTGCCT	CCGGGCGCTG	CAGGAGCAGA	960
	TCGAAGCCCT	GCTGGAGTCA	AGCCTGCGCC	AGGCCAGCA	GAACATGGAC	CCCCAGGCCG	1020
25	CCGAGGAGGA	GGAGAGGAGG	GAGGAGGAGG	TGGACCTGGC	TTGCAACCCC	ACCGACGTGC	1080
	GGAGCTGGGA	CATCTGAGGG	CGCCAGGCAG	GCGGGCGCCA	CGGCCACCCG	CAGCGAGGGC	1140
	GGAGCGGCC	CCAGGTGCTC	CCCTGACAGT	CCCTCCTCTC	CGGAGCATTT	TGATACCAGA	1200
	AGGGAAAGCT	TCATTCTCCT	TGTTGTGGT	TGTTTTTCC	TTTGCTCTTT	CCCCCTTCCA	1260
	TCTCTGACTT	AAGCAAAAGA	AAAAGATTAC	CCAAAACTG	TCTTTAAAG	AGAGAGAGAG	1320
30	AAAAAAGAAA	TAGTATTGCG	ATAACCTTGA	GCGGTGGGGG	AGGAGGGTTG	TGCTACAGAT	1380
	GATAGAGGAT	TTTATACCCC	AATAATCAAC	TCGTTTTTAT	ATTAATGTAC	TTGTTTCTCT	1440
	GTTGTAAAG	TAGGCATTAA	CACAAGGAG	GCCTCTCGGG	AGAGGATTAG	GTTCATCCTT	1500
	TTACGTGTTT	AAAAAAAGC	ATAAAACAT	TTTAAAAACA	TAGAAAAATT	CAGCAAAACCA	1560
	TTTTTAAAGT	AGAAAGAGGT	TTTAGGTAGA	AAAACATATT	CTGTGCTTTT	TCCTGATAAA	1620
35	GCACAGCTGT	AGTGGGGTTC	TAGGCATCTC	TGTACTTTTG	TTGCTCATAT	GCATGTAGTC	1680
	ACTTTATAAG	TCATTGTATG	TTATTATATT	CCGTAGGTAG	ATGTGTAAAC	TCCTCACCTT	1740
	ATTTCATGGCT	GAACTCACCT	CTTGGTTACA	GTAGCGTAGC	GTGGCGCTGT	GCATGTCTCT	1800
	TGCGCCTGTG	ACCACCAACC	CAACAAACCA	TCCAGTGACA	AACCATCCAG	TGGAGGTTTG	1860
40	TCGGGCACCA	CCAGCGGTAG	CAGGTCGGG	AAAGGCCACC	TGTCCCACTC	CTACGATACG	1920
	CTACTATAAA	GAGAAGACGA	AATAGTGACA	TAATATAATC	TATTTTATA	CTCTCTCTAT	1980
	TTTTGTAGTG	ACCTGTTTAT	GAGATGCTGG	TTTTCTACCC	AACGCCCTTG	CAGCCAGCTC	2040
	ACGTCCAGGT	TCAACCCACA	GCTACTTGGT	TTGTGTTCTT	CTTCATATTC	TAAACCAATT	2100
	CCATTTCCAA	GCACTTTCAG	TCCAATAGGT	GTAGGAAATA	GCGCTGTTTT	TGTTGTGTTG	2160
45	GCAGGGAGGG	CAGTTTTCTA	ATGGAATGGT	TTGGGAATAT	CCATGTACTT	GTTTGCAAGC	2220
	AGGACTTTGA	GGCAAGTGTG	GGCCACTGTG	GTGGCAGTGG	AGGTGGGGTG	TTTGGGAGGC	2280
	TGCGTGCCAG	TCAAGAAAGA	AAAGGTTTGC	ATTCTCACAT	TGCCAGGATG	ATAAGTTCTC	2340
	TTCCCTTTCT	TTAAGAAAGT	TGAAGTTTAG	GAATCCTTTG	GTGCCAACTG	GTGTTTGAAG	2400
	GTAGGGACCT	CAGAGGTTTA	CCTAGAGAAC	AGGTGGTTTT	TAAGGGTTAT	CTTAGATGTT	2460
50	TCACACCGGA	AGGTTTTTAA	ACACTAAAT	ATATAATTTA	TAGTTAAGGC	TAAAAAGTAT	2520
	ATTTATTGCA	GAGGATGTC	ATAAGGCCAG	TATGATTAT	AAATGCAATC	TCCCTTGTAT	2580
	TTAAACACAC	AGATACACAC	ACACACACAC	ACACACACAC	AAACCTTCTG	CCTTTGATGT	2640
	TACAGATTTA	ATACAGTTTA	TTTTTAAAGA	TAGATCCTTT	TATAGGTGAG	AAAAAACA	2700
	TCTGGAAGAA	AAAAACCA	CAAGACATT	GATTACGCTT	GTTTGGCGTT	TCCCAGAGTC	2760
	ATCTGATTGG	ACAGGCTAGG	GTGCAAGGAA	AATTAGGGTA	CTCAACCTAA	GTTGCGTTCC	2820
55	GATGAATTCT	TATCCCTGCG	CCCTTCTCTT	AAAAAACCCTA	GTGACAAAAT	AGACAAATTG	2880
	CACATCTTGG	CTATGTAATT	CTTGTAAATT	TTATTATAGG	AGTGTGTAAG	GGAGGTGGCA	2940
	AGAGTGTGGA	GGCTGACGTG	TGAGGGAGGA	CAGGCGGGAG	GAGGTGTGAG	GAGGAGGCTC	3000
	CCGAGGGGAA	GGGGCGGTGC	CCACACCGGG	GACAGGCCGC	AGCTCCATT	TCTTATTGCG	3060
	CTGCTACCGT	TGACTTCCAG	GCAAGGTTTG	GAAATATTCA	CATCGCTTCT	GTGTATCTCT	3120
60	TTACATATGT	TTGCTGCTAT	TGGAGGATCA	GTTTTTGTG	TTACAAATGC	ATATACTGCC	3180
	ATGTACTAGT	TTTAGTTTTC	TCTTAGAACA	TTGTATTACA	GATGCCCTTT	TTGTAGTTTT	3240
	TTTTTTTTTT	ATGATATCAA	TTTTGACTTA	ATGTGATTAC	TGCTCTATT	CAAAAAGGTT	3300
	GCTGTTTAC	AATACCTCAT	GCTTACCTTA	GCCATGGTGG	ACCCAGCGGG	CAGGTTCTGC	3360
	CTGCTTTGCG	GGGAGACAC	GCGGGCGCGA	TCCCACACAG	GCTGGCGGGG	GCGGGCCCCG	3420
65	AGGCGCGGTG	CGTGAGAACC	GCGCGGTGT	CCCCAGAGAC	CAGGCTGTGT	CCCTCTTCTC	3480
	TTCCCTGCGC	CTGTGATGCT	GGGCACCTCA	TCTGATCGGG	GCGGTAGCAT	CATAGTAGTT	3540
	TTTACAGCTG	TGTTATTCTT	TGCGGTAGC	TATGGAAGTT	GCATAATTAT	TATTATTATT	3600
	ATTATAACAA	GTGTGCTCTA	CGTGCCACCA	CGGGTTTGTA	CCTGTAGGAC	TCTCATTCGG	3660
	GATGATTGGA	ATAGCTTCTG	GAATTGTGTC	AAGTTTGGG	TATGTTTAAT	CTGTTATGTA	3720
70	CTAGTGTTCT	GTTTGTATT	GTTTGTATA	TTACACCATA	ATGCTAATT	AAAGAGACTC	3780
	CAAACTCTCA	TGAAGCCAGC	TCACAGTCT	GTGTGCCCCG	GTCACTAGC	AAGCTGCCGA	3840
	ACCAAAAGAA	TTTGACCCCC	GCTGCGGGCC	CACGTGGTGG	GGGCCCTGCG	CTGCGAGGGT	3900
	CATCCTGTGC	TGAGAGGCCA	TCTGCGGCAC	AGGCCACCCC	CGCCCCACCC	CTCCAGAA	3960
	CGGCTCACGC	TTACCTCAAC	CATCCTGGCT	GCGCGTCTG	TCTGAACAC	GCGGGGGCCT	4020
75	TGAGGGAGCG	TTTGTCTGTC	GTGATGGGGC	AAGGGCACAA	GTCCTGGATG	TGTGTGTAT	4080
	CGAGAGGCCA	AAGGCTGGTG	GCAAGTGAC	GGGGCACAGC	GGAGTCTGTC	CTGTGACGCG	4140
	CAGTCTGAG	GGTCTGGGGG	GCGGGCGGCT	GGGTCTGTGC	ATTCTGCTG	GCAACCGGGC	4200
80	GCTTCCAGC	ACCAACATGT	AACCGCATG	TTTCCAGCAG	AAGACAAAA	GACAAACATG	4260
	AAAGTCTAGA	AATAAACTG	GTAAAAACCC	AAAAA			

Seq ID NO: B2 Protein sequence
Protein Accession #: NP_444284.1

1 11 21 31 41 51
797

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 MEHQLLCEV ETIRRAYPDA NLLNDRVLRA MLKARETCAP SVSYFKCVQK EVLPSPMRKIV 60
 ATWMLVECEE QKCEBEVFPF AMNYLDRFLS LEPVKKSRLO LLGATCMFVA SKMKETIPLT 120
 AEKLCIYTDN SIRPEELLQM ELLLVNKLKW NLAAMTPHDF ISEPLSKMPE ASENKQIIRK 180
 HAQTFVALCA TDVKFISNPP SMVAAGSVVA AVQGLHLRSP NNFLSYRYLT RFLSRVIRCD 240
 PDCLRAQCEQ IEALLESSLR QAQONMDPKA AEEEEEEEE VDLACTPTDV RDVDI

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 Seq ID NO: B3 DNA sequence
 Nucleic Acid Accession #: XM_044166
 Coding sequence: 1..1576

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 CAGGGCGGGC GAGGACGGGG GAGGTGGGGG GGGGGGCGCC CCGCGCGAGC CGACAGCCCC 240
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 TCCCGTGGCC ACCTCGGAGC ACGTGGCGGA GATCGTGGGC AGGCAAGGCT GCAAGATTAA 480
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 CATTCTTCT GATGGAGCA GGTGGAGGTG CAGAGGGGAT TTCTCTCTCT CCTTCTCTCT 2940
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75
 Seq ID NO: B4 Protein sequence
 Protein Accession #: XP_044166.2

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 FMTVGRREDV ATARREIISA AEHFSEIRAS RNKSGAAGV APALPGQVTI RVRVYRVVG 240
 LVVGRKGTI KRIQQTNTY IITPSRDRDP VPEITGAPGN VERAREEIEI HIAVRTGKIL 300
 EYNNENDPLA GSPDAIDSR YSDAMRVHQP GCKPLSTFRQ NSLGCIGECG VDSGFEPRL 360
 GEQGGDFGYG GYLFPYGVG KQDVYGVAE TSPPLMAGQE NATPTSVLFS SASSSSSSA 420

KARAGPPGAG RSPATSAGPE LAGLPRRPPG EPLQGFSLKG GGGLRSPGGG RDCMVCFESE 480
VTAALVPCGH NLFMCACAVR ICERTDPECP VCHITATQAI RIFS

5 Seq ID NO: B5 DNA sequence
Nucleic Acid Accession #: NM_000909.1
Coding sequence: 209..1363

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ATAATCTATA ACAACCAAAC CAATCAAAAT GAATTCACAA TTATTTTCCC AGGTTGAAA 240
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Seq ID NO: B6 Protein sequence
Protein Accession #: NP_000900.1

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70 Seq ID NO: B7 DNA sequence
Nucleic Acid Accession #: NM_002590.2
Coding sequence: 204..3416

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Seq ID NO: B8 Protein sequence
 Protein Accession #: NP_002581.2

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Seq ID NO: B9 DNA sequence
Nucleic Acid Accession #: AL121939.12
Coding sequence: 185..1426

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Seq ID NO: B10 Protein sequence
Protein Accession #: CAC35071.1

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Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: NM_002035.1
Coding sequence: 108..1106

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Seq ID NO: B12 Protein sequence
Protein Accession #: NP_002026.1

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Seq ID NO: B13 DNA sequence
Nucleic Acid Accession #: CAT Cluster

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Seq ID NO: B14 DNA sequence
Nucleic Acid Accession #: XM_086767.1
Coding sequence: 276..611

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Seq ID NO: B15 Protein sequence
Protein Accession #: XP_086767.1

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Seq ID NO: B16 DNA sequence

Nucleic Acid Accession #: CAT cluster

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Seq ID NO: B17 DNA sequence

Nucleic Acid Accession #: NM_022898.1

Coding sequence: 268..2739

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Seq ID NO: B18 Protein sequence
 Protein Accession #: NP_075049.1

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Seq ID NO: B20 Protein sequence
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 IRIHTGKHP QCRICMNFBS RSDHLTHIR THTGKPFAC DYCGRKFPARS DERKRTKH 420
 LRQKERSA PSASVPAPST ASCSGVQPG GTLCSSNSSS LGGGPLAPCS SRTTTP

Seq ID NO: B21 DNA sequence
 Nucleic Acid Accession #: NM_004962.2
 Coding sequence: 457..1893

1 11 21 31 41 51
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5 CACACACGGG GGCAGCACA CGGCAGCCGG GCCAGGAGG ACCCTGTGAG CTGCAGCCCC 60
 AGAGGTTCGG GGCAGCAGC GGGTCCCTT CGAGGGCGCA GCGGCGCGCC CGGCCCCGCC 120
 CCTCGAAGCA GCGGGGCGGG GCGCGCAGTG GGCTACAAAC TTTCGACAGG CGAGTCCGGC 180
 AAGGCAGCGC GCGGACTCGG GCTCGGCTCG GCTCTGCGCT GCTCCGAGCG GCTGTGACCG 240
 CTGGCCGGGG GCTCGGGCCG CGGATACCA CGGACCGCGC GCGCGGCTGC CTGCTCCGCT 300
 AAGCCCTCGC CCGCGCGCGG ACCTCGGTAT CCAGCGCCCT GCTGCGCGGG CTCTCCCGCG 360
 GCGCCCTACT GCGCGAGGT CAGTCCGCG CCTCGGTGC GCCAGCGCTC GCCTTCCTCC 420
 TCCTGGACTT CGGCCCTTTG CCGCCCTCAC CACGCCATGG CTCTGTCCCG CGCTCGGACC 480
 AGCCCGGGAG CCGGGCCCCA GCTGCTGCTG CTGCTGCTGC GGTGTGTTCT GCTGTTGCTC 540
 CGGGATGTGG CGGGCAGCCA CAGGGCCCCC GCCTGTTCGG CACTGCCCGC GCGCGCGGAC 600
 GGCTGCGAGG GGCAGACGGA TCTCCAGCGG CACCTGGGG ACGGGCGCGC CACGTTGGGC 660
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 CAGGGCGCGC GCGCGGGAGG GGGCAACAG GTCCGAGCT TCAGGGCCAG GCTGGAAGTG 780
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 CTATGCAAGC CGGGGCGCAA GAACGCTTCA GCGCGCCCGC TGCCCTCGGG CCGGCCCA 960
 CGCCAGCACC TGCTCTTCGG CAGCTCTCG CAGAACAGG CCACACAGGG GCTACTCCCG 1020
 GGGGCCATGG CCTTGCGGCC CCCACCGCGC GGCCTGTGGC AGGCCAAGGA CATCTCCCCC 1080
 ATCGTCAAGG CGGCGCGCGG GGTATGGGAG CTGCTCTCTT CGGCCAGCTT GGATTCTGAG 1140
 20 GAGAGGAGCC CGGGGCTGCC CCGGCCGAGC CCTATGCGC CTACATCTCT AGTCTATGCC 1200
 AAGCATCTGG CCATCTCGGA GCCCAACAGC GTGGCAGTGA CGCTGCAGAG ATACGACCCC 1260
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 CGCGAGCGCG CGCAGGCCAC TGGGCCCTTC CAGGACAAAG AGCTGCCGGG GCTGGATGAG 1380
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 30 GTCAGGCTCG TGGGCTATCT CCTGGCATC CCAGAGCCCT GCTGTGTTCC CGATAAGATG 1800
 AACTCCCTTG GGGTCTCTTT CCGTGGATG AATCGGAATG TGGTTCTGAA GGTGTACCCC 1860
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 AGGCTTGAAA ACAAAACATA TCCACAACAT TGGCTTGATG TGATCATCAT CTCATAACTG 2220
 AGCAAGAGGA CTATGCAAAAT CTTAGGGGCG TCGCTCCCTG CACACGGAAG GAACCTCTGT 2280
 40 TAAATGCTCA GTTCAGAAAC CTTTGGGCCA CATAGTGATT TTGGAAGAAA GGATAATCGT 2340
 GGTGTAAATG AGTGTTTCTT TTCAAAGTCC ACTGCAGAGC TTTTATCCAT ATGGTATGCA 2400
 CATGTAGCCA ATATTGGTTT CTTTCTTCTA ATATATATAT TTTATTTTAA AACAACAAAA 2460
 AGGGAGGGCG TTGACACCAT TCCCCACAGA GATAGTCATG CTGAGTGTGG GTTGTATAA 2520
 CATGCATATT GAAATAACAC ATATAGTAAC GTGGGAATAC TAAAAAATAA CCAAGATTIT 2580
 45 ATATTTTGT AATATATACT TTCTATCTG TAGATTGTGT ATGTTATGTG TTTTATGGA 2640
 AAGCTAATAA ATTAAAGGTA CAGTGGTATC TTGA

Seq ID NO: B22 Protein sequence
 Protein Accession #: NP_004953.1

50 1 11 21 31 41 51
 MAHVPARTSP GPGPQLLLLL LPLFLLLLRD VAGSHRAPAW SALPAAADGL QGDRDLQRHP 60
 GDAANTLGPS AQDMVAHVHM RLYEKYSRQG ARPGGGNTVR SFRARLEVVD QKAVYFPNLT 120
 55 SMQDSEMLT ATFFHYSEPP RWPRALEVL KPRAKNASGR PLPLGPPTTQ HLLFRSLSQN 180
 TATQGLLRGA MALAPPFRGL WQAKDISPIV KAARRDGEILL LSAQLDSEER DPGVPRPSY 240
 APYILVYAND LAISEPNSVA VTLQRYDFFP AGDPEPRAAP MNSADPRVR AAQATGFLQD 300
 NELPLGLDERP PRAHAQHFKH HQLWPSFPRA LKPRPGRKDR RKGQEVFMA ASQVLDLDEK 360
 TMQKARRKQW DEPRVCSRRY LKVPFADIGW NEWIISPKSF DAYYCAGACE FPMPIKIVRPS 420
 NHATIQSIVR AVGIIPGIPE PCCVPDKMNS LGVLFLEENR NVVLKVYPNM SVDTCACR

Seq ID NO: B23 DNA sequence
 Nucleic Acid Accession #: AK026322.1

65 1 11 21 31 41 51
 ATTCTTTAAA TACTTAAACA TGGTTATAAC AGCTGTGTTT TAAGCTCCTT GTCTGTTAAT 60
 TCCATCATCT GTCATTTTTG CATCTGTTTT TATGACTTAA CTTTCTTCTT CATCATGGTC 120
 ACATATCCTT GCTTCTTCCC ATATTAGTA AAGTTTAGTT GGATGCTGGA TTGTTTAAAT 180
 70 TTAGCATTTT GAGTGAAGTG CTTTGCAGT TGCCCTTAAA AGTATTTGAC TTCGTTTGA 240
 TAGTTGAATT ACTTGCAGAT CAGCTTGATC ATTCTGAGAC TTGTTTAAAT CTTTGTGGA 300
 AAGGGCTATG CTACTTCAAG TATAATAAAA CCTAGTTTAA GTTTTATCCT ATAACTAAGG 360
 CATGTGTTCA ATTTGAATGT CTCCAACCTT GTGTGAATC TGAATAATGT TCAGTCCCA 420
 ATTTGCGAGT AATTTTTTTT GTTCAGCCTT GCAGTCTCAT CCTACTCAAG TGTGGCTCTG 480
 TATCCAAACA CAGTCTTGGG GATCTCATGA AGATTCTGTA AACTTTTGCT CTGCAGGATA 540
 75 CCTTCTTTTG TGGTTATGTG CCTGAAAAC TCCAGCCTCC GTGCTTCAAA TTCAGTGAAA 600
 CTACTACTCT GCTTGGATTC CCTCTTATA CAATGGTCTA CCAAGTGACT GCAACAGAAA 660
 ATCTAAGGGA ATTTCAGGAG TCACCTCAT TATTTTCTT TTTTTCAGG ATTATAGTAG 720
 TACTATACCA CCGTTCAGCC AATGTGTGAG AATGGTGGTT TCATACATT TCTCCAATTC 780
 TTTCTGTTA CAGGAGCCTC CATTACTTTT CAAACAGTAA TGCAAGTGCA GTTGCTCTC 840
 80 CTTTCTTTCA TATGTGTTT ATCTCTGGCA GTTTGAGCCA AGAGAGGGCA CGGAGAAGTA 900
 CAATGACTAG AGAGCACTTC TGTGAGGCT CATTCAATGA CCCCTACCCC AGTGCTTTAT 960
 GAATGTGTGC TGCAGATGTC ATACAGCATC ACAGCTTCTT CTCTAATTTA TGAGCCATAA 1020
 TTTTCTTTT TGTATTTTAA TTGATTACC TGCTTGGTGG CAAGAGGATG ATGAGGAGGA 1080
 CTACTATAGG ATAAATTGTT TTTTATAGAG CAATTCTCA TGGGTACAGA GGGATAGTAC 1140

TCCATTTTCC TCACGTGATAT CGGCTTGATC ATCTGAGTCA GTGGGCTCAT TGTGGAAACA 1200
 TATGGAATCC TTTATGCTTT TTCTCAGGCT GCTTCTGTTA CATGAAATAA AGCCAGAGTT 1260
 GATTGTGAAA AAAAAAAAAA AAAA

5 Seq ID NO: B24 DNA sequence
 Nucleic Acid Accession #: cat cluster

	1	11	21	31	41	51	
10	TGTATACATT	CCTTTCAAAT	AAAGACCTTG	AGAAAAACAGC	AGAGCCCAAGT	GAAGATCACC	60
	TAAAGAACTT	TGTGGCTTAAT	TTATACCTCA	TGTAGTAGCA	GTGGGTACTG	GGCAGGGTCT	120
	CTTTCCCACT	CTGATGATTT	GTGCTCTTAT	TTTTCTCTAGA	TTTACCTCAT	CTAGGGCATA	180
	TTCTTTTCCC	TCTTCTCTTT	TACCTTTCCT	GGTCTGATC	CCTCTGTACT	CAGTTCCCTT	240
	AAATTATTGG	ACTACAAAT	AATATACTAG	AAAAGCATAC	ACTTATTTTA	TTTGAATGCA	300
15	GAAATGCTAT	CTATCAGTAT	ATATACATAA	GAATGTATAT	TACAGTATAT	CTATATATAC	360
	TTAACACTGT	AACCTTTCAGT	ATTCCCCAGT	TAGCGTACCT	AACCTCTCTG	TGGGTTATGT	420
	TAATTCCTAT	TAGACTACTA	GAGAAAAACC	AACCTGGCAGT	TTGCTAAGCA	TATCTACTGG	480
	TGTTGTCTCT	GCGCCCTCTT	TTGGCTAATT	GATGTAATTA	TACTGGCTCT	AAAGATTAC	540
	TGCCCCATAA	GTAAATAGTA	TAGCCACATT	CTGAACATAT	CAAAAAGTACA	AACCTAGGAG	600
20	GAGTGTATGT	ACAAAAATGT	AAAATTTTAT	GAATTTTAT	ATGTTTATAT	GATGTTATTT	660
	CTAGTTCATA	AGAAATGTAT	GACTGCTTTG	CTTCAATTTT	GTACGTTCCC	ATTATATCTT	720
	TGCTGTCAAT	CAATCACTAA	TTTATATCAG	ATTAGGATAA	ACTAAGCCAT	TTTATGTATT	780
	TTATTTTAAA	CCTTATTTTG	GCAGAGTAAT	TCCTTAGAAT	TGGAAGAGCT	GTTACTTTGA	840
	AATTACCAAT	TTATTACAAA	ACATAGAAAT	GTATTTAGTC	TACAAAGACA	ACCAAGCATT	900
25	TTCTGTGTTT	TAATGAATAT	CTAAAAACT	ACATTTAGTT	TATTTTACTC	AGTTTGTAAA	960
	TGATTTTTTT	ACTGGCTCTA	TTGCCTTAAA	ATACTAAGA	GATTATATAT	TCCTTTGATA	1020
	ATTTTCTCTT	TCCTTGTCTT	TTTTTTTACA	TTTGCAGAG	TTATATCTAT	AGTTTGTATA	1080
	ACAAATTTCT	ATGTATTTCT	GATAACTGAA	AACAATAAAA	GGTGTGGGCT	ATTAGAAAAT	1140
30	AATTGTGAGC	ATGAAGATTA	CTGATGTAAT	ATGTATGTTG	GACTGAAGTA	TTTCTTTATA	1200
	AACATTCTAT	TTGATTTTAA	GCAAAATGTA	TGTTAAAGCA	TGTTTATACA	TCAGTAAAGT	1260
	CAATTGTGCA	CCTTCTGGAA	ATGAAAGGTT	TTTACCTAGA	TACTGTAAAT	TACACCTCCT	1320
	TAACATCAT	ATTGTCTATT	GTGTTTCTT	GCAACAAAAA	ATGTTTATGG	GCTTCATGTA	1380
	GGCTTAAGAT	TGTAGGCAAA	AATGGACTGA	GTTCAGGACC	CTTCAAGCAG	TAGGCATTCA	1440
	GTACAGAGC	AGTTGGTACT	TTGTAAACCA	GACTTACAGT	TTAAATAATAT	CAAGTTAGCT	1500
35	GATGTTTCAT	TATATATAAA	ATACTATTTT	GCTTAAAGAT	TGTATTACAA	ATATTGTGTC	1560
	TTAACATTAG	AAATAGCTGT	TTTAAATGTT	AGTTAACATA	TTAACTTTT	CAGAAAAAAA	1620
	GCATGGTTTA	TTTTTAATAA	TGAATATAGG	AACATAATAC	GTAATGTCTA	GTATAACAGC	1680
	TGAGTTAAAA	CATCTGCCAG	GATTAACTC	AGTGGGTTTT	TGCCAATGCA	TAGAGGCATT	1740
40	TTTCTCTAAG	TATGATGGCT	AATGATAACT	ATTCTTTGTT	ACACATTCAA	GTCACTCCCA	1800
	TACAAGTAAC	TATGTTTCTC	TCCAAGGGT	GTATTAAATC	TGAATGCTAA		1860
	TCATGAAGAC	TTAAGTTAGG	ACAACTCTTC	AAACCAGGAA	GTGTGAACGT	ATTTA	

Seq ID NO: B25 DNA sequence
 Nucleic Acid Accession #: FGENSESH predicted
 Coding sequence: 1..1144

	1	11	21	31	41	51	
50	ATGGAGCGCG	GGATGCACCT	CGGTGCACCG	GCCGCGCGCG	AGGACGACCT	CTTCTGCGAC	60
	AAGAGCCTGA	GCGCTCCAC	CTCCAAGCGC	TTGGAAGCGG	CTTTCGCTC	CACGCCCCCG	120
	GGCATGGACC	TGTCCCTGGC	GCCGCGCGCT	CGGGAACGCC	CGGGTCTCT	CTCTCTGTG	180
	CCCTGGGCT	GCTTCGAGCC	GGCTGACCCC	GAGGGGGCAG	GGCTGCTGTT	GCCGCGCGCT	240
	GGAGGAGGCG	GCGGCGGCG	GCGGGAAGT	GCGGCGGCG	GCGGCGGCG	GGTGGGTGTC	300
	CCCGGCTGTC	TAGTAGGTTT	AGCGGCGGTT	GCGGCGGACC	CTAGCCTAAG	CAGCCTGCGG	360
55	GCGGGGCGCG	CCCTTTGCTT	CAAGTACGGC	GAAAGCGCGA	GCGGGGCTC	GGTGGCGGAG	420
	AGCAGCGCGG	GCGAGCAGAG	CCCGGACGAC	GACAGCGAG	GTGCTGCGA	GCTCGTGTG	480
	CGGGCGGAG	TAGCGGACCC	GCGGGCTTCC	CGGGGAGCGG	GAGGTGGTGG	CGCGAAGGCA	540
	GCGAGGGCT	GCTCCAATGC	CCACCTCCAC	GGCGGCGCCA	GCGTCCCTCC	GGGGGGGCTG	600
	GGCGGCGCG	GCGGCGGGG	TAGCAGCAGC	GGTAGCAGTG	GCGGCGGTTG	CGGTAGCGGT	660
60	AGCGGCGAG	GCGGCGGCG	CAGCAGCAGC	AGCAGCAGCA	GCAAGAAATC	CAAAGAGCAA	720
	AAGGCGCTGC	GGCTTAACAT	CAATGCCCGA	GAGCGCGCGC	GGATGCAAGA	CCTGAACGAC	780
	GCGCTGGAGC	AGCTGCGCGC	GGTGATCCCC	TACGCGCACA	GCCCTCGGTT	GCGAAAGCTC	840
	TCCAAGATCG	CCAGCTGCTT	GCTGCGCAAG	AACTACATCC	TCATGCGAGC	GCAAGGCGCT	900
	GAGGAGATGC	GCGGCTGAGT	CGCTACCTCC	AACGAGGGCC	AGGCCATCTC	GGCTGCTCTC	960
65	CTGCCAGCT	GCGGCGGCTG	AGCGGCGAGCA	GCTGCTGCCC	TGCACCCGCG	GCTCGGCGCC	1020
	TACGAGCAGG	CAGCGGCTA	CCCGTTCAGC	GCGGAGCTGC	CCCGGCTGCG	CTCCTGCCCC	1080
	GAGAAGTGGC	CCCTGTTTAA	CAGGCTCTCC	TCCAGCTCTT	GCAACAGTGC	CACGGAGAGG	1140
	CCTT						

70 Seq ID NO: B26 Protein sequence
 Protein Accession #: FGENSESH predicted

	1	11	21	31	41	51	
75	MERGMHLGAA	AAGEDDLFLH	KSLASSTSKR	LEAAPRSTPP	GMDLSLAPPP	RERPASSSSS	60
	PLGCFEPADP	EGAGLLLPFP	GGGGGGSAGS	GGGGGGGVGV	PGLLVGSAGV	GGDPSLSLPP	120
	AGRALCLIKY	ESASRGSVAE	SSGGEQSPDD	DSGRCCLVL	RAGVADPRAS	PGAGGGGAKA	180
	AEGCSIAHLH	GGASVPPGGL	GGGGGGSSSS	SSSGGGGGSG	SGSGSSSSSS	SSSSSKSKSE	240
	KALRLININAR	ERRRMHDLND	ALDELRAVIP	YAHSPSVRLK	SKLATLLLLAK	NYILMQAAL	300
80	BEHRLVAVL	NQQQAISAAS	LPSSAAAAAA	AAALHPALGA	YEQAAGYPPS	AGLPPAASCP	360
	EKCALFNSVS	SSLCKQCTEK	P				

Seq ID NO: B27 DNA sequence
 Nucleic Acid Accession #: cat cluster

	1	11	21	31	41	51	
5	TTTTTTTTT	TTTTTTTTTAA	ATGTTTGATC	AAAATATTTT	AATAAGATT	CTTCTGACA	60
	TAGATACACA	TACAAATGGT	CGTACATAGC	TGTCATAGTC	TGATTGACCT	ATTTAATATA	120
	TATATCATT	TTTACACATC	CAAAACCCGC	CAACAGATCC	ATCAGAGCTC	CCAACCTACC	180
	ATCCAACCTG	ACAAACTGAA	TTTGTAATTAT	CTGCAAGGAG	TGGAAAATAG	CAGGACTCCA	240
	TTTTTAAAAA	AGATTTTCTT	GATTTTCATA	GGCGGAAAG	GCAGTCAAAC	AGCCATGCAA	300
	AACTAAAACT	GAAGCTCAC	TTTGGGTAAA	TAGCTTCTTG	TTCTTCTTTA	GTITTTCTTC	360
10	TTTTTAAATT	TTATTTTTTT	AGAAAAATAA	CAAAGGATTT	CACACCATAG	GCAAACTCAA	420
	CCAGTCTTTT	AACTTAAATA	ATTCTCCACA	GTTAAAAATA	CATATATGTA	CATATATATT	480
	AAAAGCAATT	AAATTAGACC	TTTTAAAAAT	GCACAGCACA	GCCTGGAAAA	ATATTTGCTT	540
	AGCATGTTCT	TACGTATAGC	AACTATTGCT	GTGATGTTTT	TCCTTTTGG	AATGTAAGG	600
	AGTCCCTTTT	CAAAAAAGAG	ATCAATTCAT	TCATCAATTA	AGAATACACC	TTTCTGTAA	660
15	TTTTTGGACT	GAAGCAATTT	ATTAAAGCTC	AATTTAAATA	CAGGGATGAT	GCAACTGAAA	720
	ATATCCAGGT	GACCTTTTAT	AAACCTAAGC	AGCTCAGATA	CATCAATATT	TCTCTTCATA	780
	CTGTGTGGCA	ATAAAACCTT	TAAACACTTG	GCACACAGCA	TAAATTAATCT	ATAAAACAAT	840
	TTTAGAGGCA	TTAAAAAAT	CTGCACATAA	GACCCATGAC	TTTAAACAT	GATAAATACT	900
	GTGTATGTGG	AAGGGTCATT	GAAGAATAAC	AAATAAATAC	CATGAATTGT	TAATACATCA	960
20	TTGCAGAGTA	GAAAGTAAACA	AGGTGCACAT	AAATATTTTT	AAATGCAATT	CTTTCAGCCA	1020
	CAGTCAGTTT	TTTTATATCA	CTCTCGCCAA	AACTTTGAGC	ATTTTCACAG	GATTAAAGTT	1080
	CAGAGACAAT	AAAAAATACA	AGTCTTTTAT	AGTAACATGT	TCTCTCTCTC	TGCTCTGGG	1140
	TTTTATTTC	CCCTCACTTA	AGTCAACATT	TCAAGTTTTT	CTCTGGCTC	AGAATCAAAA	1200
25	TTTTATTTC	AGTGCCCTTT	CTGATTTGTC	TGAATGAATA	TTCCATCTCT	CATGCTACCG	1260
	ATCCGCT						

Seq ID NO: B28 DNA sequence
Nucleic Acid Accession #: NM_002581.2
Coding sequence: 368..5251

30	1	11	21	31	41	51	
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35	CAGATAAAAG	AGCGGGGAGA	GAAATTAAAT	GCCCAACCAGG	AGGAGTTGGG	CTGTATTTTT	180
	CAAGAGTGGG	GAGAGTGGAG	CACACACCTT	GAGGAGGAAA	GCGAGAAAGA	AAAGAAAAAA	240
	GCAAGTGAAG	GGGGGCTCGC	CCAAGAAGGG	TGAAGAAGCG	AAGAAAGTCG	AGGCGCCGAG	300
	GCTCCCAAAG	CTGGCAGCTC	CGGGTGGCGG	TGCAGGGGCG	AAGGGGGGGG	CGGGGGGAAC	360
	GTGCGACATG	CGGCTCTGGA	GTGCGGTGCT	GCACCTGGGG	CTGCTGAGCG	CGCGCTGGG	420
40	CTGCGGGCTG	GCAGAGCGTC	CCCGCCGGGC	CCGAGAGAGC	CCGCGGGCGG	GCGAGCCCCC	480
	GCGCCCCCGC	GCGGGCCCGG	CCACCTGCGC	CACCCGCGGC	CCGCGGCGCG	CGCGCTCGC	540
	CGCGCGCGCC	GCGCGCGCGG	GGCGTGCGTG	GGAAGCCGTG	CGCGTCCCGC	GGCGCGGCGA	600
	GCAGCGGGAG	GCGAGGGGCG	CCACCGAGGA	GCCGAGCCCG	CCGAGCGGGG	CGCTCTATTT	660
	CAGCGGGCGA	GGCGAGCAGC	TGCGAGTCTT	CCGGGCGGAC	CTCGAGCTGC	CCCGGGAAGC	720
45	GTTCAGCTG	CAAGTGTGGC	TGCGAGCGGA	GGGGGGCCAG	AGGTCTCCGG	CAGTGATCAC	780
	AGGCCTGTAT	GACAAATGTT	CTTATATCTC	ACGTGAACCGA	GGATGGGTGG	TGGGCATTCA	840
	CACCATCAGT	GACCAAGACA	ACAAAGACCC	ACGCTACTTT	TTCTCTTTGA	AGACAGACCG	900
	AGCCCGGCAA	GTGACCACCA	TCAATGCCCA	CCGACAGTAC	CTCCAGGCCC	AGTGGGTATA	960
	CCTAGCTGGC	ACCTATGATG	GGCAGTTTAT	GAAGCTCTAT	GTGAATGGTG	CCCAGGTGGC	1020
50	CACCTCTGGG	GAAACAAGTG	GTGGCATATT	CAGCCCACTG	ACCCAGAAGT	CCAAAGTGCT	1080
	CATGTTAGGG	GGCAGTGCCC	TGAATCAACA	CTACCGGGGC	TACATCGAGC	ACTTCAGTCT	1140
	GTGGAAGGAT	GCCAGGATGC	AGCGGGAGAT	ACTGTCTGAC	ATGGAACCC	ATGGCGCCCA	1200
	CAGTGTCTTA	CCTCAGCTCC	TCTCCAGGA	GAACTGGGAC	AATGTGAAGC	ATGCTGTGTC	1260
55	CCCCATGAAG	GATGGCAGCA	GCCCCAAAGT	GGAATTCAGC	AATGCCCAAG	GCTTTCTGCT	1320
	GGACACAGAG	CTGAGGCTTC	CTCTGTGCGG	ACAGACATTG	TGTGACAACA	CAGAGGTGAT	1380
	TGCCAGCTAC	AATCAGCTCT	CAAGTTTCCG	CCAGCCCAAG	GTGGTGCGCT	ACCGCGTGGT	1440
	CAACTCTAT	GAAGATGATC	ATAAGAACC	GACGGTGACG	CGGAGCAGGG	TGGACTTCCA	1500
	GCACCATCAG	CTGGCTGAGG	CCTTCAAGCA	ATACAACATC	TCTGGGAGC	TGGACGTGCT	1560
60	GGAGGTGAGC	AACTCTCTCC	TTGCGCGCGG	CCTCATCCTG	GCCAACTGTG	ACATCAGCAA	1620
	GATTGGGGAT	GAGAACTGTG	ACCCCGAGTG	CAACCAACAG	CTGACGGGCC	ACGACGGCGG	1680
	GGATTGCGCG	CACCTGCGCC	ACCCTGCGCT	OGTGAAGAAG	CAGCAACAAG	GGGTGTGTGA	1740
	CATGGAGCTG	AACTATGAAC	GGTTCAACTT	TGATGGTGA	GAGTGTCTGT	ACCTGAAAT	1800
	CACCAATGTC	ACTCAGACTT	GCTTTGACCC	CGACTCTCCA	CACAGAGCCT	ACTTGGATGT	1860
	TAATGAGCTG	AAGAATCTTC	TTAAATTTGA	TGGATCAACA	CATCTCAATA	TTTTCTTTGC	1920
65	AAAATCCTCA	GAGGAGGAGT	TGGCAGGAGT	AGCAACTTGG	CCATGGGACA	AGGAGGCCCT	1980
	GATGCACTTA	GGTGGCATTG	TCTTGAACCC	ATCTTTCTAT	GGCATGCCTG	GGCACACCCA	2040
	CACCATGATC	CATGAGATTG	GTCAAGGCTT	GGGCTCTTAT	CAGTCTTCC	GAGGCATCTC	2100
	AGAAATCCAG	TCCTGCAGTG	ACCCCTGCAT	GGAGACAGAG	CCCTCTCTCG	AGACTGGAGA	2160
	CCTCTGCAAT	GATACCAACC	CAGCCCTTAA	ACACAAGTCC	TGTGGTGACC	CAGGGCCAGG	2220
70	AAATGACACC	TGTGGCTTTC	ATAGCTTCTT	CAACTCTCTT	TACAACAAC	TCATGAGCTA	2280
	TGCAGATGAC	GACTGTAGGG	ACTCTTTCAC	GCCCCAATCA	GTGCGCAGAA	TGCACTGTTA	2340
	CTGTGACCTG	GTCTACAGAG	GCTGGCAGCC	CTCCAGGAAA	CCAGCGCCTG	TTGCCCTCGC	2400
	CCCCCAAGTT	CTGGGCCACA	CAACGAGCTC	TGTGACACTG	GAGTGGTTCC	CACCTATAGA	2460
	TGGCCATTTC	TTTGAAGAGG	AATTGGGATC	AGCATGTCTAT	CTTTGCTTGG	AAGGGAGAAT	2520
75	CTGCTGAGC	TATGCTTCCA	ACGCTTCTCT	CCCAATGCCC	TGCAGCCCAT	CAGGACACTG	2580
	GAGCCCTCGT	GAAGACAGAG	GTCACTCTGA	TGTGAAACAG	CCCTGTAAAT	CCAGTGTCCG	2640
	CACCTGGAGC	CCAAATTCTAG	CTGTCAACCC	ACACAAGGTT	CCTCCAGCCT	GCCCTGAGCC	2700
	TCAAGGCTGC	TACCTGAGGC	TGGAGTTCTT	CTACCCCTTG	GTCCCTGAGT	CTCTGACCAT	2760
	TTGGGTGACC	TTTGTCTCCA	CTGACTGGGA	CTCTAGTGGG	GCTGTCAATG	ACATCAAAC	2820
80	GTTGGCTGTG	AGTGGGAAGA	ACATCTCCCT	GGGTCTCTCG	AATGTCTTCT	GTGATGTCCC	2880
	ACTGACCATC	AGACTCTGGG	ACGTGGGCGA	GGAGGTGTAT	GGCATCCAAA	TCTACACGCT	2940
	GGATGACAC	CTGGAGATCG	ATGCTGCCAT	GTGACCTTCC	ACTGCAGACA	CCCACTCTG	3000
	TCTACAGTGT	AAGCCCTCGA	AGTATAAGGT	GTCGCGGAC	CCTCTCTTCC	AGATGGATGT	3060
	GGCTCTCATC	CTACATCTCA	ATAGGAAATT	CGTAGACATG	GATCTAAATC	TTGGCAGTGT	3120

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GTACCAAGTAT TGGGTCATAA CTATTTTCAGG AACTGAAGAG AGTGAGCCAT CACCTGCTGT 3180
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ACAATGCGAC GACATGAATA AGATCAATGG TGATGGCTGC TCCCTTTTCT GCCGACAAGA 3300
AGTCTCCTTC AATGTATTGG ATGAACCCAG CCGGTGCTAT TTCCATGATG GTGATGGGGT 3360
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ATTCTCTGAT CAGTGGGCAT CCAATGCTTC AGTATCTCAT CAAGACCAGC AATGCCCAAG 3480
CTGGGTCTATC ATCGGACAGC CAGCAGCATC CCAGGTGTGT CGAACCAAGG TGATAGATCT 3540
CAGTGAAGGC ATTTCCCAAGC ATGCCTGSTA CCCTTGACCC ATCAGCTACC CATATTCCCA 3600
GCTGGCTCAG ACCACTTTT GGTCTCGGGC GTATTTTCTT CAACCAATGG TTGCGCAGC 3660
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CAGCGTCGAC CTGCTTGATA CCAAGATCA GAGCCACGAT CTAGGCCTCC ATGCTCTGAG 3780
CTGCAGGAAC AATCCCCTGA TTATCCCTGT GGTCCATGAC CTCAGCCAGC CCTTCTACCA 3840
CAGCCAGGCG GTACGTGTGA GCTTCAGTTC GCCCTGCTC GCCATCTCGG GGGTGGCCCT 3900
CCGTTCTCTC GACAACTTTG ACCCGTCCAC CCTGAGCAGC TGCCAGAGAG GGGAGACCTA 3960
CAGCCCTGCC GAGCAGAGCT CGGTGCACTT CGCATGTGAG AAAACTGACT GTCCAGAGCT 4020
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TACTGTGAGC TGCCGACAGC GCTACGTGCT CCAGATACGG CGGGATGATG AGCTGATCAA 4140
GAGCCAGACG GGACCCAGCG TCACAGTGAC CTGTACAGAG GGCAAGTGA ATAAGCAGGT 4200
GGCCTGTGAG CCACTGCTAT GCAGCATCCC AGATCACCAT CAAGTCTATG CTGCCTCCTT 4260
CTCCTGCCCT GAGGGCAGCA CCTTTGGCAG TCAATGTTCC TTCCAGTGCC GTACCCCTGC 4320
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GACCGCCCGG TGCCGAGAGA ATAAGCACAA GGTGGGCTCC TTCTGCAAT ACAAAATGCA 4500
GCCTGGATAC CATGTGCTCG GATCCTCTCG GAAGTCAAG AAACGGGCTC TCAAGACTCA 4560
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TAGGATCAAG TGTGAAGACA GTGATGCCTC CCAGGGACTT GGGAGCAATG TCACTTCTTG 4740
CCGGAAGATG GGCACCTGGA ACGGCTCCTT CCATGTCTGC CAGGAGATGC AAGGCCAGTG 4800
CTCGGTCCA AACAGCTCA ACAGCAACCT CAAACTGCAG TGCCCTGATG GCTATGCCAT 4860
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GAAAGTGACC GTGGGTGACA TCCCCCACTG GCTGAACCCC ACACGGGTAG AGAGAGTTGT 4980
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TGAGCCCTTC ATGGGAGACA ATTATTGTGA TGCCATCAAC AACCGAGCCT TTTGCAACTA 5100
TGACCGTGGG GATTGCTGCA CCTCCACAGT GAAGACCAAA AAGGTCAACC CATTCCCTAT 5160
GTCTGTGATC CTACAAGGTG ACTGTGCTTG TCGGACCCCG CAGGCCCAAG AACACAGCGG 5220
GAAAGACCTC CGGGATACA GCCATGGCTA AGGAAGGACA AGAAGTGTG AAAGAATTCC 5280
CAACGCCAGG ACCACATCCC CTTTGGTATT GATTTCACAG TCAGCTGTG AACGGAATGG 5340
CCTCTCCACA CCAGGGATCC TTAGCACCCA ACCGGTCTGC CTTTAATTTT ACCCAGGAAG 5400
GACTCACATT GGGGCGAATG AACCAAGTTT CGCATGCTG GATGATGAAA TGGATTCCCA 5460
TCCCAAGTCT TGAGATGGAT TGCATATACA GTGTGCAGTC CCAGAGCCTC CTAAAATCTT 5520
AGCCATTGTT GACACAACCA CAGCAAAAAA AAA

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Seq ID NO: B29 Protein sequence
Protein Accession #: NP_002572.1

45
50
55
60
65
70
75

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1 11 21 31 41 51
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LQVWLRABEG QRSFAVITGL YDKCSYISRD RGVVVGHTI SDQDNKDPRY FFSKLTDRAR 180
QVTTINAHRS YLPQWVYLA ATYDQPMKL YVNGAQVATS GEQVGGIFSP LTQKCKVLAH 240
GGSAIHNHYR GYIEHFLMK VARTQREILS DMETHGARTH LPQLLLQENW DNVKHAMSEW 300
KDGSSPKVEF SNAHGFLDIT SLEPPLCGQT LCDNTEVIAS YNQLSSFRQP KVVRVRYVNL 360
YEDDHKNPTV TREQVDFQHH QLABAFQYN ISWELDVLEV SNSSLRRLI LANCDISKIG 420
DENCPEPCNH TLTGHDGQDC RHLRHPAFVK QHNGVCDMD CNYERPNFDG WFPWDKEALMH 480
VTGTCPDPS PHRAYLDVNE LKNIKLDGS THLNIFFAKS SEELAGVAT WFPWDKEALMH 540
LGGIVLNSPF YGMPGHTHTM IHEIGHSLGL YHVFRGISEI QSCSDPCMET EPSFETGLDC 600
NDTNPAKPKK SCGDPGPGND TCGFHSFPNT PYNNFMSYAD DDCTDSPTPN QVARMHCYLD 660
LVYQGWQPSR KPAPVALAPQ VLGHTDTSVT LEWFPPIIDG FFERELGSAC HLCLEGRILV 720
QYASNASPFM PCSFSGHNSP REAEGHPDVE QPCKSSVRTW SPNSAVNPHT VPPACPEPQG 780
CYLELEFLYP LVPESLTIWV TFVSTDWDS GAVNDIKLLA VSGKNISLGP QNVFCDVPLT 840
IRLWDVGEV YGIQIYITLDE HLEIDAAMLT STADTPLCLQ CKPLKYKVR DPPLQMDVAS 900
ILHLNRKFPD MDLNLGVSQ YWVITISGTE ESEFSPAVTY IHGRGYCGDG IIQNDQGEQC 960
DDMNKINGDG CSLFCRQEV FNCIDEPSRC YFHDGQVCE EFBQKTSIKD CGVYTPQGF 1020
DQWASNASVS HQDQCFGWV IIGQPAASQV CRTKVIDLSE GISQHWYFC TISYPYSQLA 1080
QTTFWLRAYF SQPMVAIAVI VHLVTDGTY GDQKQETISV QLLDTKDQSH DLGLHVLSCR 1140
NNPLIIPVHV DLSQPPYHSQ AVRVSFSSPL VAISGVALRS FDNFDPVTL SQRGETYSP 1200
AEQSCVHFAC EKTDCPELAV ENASLNCSS DRYHGAQCTV SCRTGYVLQI RRDELISQ 1260
TGPSVTCTCT EGKWNKQVAC EPVDCSIPDH HQVYASFPSC PBGTTFGSQC SFQCRHFAQL 1320
KGNNSLTCM EDGLWSPFEA LCELMCLAPP FVPNADLQTA RCRENKHKVG SFCKYKCKPG 1380
YHVFGSSRKS KRAFKTQCT QDGSWQEGAC VPVTCDEPPP KPHGLYQCTN GFQFNSECI 1440
KCEDSDASQG LGSNVICRK DGTWNGSFHV CQEMQGCQSV PNEIENSLKL QCPDGYAIGS 1500
ECATSCLDHN SESIILPMNV TVRDIPWHLN PTRVERVCT AGLKWFHPA LIHCVKCEP 1560
FMGDNYCDAI NNRAFCNYDG GDCCTSTVKT KKVTPFPMSC DLQGDCAED PQAQEHSRKD 1620
LRGYSHG

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Seq ID NO: B30 DNA sequence
Nucleic Acid Accession #: NM_032808.1
Coding sequence: 61..1008

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1 11 21 31 41 51
CTAGTCTATC TCGGCTTCTT CAACCTCTCC TACAACCCCA TCAGCAACCAT TGAGGGCTCC 60
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5 GTGGAGCCCT ATGCCCTCCG CGGCTTCAAC TACCTGCGCG TGCTCAATGT CTCTGGCAAC 180
 CAGCTGACCA CACTGAGAGA ATTAGTCTTC CACTGGGTGG GCAACCTGGA GACACTCATC 240
 CTGGACTCCA ACCCGCTGGC CTGCGACTGT CGGCTCTCTG GGGTGTTCGG GCGCGGCTGG 300
 CGGCTCAACT TCAACCGGCA GCAGCCACAG TGCGCCACGC CCGAGTTTGT CCAGGGCAAG 360
 GAGTTCAAGG ACTTCCCTGA TGTGCTACTG CCCAACTACT TCACCTGCGG CCGGCGCCGC 420
 ATCCGGGACC GCAAGGCCCA GCAGGTGTGT GTGGACGAGG GCCACACGGT GCAGTTTGTG 480
 TGCCGGGCGG ATGGGAGCCC GCGGCGCGCC ATCCTCTGGC TCTCACCCCG AAAGCACTG 540
 GTCTCAGCCA AGAGCAATGG GCGGCTCACA GTCTTCCCTG ATGGCACTCT GGAGGTGGCG 600
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 GACTCCATGC CCGCCCACTT GCATGTGGCG AGCTACTGCG CCGACTGGCC CCATCAGCCC 720
 AACAGAACCT TCGCTTTCAT CTCCAACAG CCGGGCGAGG GAGAGGCCAA CAGCACCCGC 780
 GCCACTGTGC CTTTCCCTTT GACATCAAG ACCCTCATCA TCGCCACCAC CATGGGCTTC 840
 ATCTCTTCC TGGGCGTGT CCTCTTCTGC CTGGTGTGCT TGTTCTCTG GAGCGGGGGC 900
 AAGGGCAACA CAAAGCACAA CATCGAGATC GAGTATGTGC CCGGAAAGTC GGAGCGAGGC 960
 10 ATCAGCTCCG CCGCCCACTT CGGCAAGTTC AACATGAAGA TGATATGAGG CCGGGCGGGG 1020
 GGGCAGGGAC CCGCGGGCGG CCGGGCAGGG GAAGGGGCGT GCGCGCCACC TGCTCACTCT 1080
 CCACTCTTCC CCACCTCTTC CCTACCTTTC TACACAGTT CTCTTCTTCC CTCCCGCTTC 1140
 CGTCCCTGCG TGCCCGCCGC CAGCCCTCAC CACCTGCCCT CCTTCTACCA GGACCTCAGA 1200
 AGCCACAGAC TGGGGACCCC ACCTACACAG GGGCATTGAC AGACTGGAGT TGAAGGCGGA 1260
 15 GGAACCGACA CCGCGCAGAG TCAATAATTC AATAAAAAAG TTACGAACTT TCTCTGTAAAC 1320
 TTGGGTTTCA ATAATTATGG ATTTTATGA AAAGTTGAAA TAATAAAAAA AGAAAAAAAC 1380
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 TCCAACCTAG TTTCTGTGTT TTTCTTCTCT CCTCTCTCTC TTTCTCTCTC TTTCTCTCTC 1500
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 20 CTGCCCAACC CCGCCAGGCG ACCATCAGGA GCAGGCTAGG GGGCAGGCT GGGCCACAGT 1620
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 CCTGTCTGCT GGGCTGCCAG GCGGCACAC TGCAAGGGGT GGGAGCCTGG CTGGGTGTG 1740
 GCTGAGACTC TGGACAGAGG CTGGGGTCTC CTGGGGGAC AGCACAGTCA GTGGAGAGAG 1800
 CCAGGGGCTG GAGGTGGGGC CCACCCAGC CTCTGTCTCC AGCTCTGCTG CTCATTGTCT 1860
 25 GTGTGGCTCT AAGCAGGTCA CTGGCTCTC TGGGCTCAG TCTCCACATC TGTACAAATG 1920
 GGAACATTAC CCCTGCCCT GCCTACCTCA CAGGGCTGTT GTGAGGAATT GATGAGATGA 1980
 TGTATGTGAA ACACCTTGTG ACCTGTAAAG CGCTGTGCAC ACGTG

35 Seq ID NO: B31 Protein sequence
 Protein Accession #: NP_116197.1

1 11 21 31 41 51
 40 MLHELLRLQE IQLVGGQLAV VEPYAFRLGN YLRVLNVSNG QLTLEELVP HSVGNLETLI 60
 LDSNPLACDC RLLWVFRFRW RLNFNRQPT CATPEFVQK EFKDPFDVLL PNYFTCRAR 120
 IRRKQAQVF VDEGHTVQVF CRADGDPPIA ILWLSPRKHL VSAKSNRGLT VPPDGLTEVR 180
 YAQVQDNGTY LCIAANAGNV DSMFAHLHVR SYSDFWPHQP NKTFAPISNQ PGEGEANSTR 240
 ATVPFPFDIK TLIIATTMGF ISFLGVVLF LVLFLWSRG KGNTKHNI EI BYVPRKSDAG 300
 45 ISSADAPRKF NMIMI

Seq ID NO: B32 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 50 CAGCACATAC AAGAAACATA CAGTGTACCT CAAAGGGGCG CTTGAAATG TCATCAAAGG 60
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 GTATTGCGTA CGAAGGAAGC CAGGCTGGTC CTGGCAGGAA GTAAATGATA ATCTTTGGGA 180
 AACCAGGACC CTGCTCCCA GCCCAGAGGT GGAGGAGGGC GGTGAGGGTG GGGTCTACAG 240
 55 TGGCAGACGA CTGACAAAGG TAGAGGGAAA TGTAAATGCA CATCTAGGCT GCAGTCTGGT 300
 GAAAGTGGCC GGGGTGGTCC TTGAAAACA GTTGGGCTGT TCTTGGCAGG AATTAGTGAC 360
 AGCCTTCCCG TCAGGGGCGG GGACGCCCTG ATTTAAAAA AATAAATAAA TAAACGCTCT 420
 GGTATAGAAA A

60 Seq ID NO: B33 DNA sequence
 Nucleic Acid Accession #: NM_006174.1
 Coding sequence: 71..1408

1 11 21 31 41 51
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 TAATACTGCT GCCACTCGGA ATTCTGATT CCCAGTCTGG GATGACTATA AAAGCAGTGT 180
 AGATGACTTA CAGTATTTTC TGATTGGGCT CTATACATT GTAACTCTTC TTGGCTTTAT 240
 70 GGGGAATCTA CTTATTTTAA TGGCTCTCAT GAAAAAGGTT AATCAGAAGA CTACGGTAAA 300
 CTCTCTCATA GGCAATCTGG CCTTTCTGA TATCTTGGT GTGCTGTTT GCTCAGCTTT 360
 CACACTGACG TCTGTCTTGC TGGATCAGTG GATGTTGGC AAAGTCAATG GCCATATTAT 420
 GCGTTTCTT CAATGTGTGT CAGTTTGGT TTCAACTTTA ATTTTAATAT CAATTGCCAT 480
 TGTCAAGTAT CATATGATA AACATCCCAT ATCTAATAAT TTAACAGCAA ACCATGGCTA 540
 75 CTCTCTGATA GCTACTGTCT GGACACTAGG TTTGCCATC TGTCTCCCG TTCCAGTGT 600
 TCACAGTCTT GTGGAACCTT AGAAACATT TGGTTCAGCA TTGCTGAGCA GCAGGTATTT 660
 ATGTGTTGAG TCATGGCCAT CTGATTCATA CAGAATTGCC TTTACTATCT CTTTATTGCT 720
 AGTTCAAGTAT ATTCTGCCCT TAGTTTGTCT TACTGTAAGT CATACAGTGT TCTGCAGAG 780
 TATAAGCTGT GGAATGTCCA ACAAAGAAAA CAGACTTGAA GAAAATGAGA TGATCAACTT 840
 80 AACTCTTCTA CCATCCAAAA AGAGTGGGCC TCAGGTGAAA CTCTCTGGCA GCCATAAATG 900
 GAGTTATTTA TTTATCAAAA AACACAGAGG AAGATATAGC AAGAAGACAG CATGTGTGTT 960
 ACCTGCTCCA GAAAGACCTT CTCAGAGAAA CCACTCCAGA ATACTTCCAG AAAACTTTGG 1020
 CTCTGTAAAG AGTCAGCTCT CTTCACTCAG TAAGTTTATA CCAGGGGTCC CCACTTGCTT 1080
 TGAGATAAAA CCTGAAGAAA ATTCAGATGT TCATGAATTG AGAGTAAAC GTTCTGTTAC 1140

AAGAATAAAA AAGAGATCTC GAAGTGTITT CTACAGACTG ACCATACTGA TATTAGTATT 1200
 TGCTGTAGT TGGATGCCAC TACACCTTTT CCATGTGGTA ACTGATTITA ATGACAACTC 1260
 TATTTCAAAT AGGCATTTC AATCCAAATC TATATGGGT TCTTAATAAT GGGATTAAAG CTGATTAGT 1320
 CTGTGTCTT AATCCAAATC TATATGGGT TCTTAATAAT GGGATTAAAG CTGATTAGT 1380
 GTCCTTATA CACTGCTTC ATATGTAATA ATTCTCACTG TTT

Seq ID NO: B34 Protein sequence
 Protein Accession #: NP_006165.1

10 1 11 21 31 41 51
 MDLELDEYYN KTLATENNTA ATRNSDFFVW DDYKSSVDDL QYFLIGLYTF VSLLGFMGNL 60
 LILMALMKKR NQKTTVNFLI GNLAFSDFLV VLFCSPTFLT SVLLDQWFMG KVMCHIMPFL 120
 QCVSVLVSTL ILISIAIVRY HMIKHPISMN LTANHGFLFI ATVWTLGFAL CSPLPVFHSN 180
 VELQETFGSA LLSSRYLCVE SWPSDSYRIA FTISLLLVQY ILPLVCLTVS HTSVCRSISC 240
 GLSNKENRLE ENEMINLTLH PSKKSQPVK LSGSHKWSYS FIKKHRRYS KKTACVLPAP 300
 ERPSQENHSR ILPENFGSVR SQLSSSSKFI PGVPTCFEIK PEENSVDHEL RVKRSVTRIK 360
 KRSRSVFYRL TILILVFAVS WMPLHLFHV TDFNDNLISN RHFKLVYCIC HLLGMMSCCL 420
 NPILYGLNN GIKADLVSLI HCLHM

Seq ID NO: B35 DNA sequence
 Nucleic Acid Accession #: NM_014279.1
 Coding sequence: 286..1689

25 1 11 21 31 41 51
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 CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGTCTGA TCCAGGCGTG 180
 GGGACACGAG CCAGGCGCGG CCGCGCGGAG CAGCGGAGCC GGGGCGAGCG CCGAGCGCG 240
 TCCGCGTCCA GCGAGCGCGC GCGCGGCGAG CACCCAGGCG CCTGCTCTCT CCTCATCTG 300
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 TTGATACCTG TGTGGAAGA GTACAAGGCC GATGCCAAAT TGGTATTGCA GTTTAAGAG 840
 GAGGTCCAGA ATCTGACGTC AGTGCTTAA CAGCTGCAAG AGGAAATTGG CGCCTATGAC 900
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 CTGTGGGCGG TGTAGCCAC CAACGAGAAC GCTGGCAACA TCGTGTGAG TAGGCTGGAG 1440
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 TGGAAACAAG GCCACAGAT CCTCTAAC CAACGCTGTG TCCAGTCTAT CCGCTCCGAC 1740
 GAGTGTAGT TCCCTCTCTC TGAAGCCAA GGGCCCAAGT CCTCACCACA AAGGACTCTC 1800
 TGTGAACCTG TGCCAAAAA GATACCAATA ACATAACAA TACGATCTT GAAAAATCAT 1860
 CAGCAGTGGG GATTCTGACA TCGAGGGATG GCAATACCTC GGTGTTTCTC CTTTGGAGC 1920
 CCGCGGGCCA CAGAGCTCGG AAGAACTTCC CGTATTGCA GCTGGAACCT CAGCCACGG 1980
 CGCCCGGTTT TTCTCCCGG CCTGTCCCT CTCTGCTCAA ACAACATACT AAAGAGGCGA 2040
 GGCATAGCT GTTGGCCAGT TCTCACCGGG GAAAAACCCA CTGTTAGGAT GGCATGAACA 2100
 TTTCTTAGA TCGTGGTCAG CTCCGAGGAA TGTGGGCTCC AGGCTCTTTG AGAGCCATGG 2160
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 TGTGTCTGTC TCTTAGATTA ACGTGTCTGA GGCTCCACAT AGCTCCTGGA CTTGTGCTA 2280
 GTACATCTG AAGCGATGGT CAGAGTGTGT AGAGTGAAGT TGCTGTGCCC ACATGTTTG 2340
 AACTCGCGTA CCGCTAGAT ACATTGTGCA ACGTTCTTCT GTTATTCTCT TGAGGTGGTA 2400
 ACTTGTATG TTCAGTTTAT GCGATGATTG TTGTAAATGC AATGCGGTAG TTTGGATTAA 2460
 TAAGTGGATG GTTTTGTGTT CTAAAAAGAA AAAAAAATC AGTGTTCACC CTTATAGAGA 2520
 CATAGTCAAG TTATGTTGA TAATAATCAA AGGAATTACT CTCTTCTGT TAAATTAGCT 2580
 AAATCATGTA ACCGAGATA GGAAGGGCTC ACCTGGGGAA ACTCTGTTT CCGATGGGAC 2640
 AGGAAAGTCA TACGGGCAAC AGTATGCGGA AAGTACGTTT TTTAAGTAA AAAACAAAG 2700
 CAAACTTGT ACTATCCAGT TATCTAAGGA ACATAAAAA CATTAGGAGA AAAAAAATA
 AAAAAAATA AAAAAAATA AAAAAAATA AAAAAAATA A

Seq ID NO: B36 Protein sequence
 Protein Accession #: NP_055094.1

1 11 21 31 41 51
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 APQOTMCSR DARTQLRLQLL EKVQNMSSQI EVLDRRTQRD LQYVEKMEHQ MKGLESKFKQ 120
 VEESHKQHLA RQFKAKAKM DELRPLIPVL REYKADAKLV LQPKKEVQNL TSVNLNLQBE 180
 IGAYDYDELO SRVSNLEERL RACMQKLACG KLTGISDFVT VKTSGSRFGS WMTDPLAPEG 240
 DNRVWMDGY HNRFPVREYK SMVDFMNTDN FTSRLPHFW SGTGQVYNG SIYPNKPQSH 300
 IIRFDLKE TILKTRSLDY AGYNMRYHA WGHSDIDL M VDESLWAVY ATNQNAGNIV 360

VSRLDPVSLQ TLQTNWTSYP KRSAGEAFII CGTLYVTNGY SGOTKVHYAY QTNASTYEYI 420
DIPFQNKYSH ISMLDYNPKD RALYAMNNGH QILYNVTLPH VIRSDEL

5 Seq ID NO: B37 DNA sequence
Nucleic Acid Accession #: NM_006334.1
Coding sequence: 286..693

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1      11      21      31      41      51
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    CCTGCCCAGC CCTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
    CGGAGGCTTC GCGCAGCAGA GCGCGCGGCG CGCCGCTCC GGGTGCTGAA TCCAGGCGTG 180
    GGGACACGAG CCAGGCGCGG CGCGCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
    TCCGCGTCCA CGCAGCGCGC GCGCGGCCAG CACCCAGGGC CCTGCATGCC AGGTGCTTGG 300
15 AGGTGGCAGC GAGACATGCA CCGGCGCCGG AAGCTCCTCA GCCTCCTCTT CCTCATCTCG 360
    ATGGGCACTG AACTCACTCA AGTGTGCTCC ACCAACCTTG AGGAGAGCTG GCAGGTGTAC 420
    AGCTCTGCCC AGGACAGCGA GGCAGGTGT ATCTGCACAG TGGTCCGCC ACAGCAGACC 480
    ATGTGTTTAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GTTGACAGAC 540
    ATGTCTCAAT CCATAGAGGT CTGGACAGG CGGACCCAGA GAGACTTGCA GTACGTGGAG 600
20 AAGATGGAGA ACCAAATGAA AGGACTGGAG TCCAAGTTCA AACAGGTGGA GGAGAGTCAT 660
    AAGCAACACC TGGCCAGGCA GTTTAAGGGC TAACTTAAAG GAGTTTTTTC AATGTCTGAG 720
    TGACTGAAGA AGCAGTCCAC TCCCATGTAA CCATGAAAGA GAGCCAGAGA GCTTTTTCGA 780
    CCATGCATTT TTACTATTAT TTCCAATAC TTAGCACCAT TTCACTAAGG AACCTTGAAT 840
    ACAACACAGG TCCTCCTTTG CATGCGAGTG TAGCTGCATT TCATGAATAG TTTGAACCTT 900
25 TGTCAATGCA TTTTTTGAAG AAGAAAGAAA AAAAAAAGT CGTGTATGTG ACTCAAAGCA 960
    TGTAACTTTA AGATGTTGCA TTCTAAACTG ACAATAAAGA CCTTTCCCC
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30 Seq ID NO: B38 Protein sequence
Protein Accession #: NP_006325.1

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1      11      21      31      41      51
35 MPGRWRWQRD MHPARKLLSL LFLILMGTEL TQVLPTNPFE SWQVYSSAQD SEGRICITVV 60
    APQQTMCSDR ARTKQLRQLL EKVQNMSSQSI EVLDRRRTQRD LQYVVKMENQ MKGLESKFKQ 120
    VEESHKQHLA RQPKG
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40 Seq ID NO: B39 DNA sequence
Nucleic Acid Accession #: NM_058199.1
Coding sequence: 286..795

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1      11      21      31      41      51
45 GCGCGGGGA GCCATTAGGA GCGAGGAGA GAGGAGGGCG CAGCTCCGCG CCAGCCCAGC 60
    CCTGCCCAGC CCTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
    CGGAGGCTTC GCGCAGCAGA GCGCGCGGCG CGCCGCTCC GGGTGCTGAA TCCAGGCGTG 180
    GGGACACGAG CCAGGCGCGG CGCGCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
    TCCGCGTCCA CGCAGCGCGC GCGCGGCCAG CACCCAGGGC CCTGCATGCC AGGTGCTTGG 300
    AGGTGGCAGC GAGACATGCA CCGGCGCCGG AAGCTCCTCA GCCTCCTCTT CCTCATCTCG 360
    ATGGGCACTG AACTCACTCA AATAAAAGA GAAAACAAAG CAGAGAAGAT GGGAGGGCCA 420
50 GAGAGCGAGA GGAAGACCCAC AGGAGAGAAG ACACTGAACG AGCTTCCTTT GTTTTGCTCG 480
    GAAGCCACAG CTGCTCTCCT GGCTCTGCCC AGGATGTGCA GTCCAAATCC CAATCCAGCA 540
    GTGGGGTTAT GTGCTCCGCG TTACCTCTCAG AGCCCTTCTC CTGGTGCTGC CCAGACGATC 600
    AGCCAGTCCC TCCTGGAGAG GTTCTGCAAT GCCTCTAGGA GAGAAGTTT CTGCGCCCA 660
    GGAAGGCTCG GTGAGGGGTG GTGGTTGTGC ACTGTTGCTG GACAGATGCA TTATTTCATG 720
55 TGACACACA CACACACACA TGACACACA GGGAGCAGA TACCTGCAGA GAAGAGCCAA 780
    CCAGGTCTCG ATTAGTGCCA AGCTGCCCCA CAAAGGGCTA TGCTGTGTC TTATTGAGAC 840
    ACCTTGGCAA AGAGATGGCT GATTCTGGGT GGTCTGGGAC ATGGCCGAC CCAAGGCGCC 900
    TCCAAGCCTT AATGGCACCC TGAAGCCTCC ATGCCCAGGC CAAAAGATGC TTTTCTCTCC 960
    TAAAAAATAA AAAAAAATAA
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60 Seq ID NO: B40 Protein sequence
Protein Accession #: NP_478106.1

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1      11      21      31      41      51
65 MPGRWRWQRD MHPARKLLSL LFLILMGTEL TQNKRENKAE KMGGPESERK TTGKTLNEL 60
    PLFCLAEHAG SLALPRMCSP NPNPAVGLCR PAYPQSPSPG AAQTISQSLI ERFCMASRRE 120
    VFLAPGRFEG GWWLCTVAGQ MHSFMCETHH THAHTGEQIP AEKSQPGPD
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70 Seq ID NO: B41 DNA sequence
Nucleic Acid Accession #: AY038071.1
Coding sequence: 1..1686

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1      11      21      31      41      51
75 ATGAGCAATC AGTACCAGGA GGAGGGCTGC TCCGAGAGGC CCGAGTGCAA AAGTAAATCT 60
    CCAACTTTTC TCTCTCTCTA CTGCATCGAC AGCATCTCTG GCCGAGGAGS CCGTGCAAA 120
    ATGCGGTTGC TGGGAGCGCG GCAGAGCTTG CCTGCTCCGC TGACACAGCG CGCGAGCCCG 180
    GAAAAGGCGG TGCAAGGCTC CCTTAAGAGC AGCAGGCGCC CGTTGAGGCC CGAGCTGCAC 240
    CTGCGGCCCA AGCTGCGGCG CCGTGTACGC CGGGGCGGGG GCGGCTCTCT TCAGGGTGGG 300
    GCAGCGGCGG CGGCGGCGCG GCGGCGGCGG GCGGAGCGGG CCGCCACGCG CACGGGGGGT 360
    CCACGCGGGG AGGCCCCCTC GCGGCCACCG CCAACCGCGC GCGCCGCGGA ACAGCGGAGC 420
    GCGCGAGGGG CCGCGCGGCG AGCGCGGCGG GCGGCGCGCG CGGCTTGGGA CACGCTCAAG 480
    ATCAGCCAGG CGCGCGCAGT GAGCATCAGC GCGCAGCAAG CGTACCGGGA GAAAGGGGGG 540
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CCCTTCGTGC CGCCGCCGCC CGCGCTGGAC GAGCTGGGCG GCCCGGGGGG CGTCACGCAC 600
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ACCGGCACCG AGGACGACGA GGAGGAGCTG CTGGAGGACG AAGAAGATGA GGACGAGGAA 720
GAGGAACCTG TGGAGGACGA CGAGGAGGAG CTGCTGGAGG ACGACGCCCG CGCGCTGTCT 780
AAGGAGCCCC GCGCTGTGTC TGTGGCCGCC ACTGGGCGCG TGGCCGCAGC AGCTGCCGCT 840
GCAGTGGCCA CAGAGGGCGG GGAGCTGTCA CCCAAGGAGG AGCTGCTGCT GCACCGGAA 900
GACGCTGAGG GCAAGGACGG CGAGGACAGC GTGTGCTCT CTGCGGGCAG CGACTCGGAG 960
GAGGGGCTGC TGAACGCAAC ACAGAGGCGC TACCGACCA CGTTCACCAG CTACCAGCTG 1020
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CTGGCCATGA GCGTGGAGCT GACCGAGGCC CGAGTCCAGG TCTGGTTCCA GAACCGTCGG 1140
GCCAAGTGGC GCAAGCGGGA GAAGGCAGGC GCGCAGACCC ACCCCCTGG GCTGCCCTTC 1200
CGCGGGCCGC TCTCCGCCAC CCACCCGCTC AGCCCTTACC TGGACGCCAG CCCCTTCCCT 1260
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TTCCCGAGCC TACCTCGCG TCCGGGCTCG GCCAGCCTCG CGCCAGCGGG GGGCGCGCTG 1380
GGCTGAGCA CTTCCTCGG AGCGGCGAGT TCCGACACC CAGCTTTCAT CAGCCGCGCA 1440
TTCCGGCAGG TCTTTTCCAC AATGGCCCC CTGACACGCG CGTGCACGCG GCGCGCGCTC 1500
CTGAGACAGC CCACACCCGC CGTGGAGGGG GCAGTGGCAT CGGGCGCCCT GCGCGACCCG 1560
GCCACGGCGG CCGCAGACAG ACGCGCTCT AGCATAGCCG CGCTGAGGCT CAAGCCCAAG 1620
GAGCAGCGCG CGCAGCTCAC GCAGCTCAAC ATCTTCCGCG GCACACGACG GGGCAAGGAG 1680
GTGTGC
  
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Seq ID NO: B42 Protein sequence
 Protein Accession #: AAK93901.1

25
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 35

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1 11 21 31 41 51
MSNQYQEEGC SERPECKSKS PTLSSSYCID SILGRRSPCK MRLLGAAQSL PAPLTSRADP 60
EKAVGSGSPKS SSAPFEAEHL LPPKLRLRYG PGGGRLLQGA AAAAAAAAAA AAAAATATAG 120
PRGEAPPPPP PTARPERPD GAGAAAAAAA AAAAAMDTLK ISQAPQVISI RSKSYRENGA 180
PFVPPPPALD ELGGPCGVTH PEERLGVAGG PGSAPAAGGG TGTEDDEEL LEDEDEDEE 240
EBLLEDDEEE LLEDARALL KEPRRCVAA TGAVAASAAA AVATEGGELS PKEILLHPPE 300
DAEGKDGEDS VCLSGAGDSE EGLLKRKQRR YRTTTSYQL EELERAFQKT HYPDVFTRFE 360
LAMRLDLTEA RVQVWFQNR AKWRKREKAG AQTHPPGLPF PGPLSATHPL SPYLDASFPF 420
PHHPALDSAW TAAAAAASAA FPLPPPPGS ASLPPSGAPL GLSTFLGAUV FRHPAFISPA 480
FGRLFTMAP LTSASTAAL LRQPTPAVEG AVASGALADP ATAAADRRAS SIAALRLKAK 540
EHAALTLQLN ILPGTSTGKE VC
  
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Seq ID NO: B43 DNA sequence
 Nucleic Acid Accession #: CAT cluster

40
 45
 50
 55

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1 11 21 31 41 51
CGCTCGCCCC CCGCTTGCTT CTCTCTCTTC CCTTCTGCGT GCGTGTCTCG CGTCTTTGG 60
TTCGCGCGGT TCCGTGCGCC CTCTCTGGGC TTCGGCTTCA CCTTCGCTCT GCGTGTGCT 120
CTGCTCTCCT CGCTCTCAT GCGCTTCTCA GCTCTTACTC TGGTGTGCTC CCCCTCCCTC 180
GCTCGTTTCT CTGTCTCTTC TCTTCCCGG TCGTGTCTCT GCTTCTTCTG GTTCCCTCTC 240
GTCTGTGTTT GTGGGTGCTC CTCTGCGTCC TGCGCTTCTC TCTTGTGTTT CCGCGCGCTT 300
CCTGTTTGG TCCCGCTGGT TCTCGCGCGG TTCTGTGTGC GCGGGCGCGC CGGTCTTTTC 360
TTGGTGTCTT GCTCTCTGTC TCTGTCTGGT GTTCTCGGCC GTCTGTGTCT TTCTCTTTT 420
ATCTTCTGTT TCTCTTTTTT CTGTCTTCTT CTGTTTTTTT TTGTCTTTT TTTCTCTTTA 480
GCTGAGGGTG GGGAGAGATA AGCTGTATAA CTTTATTTT TCAGGAATC TGAAGAACTA 540
CAGTCTCCAT GCGTCTCAG CCAAGAAGGA GCTCACTGTG GGCACAGAG ACAGGGACCC 600
AATGTGGAGA CCGTGTGAGC TGTGTCCGGC CCGTCACTCT CAAGCACAGG GCAGGCTTCC 660
TGAGCATGTA AGAGAAATAT TGGGAGAAAC AAACAGAAAC TGAAGAATA TGAAGGTGT 720
CTTCTCTGGA TGTATTCCA TGATAGATAG TAGGGGCGAG AGTGAGAGAG GCTGACTAGG 780
TCTGGACATG GAGGCTGGAA GAGTCAGGAT GTGATTCCGA GAGGCGCATG AGAAGGAAGG 840
TGGATTTTAA GGCTGGAAT CTGAGGTTCA GTGTCCAG TCACTCAGAG ACAGAATCAC 900
AGCATAGCCC TTGCTGATGG CAA
  
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60
 Seq ID NO: B44 DNA sequence
 Nucleic Acid Accession #: NM_014421.1
 Coding sequence: 718..1497

65
 70
 75
 80

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1 11 21 31 41 51
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GCGTGGCGAG CGATTGCTG TCTCTTGTGA GTCAGGGGAC AACGCTTCGG GGCAACTGTG 120
AGTGGCGGTG TGGGGGACCT CGATTCTCTT CAGATCTCGA GGATTGCTC CGGGGACGTC 180
TCTGATCCCC TACTTAAAGC GCGTGTCTAC TTTGAAAAGG AGCACTGTGT CTTGCAAGT 240
TTGACACATA AAGGATAGGA AAAGAGAGGA GAGAAAAGCA ACTGAGTGA AGGAGAGGA 300
GCTGATCGCG GCGTCTGAT CAATTAAGAG GAGAGTTAAA CCGCCGAGAT CCCGCGCGGA 360
CCAAGGAGGT GCGGGGCAAG AAGGAACGGA AGCGGTGCGA TCCACAGGGC TGGGTTTTCT 420
TGACCTTGG TCAAGCCTTC CTGCGGAGA AAGCGCTCG CATTGTATTG CTTCCAGTTA 480
TTGCAAGACT TCTGTCTCT GTGGAGAGGC GGGTCTCGCT TGGGTTCGCG TAATTCTGT 540
CCTGAGGCGT GAGACTAGT TCATAGGGTC CTGGTCCCC GAACAGGAA GGGTTGAGG 600
AACACAATCT GCAAGCCCCC GCGACCCAGG TGAGGGGCCC CGTGTGTGGG TCCTCCCTCC 660
CTTTGCAITC CACCCCTCC GGGCTTTGCG TCTTCTGCG GACCCCTCG CGGGAGATG 720
GCGCGTTGA TGGGAGCAA GGATTGTGTC TGCTGCTGCG TCCTACTGCG CGCGTGTCTG 780
ATGGTGGAGA GCTCAGAGAT CGCGAGTTCC CGGGCCAAAC TCAACTCCAT CAAGTCTCT 840
CTGGGCGGGG AGACGCTGCG TCAGGCGGCC AATCGATCTG CGGCGATGTA CCAAGGACTG 900
GCATTGCGCG GCAATGAAGA GGGCAAAAC CTGGGCGAGG CTAACCTTGG TAGCAGTAT 960
AAGGAGTGTG AAGTGGGAG GTATTGCCAC AGTCCCCACC AAGGATCATC GGCCTGCATG 1020
GTGTGTCGGA GAAAAAGAA GCGCTGCCAC CGAGATGGCA TGTGCTGCC CAGTACCGCG 1080
TGCAATAATG GCATCTGTAT CCCAGTTACT GAAAGCATCT TAACCCCTCA CATCCCGCT 1140
  
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CTGGATGGTA CTGGCACAG AGATCGAAAC CACGGTCATT ACTCAAACCA TGAATTGGGA 1200
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 5 AAAATCTGCA AACCACTGCT CCATCAGGGG GAAGTCTGTA CCAACAACG CAAGAAGGGT 1380
 TCTCATGGGC TGGAAATTTT CCAGCGTTGC GACTGTGCGA AGGGCCTGTC TTGCAAGTA 1440
 TGGAAAGATG CCACCTACTC CTCCAAAGCC AGACTCCATG TGTGTCAGAA AATTGATCA 1500
 CCATTGAGGA ACATCATCAA TTGCAGACTG TGAAGTTGTG TATTTAATGC ATTATAGCAT 1560
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 10 AGATGATCAC AAAAAGGGAG AAAGAAAACA TGAAGTGAAT AGATTAGAAT GGGTGACAAA 1680
 TGCAGTGCAG CCAGTGTTC CATTATGCAA CTGTCTATG TAAATAATGT ACACATTGT 1740
 GGAAATGCT ATTATTAAGA GAACAGCAC ACAGTGGAAA TTAATGATGA GTAGCATGTG 1800
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 15 AATAACTTGT TATACAATAG GTTCTAAAAA TAAATTTGCT AAACAAGAAA TGAACACATG 1980
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 25 GGATCTGTAG TGCAGTGGAG TAAGCAAGAA AATTGGGAAA ACTTTTCTGT TTGTTCAAGT 2580
 TTTGGCAACA CATTGATCAT ATGTCTGAGG CACAAGTTGG CTGTCTATC TTGAAACAGG 2640
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 30 TTCTTCCAA ACCTCTGCAG CATCTGCTTT ATTGCCAAAG GGCTAGTTTC GGTTTTCTGC 2940
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 35 TTTAACTTT TGTAGACCAC AATTCATTT TTAGTTTCT TTTACTTAA TCCCATCTGC 3180
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 40 TTATATTAC AATTGTGTT CTGCAATATT TTCTTATGT CCACCTTTT AAAAATTATT 3480
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 AAAAAAAA A

45 Seq ID NO: B45 Protein sequence
 Protein Accession #: NP_055236.1

50 1 11 21 31 41 51
 MAALMRSDS SCCLLLLAIV LMVSSQIGS SRALNSIKS SLGGTTPGQA ANRSAGMYQG 60
 LAPGSSKKR NLQAYPCSS DKECEVGRYC HSPHQSSAC MVRKRKKRC HRDGMCCPST 120
 RCNNGICIPV TESILTPHIP ALDGRHRDR NHGHYENHDL GWQNLGRPH KMSHIKHEG 180
 DPCLRSSDCI EGFPCARHPW TKICKPVLHQ GEVCTKQRK GSHGLEIFQR CDCAKGLSCK 240
 VWKDATYSSK ARLHVQKI

55 Seq ID NO: 46 DNA sequence
 Nucleic Acid Accession #: NM_019885.1
 Coding sequence: 1..1539

60 1 11 21 31 41 51
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 65 GAGACCGGCC ACTGGCTGCT GCAGGGTTCT GGCTTCCAGT CGTGGCGGAG GGAGAAGTAT 240
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 AACGTGCGCA AGATCCTCAT GGGCGAGCAC CACCTCGTGA GCACCGAGTG GCCTCGCAGC 360
 ACCGCGATGT TGCTGGGCCC CAACACGGTG TCCAATTCCA TTGGGACAT CCAACGCAAC 420
 70 AAGCGCAAGG TCTTCTCCAA GATCTTCAGC CACGAGGCC TGGAGAGTTA CCTGCCCAAG 480
 ATCCAGCTGG TGATCCAGGA CACACTGCGC GCCTGGAGCA GCCACCCGGA GGCCATCAAC 540
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 75 CAGATCTCGC AGAAGGGGCT GGAGAAGGCC ATCCGGGAGA AGCTGCACTG CACACAGGGC 780
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5 ACCAGCCGCT TTGAGCTGGC TACACGGACC TTCCCCGCA TCACCTTGGT CCCCGTCTG 1440
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 10 GAACTGCTCC CTTCCTCCG TTCTTTTCG ACCCTTTTAG CTGGGGTTGG GGGACGGGAA 1920
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 15 GCCCCAGGCC CTGTCTCCC AGCATCTCC CTGTGGGCC TGGGCAAGTG CACTGACACC 2220
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 20 GAAAGCCTTC CCGGCTCCG GGCATTATTT GGGTTTAATC TCGGAGCCTC ACTCCTGGAC 2520
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 30 ATTGGGATG CCTCCTGGG AAGGTTTCCG GCGTCTTGGT GAGTCTCTAG ATTTTTCCTT 3120
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 35 TGAGTCTAG ATGTTTCATT TATTCTCTAC TTTTCCACTA CTAATAAACA GTGTGGAATA 3420
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 40 AATTGTTTT GACTGAGTAT CTAGGAGAGC AGTAAGTGA ACTTCAGACA AGCCACTGG 3660
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 45 AGATGCCCGT GTCTGTGCGT GTGCTGTGT GTTTCATACA GCTAGCATT AAAAAGACAA AACCCACAA 4020
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 50 TTTGTTATAA TTCAAATAG ATATTAGTA TAAAGTTTT GCTGTTAAAT ATTGTTTATT 4320
 TAGTAAATA TGAATTTTC TCTATTGTA ACATGGTTCA AAATATTAAT ATGTTTATT 4380
 CACAGTCTT TTAATTATGA AAAAGCACTT GTGTGTTTG TTTGTATG AAACTGGTAC 4440
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Seq ID NO: B47 Protein sequence
 Protein Accession #: NP_063938.1

55
 1 11 21 31 41 51
 60 MLFEGLLDVS ALATLAACLV SVTLALLAVSQ QLWQLRWAAT RDKSCKLPPI KSGMGFPLIG 60
 ETGHWLLQGS GFQSSRREKY GNVFKTHLIG RPLIRVTGAE NVRKILMGEH HLVSTWPRPS 120
 TRMLLGHNTV SNSIGDIHRN KRKVFSLKPS HEALESYLPK IQLVIQDTLR AWSHPPEAIN 180
 VYQEAQKLTF RMAIRVLLGF SIPEEDLGLH FEVYQFVDN VFSLPVDLFP SGYRRGIQAR 240
 QILQKGLEKA IREKLQCTQG KDYLDALDLI IESSKEBEGE MTMLQELKDT LELIFAAYAT 300
 65 TASASTSLIM QLLKHPTVLE KLRDELRAHG ILHSGGCPCE GTLRDLDTLSG LRYLDCVIKE 360
 VMRLFTPISG GYRTVLQTFE LDGFQIPKGV SVMYSIRDTH DTAPEVFKDVN VFDPDRFSQA 420
 RSEDKDGRPH YLPFGGGVRT CLGKHLAKLF LKVLAVELAS TSREELATRT PPRITLVFVL 480
 HPUVGLSVKF PGLDSNQNEI LPETEAMLSA TV

70 Seq ID NO: B48 DNA sequence
 Nucleic Acid Accession #: AB040527.1; AL136582.1
 Coding sequence: 94..2319

75 1 11 21 31 41 51
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 CGACGAAGTC GGGGAGGAAG AGATGTTTGA AGGCAACGAC TATGAAGAAT TOGGTGCCTT 180
 TGGTGGCTAT GGCACCTTCA CCAGCTTTGA CATCCATATC CTCAGAGCCT TCGGAAGCTT 240
 80 GGGTCCAGGC CTTCGATCT TATCGAATGA TCCAGCTGGA TCCGGAACA CTTCGCAATG AGACGGCCGC 300
 CCAGACCCCTG GTGGAGGCAT TGCAGCTGGA TCCGGAACA CTTCGCAATG AGACGGCCGC 360
 CGGTGCTGCC AACGTAGCCC GCGCCGCCGC CTCCAAACCT GCGGCTCGGG CCGCTGCCGC 420
 CGCTGCCCGT ACCGCTTCA GTCAAGTGGT CGTAGCCAC CGGGTGGCCA CGCGCAGGT 480
 CTCAGGAGAG GATACCCAGC CCAGACCTA CGCCGCGAG GCTCAGGGGC CCACCCCTGA 540
 GCCACCCCTT GCTTCTCCG AGACCTCCCA GATGTTAGTC ACCAGTAAGA TGGCTGCCCC 600

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CGAGGCTCCG GCAACCTCCG CACAGTCCCA GACAGGCTCC CCGGCCAGG AGGCTGCTAC 660
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CAACCGGCCC AGCAGAGCCT TCCTGGGCCA GAATGATGTC TCGATTTC A CTGAGCGGC 780
AGTGTCACT GGCATGGCCT TCCCGCGCCC CAAGAGACCT GCCCAGCCC AAGAGGCTGC 840
CACAGAGGGC CCCAGTGGTG CTTCTGGTGT GCCCAGAGC GACCTGGCA GGGAGGTGGC 900
AGCCACCCGG CCCAAGACCA CCAAGTGGGG GAAGGCGCTG GCCAAGACTC GGTGGGTGGA 960
GCTCTGCTTC GTTGTGGCAG CAGCTGCTGC CAAGGCCAAG ATGGCCACGA GCATCCCTGA 1020
GCGGAGGGGT GCAGCTGCTG CCACTGCTCA GCACAGTGTG GAGCCCTGGG CCAGGATGGG 1080
AGGCAAGAGG ACCAAGAAGT CCAAGCACCT GGATGATGAG TATGAGAGCA GCGAGGAGGA 1140
GAGAGAGACT CCGCGGGTCC CACCCACCTG GAGAGCATCA CAGCCCTCAT TGACGGTGGG 1200
GGCTCAGTTG GCCCTCGGCG CCGCGATGGC CCGGAGGTCC CAGATACCTT CAAGGCACGT 1260
ACTGTGCTCG CCCCCTCGCA ACGTGACCTT TCTGCAGGAG AGGGCAATA AGTTGGTGAA 1320
ATACCTGATG ATTAAGGACT ACAAGAAGAT CCCCATCAAG CGCGCAGACA TGCTGAAGGA 1380
TGTCATCAGA GAATATGATG AACATTTCCT TGAGATCAIT GAACGAGCAA CGTACACCTT 1440
GGAAAAGAGG TTTGGGATCC ACCTGAAGGA GATCGACAAG GAAGAACACC TGTATATTCT 1500
TGTCATCACA CGGAGCTCCT CAGCTCGCCT CCTTGGAAAA ACCAAGGACA CTCCCAGGCT 1560
GAGTCTCTCT CTTGTGATTTC TGGGCGTCAT CTTATGAAT GGCAACCGTG CCAGCGAGGC 1620
TGTCCTCTGG GAGGCACTAC GCAAGATGGG ACTGCGCCCT GGGGTGAGGC ACCCATTCCT 1680
CGGCGATCTG AGGAAGCTCA TCACAGATGA CTTTGTGAAG CAGAAGTACC TGGAAATACAA 1740
GAAGATCCCC AACAGCAACC CACCTGAGTA TGAATTCCTC TGGGGCTGCG GAGCCCGCCA 1800
TGAGACCAAG AAGATGAGG TCCTGAGATT CATGCCAG AATCAGAACCC GAGACCCCGG 1860
GGAATGGAGG GCTCATTTCT TGGAGGCTGT GGTATGATGT TCAAGACAA TGGATGTGGA 1920
TATGGCCGAG GAACATGCCA GGGCCAGAT GAGGGCCAG ATGAATATCG GGGATGAAGC 1980
GCTGATTGGA CGTGGAGCT GGGATGACAT ACAAGTCGAG CTCTGACCT GGGATGAGGA 2040
CGGAGATTTT GCGATGCTCT GGGCCAGGAT CCCCTTTGCT TTCTGGGCCA GATACCATCA 2100
GTACATTTCT AATAGCAACC GTGCCAACAG GAGGGCCAGG TGGAGAGCTG GCGTCAGCAG 2160
TGGCACCAAT GAGGGGCCCA GCACCAAGCT CCTAGATGGC CCCAGCACA GCTCCACCAT 2220
CGGACCCAGA AATGCTGCCA GAGCTGGGCG CAGCTTCTTC TCCTGATGCC AGCACCGTTG 2280
ACGAATGCA GCGATCTTAC TGGCCAAGCC AGAGCGCCTC CTCTCAGATT CCTTCTGAC 2340
ACAGCACCTT AGGCGGCTTC TTCCTGTGAG TCGGAGGTGG CATGCAAGAT GAAGCTCTCT 2400
TTGCTCTCC TGCTTTCATT TTGTGCTTTT CCTTGTGTTT TCATGTTTGG GGTATCAGTG 2460
TTACATTAAG GTTGCATAAT TAAA
  
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35
 Seq ID NO: B49 Protein sequence
 Protein Accession #: BAB33378.1, CAB66517.1

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1 11 21 31 41 51
MAEGSPFSVQS ESYSVEDMDE GSDEVGEEEM VEGNDYEEFG AFGGYGTILTS FDIHILRAFG 60
SLGPGLRILS NEPWLEENPV LAQTLVEALQ LDPETLANET AARAANVARA AASNRAARA 120
AAAARTAFSQ VVASHRVATP QVSGEDTQPT TYAAEAQGPT PEPPLASPT SQMLVTSKMA 180
APEAPATSAQ SQTGSPAQEA ATEGFPSSACA FSQAPCAREV DANRPSTAFI QMDVDFPTQ 240
PAGVSGMAPP RPKRPAPAQE AATEGPSAAS GVPTGPGRE VAATRPKTKK SKKALAKTRW 300
VEPQNVVAAA AAKAKMATSI PEPEGAAAAT AQHSAEPWAR MGGKRTKSK HLDDEYESSE 360
EERETPAVFP TWRASQPSLT VRAQLAPRPP MAPRSQIPSR HVLCLPPRNV TLLQERANKL 420
VKYLMIKDYK KIPKIRADML KDVIREDYEH FPEITERATY TLEKKFGIHL KEIDKEEHL 480
ILVCTRDSSA RLLGKTKDTP RLSLLLVILG VIFMNGNRAS EAVLWEALRK MGLRPGVRHP 540
PLGLRLKIT DDFVKQKYLE YKKIPNSNPP EYEFWGLRA RHETSOMRVL RFLAQNQNRD 600
PREWKAHFL EAVDDAFKTM DVMABEHARA QMRAQMNIGD EALIGRWSND DIQVELLTWD 660
EDGDFGDWA RPPAPFWARY HQYILNSNRA NRRATWRAGV SSGTNGGAST SVLDGPSTSS 720
TIRTRNARA GASFFSWIQH R
  
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55
 Seq ID NO: B50 DNA sequence
 Nucleic Acid Accession #: XM_084965.1
 Coding sequence: 356..2014

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1 11 21 31 41 51
GACCTAGCGT GTGCTCAGCT CTGGACAAGA CATGATGTA GGCAGACATG CTTCTGCTCT 60
GCTGGGCTTA GTGCACCAAT GCTAAGGACA GACATGAAGG GCTTGGGAAA GGCATGAAGA 120
TGCAGGGAGT CTAGGAGAGA GGATAAGAAA AACAAGCATT TTGTGGTGGG TTGAATTGCG 180
TTGTGTTTTT TAGAGGCATT TCCTGATCCA TGGTTGCGCT CCGGTGAAGA GCGAGTCTAG 240
AGAAGGAATC CGAAGCGGCG GCGGCGAGCG CGGCTCAGGT TGATTTAGAA TACGGGTGAC 300
AGTGGCTTGG CGGAGGCCCA CTGCTGACGA AAGCGGCTTA TCCGCGCGG TTTCCATGGA 360
GACGAGCCGG AGCGCGGCGG GCGGCGGGCG GTTCAGCGAG CGCGGCGGAG CTGCGCGCTC 420
CGTGGGGGTC TGCAGGAGGA AGGCGGAGGC CGGGCGCGGG ACCGGGACCT TCGCGGCAGA 480
CATGGACTTG CATTGTGACT GTGCCGCCGA AACGCGGCGC GCGAGCGCGC GGTGCGGGA 540
GATTAATAAA GCTGCCCTCA AATTATTCAA GAAGAGGAAA TCGGGTGGCA CCATGCCAG 600
CATTTTTGGG GTCAAAAACA AAGGGGACGG GAAAGCTCG GTTCCGACGG GGTGCTGAG 660
GAGCAGGACC CACGACGGAC TTGCCGAGGT GCTGGTGTCT GAGAGCGGCA GGAAGGAGGA 720
GCGCGCGCGC GGGGCGGAGA GCGGCGGGGG CGGCGGGGG CGGCGGAACC CGGGGCCCC 780
CAGAGCCGCA GGGCGCGGCG GGGGCTCCCT CGCCAGCAGC TCGGTGGCCA AGTCGACAG 840
CTTCTTCTCG CTGCTGAAGA AGAACGGGCG CTGCGAAAAC GGCAGGGGAG AGCCTGTGGA 900
CGCGAGCAAG GCGGCGGCGA AACAAAAGCG GGGCTGCGCG GGGCTGTCTA GCGGCATGCG 960
CTGCGACAGG AAGACAAGC GGGCCAAGGC GAGGCGCGCG GAGGGGCGCG CGCCCGGGG 1020
CGCTTGTGCT CTACCCGGCT CGCTCACGCG CAGCTTGGAG TGGTCAAGG AGGAGACGCC 1080
CAGAGCCGCG CGCGAGCGCG AGGAGCCGAG CCAGGACGCC CGCGAGACC CAGCAGGCTG 1140
TGDAGATATT ATTGCAGACC AAGAGGAAGA GGCAGGTCCC AGCTGTGACA AGCATGTCCC 1200
CGGGCCAGGC AAGCGGCTCT TGTCTAAAAA GAACCCCGGC GTGGTGGCCT ACCAAGGAGG 1260
CGGGGAAGAG ATGGCCAGCC CGGACGAGGT GGACGACACC TATCTACAGG AGTTCTGGA 1320
CATGCTCTCC CAGACCGAGG AGCAGGGACC CGAGCCCCAG GAGGGGCGCG CTAAGGTGCG 1380
AGCTGCGCTG GAAACCAAGG TGGTGCCGGA GACCCCAAAA GACACCAAGT GTGTGGAAGC 1440
GGCCAAGGAC GCGTCTCTCG TCAAGCGCAG GAGGCTCAAC CGGATTCCCA TCGAGCCCCA 1500
TCCTAAGGAG GAGCCCAAGC ACCCGAGGAA GGAGCAGCAG GAAGCGCTCC CCAAGACGGA 1560
  
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CGAGGGCTAC TGGGACTCCA CCACGCCAGG CCCAGAGGAA GACAGCTCGA GCAGCGGGAA 1620
 GAAGGCGGGC ATCCCCCGGG ATAGCTACAG CGGGGACGCG CTCTATGATC TCTATGCTGA 1680
 CCCGGACGGA AGTCCAGCAA CCCTTCCTGG AGGGAAGGAC AACGAGGAGA CGTCTCCCT 1740
 GTCCCGGTTA AAGCCGTAT CTCCAGGCAC CATCACTGT CCACTGCGAA CACCAGGCAG 1800
 CTTGCTGAAG GACTCTAAGA TCCCTATTAG CATCAAGCAC CTGACCAACC TTCCATCTAG 1860
 CCATCCCGTG GTGCACCAGC AACCTCCAG GAGTGAGATG CCCAGAACAA AAATCCCGGT 1920
 TTCCAAAGTG CTGGTCCGCA GAGTCAGCAA CCGGGGCTTG GCTGGGACCA CCATCAGAGC 1980
 AACGGCCTGC CACGACAGTG CCAAAAAGTT GTGAGGTCTT CCAGGCCAAG GTGGATGGGC 2040
 CCCATGCCAA GGAATAACA TTTTCCCTGG AAACCACTAA AGTAAGTTT GCTTTTCCTA 2100
 AAGAAAGTCT TTTAGGACAC CACCGTCCC CCGCCCTGCT CCAGAGCGTG GACCGAGGAG 2160
 GTCTTTGTGC CCTGAGCAGG GACCGGATAA CACCAGAAAG AGGGATGCTA CACGGGGTT 2220
 TCTCTCTCA AGATAAGTCC CTGAGAATTA TTTTCAAGCA CTTTTCCTT TTTTACCTT 2280
 AAGTTTTTCT TCCTTTTGTCT TTAATATACT GAACACTTGG AAGTCACCTT TACTTGCTT 2340
 TGCAGAAAC AGAAGTACG CAAACCTAAG TAAGAGTCAT GCCTGGATAT TGGGATAAGC 2400
 CAGTGTCTAG AGGCGTGAAG GAACCGCTGA AGAACCCAGG GAGATCTCCT CTTCCAAGAC 2460
 ACGTTTCCTT CCTCCCTTC TTTCTCTTT CTTTCCAGT T

Seq ID NO: B51 Protein sequence
 Protein Accession #: XP_084965.1

1 11 21 31 41 51
 METSRSRGGG GAVSERGGAG ASVGVCRKKA EAGAGTGTLA ADMDLHCDA AETPAAEPPS 60
 GKINKAAFKL FKRRKSGGTM PSIFGVKNKG DGKSSSGPTGL VRSRTHDGLA EVLVLESGRK 120
 EEPRGGGDSG GGGGGRPNPG PPRAAGPGGG SLASSSVAKS HSFFSLKKK GRSENGKGEP 180
 VDASKAGGKQ KRGLRGLFSG MRWHRKDKRA KAAAEGRAP GGLILPGSL TASLECVKEE 240
 TPRAAREPEE PSQDAPRDPG GCGDILADQE EAGPSCDKH VPFGPKPALS KKNPGVAVYQ 300
 GQSEMAPSPD EVDVTYIQEF WDMLSQTEBQ GPEPQEGAAK VAAALETKVV PETPKDTRCV 360
 EAAKDASSVK RRRINRIPE PPKKEEPKHP EKEQQEGVFN SDEGWDSTT PGPEEDSSSS 420
 GKKAIGPRDS YSGDALYDLY ADPDGSPATL PGKDNETS SLRLKPVSP GTITCPLRTP 480
 GSLLKDSKIP ISIKHLTNLF SSHPVVHQOP SRSEMPRTKI FVSKVLVRRV SNRGLAGTTI 540
 RATACHDSAK KL

Seq ID NO: B52 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..2016

1 11 21 31 41 51
 ATGGAGACGA GCCGGAGCCG CGCGCGCGGC GGGGCTGTCA GCGAGCGCGG CGGAGCTGGC 60
 GCGTCCGTGG GGGTCTGCAG GAGGAAGGCG GAGGCGGGGG CCGGGACCGG GACCTCGCG 120
 GCAGACATGG ACTTGCTATG TGACTGTGCC GCCGAAACGC CGCGCGCGGA GCGCGCGTGG 180
 GGGAGAGTTA ATAAAGCTGC CTTCAAATTA TTCAAGAAGA GGAATCTCGG TGGCACCATG 240
 CCCAGCATTT TTTGGGTCAA AAACAAAGGG GACCGGAAAA GCTCGGGTCC GACGGGGCTG 300
 GTGAGGAGCA GGACCCACGA CGGACTTGCC GAGGTGCTGG TGCTGGAGAG CGCAGGAAG 360
 GAGGAGCCGC GCGCGGGGGG CGACAGCGCG GGGGGCGGGG GGGGGCGGGC GAACCCGGGG 420
 CCGCCAGAGC CCGCAGGGGC CGCGGGGGGC TCCTCGCGCA AAAACCGCAA GGGAGAGCCT 480
 CACAGCTTCT TCTCGCTGCT GAAGAAGAAC GGGCGCTCGG AAAACCGCAA GGGAGAGCCT 540
 GTGAGCGCGA GCAAGGCGCG CGGCAACAAA AAGCGGGGGC TGCGGGGGCT GTTCAGCGGC 600
 ATGCGTGGCG ACAGGAAAGA CAAGCGGGCC AAGCGGAGG CCGCGGAGGG GCGCGCGGCC 660
 GGGGGCGGCT TGATCTTACC CGCTCGCTCC ACCCGCAGCC TGGAGTGGCT CAAGGAGGAG 720
 ACGCCAGAGC CCGCGCGCGA GCGCGAGGAG CCCAGCCAGG ACGCCCGCGG AGACCCAGCA 780
 GGTGAGCCCG CAGGGGGAGA GGAGGTGCCC GCGCCCGCGG ACCCGCGCCC AGCGCGGAGC 840
 TGCGGAGAGG CAGAGGGGCT CGCGCACCCC GCGCACACCG GCGCCCGGGG AGAGGACGCC 900
 GCGGGGCATC GCGCGCGCGA GCGGGGGCCC GGGGAGGTCC GCAAGCGAGA GGAAGCTTCC 960
 AGGACGCGGG CGTTCGCGT AAAGACGGTC CCGCTTGTGG ACTCCGAAGG CGGCAGCGGC 1020
 CCGGCGCGCG CCGCGCCAGA COCTGCTCT GTGACTCCAC CCTCAGACCC GTGCGCAGAT 1080
 CGTATTGTGT TGATGTTTTG TGACGTGACT TCACTGAAAA GCTTTGACTC TCTTACAGGC 1140
 TGTGGAGATA TTATTGCAAG CCAAGAGGAA GAGGCAGGTC CCAGCTGTGA CAAGCATGTC 1200
 CCGCGGCCAG GCAAGCCGCG TCTGTCTAAA AAGAACCCTG GGTGTGTGGC CTACCAAGGA 1260
 GGCGGGGAG AGATGGCCAG CCGGACGAG GTGACGACA CCTATCTACA GGAGTTCTGG 1320
 GACATGTCTT CCCAGACCGA GGAGCAGGGA CCGGAGCCCC AGGAGGGCGC GGCTAAGGTG 1380
 GCAGCTGCGC TGGAAACCAA GGTGTGCGCC GAGACCCCCA AAGACACCAG GTGTGTGGAA 1440
 GCGGCCAAGG ACGCGTCTCT GGTCAAGGCG AGGAGGCTCA ACCGATTCC CATCGAGCCC 1500
 CATCCTAAGG AGGAGGCCAA GCACCGGAG AAGGAGCAGC AGGAAGGCGT CCCCACAGC 1560
 GACGAGGGCT ACTGGGACTC CACACGCCCA GGCCAGAGG AAGACAGCTC GAGCAGCGGG 1620
 AAGAAGGCGG GCATCCCCCG GATAGCTAC AGCGGGGACG CGCTCTATGA TCTCTATGCT 1680
 GACCGGAGC GAAGTCCAGC AACCTTCTCT GGAGGGAAGG ACAAAGGAGA GACGCTCTCC 1740
 CTGTCCCGGT TAAAGCCCTT ATCTCCAGGC ACCATCACTT GTCCACTGCG AACACAGGC 1800
 AGCTTGCTGA AGGACTCTAA GATCCCTATT AGCATCAAGC ACCTGACCAA CCTTCCATCT 1860
 AGCCATCCCG TGGTGACCA GCAACCTTCC AGGAGTGAGA TGCCAGAAC AAAATCCCG 1920
 GTTTCCAAAG TGCTGGTCCG CAGAGTCAGC AACGGGGGCT TGGCTGGGAC CACCATCAGA 1980
 GCAACGCGCT GCCACGACAG TGCCAAAAG TTGTGA

Seq ID NO: B53 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 METSRSRGGG GAVSERGGAG ASVGVCRKKA EAGAGTGTLA ADMDLHCDA AETPAAEPPS 60
 GKINKAAFKL FKRRKSGGTM PSIFGVKNKG DGKSSSGPTGL VRSRTHDGLA EVLVLESGRK 120
 EEPRGGGDSG GGGGGRPNPG PPRAAGPGGG SLASSSVAKS HSFFSLKKK GRSENGKGEP 180
 VDASKAGGKQ KRGLRGLFSG MRWHRKDKRA KAAAEGRAP GGLILPGSL TASLECVKEE 240
 TPRAAREPEE PSQDAPRDPG GEPAGGEEVP APADRAPARS CREAGLAHP GDTGARGEDA 300

5 AGHRRASFGP GEVRTAEDAS RTGAVPVKTV PLVDSEGGSG RAPAAPDPAS VDPSPDPSAD 360
 RICLMFSDVT SLKSPDSLTV CGDILADQEE BAGPSCDKHV PGPGKPAISK KNPVVVAYQG 420
 GGEEMASFDE VDDTYLQEFW DMLSQTEBQG PEPQEGAAKV AAALETKVVP ETPKDRVCVE 480
 AAKDASSVKR RRLNRIPIEP HPKEEPKHPE KEQQEGVPNS DEGYWDSTTP GPEEDSSSSG 540
 KKAGIPRDSY SGDLYDLIA DPDGSFATLP GGDNEETSS LSRLKPVSPG TITCPLRTPG 600
 SLLKDSKIPI SIKHLTNLPS SHPVVHQQPS RSEMPRTKIP VSKVLVRRVS NRGLAGTTIR 660
 ATACEDSAKK L

10 Seq ID NO: B54 DNA sequence
 Nucleic Acid Accession #: NM_014138.1
 Coding sequence: 60..854

15 1 11 21 31 41 51
 CTGCAGAGAC TTCCAGGAA GGTCCAGGCG CCTCTCAGCC TTCTACTCA GAACAGCCGA 60
 TGATGGGCTC CAGTAACCTG AGCCCCGCTC CTGGCCCCAG CCAGGCCGTG CCTCTCCAG 120
 AGGGGCTGCT CGCCACGCGG TACAGAGAGG AGAAGACCTT GGAGAGCGG CGGTGGGAGA 180
 GGCTGGAGTT CCTTCAGAGG AAGAAAGCAT TCCTGCGGCA TGTGAGGAGG AGACACCGCG 240
 ATCACAATGC CCCTATGCT GTTGAGGAGG AAGCCAGAAT CTCCCCATTA GGTGACAGAA 300
 20 GCAGAAATCG ATTCCGATGT GAATGTGAT ACTGCCAGAG CCACAGGCCG AATCTTTCTG 360
 GGATCCCTGG GGAGAGTAAC AGGGCCCCAC ATCCCTCTCT CTGGGAGAGG CTGGTGACGG 420
 GCCTCAGTGG CTTGACTCTC AGCCTAGGCA CCAACCAAGC CGGGCCTCTG CCTGAAGCGG 480
 CACTCCAGCC ACAGGAGACA GAGGAGAAGC GCCAGCGAGA GAGGCAGCAG GAGAGCAAAA 540
 TAATGTTTCA GAGGCTGCTC AAGCAGTGGT TAGAGGAAAA CTGAGACGTG CACCCCATG 600
 25 GGATGGAGAC CCGAAGGGAC TCAGACGGAG CGCGCGTGTI GGCAGCGCCT GGGTGTGGGC 660
 CCATTTTGGG GACCAACAG CAAGCTGTGG TCGGATGAGT GCCAGGACCT GTGTACCGGG 720
 ACACGTGGGA GTCTCTCCAG CATGATGCTT GACTGACCGG AGGAAGTCTC TCATGTTTCG 780
 TGCTGTCTAT TCTCGGATGG CTGTGAGGCA TTCTTGGCA AGGACGCTG CTGACACGG 840
 30 TGCTCACCAG CATCTCACAT GGCTCCTGTG ATGCATGTTG TCGCTTTTCC ACCCGGGATC 900
 TCCATCTCTC TCCCTTCTCT GCTGTGAGTA AGAGATCACA TGCTGTGTA GTGTGAATGC 960
 CTGTGTGCTG TCCTGTGCTT TTGACCAATT GAGTTGACTG CCTCTGAGAA GCAGCACTAG 1020
 GCCTGTGCTG ATGCAATGTG CTGCCCTGAG ATCCAGTTTC AAGAATGGGC AGGTAAACGC 1080
 AGTGTGGGAA AGGAATGTGG AATGAGAACT TGGTGTGTCA CCGCTGTACT ATTGTGTAA 1140
 ATGTTTAAGT ATGTGATAAG CTACATGTAT GTAAATGTTG CAATACCCCT AACAGTCGAG 1200
 35 TAGTAGTCTC CCTTACAGGA ATTTTTCAGG GGGTTCCTCA TCATCAATAC CAAATAAATA 1260
 TATGTAGGAA TGGAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1320
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA

40 Seq ID NO: B55 Protein sequence
 Protein Accession #: NP_054857.1

45 1 11 21 31 41 51
 MMGLSNLSPG PGPSQAVPLP EGLLRQRYRE EKTLEERRWE RLEFLQRKKA FLRHVRRHR 60
 DIMAPYAVGR EARISPLGDR SQNRFRCECR YCQSHRPNLS GIPGESNRAP HPSWETLVQ 120
 GLSGTLTSLG TNQPGFLPEA ALQPQETEEK RQRERQESK IMFQRLKQW LLEN

50 Seq ID NO: B56 DNA sequence
 Nucleic Acid Accession #: NM_000025.1
 Coding sequence: 198..1424

55 1 11 21 31 41 51
 GCTACTCTCT CCCCAGAGAC GGTGGCACCG AGGAGTTTGG GGTGGGGGGA GGCTGAGCGC 60
 TCTGGCTGGG ACAGCTAGAG AAGATGGCCG AGGCTGGGGA AGTGCCTCTC ATGCCCTTGT 120
 GTCCCCCTCC CTGAGCCAGG TGATTTGGGA GACCCCTCTT TCTCTCTTT CCTACCGCC 180
 CCAAGCGGGA CCGGGGATG GCTCCGTGGC CTCACGAGAA CAGCTCTCTT GCCCATGGC 240
 CGGAACCTCC CACCTGGCG CCCAATACCG CCAACACCG TGGGCTGCCA GGGGTTCGGT 300
 60 GGGAGGCGGC CCTAGCGGGG GCCCTGCTGG CGCTGGCGGT GCTGGCCACC GTGGGAGGCA 360
 ACCTGCTGGT CATCGTGGC ATCGCCTGGA CTCGAGACT CCAGACCATG ACCAACCTGT 420
 TCGTACTTCT GCTGGCCGCA GCGAACCTGG TGATGGGACT CCTGGTGGTG CCGCGGGGG 480
 CCACCTTGGC GCTGACTGGC CACTGGCCGT TGGGCGCCAC TGGCTGCGAG CTGTGGACCT 540
 CGGTGAGCT GCTGTGTGT ACCGCCAGCA TCGAAACCTT GTGCGCCCTG CGCGTGACCC 600
 65 GCTACCTGGC TGTGACCAAC CGCTGCGTT ACGGCGCACT GGTCAACAG CGCTGCGCCC 660
 GGACAGCTGT GGTCTGGTG TGGGTGTGT CGGCGCGGT GTCTTTTGG CCCATCATGA 720
 GCCAGTGGTG GCGGTAGGG GCGAGCGCG AGGCGCAGCG CTGCCACTCC AACCGCGCT 780
 GCTGTGCTCT CGCTCCCAAC ATGCCCTACG TGCTGCTGTC CTCTCTCTCT TCTTCTTACC 840
 TTCTCTCTCT CGTATGCTC TTCTGTACG CGCGGTCTT CTGTGTGGCT ACGCGCCAG 900
 70 TGCGCTTGTCT GCGCGGGGAG CTGGGCGGCT TTCCGCGCGA GGAGTCTCG CGGCGCGCT 960
 CGCGCTCTCT GCGCGCGGCC CGGTGGGGA CGTGCGCTCC GCCGAAAGG GTGCGCGCT 1020
 GCGGCGCGCG GCGCGCGGCT CTCTGCTCT TCGGGAACA CGGGCCCTG TGCACTTGG 1080
 GTCTCATCAT GGGCACCTTC ACTCTCTGCT GTTTCGCTT CTCTCTGCT AACGTGCTGC 1140
 GCGCCCTGGG GCGGCGCTCT CTAGTCCCGG GCGCGGCTT CCTTGCCTG AACTGGCTAG 1200
 75 GTTATGCCAA TTCTGCTTTC AACCGCTCA TCTACTGCG CAGCGCGAG TTTCGAGCG 1260
 CCTTCCGCG TCTTCTGTG CGCTGCGGCC GTGCGCTGCC TCGGAGAGCC TGGCGCGCG 1320
 CCGCGCGGCC CCTCTTCCCG TCGGCGGTT CTGCGCGCG GAGCAGGCCA GCGCAGGCCA 1380
 GCGTTTGCCA ACGCTGTGAG GGGGCTTCTT GGGGAGTTTC TTAGGCTGGA AGGACAAGAA 1440
 80 GCAACAATC TGTGTATCAG AACCTGTGGA AACCTCTGG CCTCTGTTCA GAATGAGTCC 1500
 CATGGGATG CCGGCGTGTG ACACTCTACC CTCAGAACCT TGACGAGTGG GCCATGTGAC 1560
 CCAAGGAGGG ATCCTTACCA AGTGGGTTTT CACCATCTCT TTGCTCTCTG TCTGAGAGAT 1620
 GTTTTCTAAA CCCCAGCTT GAACCTTCACT CCTCTCTAG TGGTAGTGTG CAGGTGCGGT 1680
 GGAGCAGCAG GCTGGCTTTG GTAGGGGAC CCATCAACCG GCTTGCCTGT GCAGTCAGTG 1740
 AGTGCTTAGG GCAAGAGAG CTCCCTGCTT TCCATCTCT CTGCCACCA AACCTGATG 1800

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AGACCTTAGT GTTCTCCAGG CTCTGTGGCC CAGGCTGAGA GCAGCAGGGT AGAAAAAGACC 1860
AAGATTGGGG GTTTTATCTC TGGTTCCTT ATTACTGCTC TCAAGCAGTG GCCTCTCTCA 1920
CTTTAGCCAT GGAATGGCTC CGATCTACCT CACAGCAGTG TCAGAAGGAC TTGCCAGGG 1980
TTTTGGGAGC TCCAGGGTTC ATAAGAAGGT GAACCATAG AACAGATCCC TTCTTTTCT 2040
TTTGCAATCA GATAAATAAA TATCACTGAA TGCAGTTCAT CCTCGGCCA CTTTCCCTCC 2100
GTTTGTTTTC TTTTCATAAT CCACTTACTC CCTTCCCTTC TACTCTGC3C TGGCTTTTGA 2160
CAGAGGCAGT AAATTAGGCC TAATCCTCAC TCTTTTCTTC CTAATCTTCA TCAACAAAA 2220
AATGAAAAAGT CTGTCTGGAC GAAGGGGAGT GAGCTTGAGC CTTGATATC TTGCTCCCC 2280
ACCTTCTCTG AAACCTCTGA AATCCAGTTG CCATTGAGTA GCAAGGCCAC GCTCCCCACA 2340
GGACTTGGAC AGAGGGGCCA CAGGGGGATG GGCTGGCTGT GGCCAGGTTT AGGGCAGGG 2400
GCATTGTGCC CCTCATGCT ATAATCCAGT GGTGCCTTAC ATGGTGTGTG TGTGTGTGTG 2460
TGGGTGTGTG TGTGTGTGTG TGTGTCTGGA GGCACAGGCA CAAAGCATTC CTTGGGTGG 2520
TCAAATGTCT TGTGTCTATA ATATATTCTG ATGTTTCCCA GCCTTTCAC AACCTCTACC 2580
TTCCCACTCA CCTTCCCGAG CTACAAAAAT CTGTATTATC CTCTAAAGT AAAACTGGAG 2640
TTAC

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Seq ID NO: B57 Protein sequence
Protein Accession #: NP_000016.1

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1 11 21 31 41 51
MAPWPHENSS LAPWPDLPFL APNTANTSGL PGVPWEAALA GALLALAVLA TVGNLLVIV 60
AIANTPRLQT MINVFTSLA AADLVMGLLV VPPAATLALT GHWPLGATGC ELMTSVDVLC 120
VTASIELTCA LAVDRYLAVT NPLRYGLVLT KRCARTAVVL VVVVSAVSEF APIMSQWVRV 180
GADABEQRCH SNPRCCAPAS NMPVVLSSS VSFYLPPLVM LFVYARVFFV ATRQLRLLRG 240
ELGRFPPEES PPAPSRSLAP APVGTICAPPE GVPACGRPA RLLPLREHRA LCTGLLIMGT 300
FTLCHLPFFL ANVLRALGGP SLVPGPAFLA LNWLYGANSF FNPLIYCRSP DFRSAFRRL 360
CRGRRLPPE PCAAARPALF PSGVPAARSS PAQRLCQRL DGASWGV

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Seq ID NO: B58 DNA sequence
Nucleic Acid Accession #: NM_032553.1
Coding sequence: 37..1038

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1 11 21 31 41 51
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ATTCTGTGTC CAGGTCTCAT AGGGAATATA TTAGCCCTGT GGGTATTCTA TGGTTATATG 180
AAAGAAACAA AAGCAGCTGT GATATTATAG ATAAACTTAG CCATTGCTGA CTTACTACAA 240
GTTCTTTCTC TGGCACTGAG GATCTTCTAC TACTTGAATC ATGACTGGCC ATTTGGGCTC 300
GGTCTCTGCA TGTCTGTGTT CTACCTGAAG TATGTCAACA TGTATGCAAG CATCTACTTC 360
TTGCTCTGCA TCACTGTGCG ACGATTTTGG TTTCTCATGT ACCCTTTTCC CTTCCATGAC 420
TGCAACAGCA AATATGACCT GTACATCAGC ATTGTGGCT GGTGATCAT CTGCTTGCC 480
TGTGTACTCT TTCCACTCCT CAGAACCACT GATGATACCT CTGGCAATAG GACCAATATG 540
TTTGTGGATC TTCCATCCAG GAATGTCAAC CTGGCCCACT CCGTTGTTAT GATGACCATT 600
GGCGAGTTGA TGGGGTTTGT AACTCCGCTT CTGATTGTCC TATATTGTAC CTGGAAGACG 660
GTTTTATCAC TGCAAGATAA ATATCCCATG GCCCAAGATC TTGGAGAGAA ACAGAAAGCC 720
TTGAAGATGA TTCTAACTCT TGCAGGGGTA TTCTTAATTT GCTTTGCACC TTATCATTTT 780
AGTTTTCTCT TAGATTTCTT GGTGAAGTCC AATGAATTA AAAGCTGCCT AGCCAGAAGG 840
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CCAGTCAATC ACTACTTTTC CACTAATGAG TTCCGAAGAC GGCTTTCAG ACAAGATTG 960
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Seq ID NO: B59 Protein sequence
Protein Accession #: NP_115942.1

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MYPRFHDCK QKXDLIYISIA GWLIICLACV LFPILRTSD TSGNRTKCFV DLPTRNVNLA 180
QSVVMTTIGB LIGFVTPLLI VLYCTWKTVL SLQDKYPMQA DLGEKQKALK MILTCAGVFL 240
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Seq ID NO: B60 DNA sequence
Nucleic Acid Accession #: CAT cluster

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 Nucleic Acid Accession #: NM_014522.1
 Coding sequence: 846..3911

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10 Seq ID NO: B62 Protein sequence
 Protein Accession #: NP_055337.1

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Seq ID NO: B65 DNA sequence
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 CGCAGCCCGA AGATTCACTA TGGTGAATAA CGCCTTCAAT ACCCTTACCG CCGTGCAAAA 180
 GGAGAGGGCG CGGCAAGACG TGGAGGCCCT CCGAGCCGCG ACGGTCAAG CTCAGATACT 240
 GACCGGCAAG GAGCTCCGAG TTGCCACCCA GGAAGAGAG GGCTCCTCTG GGAGATGTAT 300
 80 GCTTACTCTC TTAGGCCTTT CATTCATCTT GGCAGGACT ATTGTTGGTG GAGCCTGCAT 360
 TTACAAGTAC TTCAATGCCA AGAGCACCAT TTACCGTGA GAGATGTGCT TTTTGTATTC 420
 TGAGGATCTC GCAAAATCCC TTCTGTGAGG AGAGCCTAAC TTCTGCTCTG TGACTGAGGA 480
 GGCTGACATT CGTGAGGATG ACAACATTGC AATCATTGAT GTGCTGTCTC CCAGTTTCTC 540
 TGATAGTGAC CCTGCAGCAA TTATTATGTA CTTTGAAAAG GGAATGACTG CTTACTGGA 600
 CTTGTGTGCTG GGGAACTGCT ATCTGATGCC CCTCAATACT TCTATTGTGA TGCTCCCAA 660

5
AAATCTGGTA GAGCTCTTTG GCAAACTGGC GAGTGGCAGA TATCTGCCTC AAACCTATGT 720
GGTTCGAGAA GACCTAGTTG CTGTGGAGGA AATTCGTGAT GTTAGTAACC TTGGCATCTT 780
TATTACCAA CTTTGCRAA ACAGAAAGTC CTTCCGCTT CGTCGCAGAG ACCTCTTGCT 840
GGGTTTCAAC AAACGTGCCA TTGATAAATG CTGGAAGATT AGACACTTCC CCAACGAATT 900
TATTGTTGAG ACCAAGATCT GTCAAGAGTA AGAGGCAACA GATAGAGTGT CCTTGGTAAT 960
AAGAAGTCAG AGATTACAA TATGACTTTA ACATTAGGT TTATGGGATA CTCAAGATAT 1020
TTACTCATGC ATTACTCTA TTGCTTATGC CGTAAAAAAA AAAAAAAAAA AAAAAAAAAA 1080
AA

10 Seq ID NO: B66 Protein sequence
Protein Accession #: NP_004858.1

15
1 11 21 31 41 51
MVKIAFNTPT AVQKEEARQD VEALLSRTVR TQILTGKELR VATQKEKSSS GRCMLTLGL 60
SFILAGLIVG GACIYKYPMP KSTIYRGEMC FFDSEDPANS LRGGEPNPLP VTSEADIRE 120
DNIAIIDVPE PSFSDSDPAA IHDPEKGMT AYLDLLLGNC YLMPINTSIV MPPKNLVLP 180
GKLASGRYLP QTVVVRDLV AVEBIRDVSN LGIFIYQLCN NRKSFRLRRR DLLLGFNRRA 240
IDKCWKIRHP PNEFIVETKI CQE

20 Seq ID NO: B67 DNA sequence
Nucleic Acid Accession #: XM_083862.1
Coding sequence: 121..813

25
1 11 21 31 41 51
ACGCGGGAGG TCTGAGCTGT GGGCTGAGGC AGCGCAGCCG CTGCGCCAGG GTGCGCGATG 60
CCTTGAACCT GGGAAACTAT GTGAAGCAAC ACTCTGGATT TTGAAAGACA TCTTTTCATC 120
ATGGGACAGC AAATTTGGGA TCAGACACAG TTGGTTATTA ACAAGTTACC AGAAAAAGTA 180
GCAAAACATG TTACGTTGGT TCGAGAGAGT GGCTCCCTAA CTTATGAAGA ATTTCTGGG 240
AGAGTAGCTG AGCTTAATGA TGTAAACGCT AAAGTGGCTT CTGGCCAGGA AAAACATCTT 300
CTCTTTGAGG TACAACCTGG GTCTGATTCC TCTGCTTTT GGAAGTGGT TGTACGGGTG 360
GTCTGTACCA AGATTACAA AAGCAGTGGC ATTGTGGAGG CATCACGAT CATGAATTA 420
TACCAGTTTA TTCAACTTTA TAAAGATATC ACAAGTCAAG CAGCAGGAGT ATCGGCACAG 480
AGCTCCACCT CTGAAGAACC TGATGAAAC TCATCCTCTG TAACATCTG TCAGGCTAGT 540
CTTTGGATGG GAAGGCTGAA GCAGCTGACC GATGAGGAGG AGTGTGTAT CTGTATGGAT 600
GGGCGGGCTG ACCTCATCTT GCCTTGTGCT CACAGCTTTT GTCAGAAGTG TATTGATAAA 660
TGGAGTGATC GACACAGGAA TTGCCCTATT TGTGCGCTAC AGATGACTGG AGCAAATGAA 720
TCTTGGGTGG TATCAGATGC ACCCACTGAA GATGATATGG CTAACATAT TCTTAAACATG 780
GCTGATGAGG CAGGCCAGCC CCACAGGCCA TGACCTTGAA GTGAAAGTCT TCTGTGCTA 840
TTGTGGGCTC AAATATTTGG TCATGCGGGA AGAATGTAGG GTTGTGGCAC TGGCAGAGAC 900
ACAGGAAAT CCAATTTCCC CACTCTTTA TTTTGTCTAT TCTGATCAT TGTCCCTCT 960
TTAAAAATA ACTTCCCATG TCTTCCAAA AAAAAAAAAA AAAAA

45 Seq ID NO: B68 Protein sequence
Protein Accession #: XP_083862.1

50
1 11 21 31 41 51
MQQISDQQTQ LVINKLPEKV AKHVLVRES GSLTYEEFLG RVARLNDVTA KVASGQEKHL 60
LFEVQPGSDS SAFKVVVVVV VCTKINKSSG IVEASRIMNL YQFIQLYKDI TSQAAGVLAQ 120
SSTSEEPDEN SSVTSQAS LMMGRVKQLT DEEECCICMD GRADLILPCA HSFCQKCIDR 180
WSDRHRNCPRI CRLQMTGANE SHVVSADAPTE DDMANYILNM ADEAGQPHRP

55 Seq ID NO: B69 DNA sequence
Nucleic Acid Accession #: NM_002975.1
Coding sequence: 180..1151

60
1 11 21 31 41 51
CGACCAACGG ACCGACAGA GACGAGGAGA GGAACAGGAA GAGAGAAGCT GGGAGAATCG 60
GGAAACCTGG GGCTAGTGAC CTGCACACAG GGCAGGGGCA CTGGCAGTT CCCAGAGGCC 120
ACCCCTCCCA CCCAGACAT CCAGACATCT GGAACCTTTG GTGCCAAGAG TCCAGCTTAA 180
TGCAAGCAGC CTGGCTTTTG GGGCTTTTGG TGGTCCCCCA GCTCTTGGGC TTTGGCCATG 240
GGGCTCGGGG AGCAGAGAGG GAGTGGGAGG GAGGCTGGGG AGGTGCCAG GAGGAGGAGC 300
GGGAGAGGGA GGCCCTGATG CTGAAGCATC TGCAGGAAGC CCTAGGACTG CCTGCTGGGA 360
GGGGGGATGA GAATCTTGCC GGAACCTTTG AGGGAAAAGA GGAAGTGGAG ATGGAGGAGG 420
ACCAGGGGGA GGAAGAGGAG GAGGAAGCAA CGCAACCCC ATCTCCGGC CCCAGCCCCC 480
CTCCACCCC TGAGGACATC GTCACTTACA TCCTGGGACC CCGTGGGAC CAGCTGACCC 540
GCCTGACCCA GCTGCACGTC CGTCTGCACG CBTGGGACAC CGCGTGGTC GAGCTGACCC 600
AGGGGCTGGG GCAGCTGGG AACGCGGAG GCGACACCCG CGATGCCGTC CAAGCCCTGC 660
AGGAGGGCCA GGGTGGGCC GAGCGCGAGC AGCGCCGCTT GAGAGGCTGC CTGAAGGGGC 720
TGGCTCTGGG CCACAAGTGC TTCTGCTCTT CGCGGACTT CGAAGCTCAG GCGGCGGCGC 780
AGGCGCGGTG CAGCGCGGCG GCGCGGAGCC TGGCGCAGCC GGCAGACCGC CAGCAGATGG 840
AGGCGCTCAC TCGGTACCTG CGCGCGGCGC TCGCTCCCTA CAATGGGCC GTGTGGCTGG 900
GGGTGCAGA TGGGCGGCC GAGGGCTCTT ACCTCTTGA AAACGGCCAG CGGCTGCTCT 960
TCTTCCCTCG GCATGCTCA CCGCGCCCG AGCTGGGCGC CCAGCCAGC GCGTGGCGC 1020
ATCCGCTCAG CCGGACCCAG CCCACCGGTG GCAAGCTCGA GAAGTGGCTG GCGCAGGCT 1080
CTGACAGCGG CTCTGGTGG GACCAGACT GCCAGCGCG TCTCTACTAC GTCTGGAGT 1140
TCCCTTCTA CGGGGCGCG TACCCGCTT CTTGCCCAT CCCACACCC GCGCTTTCCC 1200
TGGCGGTC CCACCTCTT CCGGAATGCG CTTTCCCTTC CTGGCCACGA ATGGCAGGT 1260
CCTCCCGAC CCCAGCTCG GCGGCTTCT GAGGGCTCT TGGGTGGCG GCACTCTTC 1320
TTGTAGTGT CTTTCTTGA AGGGGCGGC ACCAGGCTAG GTCGCTGCC AATAATCTT 1380
TGTGAATCTT GAAAAA AAAAAA

Seq ID NO: B70 Protein sequence
Protein Accession #: NP_002966.1

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5      1      11      21      31      41      51
MQAANLLGAL VVPQLLGFPH GARGAEREWE GNGGGAQEEE REREALMLKH LQEALGLPAG 60
RGDENPAGTV BGKEDWEMRE DQGEEREEEA TPTPSSGSPS SPTPEDIVTY ILGRLAGLDA 120
10     GLHQLHVRHL ALDTRVVELT QGLRQLRNAA GDTRDAVQAL QEAQGRABRE HGRLEGCLKG 180
LRLGHKCFLL SRDPFAQAAA QARCTARGGS LAQPADRQQM BALTRYLRRA LAPYNWFWNL 240
GVHDDRABGL YLPENGQRVS FFAWHRSRPR ELGAQPSASP HPLSPDPQNG GTLENCVAQA 300
SDDGSWMDHD CQRRLYYVCE FPF
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Seq ID NO: B71 DNA sequence
Nucleic Acid Accession #: BC000839.1

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15      1      11      21      31      41      51
CTGGCCAGGG CGACTGGCGG ATAAGGTCTT GTGCGTGGCC TCGAGGCTTA AAAGTAGCAG 60
20     TGGGGCTTTG TGAAGGACAA AATGGCGATG GCGGGCCGTG TAGGTCCCCC TTCCTATGAT 120
GAGGACCTTT TCACAGACCT GTACTGAGCT CCGTGAGGAT AAGTAACCTC GAGGAGATGG 180
GCCCTGCAAG CCTCTTCTT AGCGGTCTGT TCAGAAAATA GCGTTTTCGA AATGCCCTGA 240
GTTGACCTAA TGCTTATTG GGCTCCTGTC TGCAGGATT ACGGGCACGT TGGAACCGAA 300
GAGAGCTCTG TTGTTGCAAT GTTCAGCCCA CAAGAGCTTA CTGGTGAAG AATGGGACAA 360
25     GACCCATCTT TATGCAAAAGC CAGCGTTACA GTAATGTTCC AGCATCTCAT AATCTATCCT 420
GGGGAATTCA GCTGCCTCCC AGGGTGAATA CAGGTATTCC TGATGACAGT CTGCCTCTAT 480
CTTACAGAGC AGCTTGTGTC TATATACCAT TGAAAAGCCT TCAGAGCTGA GAGGTACTAC 540
TAACCAATAA CCTGCTTGCG TCAAAGGGCC AGCACCTTCT CTCTAAAGCC CAAGAGGAGT 600
TTGAGGAAAA CTAGGTGTCT GTGTTCACCT CAGGCTGAAG TTACAGTCT GAGCAATAA 660
30     GGTGTATAAA AATGGAATC TGCTTGGAG GACATCAGAA GGTGAATTTT CCAAGTCTT 720
GGACAACCTA GCTGTGAAA AGCTTCTCG GTTTGGGGGG TATTTTCAGT GTACCTTAAA 780
GTGTAGCAG AGATGACCAC AGACACTGGG AGCCAATGAA ACAGCAGTTG AGGGTTTGCT 840
GTGTATCACA TTTCTGTATT TTATCACCCC CTCTCTGCAA CATTATTAT CTGGAATCTA 900
CCTGCCCTTT TGTTTTTTAG ATACAGGGCC TTGGTTTTGT TACCCAGGCT GGTTCAGG 960
35     CCATAGCTTT AAGAGATCCT CTCACCACAG ATTTCCAAAG TGCTGGGATT GCAGGTGTA 1020
TTATGGCAC CCAGACTTTG CTGCTTTCT TACATGATCC AGGCCAGAA CCCAACTCA 1080
GGCACTGTAT AGATGACCAC TTCTGTAAAC TACTGACCTA GCTTGTGCCC AATTGTTGCT 1140
TGAACCTCCC ATAACCTCAC TTCTGTCTG TTCTCTGTA TACAGCCACC TTCTGTTCCC 1200
40     GTCATGAGCC TTTAGGTCTC CATTTGCATA TTGCAAATAC TATGTTCCAT GTAGGTAGCT 1260
CAITCAGGGC CTGTCTCTTC ACTTCAAAA AGGTTCCCTT GAGGACTGGC TGTCAATTTG 1320
TGTGCTGTG TTGTTGTG ATGAAAAATA TAAATGATT GATTACATA AAAAAAAAAA 1380
AAAAAA
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Seq ID NO: B72 DNA sequence
Nucleic Acid Accession #: CAT cluster

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45      1      11      21      31      41      51
TGCTAGTAGG GCCTGGGTTA ATCGGCCGAG GGTGGCTTCG TGGTCTTTAT AGCTGTACT 60
50     CTTTGTACTT GTCTTTTCT TTTATTTCT TTTGAGCGAT TGTGCGAACA TAGCATAGCA 120
CGCACTATGG CACGAGGCTC GTGCTGCCGT GCCAGGGCGA CTGGCGGATA AGGTCTTGTG 180
CGTGGCCTCG AGGCTTAAAA GTAGCAGTGG GCGCTTGTGA AGGACAAAAT GCGATGGCG 240
GGCCGTGTAG GTCCCCCTTC CTATGATGAG GACCTTTTCA CAGACCTGTA CTGAGCTCG 300
TGAGGATAAA TAACTCTGAG GAGATGGGCC CTGCAAGCCT CTGCTTAGC CGTCTGTTCA 360
55     GAAAAATAGCG TTTTCGAAAT GCCCTGAGTT GACCTAATGT CTTATTGGGC TCCTGTCTGC 420
AGGATTTACG CGCACTTTGG AACCGAAGAG AGCTCTGTG TTGCAATGTT CAGCCACAA 480
GAGCTTACTG GTGAAGGAAT GGGACAAGAC CCATCTTTAT GCAAAGCCAG GGTACAGTA 540
ATGTTCCAGC ATCTCATAAT CTATCCTGGG GAATTCAGCT GCCTCCAGG GTGAATACAG 600
GTATTCTCGA TGACAGTCTG CCTCTATCTT ACAGAGCAGC TTGTTGCTAT ATACCATTGA 660
60     AAAGCCTTCA GAGCTGAGAG GTACTACTAA CCAATAACCT GCTTGGCTCA AAGGGCCAGC 720
ACCTTCTCTC TAAAGCCCAA GAGGAGTTTG AGGAAAACCT GGTGTCTGTG TTCACTCCAG 780
GCTGAAGTTA CAGGTCTGAG CAAATAAGGT GTATAAAAAA TGGAACTCTG CTTGGAGGAC 840
ATCAGAAGGT GAATTTTCCA AGTCTTGGG CAACCTAGCT GTTGAAAGC TTTCTGGGTT 900
TGCGGGGTAT TTCAGATGTA CCTTAAAGTG TTAGCAGACA CAGATTAAGA CACTGGGAGC 960
65     CAATGAAACA GCAGTTGAGG GTTTGCTGTG TATCACATTT CTGTATTTTA TCACCCCTTT 1020
CCTGCAACAT TATTTATCTG GAATCTACCT GCCCTTTTGT TTTTAGATA CAAGGGCTTG 1080
GTTTGTGTTAC CCAGGCTGGT TTCAAGGCCA TAGCTTTAAG AGATCCTCTC ACCACAGATT 1140
TCCAAAGTGC TGGGATTGCA GGTGTGATTC ATGGCACCCA GACITTGCTG CCTTCTTAC 1200
70     ATGATCCAGG CCCAGAACCC AAACCTCAGG ACTGTATAGA TGACCACTTT CGTAAACTAC 1260
TGACCTAGCT TGTTCGCAAT TGTGATTTGA ACTTCCCAT ACTCCACTTC GTGTCTGTT 1320
CTCTGTATAC AGCCCACTTC TGTCCCGTC ATGAGCCTTT AGGTCTCCAT TTGCATATTG 1380
CAAACTACTAT GTTCCATGTA GSTAGCTCAT TCAGGGCCTT GCTCTTCACT TCAAAAAAGG 1440
TTCCCTTGAG GACTGGCTGT CAATTTGTGT TGCTGTGTTG GTTGTGTATG AAAAAATAA 1500
75     AATGATTGAT TACATAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAACAA CAAAAAAC 1560
GCGCGGCTTT TTTCCCGGCC GCACAAAGTT ATAAAAAGCC GTCCATC
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Seq ID NO: B73 sequence
Nucleic Acid Accession #: NM_000222.1
Coding sequence: 22..2952

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80      1      11      21      31      41      51
GATCCCATCG CAGCTACCGC GATGAGAGGC GCTCGCGGCG CTGGGATTT TCTCTGCGTT 60
CTGCTCTCTAC TGCTTCCGGT CCAGACAGGC TCTTCTCAAC CATCTGTGAG TCCAGGGGAA 120
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WO 03/042661

5 CCGTCTCCAC CATCCATCCA TCCAGGAAAA TCAGACTTAA TAGTCCGCGT GGGCGACGAG 180
 ATTAGGCTGT TATGCACTGA TCCGGGCTTT GTCAAATGGA CTTTGGAGAT CCTGGATGAA 240
 ACGAATGAGA ATAAAGCAGAA TGAATGGATC ACGAAAAAGG CAGAAGCCAC CAACACCGGC 300
 AAATACACGT GCACCAACAA ACACGGCTTA AGCAATTCCA TTTATGTGTT TGTTAGAGAT 360
 CCTGCCAAGC TTTCTCTGTT TGACGGCTCC TTGTATGGGA AAGAAGACAA CGACACGCTG 420
 GTCCGCTGTC CTCTCACAGA CCCAGAAGTG ACCAATTATT CCCTCAAGGG GTGCCAGGGG 480
 AAGCCTCTTC CCAAGGACTT GAGGTTTATT CCTGACCCCA AGGCGGGCAT CATGATCAAA 540
 AGTGTGAAC GCSCCTACCA TCGGCTCTGT CTGCAATTGT CTGTGGACCA GGAGGGCAAG 600
 TCAGTGTCTGT CGSAAAAATT CATCTGAAA GTGAGGCCAG CCTTCAAGCT TGTGCTGTT 660
 10 GTGTCTGTGT CCAGAGCAAG CTATCTCTTT AGGGAAGGGG AAGAATTCAC AGTGACGTGC 720
 ACAATAAAG ATGTGCTAG TTCTGTGTAC TCAACGTGGA AAAGAGAAAA CAGTCAGACT 780
 AAATACAGG AGAAATATAA TAGCTGGCAT CACGGTGACT TCAATTATGA ACGTCAGGCA 840
 ACGTGTACTA TCAGTTCAGC GAGAGTTAAT GATTCTGGAG TGTTCATGTG TTATGCCAAT 900
 15 AATACTTTTG GATCAGCAAA TGTCAACA ACCTTGGGAG TAGTAGATAA AGGATTCATT 960
 AATATCTTCC CCATGATAAA CACTACAGTA TTTGTAAACG ATGGAGAAAA TGTGATTG 1020
 ATTGTGAAT ATGAAGCAT CCCCAACCTT GAACACCAGC AGTGGACTTA TATGAACAGA 1080
 ACCTTCACTG ATAAATGGGA AGATTATCCC AAGTCTGAGA ATGAAAGTAA TATCAGATAC 1140
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 20 GTGTCCCAAT CTGACGTCAA TGCTGCCATA GCATTAAATG TTTATGTGAA TACAAAACCA 1260
 GAAATCTGTA CTTACGACAG GCTCGTGAAT GGCATGCTCC AATGTGTGGC AGCAGGATTC 1320
 CCAGAGCCCA CAATAGATTG GTATTTTGTG CCAGGAAGCT AGCAGAGATG CTCTGCTTCT 1380
 GTACTGCCAG TGGATGTGCA GACACTAAAC TCATCTGGGC CACCGTTTGG AAAGCTAGTG 1440
 GTTCAGAGTT CTATAGATT TAGTGCAATC AAGCACAATG GCACGGTGA ATGTAAAGCT 1500
 25 TACAACGATG TGGCAAGAC TTCTGCTAT TTTAACTTTG CATTAAAGG TAACAACAA 1560
 GAGCAATCC ATCCCCACAC CCTGTTCACT CCTTGTCTGA TTGGTTTGT AATCGTAGCT 1620
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 30 ACCCTGGGTG CTGGAGCTTT CGCTGTAAG ATGCTCAAGC CGAGTGCCCA TTTGACAGAA 1860
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 35 CAGGAAGATC ATGCAAGAC TGCACTTTAT AAGATCTTC TGCACTCAA GGAGTCTTCC 2160
 TGCAGCGATA GTACTAATGA GTACATGGAC ATGAAACCTG GAGTTCTTA TGTGTGCCA 2220
 ACCAAGGCCG ACCAAGGAG ATCTGTGAGA ATAGGCTCAT ACATAGAAAG AGATGTGACT 2280
 CCGCCATCA TGGAGGATGA CGAGTTGGCC CTAGACTTAG AAGACTTGCT GAGCTTTTCT 2340
 40 TACCAGGTGG CAAAGGGCAT GGCTTTCTCT GCCTCCAAGA ATTGTATTCA CAGAGACTTG 2400
 GCAGCCAGAA ATATCTCTCT TACTCATGTT CGGATCAAAA AGATTGTGA TTTTGGTCTA 2460
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 45 CACGCACCTG CTGAATATGA TGACATAATG AAGACTTGCT GGGATGCGA TCCCTTAA 2760
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 55 GGTAGTAATC ACAGTTGGCC TTCAGAACCA TCCATAGTAG TATGATGATA CAAGATTAGA 3360
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 60 GCTTCCCTAG CCAGCACTTG TATATACGCA TCTATAAAT GTCCGTGTTT ATACATTGA 3660
 GGGGAAACCA CCATAAGGTT TCGTTCTGT ATACAAACCT GGCATTATGT CCACTGTGTA 3720
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 65 GATGCTGTTT GACAAAGTTA CTGATTCAT GCATGGCTCC CACAGGAGTG GGAACACACT 3960
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 70 TAGCTTACCA GAGCTTCCA TAGTGTGCA GAGGAAGTGG AAGGCATCAG TCCCTATGTA 4260
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 75 TTGTCTTGAA AGATTGAGGT ATGTTGCTCT TATGTTTCC CCTTCTACA TTTCTTAGAG 4560
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 80 TTGCCATACT TTGTCTGAAA AATTCCTTTG TGTTCCTATT GACTTCAATG ATAGTAAGAA 4860
 AAGTGGTTGT TAGTTATAGA TGTCTAGGTA CTTCAGGGGC ACTTCATTGA GAGTTTGTG 4920
 AATGCTCTTT GAATATTCCC AAGCCCATGA GTCCCTGAAA ATATTTTTAT TATATACAGT 4980
 AACTTTATGT GTAAATACAT AAGCGCGTA AGTTTAAAGG ATGTTGGTGT TCCAGTGT 5040
 TTATCTCTGT ATGTTGTCCA ATTGTGACA GTTCTGAAGA ATTC

Seq ID NO: B74 protein sequence
Protein Accession #: NP_000213.1

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5 1      11      21      31      41      51
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MRGARGAMDF LCVLLLLLRV QTGSSQPSVS PGEPSPPSIH PGKSDLIVRV GDEIRLLCTD 60
PGFVKWTFBI LDETNNKQN EWITEKAEAT NTGKYTCNKH HGLSNSIYVF VRDPKRLPLV 120
DRSLYGEKEDN DTLVRCPLTD PEVTNYSLEK CQKPLPKDL RFIPDPKAGI MIKSVKRAYH 180
RLCLHCSVDQ EGKSVLSEKF ILKVRPAPKA VPVSVSKAS YLLREGEBFT VTCTIKDVSS 240
10 SVYSTNKRKN SQTQLQEKYN SWHHGDFNYE RQATLTISSA RVNDSGVFMC YANNTPGSAN 300
VTTTLEVVDK GFNIFPMIN TTVFVNDGEN VDLIVEYEF PKPEHQWYI MNRTFTDKWE 360
DYFKSENEEN IRYVSELHLT RLKQTEGGTY TFLVNSDVN AAIAPNVYVN TKPEILTIDR 420
LVNGLMQCVA AGFPEPTIDM YPCPGTEQRK SASVLPVDVQ TLNSSGPPFG KLVVQSSIDS 480
SAFKHNGTVE CKAYNDVGKT SAYFNPAFKG NNKEQIHPT LFTPLLIGFV IVAGMCIIV 540
15 MILTYKYLQK PMYEVQWKV EERINGNYVY IDPTQLPYDH KWEFFPNRLS PGKTLGAGAP 600
GKVVETATYG LIKSDAAMTV AVKMLKPSAH LTEREALMSE LKVLSTYLNH MNIVNLLGAC 660
TIGGPTLVIT EYCCYGDLLN FLRRKRDSFI CSKQEDHAEA ALYKLLHSHK ESSCSDSTNE 720
YMDMKRGSVY VVPTKADKRR SVRIGSYIER DVTPAIMEDD ELALDLEDLL SFSYQVAKGM 780
APLASKNCIH RDLAARNILL THGRITKICD POLARDIKND SNYVVKGNAR LPVKKMAPES 840
20 IFNCVYTFES DVMSYGIPLW BLFSLGSSPY PGMFVDSKFI KMIKEGFRML SPEHAPAEY 900
DIMKTCWDAD PLKRPPTFKQI VQLIEKQISE STNHIYSNLA NCSFNRQKPV VDHSVRINSV 960
GSTASSSQPL LVHDDV

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Seq ID NO: B75 DNA sequence
Nucleic Acid Accession #: NM_004456
Coding sequence: 58..2298

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30 1      11      21      31      41      51
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GGCCAGACTG GGAAGAAATC TGAGAAGGGA CCAGTTTGTG GCGCGAAGCG TGTAAATATCA 120
GAGTACATCG GACTGAGACA GCTCAAGAGG TTCAGACGAG CTGATGAAGT AAAGAGTATG 180
TTTAGTTCCA ATCGTCAGAA AATTTTGGAA AGAACGGAAA TCTTAAACCA AGAATGGAAA 240
CAGCGAAGGA TACAGCCTGT GCACATCCTG ACTTCTGTGA GCTCATTGCG CGGGACTAGG 300
35 GAGTGTTCGG TGACCACTGA CTTGGATTTT CCAACACAAG TCATCCCATG AAAGACTCTG 360
AATGCAGTTG CTTAGTACC CATAATGTAT TCTTGTCTC CCCTACAGCA GAATTTTATG 420
GTGGAAGATG AAACGTGTTT ACATAACATT CCTTATATGG GAGATGAAGT TTAGATCAGC 480
GATGGTACTT TCATTGAAGA ACTAATAAAA AATTATGATG GGAAAGTACA CGGGGATAGA 540
GAATGTGGGT TTATAAATGA TGAAATTTTT GTGGAGTTGG TGAATGCCCT TGGTCAATAT 600
40 AATGATGATG ACGATGATGA TGATGGAGAC GATCCTGAAG AAAGAGAAGA AAAGCAGAAA 660
GATCTGGAGG ATCACCAGGA TGATAAAGAA AGCCGCCAC CTOGGAATTT TCCTTCTGAT 720
AAAATTTTGG AGGCCATTTC CTCAATGTTT CCAGATAAGG GCACAGCAGA AGAACTAAGG 780
GAAAATATAA AAGAACTCAC CGAACAGCAG CTCCAGGCG CACTTCTCC TGAATGTACC 840
CCCAACATAT ATGGACCAAA TGCTAAATCT GTTCAGAGAG AGCAAGGCTT ACACCTCCTT 900
45 CATAAGCTTT TCTGTAGGCG ATGTTTAAA TATGACTGCT TCCTACATCC TTTTCATGCA 960
ACACCCAAAC CTTATAAGCG GAAGAACACA GAAACAGCTC TAGACAACAA ACCTTGTGGA 1020
CCACAGTGTG ACCAGCATTT GGAGGGAGCA AAGGAGTTTG CTGCTGCTCT CACCGCTGAG 1080
CGGATAAAGA CCCCAACAAA ACGTCCAGGA GCGCGCAGAA GAGGACGGCT TCCCAATAAC 1140
AGTAGCAGCG CCAGCACCCC CACCATTAAT GTGCTGGAAT CAAAGGATAC AGACAGTGAT 1200
50 AGGGAAGCAG GGAGTGAAC GGGGGGAGAG AACAAATGATA AAGAAGAAGA AGAGAAGAAA 1260
GATGAACCTT CGAGCTCCTC TGAAGCAAT TCTCGGTGTC AAACACCAAT AAAGATGAAG 1320
CCAAATATGG AACCTCCTGA GAATGTGGAG TGGAGTGGTG CTGAAGCCTC AATGTTTGA 1380
GTCTCATTTG GCACTTACTA TGACAATTTT TGTGCCATTG CTAGGTTAAT TGGGACCAAA 1440
ACATGTAGAG AGGTGTATGA GTTTAGAGTC AAAGAATCTA GCATCATAGC TCCAGTCTCC 1500
55 GCTGAGGATG TGGATATCTC TCCAAGGAAA AAGAAGAGGA AACACCGGTT GTGGGCTGCA 1560
CACTGCAGAA AGATACAGCT GAAAAAGGAC GGCTCCTCTA ACCATGTGTA CAATATCAA 1620
CCCTGTGATC ATCCACGGCA GCCTTGTGAC AGTTCGTGCC CTGTGTGAT AGCACAAAAT 1680
TTTTGTGAAA AGTTTGTGCA ATGTAGTTCA GAGTGTCAAA ACCGCTTTCC GGGATGCGC 1740
TGCAAGACAC AGTGCAACAC CAAGCAGTGC CGTGCTTACC TGGCTGTCCG AGAGTGTGAC 1800
60 CCTGACCTCT GTCTTACTTG TGGAGCGGCT GACCATGGG ACAGTAAAAA TGTGTCTGCG 1860
AAGAACTGCA GTATTTCAGG GGGCTCCAAA AAGCATCTAT TGCTGGCACC ATCTGACGTG 1920
GCAAGCTGGG GGAATTTTAT CAAAGATCCT GTGCAGAAAA ATGAATTCAT CTCAGAATAC 1980
TGTGGAGAGA TTATTTCTCA AGATGAAGCT GACAGAAGAG GGAAAGTATA TGATAAATAC 2040
ATGTGCAGCT TTCTGTTCAA CTGGAACAAT GATTTTGTGG TGGATGCAAC CCGCAAGGGT 2100
65 AACAAAATTC GTTTTGCAAA TCATTGCGTA AATOCRAACT GCTATGCAAA AGTTATGATG 2160
GTTAAGCGTG ATCAGAGAT AGGTATTTT GCCAAGAGAG CCATCCAGAC TGGCGAAGAG 2220
CTGTTTGTGG ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTGCG CATCGAAGAG 2280
GAAATGGAAA TCCCTTGACA TCTGCTACCT CTTCCCTCTC CTCTGAAACA GCTGCTTAG 2340
CTTCAGAAAC CTCGAGTACT GTGGGCAATT TAGAAAAAGA ACATGCAGTT TGAATTTCTG 2400
70 AATTTGCAAA GTACTGTAAG AATAATTAT AGTAATGAGT TTAATAATCA ACTTTTATT 2460
GCCTTCTCAC CAGCTGCAAA GTGTTTGTGA CCAAGTAATT TTTGCAATAA TGCAATATG 2520
TACATTTTTC AACTTTGAAT AAAGAATACT TGAAGTTGAA AAAAAAAA AAAAAA

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Seq ID NO: B76 Protein sequence
Protein Accession #: NP_004447

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80 1      11      21      31      41      51
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MQQTGKKSEK GFVCRKRVK SEYMRLRQLK RFRRADEVKS MFSSNRQKIL ERTEILNQEW 60
KQRRIQVVEI LTVSVSLRGT RECSVTSLDL PPTQVIPLKT LNAVASVPIM YSNVPLQONF 120
MVEDETVLEN IPYMGDEVLQ QDGTFIIEELI KNYDGKVEHD RECGFINDEI FVELVNALGQ 180
YNDDDDDDDG DDPBEREEKQ KDLEDRDDK ESRPFRKFPK DKILEAIGSM FPDKGTASEL 240
KRYKELTEQ QLPGLALPPEC TPNIDGPNK SVQREQSLHS FHTLPCRRCF KYDCFLHPPH 300
ATPNTYIKRN TETALDNKPC GPQCYQHLEG AKEFAAALTA ERIKTPPKRP GGRBRGLFVN 360

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NSSRPSTPTI NVLESKOTDS DREAGTETGG ENNDKEEBEK KDETSSSSEA NSRCQTPIMK 420
 KPNIPEPPV EWSGAESMF RVLIQTYDIN FCAIARLIGT KTCRQVVEFR VKESSIIAPA 480
 PAEDVDTPPR KKKRKHRLWA AHCRIQLKK DGSSNHVYNY QPCDHPQPC DSSCPVIAQ 540
 NFCEKFCQCS SECQNRFPQC RCKAQCNTRK CPCYLAVREC DPDLCLTGA ADHWDSKNVS 600
 CKNCISQKRS KKHLLAPSD VAGWGFIDK PVQNEFISE YCGEIIISQDE ADRRGKVYDK 660
 YMCSPFLNINL NDFVVDATRK GNKIRFANHS VNPNCYAKVM MVNGDHRIGI FAKRAIQTGE 720
 ELFVDYRYSQ ADALKVVGIE REMEIP

Seq ID NO: B77 DNA sequence
 Nucleic Acid Accession #: NM_007015
 Coding sequence: 1..1005

1 11 21 31 41 51
 15 | | | | |
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 TGCAGCCCC CGGCGTACGC TACGCTGACG GTGAAGCCCT CCAGCCCCGC GCGGCTGCTC 120
 AAGGTGGGAG CCGTGGTCTT CATTTCCGGA GCTGTGCTGC TGCTCTTTGG GGCATCGGG 180
 GCCTTCTACT TCTGGAAGGG GAGCGACAGT CACATTACA ATGTCCATTA CACCATGAGT 240
 ATCAATGGGA AACTACAAGA TGGGTCAATG GAAATAGACG CTGGGAACAA CTTGGAGACC 300
 TTTAAATGG GAAGTGGAGC TGAAGAAGCA ATTGCAGTTA ATGATTTCCT GAATGGCATC 360
 ACAGGAATTC GTTTTGCTGG AGGAGAGAAG TGCTACATTA AAGCGCAAGT GAAGGCTCGT 420
 ATTCTGAGG TGGGCGCGCT GACCAACAG AGCATCTCCT CCAACTCGGA AGGCAAGATC 480
 ATGCCAGTCA AATATGAAGA AAATTCTCTT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG 540
 GACACAGCT TCTTGAGTTC TAAGGTGTTA GAACCTCTCG GTGACCTTCC TATTTTCTGG 600
 25 CTTAAACCAA CCTATCCAAA AGAAATCCAG AGGGAAGAA GAGAAGTGGT AAGAAAAATT 660
 GTTCCAACTA CCACAAAAG ACCACACAGT GGACCACGGA GCAACCCAGG CGCTGGAAGA 720
 CTGAATAATG AAACAGAGCC CAGTGTTCCT GAGGACTCAC AAGCCTTCAA TCCTGATAAT 780
 CCTATCATC AGCAGGAAGG GGAAAGCATG ACATTGACG CTAGACTGGA TCACGAAGGA 840
 ATCTGTGTGA TAGAATGTAG GCGGAGCTAC ACCCACTGCG AGAAGATCTG TGAACCCCTG 900
 30 GGGGGCTAAT ACCCATGGCC TTATAATTAT CAAGGCTGCC GTTCGGCCTG CAGAGTCATC 960
 ATGCCATGTA GCTGTGGGGT GGCCCGTATC TTGGGCATGG TGTGAAATCA CTTTATATAT 1020
 CACGTGCTGT AAAATAAGAA CTAGCTGAAG AGACAACCAA AGAAGCATTA AGGCAGGTTG 1080
 ATGCTGATGG GACCATAAAA TATTTTACA CGCAGCTGA GCGGTATTTC TTGACACTCT 1140
 TAACAGATT TTTTAAATCG TTTTCCAGAA CTTTAGTATA TGCAATGCA CTGAAAGGGT 1200
 35 AGTTCAAGTC TAAATGCCA TAACCCGTT ATTGTATT TTTTATTTC ATTGATTTC 1260
 CATAGTCTT CCCTTGCTTG CATCTTCCA AGCTATTTC AAATAACAC GAAAAATTAC 1320
 AGTTTGCC

Seq ID NO: B78 Protein sequence
 Protein Accession #: NP_008946

1 11 21 31 41 51
 45 | | | | |
 MTENSQKVPD ALVGPDDVEF CSPPAYATLT VKPSSPARLL KVGAVVLISG AVLLLFGAIG 60
 AFYFWKGSIS HIYNVHYTMS INKQLQDGM EIDAGNNLET FRMGSGABEA IAVNDFQNGI 120
 TGRFAGGDEK CYIKAQVKAR IPEVGAATKQ SISKLEGI MPVKYEENSL IWVAVDQPVK 180
 DNSFLSKVL ELCCDLPIFW LKPTYKPIQ RERREVVRI VPTTTKRPHS GPRSNPAGR 240
 LNNETRPSVQ EDSQAFNPDN PYHQBGESM TFDRLDHEG ICCIECRRSY THCQKICEPL 300
 GGYYPWFYNY QGCRSACRVI MPCSWVARI LGMV

Seq ID NO: B79 DNA sequence
 Nucleic Acid Accession #: NM_012449.1
 Coding sequence: 66..1085

55 1 11 21 31 41 51
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 CGGAGACTCA CGGTCAAGCT AAGGCGAAGA GTGGGTGGCT GAAGCCATAC TATTTTATAG 60
 AATTAATGGA AAGCAGAAAA GACATCACAA ACCAAGAGA ACTTTGGAAA ATGAAGCCTA 120
 GGAGAAATTT AGAAGAAGAC GATTATTTC ATAAGGACAC GGGAGAGACC AGCATGCTAA 180
 60 AAAGACCTGT GCTTTTGAT TTGCACCAA CAGCCCATGC TGATGAATTT GACTGCCCTT 240
 CAGAAGTCA GCACACAGG GAACCTTTC CACAGTGGCA CTTGCCAATT AAAATAGCTG 300
 CTATTATAGC ATCTCTGACT TTCTTTTACA CTCTCTGAG GGAAGTAATT CACCCCTTAG 360
 CAACCTCCCA TCAACAATAT TTTTATAAAA TTCAATCCT GGTCTATCAC AAAGCTCTGC 420
 CAATGGTTTC CATCACTCTC TTGGCATTGG TTTAAGTGGC AGGTGTGATA GCAGCAATTG 480
 65 TCCAACCTCA TAATGGAACC AAGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT 540
 TAACAAGAAA GCAGTTTGGG CTCTCTGAGT TCTTTTTTGC TGTAAGTGGC GCAATTTATA 600
 TACGCTCTTA CCAATGAGG CGATCTTACA GATACAGAT GCTAAACTGG GCATATCAAC 660
 AGGTCCAACA AAATAAGAA GATGCTTGA TTGAGCATGA TGTTTGAGA ATGGAGATT 720
 ATGTGTCTCT GGGAAATGTG GGAATGGCAA TACTGGCTCT GTTGGCTGTG ACATCTATT 780
 70 CATCTGTGAG TGACTCTTTG ACATGGAGAG AATTCTACTA TATTCAGAGC AAGCTAGGAA 840
 TTGTTTCCCT TCTACTGGC ACAATACAGC CATTGATTTT TGCTGGAAT AAGTGGATAG 900
 ATATAAACA ATTGTATGG TATACACCTC CAACCTTTAT GATAGCTGTT TTCCTTCCAA 960
 TTGTTGCTCT GATATTTAAA AGCATACTAT TCCTGCCATG CTTGAGGAAG AAGTACTGA 1020
 75 AGATTAGACA TGGTTGGGAA GAGTCAACA AAATTAACAA AACTGAGATA TGTTCACAGT 1080
 TGTAGATTA CTGTTTACAC ACATTTTGT TCAATATTGA TATTTTAT CACCAACATT 1140
 TCAAGTTGT ATTGTATAT AAATGATTA TTCAAGGAAA AAAAAA AAAAA

Seq ID NO: B80 Protein sequence
 Protein Accession #: NP_036581.1

80 1 11 21 31 41 51
 | | | | |
 MESRKDITNQ BELWQKPRR NLEEDDYLRK DTGETSMLKR FVLLHLHQTA HADEFDCPSE 60
 LQHTQELFPQ WLPPIKIAAI IASLTFLYTL LREVIHPLAT SHQQYFYKIP ILVINKVLPM 120

VSITLLALVY LPGVIAIVQ LHNGTKYKFP PHWLDKMLT RKQFGLLSFP FAVLHAIYSL 180
 SYPMRRSYRY KLLNWAYQQV QQNKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS 240
 VSDSLTWREB HYIQSKLGIV SLLGLTIHAL IFAWNKWIDI KQFVWYTPPT FMIAVFLPIV 300
 VLIPKSLIFL PCLRRKILKI RHGWEDVTKI NKTBICSQL

5

Seq ID NO: B81 DNA sequence
 Nucleic Acid Accession #: NM_000684
 Coding sequence: 87..1520

10 1 11 21 31 41 51
 TGCTACCGCG GCCCGGGCTT CTGGGGTGTT CCCCAACCAC GGCCAGGCC TGCCACACCC 60
 CCGCCCCCG GCGTCCGAG CTGGGCATGG GCGCGGGGGT GCTCGTCTTG GCGCCCTCCG 120
 AGCCCGGTAA CCGTCTCTCG GCCGCACCGC TCCCGACCG GCGCGCCACC GCGCGCGGCG 180
 15 TGCTGGTAGC CCGTCTCGCG CCGCCCTCGT TGCTGCTCC CCGCAGCGAA AGCCCGGAGC 240
 CGCTGTCTCA GCAGTGACA GCGGGCATGG GTCTGTGAT GCGCTCATC GTGCTGCTCA 300
 TCGTGGCGGG CAATGTGCTG GTGATCGTGG CCATCGCCAA GACGCGCGG CTGCAGACGC 360
 TCACCAACT CTTCATCATG TCCCTGGCCA GCGCGACCT GGTCTGGGG CTGCTGGTGG 420
 TGCGGTTCGG GCGCACCATC GTGGTGTGGG GCGCTGGGA GTACGGCTCC TTCTTCTGG 480
 20 AGCTGTGGAC CTCACTGGAC GTGCTGTGGG TGACGGCCAG CATCGAGACC CTGTGTGTCA 540
 TTGCCCTGGA CCGCTACCTC GCCATCACT CCGCTTCCG CTACAGAGC CTGCTGAGCG 600
 GCGCGCGGCG CCGGGGCTTC GTGTGACCG TGTGGGCCAT CTGCGCCCTG GTGTCTTCC 660
 TGCCCATCTC CATGCACTGG TGGCGGGCGG AGACGACGA GCGCGCGCG CTGTACAAAG 720
 ACCCCAGTG CTGCGACTTC GTACCAACC GGCCTACGC CATCGCTCG TCGTAGTCT 780
 25 CTTTCTAGT GCCCTGTGC ATCATGGCCT TCGGTACCT GCGGGTGTTC CCGAGAGCCC 840
 AGAAGCAGT GAAGAAGAT GACAGCTCGG AGCGCGTTC CCGCGCGCG CCAGCGCGCG 900
 GCGCTCGCC CTGCGCTCG CCGCTCCCG CCGCGCGCC GCGCGCGGA CCGCGCGCG 960
 CCGCGCGCG CCGCGCGCG CCGCGCTGG CCAACGGCG TCGGGTAAG CCGCGCGCT 1020
 CCGCGCTCGT GCGCCTACGC GACGAGAAG CCGTCAAGAC GCTGGGCATC ATCATGGCG 1080
 30 TCTTCACTG CTGCTGGCTG CCGTCTTCC TGGCAACGT GGTGAAGGCC TTCCACCGCG 1140
 AGCTGGTGCC CAGCGCCTC TTCTCTTCT TCACTGGCT GCGCTACGCC AACTCGGCT 1200
 TCAACCGAT CATCTACTGC CCGAGCCCG ACTTCGCAA GCGCTTCCG GACTGCTCT 1260
 GCTGCGCGCG CAGGGCTGCC CCGCGCGCG CCGGAGCCCA CCGGAGCCCG CCGCGCGCT 1320
 CGGGCTGTCT GCGCGCGCG GCGCGCGCG CATCGCGCG GCGCGCGCT GCGCGCTGCA 1380
 35 ACGACGATG CCGCGCGCG CCGCGCGCG CCGCGCTGCT GCGCGCTGCT GCGCGCTGCA 1440
 ACGCGCGGCG GCGCGCGGAC AGCGACTCGA GCGTGGACGA GCGTGGCGC CCGCGCTTGG 1500
 CCGCGCGGCG CAGGGTGTAG GCGCGCGCG GCGCGCGCG CCGCGCGCG GCGCTTCCAG 1560
 40 GCGAAGCAG AGATCTGTGT TTAATAAGA CCGATAGCAG GTGAATCGA AGCCCAAT 1620
 CCGCTGTGTA ATCATCGAG GCAAGAGAA AAGCCACGA CCGTTCACA AAAAGAAAG 1680
 TTGGGAAGG GATGGGAGAG TGGCTTGTG ATGTCTCTG TTG

Seq ID NO: B82 Protein sequence
 Protein Accession #: NP_000675.1

45 1 11 21 31 41 51
 MGAGVLVLA SEPGNLSSAA PLFDGAATAA RLLVPASPPA SLLPPASESP EPLSQWNTAG 60
 MGLLMALIVL LIVAGNLVI VAIKTPRLQ TLINLPIMSL ASADLVMLGL VVPFGATIVV 120
 50 WGRWEYSFP CELWTSVDVL CVTASIELIC VIALDRYLAI TSPFRYQSL TRARARGLVC 180
 TWALISALVS FLFILMHWR ABSDBARRCY NDFKCCDFVT NRAYAIASSV VSPYVPLCIM 240
 AFVYLVRFRE AQKQVKIKDS CERRFLGGPA RPPSPSPSPV PAPAPPPGPP RPAAAAATAP 300
 LANGRAGRRL PSRLVALREQ KALKTLGIIM GVPTLCWLEP FLANVVKAPH RELVPRDLFV 360
 FFMWLGYSN AFNPYICRS PDKKAFQGL LCCARRAARR RHATHGDRFR ASGLARPGP 420
 55 PPSGGAASDD DDDVVGATP PARLLEPWAG CNGGAADSD SSLDEPCRPG PASESKV

Seq ID NO: B83 DNA sequence
 Nucleic Acid Accession #: NM_000729.2
 Coding sequence: 2..421

60 1 11 21 31 41 51
 GGCTCAGCTG CCGGGCTGCT CCGGTTGGAA ACGCCAAGCC AGCTGCGGTC CTAATCCAAA 60
 AGCCATGAAC AGCGCGGTGT GCGTGTGCGT GCTGATGGCG GTACTGGCGG CTGGCGCCCT 120
 GACGAGCGCG GTGCTCCCG CAGATCCCGC GGGCTCCGGG CTGACGCGG CAGAGGAGGC 180
 65 GCGCGGTAGG CAGCTGAGGG TATCGCAGAG AACGGATGGC GAGTCCCGAG CGCACCTGGG 240
 CCGCTGCTG GCAAGATACA TCCAGCAGGC CCGGAAAGCT CCTTCTGGAC GAATGTCCAT 300
 CGTTAAGAAC CTGCAGAAC TGGACCCAG CCACAGGATA AGTGACCGGG ACTACATGGG 360
 CTGGATGGAT TTTGGCGGTC GCAGTGGCGA GGAGTATGAG TACCCCTCCT AGAGGACCCA 420
 70 GCGCCATCA GCCCAACGGA AGCAACCTCC CAACCCAGAG GAGGCAGAT AAGACAACAA 480
 TCACACTCAT AACTCATTTG CTGTGGAGTT TGACATTGAA TGTATCTATT TATTAAGTTC 540
 TCAATGTGAA AATGTGTCT GTAAGATTGT CCACTGCAAC CACACAGCT CACCAGAAAT 600
 TGTGCAACT GAAGACAAA CTGTTTCTT CATCTGTGAC TCCTGTTCTG AAAATGTGT 660
 TATGCTATTA AAGTGATTTC ATTCTGCC

75 Seq ID NO: B84 Protein sequence
 Protein Accession #: NP_000720.1

80 1 11 21 31 41 51
 MNSGVCLCVL MAVLAAGALT QVPPADPAG SGLQRAEAP RRQLRVGQRT DGESEAHLAG 60
 LLARYIQQR KAPSGRHSIV KNLQNLDPH RISDRYMGW MDPGRRAER YEYPS

TABLE 74 Gene Sequences Up- or Down-Regulated in Cancer

Angiogenesis

5	A1 DNA SEQUENCE	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Gene name:	Hs.154210
	Unigene number:	M31210
	Probeset Accession #:	M31210
10	Nucleic Acid Accession #:	251-1396
	Coding sequence:	
15	TCTAAAGTTC GGGGGCAGCA GCAAGATGCG AAGCGAGCCG TACAGATCCC GGGCTCTCCG 60	
	AACGCACTTT CGCCCTGCTT GAGCGAGGCT GCGGTTTCCG AGGCCCTCTC CAGCCAAGGA 120	
	AAAGCTACAC AAAAAGCCTG GATCACTCAT CGAACCACCC CTGAAGCCAG TGAAGGCTCT 180	
	CTGCGCTCGC CCTCTAGGCT TCGTCTGGAG TAGCGCCACC CCGGCTTCTT GGGGACACAG 240	
	GGTTGGCACC ATGGGGCCCA CCAGGCTCCC GCTGGTCAAG GCCCACCACA GCTCGGTCTC 300	
	TGACTACTTC AACTATGATA TCATGTTCCG GCATTACAAC TACACGGGAA AGCTGAATAT 360	
	CAGCGCGGAC AAGGAGAACA GCATTAAACT GACCTCGGTG GTGTTTCATC TCATCTGCTG 420	
	CTTTATCATC CTGGAGAACA TCTTTGTCTT GCTGACCATT TGGAAAACCA AGAAATTCCA 480	
20	CCGACCCATG TACTATTTTA TTGGCAATCT GGCCCTCTCA GACCTGTGG CAGGAGTAGC 540	
	CTACACAGCT AACCTGCTCT TGCTGGGGCC CACCACCTAC AAGCTCACTC CCGCCCACTG 600	
	GTTCCTGCGG GAAGGGAGTA TGTTTGTGGC CCTGTCAGCC TCCGTGTTCA GTCTCTCGC 660	
	CATCGCATTT GAGCGCTATA TCACATGCTT GAAAATGAAA CTTCCACACG GGAGCAATAA 720	
25	CTTCGCGCTC TTCTGCTTAA TCAGCGCCTG CTGGGTCTAT TCCCTCATCC TGGTGGCCT 780	
	GCCTATCATG GCTCTGGAAT GCATCAGTGC GCTGTCCAGC TGCTCCACCG TGCTCCCGCT 840	
	CTACCAAGC CACTATATCC TCCTCTGCAC CACGCTCTTC ACTCTGCTTC TGCTCTCCAT 900	
	CGTCATTCTG TACTGCAGAA TCTACTCCTT GGTCAAGACT CGGAGCGCCG CCGTGAAGTT 960	
	CCGCAAGAAC ATTTCCAAGG CCAGCCGCGC CTCTGAGAAC GTGGCGCTGC TCAAGACCGT 1020	
	AATTATCGTC CTGAGCGTCT TCATCGCCTG CTGGGCACCG CTCTTCATCC TGCTCTGCT 1080	
30	GGATGTGGGC TGCAAGGTGA AGACCTGTGA CATCTCTTTC AGAGCGGAGT ACTTCTGGT 1140	
	GTTAGCTGTG TCAACTCCCG GCACCAACCC CATCAATTAC ACTCTGACCA ACAAGGAGAT 1200	
	GGGTGCGGCC TTCTATCCGA TCATGTCTCTG CTGCAAGTGC CCGAGCGGAG ACTCTGCTGG 1260	
	CAAAATTCAAG CGACCCATCA TCGCGGCGAT GGAATTGAGC CGCAGCAATC CGGACAATTC 1320	
	CTCCACCCCC CAGAAAGACG AAGGGGACAA CCCAGAGACC ATTATGTCTT CTGGAACGTT 1380	
35	CAACTCTTCT TCTAGAACT GGAAGCTGTC CACCCACCGG AAGCGCTCTT TACTTGGTGG 1440	
	CTGGCCACCC CAGTGTGTTG AAAAAATCT CTGGGCTTCG ACTGCTGCCA GGGAGGAGCT 1500	
	GCTGCAAGCC AGAGGGAGGA AGGGGGAGAA TACGAACAGC CTGGTGGTGT CCGGTGTTGG 1560	
	TGGGTAGAGT TAGTTCCTGT GAACAATGCA CTGGGAAGGG TGGAGATCAG GTCCCGGCT 1620	
40	GGAATATATA TTCTACCCCC CTGGAGCTTT GATTTTGCAC CTATGTCTCC CATGTGAAAG 1740	
	GTCAAGCTCC TAAAGGGTTC ATTTGGCCCC TCCTCAAGA CTAATGTCCC CATGTGAAAG 1800	
	CGTCTCTTTG TCTGGAGCTT TGAGGAGATG TTTTCTTCA CTTTAGTTTC AAACCAAGT 1860	
	GAGTGTGTGC ACTTCTGCTT CTTTAGGGAT GCGCTGTACA TCCACACACC CACCTCCCT 1920	
	TCCCTTCTCA CCGCTCTCTA ACGTCTCTTT ACTTTTACT TTAACCTACT GAGAGTTATC 1980	
45	AGAGCTGGGG TTGTGGAATG ATCGATCATC TATAGCAAT AGGCTATGTT GAGTACGTAG 2040	
	GCTGTGGGAA GATGAAGATG GTTTGGAGGT GTAAAAACAT GTCCTTGGCT GAGGCCAAAG 2100	
	TTTCCATGTA AGCGGATGCC GTTTTGTGGA ATTTGGTTGA AGTCACTTTG ATTTCTTTAA 2160	
	AAAACATCTT TTCAATGAAA TGTGTTACCA TTTCAATACC ATTGAAGCCG AAATCTGCAT 2220	
	AAGGAAGCCC ACTTTATCTA AATGATATTA GCCAGGATCC TTGGTGTCTT AGGAGAAACA 2280	
50	GACAGCAAAA ACAAAGTGAA AACCGAATGG ATTAACTTTT GCAAAACCAAG GGAGATTTC 2340	
	TAGCAATGTA GTCTAACAAA TATGACATCC GTCTTTCCCA CTTTGTGTTA TGTTTATTC 2400	
	AGAATCTTGT GTGATTCAAT TCAAGCAACA ACATGTTGTA TTTTGTGTTG TTAAGATAC 2460	
	TTTTCTTGAT TTTTGAATGT ATTTGTTTCA GGAAGAAGTC ATTTTATGGA TTTTCTAAC 2520	
	CCGTGTTAAC TTTTCTAGAA TCCACCTCTT TGTGCCCTTA AGCATTACTT TAACGTGATG 2580	
55	GGAAAGCCAG AACTTTTAAAG TCCAGCTATT CATTAGATAG TAATTGAAGA TATGTATAAA 2640	
	TATTACAAAG AATAAAAAATA TATTACTGTC TCTTTAGTAT GGTTTTCAGT GCAATTAAAC 2700	
	CGAGAGATGT CTGTGTTTTT TAAAAAGAA AGTATTTAAT AGGTTTCTGA CTTTGTGGA 2760	
	TCATTTTGCA CATAGCTTTA TCACTTTTAA AACATTAATA AACTGATTTT TTTAAAG	
60	A2 Protein sequence:	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Gene name:	Hs.154210
	Unigene number:	M31210
	Probeset Accession #:	AAA52336
65	Protein Accession #:	none found
	Signal sequence:	50-71, 92-110, 122-140, 160-177, 202-222, 251-269, 283-301
	Transmembrane domains:	plasma membrane
	Cellular Localization:	
70	1 11 21 31 41 51	
	MGPTSVPLVK AHRSSVSDYV NYDIIVRHYN YTGKLNISAD KENSILTSV VFILICCFII 60	
	LENIPVLLTI WTKKPKHRPM YYFIGNLALS DLLAGVAYTA NLLLSGATTY KLTFAQWFLR 120	
	EGSMFVALSA SVFSLIAIAI ERYITMLKMK LEHNSNNFRL PLLISACWVI SLILGGLPIM 180	
75	GWNCISALSS CSTVLPLYHK HYILFCTTVF TLLLSIVIL YCRIYSLVRT RSRRLTFRKN 240	
	ISKASRSSEN VALLKTVIIV LSVFIACNAP LFILLLLDVG CKVKTCDLIF RAEYFLVLAV 300	
	LNSGTNPFIY TLTNKEMRRA FIRIMSCCKC PSGDSAGKFK RPIIAGMEFS RSKSDNSHP 360	
	QKDEGDNPET IMSSGNVNSS S	
80	A3 DNA SEQUENCE	G protein-coupled receptor 51
	Gene name:	Hs.198612
	Unigene number:	AA452928
	Probeset Accession #:	NM_004624.1
	Nucleic Acid Accession #:	

	1	11	21	31	41	51	
5	ATGGCTTCCC	CGCGGAGGTC	CGGGCAGCCA	GGGGGGGCGC	GGCGCGCGCC	ACCGCGCGCC	60
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	GCGCTGGGCG	CGGGCGCGCC	CGCGCGCGCG	CCCGCAGCGC	CGCGCGCTCT	CATCATGGGC	180
	CTCATGTCCG	TCACCAAGGA	GGTGGCCAA	GGGAGCATGT	GGCGCGGTGT	GCTCCCCGCG	240
10	GTGGAACTGG	CCATCGAGCA	GATCGCGCA	GAGTCACTCC	TGCGCCCCAT	CTTCTCGTAC	300
	CTGCGGCTCT	ATGACACGGA	GTGCGACAG	CCAAAGGGGT	GGAAAGCCCT	TCAGATGTGA	360
	ATAAATATCG	GGCGGAACCA	CTTGATGGTG	TTTGGAGGCG	TCGTGTCCAT	CGTCAATCC	420
	ATCATTTCTG	AGTCCCTCCA	AGGCTGGAAT	CTGTGTGAGC	TTTCTTTTGC	TGCAACCACG	480
	CGTGTCTTAG	CGGATAAGAA	AAAATCAACT	TATTTCTTCT	GGACCGCTCC	ATCAGACAAT	540
15	GCGGTGAATC	CAGCCATTCT	GAGTTTGCTC	AGACACTACC	AGTGGGAAGC	CGTGGGCAGC	600
	CTGACGCGAG	ACGTTTCAGAG	GTGCTCTGAG	GTGCGGAATG	ACCTCAGTCG	AGTTCTGTAT	660
	GGCGAGGACA	TTGAGATTTC	AGATCCAGAG	AGCTTCTCCA	ACGATCCCTG	TACCAGTGTC	720
	AAAAAGCTGA	AGGGGAATGA	TTGTGGGATG	ATCTTTGGCC	AGTTTGACCA	GAATATGGCA	780
	CCAAAGATGT	TCGTGTATGC	ATACGAGAGT	ACACATGTAT	TAGTAGTAAT	TCAGTGATC	840
20	ATTCCGGGCT	GGTACGAGCC	TTCTTGGTGG	GAGCAGGTGC	ACACGGGAAG	CAACTCATCC	900
	CGCTGCTCTC	GGAGAATCTT	CTGTGCTGCC	ATGGAGGGCT	ACATTGTGGT	GGATTTGAGT	960
	CCCGCTGAGT	CCAGACGAGT	CAGACAGATC	TCAGGAAGA	CTCCACAGCA	GTATGAGAGA	1020
	GAGTACAACA	ACAAGCGGTC	AGGCGTGGGG	CCCGACCAAT	TCACCGGTGA	CGCTCATGAT	1080
	GGCATCTGGG	TCATCGCCAA	GACACGTGAG	AGGGCCATGG	AGACACTGCA	TGCCAGCAGC	1140
25	CGGCACCTGG	GGATCCAGGA	CTTCAACTAC	ACGGACCACA	CGCTGGGCAG	GATCATCTCT	1200
	CGGCACCTGG	GGATCCAGGA	CTTCAACTAC	ACGGACCACA	CGCTGGGCAG	GATCATCTCT	1260
	AAGTGCATGA	ACGAGACCCA	CTTCTTCGGG	GTACCGGGTC	GAAGTTGTAT	CGGAATGGG	1320
	GATGCAATGG	GGACATTATA	ATTACTCTAA	TTTCAAGACA	CGAGGAGGCT	GRAAGTGGGA	1380
	GAGTACAACG	CTGTGGCCGA	CACACTGGAG	ATCATCAATG	ACACCATCAG	GTTCCAAGGA	1440
30	TCGGAACACC	CAAAAGTACA	GACCATCATC	CTCGGGATGA	TCATGGCCAG	TGCTTTTCTC	1500
	CTCTACAGCA	TGCTTCTGCG	CCTCACCATC	CTCATAAAGA	TGTGAGTGAT	ATACATGAAC	1560
	TTCTTCAACA	TCAAGAAACG	GAATCAGAAG	TATCTATCCA	TATTTCTCTT	TGCGCTTGAT	1620
	AATCTATATC	TCCTTGGAGG	GATGCTCTCC	GTGCTTCCA	CGGTGAGGAC	CTGGATTCTC	1680
	GGATCCTTTG	TCTCTGAAAA	GACCTTTGAA	ACACTTTGCA	AGACTGGAAG	AGTCAAGCCG	1740
35	ACCGTGGGCT	ACAGCAGCCG	TTTTGGGGCC	ATGTTTGGCA	ACCAGAAACT	GCTTGTGATC	1800
	ATCTTCAAAA	TGTGTAAAT	GAGAAGAATG	ATCATCAAGG	ACCAGAAACT	GCTTGTGATC	1860
	GTGGGGGGGA	TGCTGTGAT	CGACTGTGTG	ATCTGGAAT	GCTGGCAGGC	TGTGGACCCC	1920
	CTGCGAAGGA	CAGTGGAGAG	TGCAGACATG	CGCGCGAACC	CAGCAGGACG	GGATATCTCC	1980
	ATCGGCCCCC	TCCTGGAGCA	CTGTGAGAAC	ACCCATATGA	CCATCTGGCT	TGGCATGCTC	2040
40	TATGCTCTACA	AGGGACTTCT	CATGTTGTTC	GGTGTGTTCT	TAGCTTGGGA	GAACCGCAAC	2100
	GTGAGCATCC	CGCGACTCAA	CGACAGCAAG	TACATCGGGA	TGAGTGTCTA	CAACGTGGGG	2160
	ATCATGTGCA	TCATCGGGGG	CGCTGTCTCC	TTCTGACCC	GGGACACGCG	CAATGTGAGC	2220
	TTCTGCTATG	TGGCTCTGGT	CATCATCTTC	TGCAGACCA	TCACCTCTTG	TCAGTTATTC	2280
	GTGCGGAGGC	TCATCACCC	GAGAACAAAC	CCAGATGCAG	CAACGAGGAA	CAGCGATGTC	2340
45	CAGTTTCACT	AGAAATCAAA	GAAGAAGAT	TTCAAAGGCT	CCACCTCGGT	CACCATGATC	2400
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	AAGATCACAG	AGCTGGATAA	AGACTTGGAA	GAGGTGACCA	TGCAGCTGCA	GGACACACCA	2520
	GAAGAAGCCA	CCTACATTAA	ACAGAACCAC	TACCAGAGC	TCAATGACAT	CTCAACCTG	2580
	GGAAACTTCA	CTGAGAGCAC	TACGAGAGGA	AGAGGCCATT	TAAAAATCA	CCTCGATCAA	2640
	AATCCCGAGC	TACAGTGGAA	CACACACAG	CCCTCTGGAA	CTCGACAGAA	TCCTATAGAA	2700
50	GATATAAACT	CTCCAGAAAC	CATCAGCGT				

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70	IKYGNHLMV	FGGVCPSVTS	IIAESLQQWN	LVQLSFAATL	PVLADKKKYP	YPPFTVPDSN	180
	AVNPAILGKL	KHYQWKRQV	LTDQDPAFSE	VRNLDLTGLV	GEDIIEISDT	SFSNDPCTSV	240
	KIKLKGNDVRI	ILGQFDQDMA	AKVFCFAYEE	NMYSKYSQMI	IPGWYEPSW	EQVTEANSS	300
	CLRLKNLLAA	MEGVIYDVDS	PLSSQKIKTI	SGKTPQOYER	EYNNKNSGVG	PSKFGVYAD	360
	GIWVIAKTLQ	RAMETLHAFB	RHQRIQDFPN	TDHLGRIIL	NAMNETNFFG	TVPGQVFRNG	420
75	ERMGTIKETQ	QSDPREKVRG	EYNVAWDTLE	IINDTIRFQG	SEPPKDKITII	LEQLRKISLP	480
	LYSILSALTI	LQMIHASAFL	PNFNTKRNKQ	LIKNSQSPMY	NIILGLGMSL	YASIFLPGLD	540
	GSFVSEKTFE	TLCTVRTWIL	TVGYTIFARG	MPAKICWAFH	IKTQWQKKK	IKTKQKLVI	600
	VGGMLIDLIC	LILICQAVDP	LRRTVEKYSM	SPDGAGBDIS	IRPLEHCEN	THMTIWLGI	660
	YAYTKGLML	GCFLVAETRN	VSIIPALNDS	EYIGMSVYNG	IMCIIGAAVS	FLTRDQPNVQ	720
80	FCIVALVIIIF	CSTITLCLVF	VPKLTITLRN	PDAAATQNRK	QFTQNKQKED	SCTSTSVTSV	780
	NQASTSRLEG	LQSENERLRM	KITELDKOLE	EVNTGLQDTP	EKTTYIKQNH	YQELMDILNL	840
	GNFTSRSDGG	KAILKNHLDL	NQLOQWNTTE	PSRTCKDPIE	DINSPEHIQR	RLSLQLPLIL	900
	WAVLPRIGDG	DASCVCPCVS	PTASPRHRHV	PSPTFRVMVSG	L		

A5 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Nucleic Acid Accession #: none found
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

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    GTGTGACGGG CTGCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
    GTCGAAATGT GCGCCAACTT TCTTCCCTTG TGCCAGCGGC ATCCATTGCA TCATTGGTCG 300
    CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
    AAACCTCTG CTTTGCTCCA CCGCCCGCTA CCACTGCAAG AACGSCCTCT GTATTGACAA 420
    GAGCTTCATC TCGATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
    AAGTTCTCAA GAACCCGCGA GTGGGCGAGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540
    TTACCCAGC ATCAGCTATG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600
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    CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGAGCA 780
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    GGGCACTGCT GAGCCAGGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080
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    TGCTCATGGG AAGCTCTTTA AGCAGCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200
    AACTATCTCT GCATTCCCTT CCTCCCCAG ACTTCAGAGA TGTTTTTCTG GCGTCTCAGT 1260
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    GAGCCCTTCC CATGATGTTA TCCAAGTTCT CAGCTCTCAA AATGCAGGCT GCCAAGACCC 1860
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    GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G
  
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A6 Protein sequence:

Gene name: ESTs

Unigene number: Hs.293616
 Probeset Accession #: AN043782
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

10 1 11 21 31 41 51
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 KNGLCIDKSF ICDGQNNQCD NSDEESCRSS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180
 15 VIPVLVVALL ALVLHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVANGIQ 240
 YVASQAQNA SEVGSPPSYS BALDQRPAN YDLPPPPYSS DTESLNQADL PPYRSRSGSA 300
 NSASSQAASS LLSVEDTSHS PQQPGPQEGT AEPDSEPSQ GTEEV

20 A7 DNA SEQUENCE
 Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
 Unigene number: Hs.149609
 Probeset Accession #: X06256
 Nucleic Acid Accession #: NM_002205
 25 Coding sequence: 1-3150 (underlined sequences correspond to start and stop codons)

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A8 Protein sequence:

5 Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
 Unigene number: Hs.149609
 Probeset Accession #: X06256
 Protein Accession #: NP_002196
 Signal sequence: 1-42
 Transmembrane domains: 998-1020
 10 Integrin alpha domains: 56-115, 268-318, 322-384, 388-444, 452-503, 1022-1036
 Cellular Localization: plasma membrane

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 20 DNFRTRILEYA PCRSDFSWAA GQGYCQGGPS AEFTKTRGVV LGPGSYFWQ GQILSATQEQ 240
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 35 YKLGPFRKSL PYGTAMEKAQ LKPPATSDA

A9 DNA SEQUENCE

40 Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)
 Unigene number: Hs.287797
 Probeset Accession #: X07979
 Nucleic Acid Accession #: NM_002211.1
 Coding sequence: 1-2397 (underlined sequences correspond to start and stop codons)

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 65 TTTGAGCTG TTTACAGGA GCTGAAAAC TTGATCCCTA AGTCAGCAGT AGGAACATTA 1080
 TCTGCAAAAT CTAGCAATGT AATTCACTTG ATCATTGATG CATACAATTC CTTTCTCTCA 1140
 GAAGTCAATT TGGAAAACCG CAAATTGTCA GAAGGAGTAA CAATAAGTTA CAAATCTTAC 1200
 TGCAAGAACG GGGTGAATGG AACAGGGGAA AATGGAAGAA AATGTTCCAA TATTTCATT 1260
 GGAGATGAGG TTCAATTGGA AATTAGCATA ACTTCAATA AGTGTCCAA AAAGGATTCT 1320
 70 GACAGCTTTA AAATTAGGCC TCTGGGCTTT ACGGAGGAAG TAGAGGTTAT TCCTCAGTAC 1380
 ATCTGTAAT GTGAATGCCA AAGCGAAGGC ATCCCTGAAA GTCCCAAGTG TCATGAGGA 1440
 AATGGGACAT TTGAGTGTGG CGGTGTCAGG TGCAATGAAG GCGCTGTGG TAGACATTGT 1500
 GAATGCAGCA CAGATGAAGT TAACAGTGAA GACATGGATG CTTACTGCG GAAAGAAAAC 1560
 AGTTCAGAAA TCTGCAGTAA CAATGGAGAG TGGCTCTGCG GACAGTGTGT TTGTAGGAAG 1620
 75 AGGGATAATA CAAATGAAT TTAATCTGCG AAATCTGCG AGTGTGATAA TTTCACTGT 1680
 GATAGCTAAT TTGCTGAGGA AATGCTGTTT GCAAGTGTG TGTGTGTGAG 1740
 TGCACCCCA ACTACACTGG CAGTGATGT GACTGTCTT TGGATACAG TACTTGTGAA 1800
 GCCAGCAACG GACAGATCTG CAATGGCCGG GGCATCTGCG AGTGTGTGT CTTGTAAGTGT 1860
 ACAGATCGGA AGTTTCAAGG GCAAACGTGT GAGATGTGTC AGACCTGCCT TGGTGTCTGT 1920
 80 GCTGAGCATA AAGAATGTGT TCAGTGCAGA GCCTTCAATA AAGGAGAAAA GAAAGACACA 1980
 TGCACACAGG AATGTTCTTA TTTAAACATT ACCAAGGTAG AAAGTCGGGA CAAATTACCC 2040
 CAGCCGCTCC AACCTGATCC TGTGTCCCAT TGTAAAGGAGA AGGATGTTGA CGACTGTG 2100
 TTCTATTTTA GTATTCACT GAATGGGAAC AACGAGGTCA TGGTTCATGT TGTGGAGAAT 2160
 CCAGAGTGTC CCATGCTGCC AGACATCATT CCAATTGTAG CTGGTGTGTT TGCTGGAATT 2220

GTTCCTATTG GCCTTGCAAT ACTGCTGATA TGGAACTTT TAATGATAAT TCATGACAGA 2280
 AGGGAGTTTG CTAAATTGTA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAAAAAT 2340
 CCTATTATATA AGAGTGCCGT AACAACTGTG GTCAATCGA AGTATGAGGG AAAATGA

A10 Protein sequence:

Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)
 Unigene number: Hs.287797
 Probeset Accession #: X07979
 Protein Accession #: NP_002202.1
 Signal sequence: 1-21
 Transmembrane domains: 732-754
 INB domain: 34-464
 PSI domain: 26-76
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
20  MNLQPIFWIG LISSVCCVFA QTDENRCLKA NAKSCGECIQ AGPNCGWCTN STFLQEGMPT 60
    SARCDLLEAL KKKGCPDDI ENPRGSKDIK KNKNVTNRSK GTAEKLPED ITQIQPQLV 120
    LRLRSGEPQT FTLKFKRAED YPIDLYLMD LSYSMKDDLE NVKSLGTDLM NEMRRITSDF 180
    RIGFGSFVEK TVMPYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLTNKG VFNELVGKQR 240
    ISGNLDSPEG GFDAIMQVAV CGSLIGWRNV TRLLVPSTDA GPHFAGDGKL GGIVLPNDGQ 300
25  CHLENNMYTM SHYYDPSIA HLVOKLSENN IQTIFAVTEE FQPVYKELKN LIPKSAVGTI 360
    SANSNNVIQL IIDAVNSLSS EVILENGLS EGVTSYKSY CKNGVNGTGE NGRKCSNISI 420
    GDEVQFEISI TSNKCPKKDS DSPKIRPLGF TEEVEVILQY ICEBCQSEB IPESPKCHEG 480
    NGTFEGQACR CNEGRVGRHC ECSTDENVSE DMDAYCRKEN SSEICSNNGE CVCQQCVRK 540
    RDMTNEIYSG KPECECNFNC DRNGLICGG NGVCKCRVCE CNPNYTGSA CDSLDTSTCE 600
30  ASHGQICNGR GICECGCKCK TDPKFGQGTG EMQQTCLGVC AEHKECVQCR AFNKGKKDT 660
    CTQECSYFNI TKVESRDKLP QFVQDPVSH CKEKDVDWC FYFTYSVNGN NEVMVHVVEN 720
    PECPTGPDII PIVAGVVAGI VLIGLALLLI WKLLMIHDR REFAKFEKEK MNAKNDTGEN 780
    PIYKSAVTTV VNPKYEGK
  
```

A11 DNA SEQUENCE

Gene name: selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Nucleic Acid Accession #: NM_000450
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
45  ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAA AGAGAGTGGA 60
    GCTTGTCTTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
    CAGCAAGGT ACACACACCT GGTTCGAATT CAACAACAAG AAGAGATTGA GTACCTAAAC 180
    TCCATATTGA GCTATTACCC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG 240
    TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAAGAG CCAAGAACTG GGCTCCAGGT 300
50  GAACCCAAAC ATAGGCAAAA AGATGAGGAC TGCCTGGAGA TCTACATCAA GAGAGAAAAA 360
    GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGTACACA 420
    GCTGCTGTA CCAATACATC CTGCACTGAC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480
    TACACTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAT TGTGAAGTGT 540
    ACAGCCCTCG AATCCCTGTA GCATGGAAGC CTGTTTGCA GTCAACCACT GGGAAACTTC 600
    AGCTACAATT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
55  ACCATGCAGT GTATGTCTCT TGGAGAAATG AGTGCTCTTA TTCCAGCCTG CAATGTGGTT 720
    GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTGGA 780
    AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTTGA ACTAATGGGA 840
    GCCCAGAGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACAGAGGCC AACGTGTAAA 900
    GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960
60  CCTGCTGGAG AGTTCACTTT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020
    TTGCAGGGAC CAGCCAGGT TGAATGCACC ACTCAAGGCC AGTGGACACA GCAATCCCA 1080
    GTTGTGAAG CTTTCCAGTG CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT 1140
    CTTCTAGTG CTTCTGCGAG TTTCCGTTAT GGTCCAGCT GTGAGTTCTC CTGTGAGCAG 1200
    GGTTTTGTGT TGAAGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260
65  GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320
    GTGAGGTGTG CTCATTCGCC TATTGGAGAA TTCACCTACA AGTCCTCTTG TGCTTCAGC 1380
    TGTGAGGAGG GATTTGAATT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440
    TGGACAGAAG AGGTTCCTTC CTGCCAAGTG GTAAAAATGTT CAAGCCTGGC AGTTCCGGGA 1500
    AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGCCA CTGTGTGCAA GTTCGCTGT 1560
70  OCTGAAGGAT GGAAGCTCAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG 1620
    TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680
    CTTCTGCTG CTGACTCTC CTCTCTGACA TTAGCACCAT TTCTCCTCTG GCTTCGGAAA 1740
    TGCTTAOCCA AAGCAAAGAA ATTTGTTCTT GCCAGCAGT GCCAAAGCCT TGAATCAGAC 1800
    GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA
  
```

A12 Protein sequence:

Gene name: Selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Protein Accession #: NP_000441
 Signal sequence: 1-22
 Transmembrane domains: 555-573
 C-lectin domain: 23-139

Cellular Localization: plasma membrane

5 1 11 21 31 41 51
 120 MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRYYHLVAI QNKKEIEYLN 60
 180 SILSYSPSY WIGIRKVN NV WVVGTQKPL TEEAKNWAPG EPNRQKDED CVEIYIKREK 120
 240 DVGMMNDERC SKKALALCYT AACTNTSCSG HGECVETINN YTCKCDPGFS GLKCEQIVNC 180
 300 TALESPHEGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEM SAPIACNVV 240
 360 ECDAVTNPAN GFVECFQNPFG SFPWNTTCTF DCEBGFELMG AQSILQCTSSG NWDNEKPTCK 300
 420 AVTCRAVRQP QNGSVRCSSHS PAGEFTFKSS CNFTCEBGFEM LQGPAAVECT TQGWNTQIIP 360
 480 VCEAFQCTAL SNPERGYMNC LPSASGSFRY GSSCEFSCEQ GFVLKGSKRL QCGPTGENDN 420
 540 EKPTCEAVRC DAVHPPKGL VRCAHSPICE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ 480
 600 WTEEVPSQOV VKCSSLAVPG KINMSSCSGEP VFGTVCKFAC PEGWTIANGSA ARTCGATGHW 540
 660 SGLLPTCEAP TESNIPVLVAG LSAAGLSLLT LAPFLWLRLK CLRKAKKFVP ASSQCSLESD 600
 GSYQKPSYIL

A13 DNA SEQUENCE

20 Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Nucleic Acid Accession #: NM_001508
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
 120 ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60
 180 CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCTTA TTCTGGTGTA CCTGATCATC 120
 240 TTCTGATGAG GCCTTCTGGG GAACAGCGCC ACCATTGCGG TCACCCAGGT GCTGCAGAAG 180
 300 AAAGGATACT TGACAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTGCGACATC 240
 360 TTGGTGTTC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTGACC 300
 420 ACGTCCAGCT ACACCCGTGC CTGCAAGCTG CACACTTTC TCTTCGAGGC CTGCAGCTAC 360
 480 GCTACGCTGC TGACCTGTCT GACACTCAGC TTGAGCGCT ACATCGCCAT CTGTACCCCC 420
 540 TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG 480
 600 GTCACTCCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTG 540
 660 GTGAAGCTGC CCAGCCACCG GGTCTCACT TGCAACCGCT CCAGCACCAG CCACCAACG 600
 720 CAGCCCGAGA CTTCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 660
 780 CAGTCCAGCA TCTTGGCGC CTTCGTGTC TACCTCGTGG TCTCTGCTCT CGTAGCCTTC 720
 840 ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGCTGCTG GCGCGGGGGC 780
 900 ACCGCGCTCT CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 840
 960 ACCATCATCT TCTTGGGCT GATTGTGTGT ACATTGGCCG TATGCTGGAT GCCCAACGAG 900
 1020 ATTCCGAGGA TCTATGCTGC GGCCTGCTGC GGCCTGCTGC GGCCTGCTGC GGCCTGCTGC 960
 1080 GCGTACATGA TCTCTCTCCC CTTCCTGAG AGTTTCTTCT ACCTCAGCTC GGTCTCAAC 1020
 1140 COGCTCTGT ACACGGTGTG CTGCGAGCAG TTTCGGCGGG TGTTGCTGCA GGTGCTGTGC 1080
 1200 TGCCGCTGT CGCTGAGCA GGCCTGCTGC GGCCTGCTGC GGCCTGCTGC GGCCTGCTGC 1140
 1260 ACCACGAGA GCGCCGCTT TGTGACGCG CCGTGTCTCT TCGCTGCTGC GCGCTGCTGC 1200
 1320 TCTGCAAGGA GAACCTGAGAA GATTTCTTA AGCACTTTC AGAGCGAGGC CGAGCCGAGC 1260
 1380 TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACGAGCC 1320
 1440 AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

A14 Protein sequence:

55 Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Protein Accession #: NM_001508, NP_001409
 Signal sequence: none found
 Pfam domains: 7tm_1 [72-172, 224-344]
 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342
 60 Cellular Localization: plasma membrane

65 1 11 21 31 41 51
 120 MASPSLPGSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNSA TIRVTQVLQK 60
 180 KGYLQKEVTD BMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLCKL HTFLFEACSY 120
 240 ATLLHVLTL FERYIAICHP FRYKAVSGPC QVKLLIGFVN VTSALVALPL LPAMGTREYPL 180
 300 VNVPSHRGLT CNRSSTRHHE QPETSNSIC TNLSSRWTFV QSSIFGAFVV YLVVLLSVAF 240
 360 MCWMMQVLM KSQKSLAGG TRPPQLRKSE SEESRTARRQ TIIFLRLLIV TLAVCMMPNQ 300
 420 IRRIMAAKP KHDWTRSYFR AYMILLPFSE TFFYLSVIN PLLYTVSSQQ FRRVFVQLC 360
 480 CRLSLQHANH EKRLRVHAHS TTDSARPVQR PLLFASRRQS SARRTEKIFL STFQSEAEPC 420
 540 SKSQSLSLSE LEPNSGAKPA NSAAENGFOE HEV

A1 ProstateA15 DNA sequence

80 Gene name: CBGP1
 Unigene number: Hs.222399
 Probeset Accession #: AA256485
 Nucleic Acid Accession #: AJ400877
 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

	GGGTCGCGG	CACACCTCCC	CGGCGCGCG	CGGCCACCGC	CGCACTCGG	CGGCTCTGC	60
	CCGCAACCGC	TGAGCCATCC	ATGGGGGTGG	CGGGCGGCAA	CGTCCCGGG	GGGGCTGGG	120
5	CGGTGCTGCT	GCTGCTGCTG	CTGCTGCGC	CCTGCTGCT	GCTGGCGGG	GCCGTCCCGC	180
	CGGGTCGGG	CGGTGCGCG	GGGCGCGAG	AGGATGTAGA	TGAGTGTGCC	CAAGGGCTAG	240
	ATGACTGCCA	TGCGGACGCC	CTGTGTGAGA	ACACACCCAC	CTCCTACAAG	TGCTCTGCA	300
	AGCCTGGCTA	CCAAGGGGAA	GGCAGGCAGT	GTGAGGACAT	CGATGAATGT	GGAAATGAGC	360
	TCAATGAGAG	CTGTGTCCAT	GACTGTTTGA	ATATTCCAGG	CAATTATCGT	TGCACTTGT	420
10	TTGATGGCTT	CATGTTGGCT	CATGACGGTC	ATAATTGTCT	TGATGTGGAC	GAGTGCTGG	480
	AGAACAATGG	CGGCTGCCAG	CATACTGTG	TCAACGTCT	GGGGAGCTAT	GAGTGCTGCT	540
	GCAAGGAGGG	GTTTTCCTG	AGTGACAACT	AGCACACCTG	CATTCAACGC	TGGAAGAGG	600
	GCCTGAGCTG	CATGAATAAG	GATCACGGCT	GTAGTCACAT	CTGCAAGGAG	GCCCCAAGGG	660
	GCAGCGTCG	CTGTGAGTGC	AGGCCCTGGT	TTGAGCTGGC	CAAGAACCCG	AGAGACTGCA	720
15	TCCTGAGCTG	TAACCATGGG	AACGGTGGGT	GCCAGCAGCT	CTGTGACGAT	ACAGCCGATG	780
	GCCCCAGAGT	CAGCTGCCAT	CCACAGTACA	AGATGCACAC	AGATGGGAGG	AGCTGCCTTG	840
	AGCGAGAGG	CAGCTGCCAT	CCACAGTACA	AGATGCACAC	AGATGGGAGG	AGCTGCCTTG	900
	ATAAACGGGT	GAAACGGCGG	CTGCTCATGG	AAACGTGTGC	TGTCAACAA	GGAGGCTGTG	960
	ACCGCACCTG	TAAGGATACT	TGACAGAGTG	TCCACTGCAG	TTGTCTCTGT	GGATTCACTC	1020
20	TCCAGTTGGA	TGGGAAGACA	TGTAAAGATA	TTGATGAGTG	CCAGACCCGC	AATGGAGGTT	1080
	GTGATCATTT	CTGCAAAAAC	ATCGTGGGCA	GTTTGTGAGT	CGGCTGCAG	AAAGGATTTA	1140
	AATTATTAA	AGATGAGAAG	TCTTGCCAAG	ATGTGGATGA	GTGCTCTTTG	GATAGGACCT	1200
	GTGACCAAG	CTGCATCAAC	CACCTGTGCA	CATTGTCTTG	TGCTTGCAAC	CGAGGGTACA	1260
	CCCTGTATGG	CTTCAACCC	TGTGGAGACA	CCAATGAGTG	CAGCATCAAC	AACGGAGGCT	1320
25	GTGAGAGCTG	CTGCTGTGAA	ACAGTGGGCA	GCTATGAATG	CCAGTGGCAC	CCTGGGTACA	1380
	AGCTCCACTG	GAATAAAAAA	GACTGTGTGG	AAAGTAAAGG	GCTCCTGCC	ACAAGTGTGT	1440
	CACCCGCTG	CTCCTGTGCA	TGCGTAAAGA	GTGGTGGAG	AGACGGGTGC	TTCTCAGAT	1500
	GTCACTCTGG	CATTCACTC	TCTTCAGATG	TCACCACCAT	CAGGACAAGT	GTAACTTTA	1560
	AGCTAAATGA	AGGCAAGTGT	AGTTTGAAGA	ATGCTGAGCT	GTTTCCCGAG	GGTCTGCGAC	1620
30	CAGCACTACC	AGAGAAAGCAC	AGCTCAGTAA	AAGAGAGCTT	CCGCTACGTA	AACCTTACAT	1680
	GCAGCTCTGG	CAGCAAGTGC	CCAGGAGCCC	CTGGCCGACC	AAGCACCCCT	AAGGAAATGT	1740
	TTATATTATG	TGAGTTTGA	CTTGAAACTA	ACCAAAAGGA	GGTGACAGCT	TCTTGTGACC	1800
	TGAGCTGCAT	CGTAAAGCGA	ACCGAGAAGC	GGCTCCGTAA	AGCCATCCGC	ACGCTCAGAA	1860
	AGGCGGTCCA	CAGGAGAGCA	TTTCACTCC	AGCTCTCAGG	CATGAACCTC	GACGTGGCTA	1920
35	AAAAGCCTCC	CAGAAACATCT	GAACGCCAGG	CAGAGTCCCTG	TGGAGTGGGC	CAGGGTCATG	1980
	CAGAAACCA	ATGTGTCACT	TGCAGGGCTG	GGACCTATTA	TGATGGAGCA	CGAGAACGCT	2040
	GCATTTATGT	TCCAAATGGA	ACCTTCCAAA	ATGAGGAAGG	ACAAATGACT	TGTGAACCAT	2100
	GCCCAAGACC	AGGAAATCTT	GGGGCCCTGA	AGACCCAGAA	AGCTTGGAA	ATGTCTGAAT	2160
	GTGGAGGTCT	GTGCTCAACT	GGTGAATATT	CTGCAGATGG	CTTTGCACTT	TGCCAGCTCT	2220
40	GTGCCCTGGG	CAGCTTCCAG	CCTGAAGCTG	GTGCAACTTC	CTGCTTCCCC	TGTGGAGGAG	2280
	GCCTTGCCAC	CAAACTCAG	GGAGCTACTT	CCTTTCAGGA	CTGTGAAACC	AGAGTTCAAT	2340
	GTTCACTGGG	ACATTTCTAC	AACACCAACA	CTCACGATG	TATTCGTTCG	CCAGTGGGAA	2400
	CATACCAGCC	TGAATTTGGA	AAAAATAATT	GTGTTTCTTG	CCCAGGAAAT	ACTACGACTG	2460
	ACTTTGATGG	CTCCACAAAC	ATAACCCAGT	GTAAAAACAG	AAGATGTGGA	GGGGAGCTGG	2520
45	GAGATTACAC	TGGGTACATT	GAATCCCCAA	ACTACCCAGG	CAATTACCCA	GCCAAACCCG	2580
	AGTGTACGTG	GACCATCAAC	CCACCCCCCA	AGCGCCGAT	CCTGATCGTG	GTCCCTGAGA	2640
	TCTTCCCTGCC	CATAGAGGAG	GACTGTGGGG	ACTATCTGGT	GATGCGGAAA	ACCTCTTCAT	2700
	CCAAATCTGT	GACAACATAT	GAAACCTGCC	AGACCTACGA	ACGCCCCATC	GCCTTCACCT	2760
	CCAGGTCAAA	GAGCTGTGG	ATTCAATTCA	AGTCCAATGA	AGGGAAACAG	GCTAGAGGGT	2820
50	TCCAGTCCCC	ATAGCTGACA	TATGATGAGG	ACTACCAAGG	ACTCATTGAA	GACATAGTTC	2880
	GAGATGGCAG	GCTCTATGCA	TCTGAGAAAC	ATCAGGAAAT	ACTTAAGGAT	AAGAAACTTA	2940
	TCAAGGCTCT	GTTTGTATGT	CTGGCCCATC	CCCAGAACTA	TTTCAAGTAC	ACAGCCGAGG	3000
	AGTCCCGAGA	GATGTTTCCA	AGATCGTTCA	TCCGATTGCT	ACGTTCCAAA	GTGTCCAGGT	3060
	TTTTGAGACC	TTACAAATGA	CTCAGCCAC	GTGCCACTCA	ATACAAATGT	TCTGCTATAG	3120
55	GGTTGTGGG	ACAGAGCTGT	CTTCTTCTG	CATGTGAGCA	CAGTGGGGA	TTGCTGCCTC	3180
	CGGTATCAGT	GACTCATTAG	AGTTCAATTT	TTATAGATAA	TACAGATATT	TTGGTAAATT	3240
	GAACTTGGTT	TTTCTTTCCC	AGCATCGTGG	ATGTAGACTG	AGAATGGCTT	TGAGTGGCAT	3300
	CAGCTTCTCA	CTGCTGTGGG	CGGATGTCTT	GGATAGATCA	CGGCTGGCT	GAGCTGGACT	3360
	TTGCTCAGCC	TAGTGTAGAC	TCACTGTCC	TTCTGGGCTC	TTACTCTCTC	TCAAGGAGTC	3420
60	TGTAGTGGAA	AGGAGGCCAC	AGAAATAAGCT	GCTTATTCTG	AAACTTCAGC	TTCTCTAGC	3480
	CGGCTCTCT	CTAAGGGAGC	CCTCTGCACT	CGTGTGAGG	CTCTGACGAG	GCAGAACGAG	3540
	CAAGAGGGGA	GGAAGGAGGA	CCCTGTCAGG	CTCCCTCCAC	CCACCTTGAG	ACCTGGGAGG	3600
	ACTCAGTTTC	TCCACAGCCT	TCTCCAGCCT	GTGTGATACA	AGTTTGTATC	CAGGAACTTG	3660
	AGTTCTAAGC	AGTGTCTGTC	AAAAAATAAA	GCAGAAAGAA	TTAGAAATAA	ATAAAACTTA	3720
65	AGCACCTCTG	GAGACAT					

A16 Protein sequence

Gene name: CEGP1
 Unigene number: Hs.222399
 Probeset Accession #: AA256485
 Protein Accession #: CAB92285
 Signal sequence: 1-31
 Transmembrane domains: none
 PFAM domains: EGF-like domains [49-84,132-167,177-213,286-321,407-442]
 CUB domain [809-918]
 Cellular Localization: may be secreted

	1	11	21	31	41	51	
80	MGVAGRNRP	AAAVLLLLL	LLPPLLLLAG	AVFPGRGAA	GPQEDVDECA	QGLDDCHADA	60
	LQNTPTSYK	CSCKPGYQGE	GRQCEDIDEC	GNEIINGCVH	DCLNIPGNRY	CTCFDGFMLA	120
	HDGHNCLDVG	ECLNNGGCG	HTCNVVMGYS	ECCKEGPFL	SDNQHTCIHR	SEBGLSCMNK	180
	DRGCSHICKE	APRGSVACBC	RPQFELAKNQ	RDCLILTCNH	NGGCQBSQDD	TADGPECSCH	240
	PQYQHTDGR	SCLEREDTVL	EVTESNTTSV	VDGDKRVKRR	LLMETCAVMN	GGDRTCKD	300

5 STGVHCSCPV GFTLQLDGKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFKLLTDEK 360
 SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGFTH CGDTNECSIN NGGQQQVCVN 420
 TVGSYEQCH PGYKLHWNKK DCVEVKGLLP TSVSFVSLH CGKSGGGDC FLRCHSGIHL 480
 SSDVTIIRTS VTFKLNKGKC SLKNAELFPE GLRPALEKH SSVKESFRYV NLTCSSGQKV 540
 PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCDLSCIVKR TEKRLRKAIR TLRKAVHREQ 600
 FHLQLSGMNL DVAKKPPRTS BRQAESCQVG QGHAENQCVS CRAGTYIDGA RERCILCFNG 660
 TFQNEEGQMT CEPCEPRPNS GALKTPBAMN MSECGLCQFP GEYSADGFAP CQLCALGTFQ 720
 10 PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSPGHFP NITTHRCIRC PVGTYQPEFG 780
 KNNCVSCPQN TTTDFDGSYN ITQCKNRRCG GELGDFGTGYI ESPNYPGNYP ANTECTWTIN 840
 PPPKRRILIV VPEIFLPIED DCGDYLVMRK TSSNSVITY ETCQTYERPI AFTSRSKLW 900
 IQFKSNEGNS ARGFQVPYVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLKALFDV 960
 LAHPQNYFKY TAQSEREMFP RSFIRLLRSK VSRFLRPYK

15 A17 DNA sequence

Gene name: ESTs
 Unigene number: Hs.293102
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272
 Nucleic Acid Accession #: none found
 20 Coding sequence: 1-489 (entire sequence is an open-reading-frame)

1 11 21 31 41 51
 CAAAAAGAAA TAGATAAAAT AAATGGAATA TTAGAAGAGT CTCCTGATAA TGATGGTTTT 60
 25 CTGAAGGCTC CTGCAGAAAT GAAAGTTTCT ATTCCAATA AAGCCTTAGA ATTGATGGAC 120
 ATGCAAACTT TCAAGCAGA GCCTCCGAG AAGCCATCTG CTTGAGAGCC TGCCATTGAA 180
 ATGCAAAAGT CTGTTCCAAA TAAAGCCTTG GAATTGAAGA ATGAACAAAC ATTGAGAGCA 240
 GATCAGATGT TCCCTTCAGA ATCAAAACAA AAGAAAGTTG AAGAAAATTC TTGGGATTCT 300
 GAGAGTCTCC GTGAGACTGT TTCACAGAA GATGTGTGTG TACCCAAGGC TACACATCAA 360
 30 AAAGAAATGG ATAAATAAG TGGAAATAA GAAGATTCAA CTAGCCTATC AAAAATCTTG 420
 GATACAGTTC ATTCTTGTA AAGAACAAGG GAACTTCAA AAGACCCCTG TGACCCACGT 480
 TCAGGAAAA

35 A18 Protein sequence

Gene name: ESTs
 Unigene number: Hs.293102
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272
 Protein Accession #: none found
 Signal sequence: none
 40 Transmembrane domains: none
 Cellular Localization: nuclear

1 11 21 31 41 51
 45 QKEIDKINK LEESPDNDGF LKAPCRMVVS IPTKALELMD MQTFKAEPPE KPSAFEPPIE 60
 MQKSVENKAL ELKNEQTLRA DQMFPSESQK KXVEENSWDS ESLRETVSQK DVCVPKATHQ 120
 KEMDKISGKL EDSTSLSKIL DTVHSCERTR ELQKDPDCPR SGK

50 Breast

55 A19 DNA SEQUENCE

Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Nucleic Acid Accession #: AB038157
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 60 ACCGGGCACC GGACGGCTCG GGTACTTTCT TTCTTAATTA GGTATGCCCC GTGTGAGCCA 60
 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACGTGGGC CTACTATCTC TTCCGTGGTG 120
 65 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCCGATGTC 180
 AGAGGTCTCG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA AGCCCCCTTC 240
 TCATTCCGAT CGCTTTTGGG CCTTGATGAT TTGAAATAAA GTCCGTGTGC ACCAGATGCA 300
 GATGCTGTGG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
 70 TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGGAAGA CCTGTGCTC CGATGACTGG 600
 AAGGTCACCT ACGCAATGT TGCTGTGCC CAATGGGTTT TCCCAAGCTA TGTGAGTTCA 660
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTCCGGG AGGAGTTTGT GTCCATCGAT 720
 75 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 TGTGCTCTCG GCCACGTGGT TACCTTGCA GTCACAGCCT GTGTCATAG AAGGGGCTAC 840
 AGCTCAGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900
 CTTCACTTCC AGGGCTACCA CTTGTGCGGG GGCTCTGTCA TCACGCCCTC GTGGATCATC 960
 ACTGCTGCAC ACTGTGTTTA TGACTGTGAC CTCCCCAAGT CATGGACCAT CCAGTGGGT 1020
 80 CTAGTPTCCC TGTGGACAA TCCAGCCCCA TCCACCTTGG TGGAGAAGAT TGTCTACAC 1080
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCTGCCCA 1140
 CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCTGCCCCA ACTCTGAAGA GAACTTCCCC 1200
 GATGGAAAAG TGTGCTGAGC GTCAAGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260
 TCCCCGTGCC TGAACACGCG GCGCGTCCCT TTGATTTCAC ACAAGATCTG CAACACAGG 1320
 GACGTGTACG GTGGCATCAT CTCCCCCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380

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 10
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 20

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GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
AAGTTAGTGG GAGCGACCCAG CTTTGGCATC GGCTGGCGAG AGGTGAACAA GCCTGGGGTG 1500
TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTTG AGGTGATGAA GACAGCCGGA 1620
TCCTCCCGTG GACTCCCGTG TAGGAAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680
TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCCCTCCA TCTGATTCCA GCACAACTTT 1740
CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTGG CCCAGGCTGG 1800
AGTGCACTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTC ACGGATTCTC 1860
TTGCCCTCAG TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCACACC CAACTAATTT 1920
TTGTATTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
CCTCAATGA TGTGCTGCTC TCAGCCTCCC ACAGTCTGG GATTACAGGC ATGGGCCACC 2040
ACGCTTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG 2160
ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
GCACCAGCCC AGAAGTGCAG AACTGCAGTC ACTGCAGTIT TTCATCTCTA GGGACCAGAA 2280
CCAAACCCAC CTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
ATGACTCGTT TAAGCCTTAT TTTTCATGAT TCTTTGTAGC ATTTGGTGCT TGACGTATTA 2400
TTGTCCITTG ATTCCAAATA ATATGTTTCC TTCCCTCAA AAAAAAAAAA AAAAAAAAAA 2460
AAAAAAA
  
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A20 Protein sequence:

25
 30

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Gene name: TMRSS3a
Unigene number: Hs.298241
Probeset Accession #: AI538613
Protein Accession #: BAB20077
Signal sequence: none found
Transmembrane domains: 43-65, 239-261
Tryp_SPC domain: 216-444
Cellular Localization: not determined
  
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35
 40

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1 11 21 31 41 51
| | | | |
MGENDPPAVE APFSFRSLFG LDDLKISFVA PDADAVAAQI LSLLPLKFPF IIVIGIILI 60
LALAIGLGIH FDCSGKYRRC SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLOVF 120
TAASWKIMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEOQFREEFV SIDHLLPDDK 180
VTALHSHVYV REGCASGHVU TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH 240
LCGGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSHYKPKR 300
LGMNDIALMKL AGPLTFNEMI QFVCLPNSEE NFPDGKVCWT SGWGATEDGA GDASPVNLHA 360
AVPLISNKIC NHRDVVGGII SPSMLCAGYL TGGVDSQQGD SGGPLVCQER RLWKLVGATS 420
FGIGCAEVNK PGVYTRVTSF LDWIHEQMER DLKT
  
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A21 DNA SEQUENCE

45
 50

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Gene name: ESTs; opposite strand to TRPS1
Unigene number: none
Probeset Accession #: AA428090
Nucleic Acid Accession #: AA428090
Coding sequence: 1-558 (underlined sequences correspond to start and stop codons)
  
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55
 60
 65
 70
 75
 80

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1 11 21 31 41 51
| | | | |
ATGAAGCCCA GTTTGAAACA CTGGGCTGAT ATAAAAATGT TTTCTGAAAT AGACCAAAGG 60
CAAGTTGTGG GAGAAGAAAT TCATCTACAA GTAGTATCTG TATCTTATCT TGTAGAAAAC 120
TTTTAGACA CAGATGATCT TATGTCCATA GTGGAGGAAT CAGACAGCTG CTACAAACGT 180
GATTCTGTTG GGCCTCCTGG TAGAGCTGGA GACAGACTGC AACCCAAGAC AAAACCCAGA 240
GGAAAAACAA CTAACTCAG CCATTTGCCC AATTTCCACC TTGCTAGTTA TCAGAGTTCA 300
CTATTGTTTA AGCTCCAGGG GTCATACTAT GGCAATCTAC TGGTGGAAAT TATTCTGAGC 360
AAGTGTITTG TTCAGCTTGC AGTATTAAAA CAAAAAAGAC ATTGCCTCCA GCTGCAAGAC 420
AAGGGCATG CCATTATGAA AGCCCTCAA AGACTCTCTG CTATTTTCAA AACATGGAAA 480
GAAAAAGGGA AAAAAGAAAA AAAATAATA ATTAGAAGGA TTGTTCCTT AATTTGGGCT 540
CCCAAAATG AGAATGAAG ATTGTATAAT GAGGGGAGAT ACTAATTATT TTAACCTCTC 600
CAAGCAAAAT TTCTGAAGCA ATCAATTATT TATATACITT ATGTTCTGTC TTTTGTATT 660
TTTCTTCTG GTTAAAAACA TGCAAGTGAG TCTTGCCAAC GTCCITTCCT ATCTGGATCT 720
GTTCTGCTC ATTTCTCTTT CAAAGTCATC TTTGAGGGAA CTGCGCTGA TTAATTGAT 780
TTTAACCAA CAAATAAGAT ATTGATATA TTAATTTAAA CTTTGTGAGA TGATTGATTA 840
GGAATTGCAT CATGTTTACA TGAGTATACC GAATTTCAAG TTAACCTTCA TAAGCAGGAG 900
TTTTTACACA TCGTAACATA ATCATTAACC AATACTCGAC ACTCAATATT TGATACTCAA 960
CTGAATGTTT TTGAATAAAA CACATTTTTA TGTATCTCT CTGGAGAAAG TAGTATATAT 1020
CTTTTACAC AAAATATATC AGTGAGAGAG TGTGTGTTA AGAAAAAAA TCAAGCACA 1080
ACAAATTGAG AGAGTCCAGG CTTTATCAAT ATAAGTAATA ATTTTGTAGA ATGGTGATTT 1140
GATTTTACCA TTTCAATTCA GCAGAGCCTG TATATATATA TATATATATA TATATATATA 1200
TATATATATA TATATATATA TATATACAA TGATCTGTAT TTCTATTG CAGAAAGGATG 1260
AAAGTGAATC CATATAAACC ATACCAACGC CGTTATGTGT AACTGTGTGT AAAACTTTAT 1320
TATTCAGCTT TAGATGTAA CAGATCTTT GCTGCTGAA GATTGTGTC ATAGAAATA 1380
CACCAGAAGC ATGTTTGTGA GTAGAAATGA ACATGCACTA TGAACACAA ATAAATATAA 1440
ACGAAAAAAT TTCAATGTGT GTAAGAACAG AACTATTATA GCCACATTC TAGTATTCAA 1500
ATCAGGACTA CAAATTGAAT TCTTTTCTT AGCAACATGA AATCATTCCA TATGAAGAGC 1560
ATTTCTGCT GGTGAATATT GCTGTAAAGT AATTTTACA TTGGCATTT GAGATGTTCC 1620
CCCTCATGC CTCCCCCAA GTTTTCCATG TGGTTGTCAA ATAGTCCG
  
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A22 Protein sequence:

Gene name: ESTs; opposite strand to TRPS1
 Unigene number: none
 Probeset Accession #: AA428090
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 113-129
 Cellular Localization: not determined

10 1 11 21 31 41 51
 MKPSLKHWD IKMFSEIDQR QVVGEEIHLQ VVSVSYLVEN PSDTDDLMSI VEESDSCYNR 60
 DSVGLPGRAG DRLQPKTKPR GKTNNLSHLF NFHLASYQSS LLFLKQSSY GNLLVEFELS 120
 KCFVQLAVLK QRKCLQLQS KGIAMKAPQ RLSAIPKTKW EKGKKEKKII IRRICSLIWA 180
 15 PKNEK

A23 DNA SEQUENCE

20 Gene name: ESTs
 Unigene number: Hs.29383
 Probeset Accession #: AW207206
 Nucleic Acid Accession #: AL133619
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
 ATGAGCGGTG CGGGGGTGGC GGCTGGGAGC CGGCCCCCA GCTCGCGAC CCCGGGCTCT 60
 CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCCT TGAGGCCGCA GAGCCCGCAG 120
 CTCAGGCAGA GCGACCCGCA GAAACGGAACT CTGGACCTGG AGAAAGCCT GCAGTTCCTG 180
 30 CAGCAGCAGC ACTCGGAGAT GCTGGCCAAAG CTCCATGAGG AGATCGAGCA TCTGAAGCGG 240
 GAAAACAAGG GTAGCGCGC GCGGGGCCCT AGGCCGCGCC TGCTCCCGCA GGCACACTCA 300
 ACACTGCCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACACG CCTGGGCTCA 360
 GGGGGAACAC AGGACGGGGA GCGCCCTCCAG ACTGTCTTGG CCCACCTGGC TGCACTGGCC 420
 CCTGTATGCC AACCCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC CGCTACCTCT 480
 35 AGCCGTGGCT GAGCATGTT ATGCAGCCAA GCACAGCAG TGCTGCTCTC GGGAGGCCCA 540
 GGGCCTGAGG TCATTGCAGG GCGCAGGTTG GCCACAGGCT GCTCCCGAGA CCTCCCTCCT 600
 CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CTGCGCTGCT TAGATCTTTG 660
 CCTCAGATTG CTGCTGTGGC CAGGCCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720
 ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780
 40 GCAGCAACCA TGGGACAAA GGGAGGAAGC AGAGTCTGTG TTCTTGCCA CTGTGCTCAAG 840
 GCACCTCCCC ATCTGACAG CGGCCCCAC CCAGCCCGAG ATCCTGGGCT GTGGTCTCAA 900
 GCTCACTTCC CATTTATCTT GGGGCTGGG GCAGCTGGG GCGCTCTCC TCCCGAGGA 1020
 TGGAGCCAGC CTGGGAACAT GCGAGCTGGG GCGAGTGCCTA GGGCTCTCC TCCCGAGGA 1080
 GACATGGAGA AGGGGGTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCAGTGTAG 1140
 45 CTGTTCTGGG CAAAGTGGG CCCAAGTGGG CAGCCCCAGC CCTGCACTGC TGGGGACGCT 1200
 GACAGGACAC GGAAGAGGCG CATGCTTTCC CTGCGGACCT GCTGTTCCAT GTGTCCCAAG 1260
 CCCCTCTGCT TTCCAGATGG CCCCTCAGGA AACCACTTT CCAGGGGCTC TGCTCCCTTG 1320
 GCGCTCGCT GGGTCTGCAT CAACGGAGTG TGGGTAGAGC CGGAGGACC CAGCCCTGCC 1380
 AGGCTGAAGG AGGGCTCCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGG 1440
 50 GCGGTAGGG CCGGACTGTG GCGCTCTCCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1500
 TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1560
 TCCTTCAACA AGCAAGATTG AAAAGCTGAC GTCTCCAGA AGGCGGACCT GGAAGAGGAG 1620
 CCCCTACTTC ACAACAGCAA GCTGGACAAA GTTCTTGGG TACAAGGCA GCGCAGAAAG 1680
 GAGAAAGCAG AGGCCTCTAA TGCAAGAGCT GCGTGTATGG GGAACAGCA GCAACAGGC 1740
 55 AGGCAGATGG GGGCGGGGCG ACACCCCCCA ATGATCCTGC CCCTTCCCTC GCGAAAGCCC 1800
 ACCACACTTA GGCAGTGGGA AGTGCTCATC CGCAGCTGT GGAATACCAA CCTCTCGAG 1860
 ACCCAAGAGC TGGCGACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGAGGCC 1920
 COGGAGGAAG CTAGCTTTCC CAGGGACCAA GAAGCCACGC ATTTCCCAA GGTCTCCACC 1980
 AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CTGTGGCGG AGCGTGCCAT CCTGCCCGCA 2040
 60 CTGAAGCAGA CCCCAGAGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCATGACG
 AAACGGCGCC TGCATCGCTC AGTGTCTTGA

A24 Protein sequence:

65 Gene name: ESTs
 Unigene number: Hs.29383
 Probeset Accession #: AW207206
 Protein Accession #: T43457
 Signal sequence: none found
 Transmembrane domains: 303-322
 Cellular Localization: not determined

75 1 11 21 31 41 51
 MSGAGVAAGT RPPSSPTPGS RRRRQRPVSV VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60
 QQQHEMLAK LHEEIEHLKR ENKGEFARGP RPALPPQAHs TLPLPQHRNT AINSSTRLGS 120
 GGTQDGEPLQ TVLAHLAALA PVQPSGYRF WGTWTDAA TS SRGWITMLCSQ AQHVLLSGSP 180
 GPEVIAGRQV ATGCSFDLPP PSRAEMGRNP WDSFPCPARSL PQIAAVARER ISSPMALSFP 240
 80 MLGAQGIWTH SIQSSLPATW AATMGTKGGS RVLFPCHLSK ALPHPDSPGH PAQDPGLNSQ 300
 AHFPLSLGLG LITSGGLTGG WSQPGNLAAG AVPRALPSQG DMEKGVBBGP FPSRCNGSSE 360
 LFWAKCGPFR QPQPCSAQDA DRTREBAMLS LGTCCSMCFK PSCFPDGPSP NHLSRASAPL 420
 GARWVCINQ VVEPGGSPSA RLKEGSSRTH RPKGKRGLA GGSADTVRSP ADSLSMSSEFP 480
 SVKSISNSAN SQGKARPQPG SFNKQDSKAD VSQKADLEE PLLENSKLDK VPGVQQAARK 540

EKABASNAGA ACNGNSQHQG RQMGAGAHPP MILPLPLRKP TTLRQCEVLI RELMNTNLLQ 600
 TQSLRLHLKSL LEGSQRPPQAA PEEASFPRDQ EATHFPKVST KSLSKKCLSP PVAERAILPA 660
 LKQTPKKNFA ERQKRLQAMQ KRRLHRSVL

5

A25 DNA SEQUENCE

Gene name: ESTs; prolactin receptor
 Unigene number: Hs.25252
 Probeset Accession #: AA057193
 Nucleic Acid Accession #: NM_000949
 Coding sequence: 285-2153 (underlined sequences correspond to start and stop codons)

10

1 11 21 31 41 51
 15 GGAGGCTGAA ATCCCCAGAC GCGGTTTTC TGGGCTGGGC TTCTGCTTA CTCACTCCTT 60
 CTCCCTCTTT CTGGATTTTA CCGACCGTTC GCGAAACAGC TTTCACACA ATGGAGCTTC 120
 ATGTCTCTGT GCGAGGAAGTA CTCATCGACT GATGTGGCAG ACTTTGCTCC CTGACAAAAC 180
 TAAAGAACTG TCCTATTTCAT GGAGGCGAAC ACTGAGGATG CTTTCCACAT GAACCCCTGAA 240
 GTGAACCTTC GATACATTTC CTGCAGCAAG AGAAGGCAGC CAACATGAAG GAAAATGTGG 300
 20 CATCTGCAAC CGTTTTCACT CTGCTACTTT TTCTCAACAC CTGCCTTCTG AATGGACAGT 360
 TACCTCTCTG AAAACCTGAG ATCTTTAAAT GTCGTTCTCC CAATAAGGAA ACATTACCTT 420
 GCTGTGGGAG GCTGGGGACA GATGGAGGAC TTCCTACCAA TTATTCAGTG ACTTACCACA 480
 GGGAAAGGAG GACACTCATG CATGAATGTC CAGACTACAT AACCGGTGGC CCCAACTCCT 540
 25 GCCACTTTTG CAAGCAGTAC ACCTCCATGT GGAGGACATA CATCATGATG GTCAATGCCA 600
 CTAACAGAGT GGGAAAGCAGT TTCTCGGATG AACTTTATGT GGACGTGACT TACATAGTTC 660
 AGCCAGACCC TCCTTTGGAG CTGGCTGTGG AAGTAAACA GCCAGAAGAC AGAAAACCTT 720
 ACCTGTGGAT TAAATGGTCT CCACCTACCC TGATTGACTT AAAAACTGGT TGGTTCACTG 780
 TCCTGTATGA AATTGCGATTA AAACCCGAGA AAGCAGCTGA GTGGGAGATC CATTTTGTCT 840
 GGCAGCAAAAC GATAGTTTAAG ATTCTCAGCC TACATCCAGC ACAGAAATAC CTTGTCCAGG 900
 30 TTGCTGTCAA ACCAGACCAT GGATACTGGA GTGCATGGAG TCCAGCGACC TTCATTGAGA 960
 TACCTAGTGA CTTCACCATG AATGATACAA CCGTGTGGAT CTCTGTGGCT GTCCCTTTCTG 1020
 CTGTCTATCT GTTGATTATT GTCTGGGCAG TGGCTTTGAA GGGCTATAGC ATGGTGACCT 1080
 GCATCTTTCC GCCAGTTCTT GGGCCAAAAA TAAAGGATTT TGATGCTCAT CTGTGGGAGA 1140
 35 AGGGCAAGTC TGAAGAACTA CTGAGTGCTT TGGGATGCOA AGACTTTCTT CCCACTTCTG 1200
 ACTATGAGGA CTGTCTGGTG GAGTATTTAG AAGTAGATGA TAGTGAGGAC CAGCATCTAA 1260
 TGTCAGTCCA TTCAAAGAA CACCCAGTTC AAGGTATGAA ACCACATATC CTGGATCCTG 1320
 ACACGTACTC AGGCCGGGGG AGCTGTGACA GCCCTTCCTT TTGTCTGAA AAGTGTGAGG 1380
 AACCCCAAGC CAATCCCTCC ACATTTCTAT ATCCTGAGGT CATTGAGAA GAGAGAAATC 1440
 40 CTGAACAAC CCACACCTGG GACCCCACTG GCATAAGCAT GGAAGGCAAA ATCCCTTATT 1500
 TTCTGTCTGG TGGATCCAAA TGTTCAACAT GGCCCTTACC ACAGCCAGC CAGCAACAAC 1560
 CCAGATCCTC TTACCAAAAT ATTACTGATG TGTGTGAGCT GGCCTGTGGC CCTGCAGGTG 1620
 CAACCGCCAC TCTGTGTAAT GAAGCAGGTA AAGATGCTTT AAAATCTCT CAAACCAATTA 1680
 AGTCTAGAGA AGAGGGAAAG GCAACCCAGC AGAGGGAGGT AGAAGGCTTC CATTTCTGAGA 1740
 45 CTGACCAGTA TACGCCCTGG CTGCTGCCCC AGGAGAAAC CCCCTTTGGC TCGCTAAAC 1800
 CCTTGGATTA TGTGGAGATT CACAAGGTCA ACAAGATGG TGCATTATCA TTGCTACCAA 1860
 AACAGAGAGA GAACAGCGGC AAGCCCAAGA AGCCCGGGAC TCCTGAGAAC AATAAGGAGT 1920
 ATGCCAAGGT GTCCGGGGTC ATGGATAACA ACATCCTGGT GTTGTGCGCA GATCCACATG 1980
 CTAACCAAGT GGCCTGCTTT GAAGATCAG CCAAGAGGC CCCACATCA CTTGAACAGA 2040
 50 ATCAAGCTGA GCAAGCCCTG GCCAACTTCA CTGCAACATC AAGCAAGTGC AGGCTCCAGC 2100
 TGGGTGGTTT GGAATTACCTG GATCCCGCAT GTTTTACACA CTCCTTTTAC TGATAGCTTG 2160
 ACTAATGGAA TGATTGGTTA AAATGTGATT TTTCTTCAGG TAACACTACA GAGTACGTGA 2220
 AATGCTCAAG AATGTAGTCA GACTGACACT ACTAAGCTC CCAGCTCCTT TCATGCTCCA 2280
 TTTTAAACCA CTTGCCCTCT TCTCCAGCAG CTGATTCCAG AACAAATCAT TATGTTTCTT 2340
 55 AACTGTGATT TGTAGATTTA CTTTTGCTG TTAGTTATAA AACTATGTGT TCAATGAAAT 2400
 AAAAGCACAC TGCTTAGTAT TCTTGAGGGA CAATGCCAAT AGGTATATCC TCTGAAAAG 2460
 GCTTTTCATGA TTTGGCATGG GACAGAGGGA AATGAAATTG TCAAAATTGT TTACCATAGA 2520
 AAGATACAAA AAGAAAATT TCCACATAGG AAAATGCCAT GAAAATTGCT TTTGAAAAC 2580
 AACTGCATAA CCTTTACAGT CCTGTCCAT TTTATTAGGA TTACCCAAAT ATAACCATTT 2640
 60 AAGAAAAGAA TGCAATCCAG AACAAATTGT TTACATAAGT TCCTATACCT TACTGACACA 2700
 TTGCTGATAT GCAAGTAAGA AAT

A26 Protein sequence:

Gene name: ESTs; prolactin receptor
 Unigene number: Hs.25252
 Probeset Accession #: AA057193
 Protein Accession #: NP_000940
 Signal sequence: 1-23
 Transmembrane domains: 237-253
 70 PN3 domains: 28-112, 127-215
 Cellular Localization: plasma membrane

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80

1 11 21 31 41 51
 MKENVASATV FTLLFLPLNTC LLNGQLPPGK PEIFKCRSPN KETFTCMWRP GTDGGGLPTNY 60
 SLTYHREGET LMRECPDYIT GGFNSCHFVK QYTSWRTYI MMVNATNQM GSPSDELYVD 120
 VTYIVQDPDP LELAVEVKQP EDRKPYLWIK WSPPTLIDLK TGMFTLLYEI RLKPEKAAEW 180
 80 EIHFAGQTE PKILSLHPGQ KYLVQVRCKP DHGYWSAWSP ATFIIQPSDF TMNDTTVWIS 240
 VAVLSAVICL IIVWAVALKG YSMVTCIPFP VPQPKIKGFD AHLLBKQKSB ELLSALGOQD 300
 FPPTSDYEDL LVEYLEVDD S EDQHLMSVHS KEHPSQGMKP TYLDPDITDSG RGSQSPSLL 360
 SEKCEEPQAN PSTFYDPEVI EKPEPFETH TWDPQCISM GRIPYFHAGG SKCSTWPLPQ 420

PSQHNPRSSY HNITDVCELA VGPAGAPATL LNEAGKDALK SSQTIKSREE GKATQOREVE 480
 SFHSETDQDT PWLLPQEKTP FGSAPLDYV EIHKVNKDG LSLLPKQREN SGKPKPGTP 540
 ENNKEYAKVS GVMONNLLVL VPDPAKQVA CFESSAKEAP PSLEQNQARK ALANFTATSS 600
 KCRLQLGGLD YLDPACTHS FH

A27 DNA SEQUENCE

Gene name: Human neuropeptide Y receptor Y1 (NPYY1)

Unigene number: Hs.169266

Probeset Accession #: L07615

Nucleic Acid Accession #: NM_000909.1

Coding sequence: 209-1363 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CATGCCACC CTTCTTCTT TAATAAGCAG GAGCGAAAAA GACAAATCC AAAGAGGATT 60
 GTTCAGTTCA AGGGAATGAA GAATTCAGAA TAATTTTGGT AAATGGATT CAATATCGGG 120
 AATAAGAATA AGCTGAACAG TTGACCTGCT TTGAAGAAAC ATACTGTCCA TTGTCTAAA 180
 ATAATCTATA ACAACCAAAC CAATCAAAAT GAATTCACCA TTATTTTCCC AGGTTGAAAA 240
 TCATTGAGTC CACTCTAATT TCTCAGAGAA GAATGCCAG CTTCTGGCTT TTGAAAATGA 300
 TGATTGTGAT CTGCCCTTGG CCATGATATT TACCTTAGCT CTTGCTTATG GAGCTGTGAT 360
 CATTCTTGGT GTCTCTGGAA ACCTGGCCTT GATCATAATC ATCTTGAAC AAAAGGAGAT 420
 GAGAAATGTT ACCAACATCC TGATTGTGAA CCTTTCCTTC TCAGACTTGC TTGTTGCCAT 480
 CATGTGTCTC CCTTTTACAT TTGTCTACAC ATTAATGGAC CACTGGGTCT TTGGTGAGGC 540
 GATGTGTAAG TTGAATCCTT TTGTGCAATG TGTTTCAATC ACTGTGTCCA TTTTCTCTCT 600
 GGTCTCTCAT CTGTCTGGAAC GACATCAGCT GATAATCAAC CCTCGAGGGT GGAGACCAAA 660
 TAATAGACAT GCTTATGTAG GTATTGCTGT GATTTGGGTC CTTGCTGTGG CTTCTTCTTT 720
 GCCTTTCCTG ATCTACCAAG TAATGACTGA TGAGCCGGTC CAAATGTAA CACTTGATGC 780
 GTACAAAGAC AAATACGTGT GCTTTGATCA ATTTCATCG GACTCTCATA GGTGTCTTA 840
 TACCACTCTC CTCTTGTGTC TGCAATATT TTGTCCACTT TGTTTATAT TTATTGCTA 900
 CTTCAAGATA TATATACGCC TAAAAAGGAG AAACAACATG ATGGACAAGA TGAGAGACAA 960
 TAAGTACAGG TCCAGTGAAA CCAAAAGAAAT CAATATCATG CTGCTCTCCA TTGTGGTAGC 1020
 ATTTCAGTCT TGCTGGCTCC CTCTTACCAT CTTTAACACT GTGTTTGATT GGAATCATCA 1080
 GATCATTGCT ACCTGCAACC ACAATCTGTT ATTCTGTCTC TGCCACTCTA CAGCAATGAT 1140
 ATCCACTTGT GTCAACCCCA TATTTTATGG GTTCTGTAAC AAAAAGCTCC AGAGAGACTT 1200
 GCAGTCTTTC TTCAACTTTT GTGATTCCG GTCTCGGGAT GATGATTATG AAACAATAGC 1260
 CATGTCCACG ATGCACACAG ATGTTTCAA AACTTCTTTG AAGCAAGCAA GCCCAGTCGC 1320
 ATTTAAAAAA ATCAACAACA ATGATGATAA TGAAAAAATC TGAAGTACT TATAGCCTAT 1380
 GGTCCCGGAT GACATCTGTT TAAAAACAAG CACAACCTGC AACATACTTT GATTACCTGT 1440
 TCTCCCAAGG AATGGGGTGG AAATCATTTG AAAATGACTA AGATTTTCTT GTCTTGCTTT 1500
 TTACTGCTTT TGTGTAGTT GTCATATTA CATTGGAAC AAAAGGTGTG GGCTTTGGGG 1560
 TCTTCTGGA ATAGTTTGA CCAGACATCT TTGAAGTGT TTTTGTGAAT TTATGCATAT 1620
 AATATAAAGA CTTTATATCT GTACTTATG GAATGAAAT TCTTTAAAT ATTACGATG 1680
 GCTGACTTCA GAAGTACCTG CCATCCAATA CGGTCAATAG ATTGGGTCTA CTTGATTAGA 1740
 TTAGATTAGA TTGATTGTG AACAGATTGG GCCATCCTTA CTTTATGATA GGCATCATTT 1800
 TAGTGTGTTA CAATAGTAAC AGTATGCAAA AGCAGCATTC AGGAGCCGAA AGATAGTCTT 1860
 GAAGTCATTC AGAAGTGGTT TGAGGTTTCT GTTTTGTGTT GGTTTTGTGTT TGTTTTGT 1920
 TTTTTCACC TTAAGGGAGG CTTTCATTTC CTCCCGACTG ATTGTCACTT AAATCAAAAT 1980
 TTAAAAATGA ATAAAAAGAC ATACTTCTCA GCTGCAAAATA TTATGGAGAA TTGGGCACCC 2040
 ACAGGAATGA AGAGAGAAAG CAGCTCCCCA ACTTCAAAAC CATTTTGGTA CCTGACAAAC 2100
 AGAGCAATTA AGAGTAATTA ATTTAATAAA GTAAATTAGT ATTGCTGCAA ATAGCTAAAT 2160
 TATATTTATT TGAATTGATG GTCAAGAGAT TTCCATTTT TTTTACAGAC TGTTCAGTGT 2220
 TTGTCAAGCT TCTGGTCTAA TATGTACTCG AAAGACTTTC CGCTTACAT TTGTAGAAAC 2280
 ACAATATGCG TTTTCCATAC AGCAGTGCCT ATATAGTGAC TGATTTTAACT TTTCAATGTC 2340
 CATCTTTCAA AGGAAGTAAAC ACCAAGGTAC AATGTTAAAG GAATATTAC TTTACTTAGC 2400
 AGGGAATAAT ACACAAAAAC TGCAGATACT TCATATAGCC CATTTTAACT TGTATAAACT 2460
 GTGTGACTTG TGGCGTCTTA TAAATAATGC ACTGTAAAGA TTAAGTAATA GTGTGTGTCAT 2520
 GTTAATGTGC CTAATTTTAT GTATCTTGTA ATCATGATTG AGCCTCAGAA TCATTGGAG 2580
 AAACATATAT TTAAGAACA AGACATACCT CAATGTATTA TACAGATAAA GTATTACATG 2640
 TGTTTGATTT TAAAGGGGCG GACATTTTAT TAAATCAAT ATTGTTTTTG CTTTCTCTGA 2700
 GGAGTCTCTT TCAGTTTCAT TTTTCTCAT CCCATCGATG GT

A28 Protein sequence:

Gene name: Human neuropeptide Y receptor Y1 (NPYY1) mRNA, exon 2-3 and complete cds

Unigene number: Hs.169266

Probeset Accession #: L07615

Protein Accession #: NP_000900.1

Signal sequence: none found

Pfam domains: 7tm_1 [57-91]

Transmembrane domains: 39-61, 77-99, 118-139, 157-179, 212-234, 264-286, 300-322

Cellular Localization: plasma membrane

1 11 21 31 41 51
 MNSTLFSQVE NHSVHNPSE KNAQLLAPEN DDCHLPLAMI FTLALAYGAV IILGVSGNLA 60
 LIIILKQKE MRNVNLIIV NLSFSDLLVA IMCLPPTFVY TLMDRHWVGE AMCKINPFVQ 120
 CYSITVSIFS LVLI AVERHQ LI INPRGWRP NNRHAYVGLA VIWVLAVASS LPPLIYQVMT 180
 DEPPQNVTL D AYKDKYVCFD QPPSDSHRLS YTTLLLVLYQ FGPLCFIFIC YFKIYIRLKR 240
 RNNMOMKMD NKYRSSETER INIMLLSIVV AFAVCWLPFL IFNTVFDWNH QIIATCNHNL 300
 LFLLCILYAM ISTCVNPIFY GFLNKNFQRD LQFFNFPCDF RSRDDYETI AMSTMETDVS 360

KTSLRQASPV AFKKINNDD NEKI

A29 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM_032551.1

Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51
 | | | | |
 ATGCACACCG TGGCTACGTC CGGACCCCAAC GCGTCCCTGGG GGGCACCCGC CAACGCCTCC 60
 GGCTGCCCGG GCTGTGGGCG CAACGCCTCG GACGCGCCAG TCCCTTGGCC GCGGCGCGTG 120
 GACGCTTGGC TCGTGCCTCG CTTCCTTCGG GCGCTGATGC TGCTGGGCGT GGTGGGGAAC 180
 TCGCTGTGCA TCTAGTCAT CTGCCGCCAC AAGCGGATGC GGACCGTGAC CAACTTCTAC 240
 ATCGCCAAAC TGGCGGCCAC GGACGTGACC TTCTCTCTGT GCTGCGTCCC CTTCACGGCC 300
 CTGCTGTACC CGCTGCCCGG CTGGGTGCTG GCGACTTCA TGTGCAAGTT CGTCAACTAC 360
 ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCCATGAG TGTGGACCGC 420
 TGGTACGTGA CGTGTGTTCCC GTTGGCGGCC CTGCACCGCC GCACGCCCCG CTGGGCGCTG 480
 GCTGTGACGC TCAGCATCTG GGTAGGCTCT GCGGCGGTGT CTGCGCCGGT GCTGCGCCCTG 540
 CACCGCCTGT CACCGCGGCC GCGCGCTTAC TGCAGTGAGG CCTTCCCCAG CCGCGCCCTG 600
 GAGCGCGGCT TCGCACTGTA CAACCTGTG GCGCTGTACC TGCTGCGGCT GCTGCCACCC 660
 TGGCGCTGCT ATGCGGCCAT GCTGCGCCAC CTGGGCGCGG TCGCGGTGCG CCGCGCGCCC 720
 GCGGATAGCG CCGTGCAGGG GCAGGTGCTG GCAGAGCGCG CAGGCGCGCT GCGGCGCAAG 780
 GTCTCGCGGC TGGTGGCGGC CGTGGTCTCT CTCTTCCCGC CTGCTGCGGG CCGCATCCAG 840
 CTGTTCTTGG TGTCTGAGGC GCTGGGCGCC GCGGCTCTCT GGCAACCCAG CAGCTACGCC 900
 GCCTACGCGC TTAAGACCTG GGCTCACTGC ATGTCTTACA GCACTCCCGC GCTGAACCCG 960
 CTGCTCTACG CCTTCTCTGG CTGCACTTCT CGACAGCGCT TCCGCGCGGT CTGCCCTTGC 1020
 GCGCGCGCGC GCGCGCGCGC CCGCGACCTT CGGACCCCGC AGCCCCACAC 1080
 GCGAGGCTGC ACCGCTCTGG GTCCCAACCG GCGCGCGGCA GCGCGGAGAG 1140
 AGTGGGCTGG CCGCGCGCGG GCTGTGCGTC CTGGGGGAGG ACACGCCCC TCTCTGA

A30 Protein sequence

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175), mRNA

Unigene number: Hs.208229

Protein Accession #: AI819198

Signal sequence: none found

Pfam domains: 7tm_1 [59-323]

Transmembrane domains: 43-65, 86-108, 122-144, 159-181, 203-225, 260-282

Cellular Localization: plasma membrane

45 1 11 21 31 41 51
 | | | | |
 MHTVATSGFN ASWGAANAS GCPGCGANAS DGPVPSRAV DAWLVPLFFA ALMLLGLVGN 60
 SLVIYVICRH KPMRTVTNFI IANLAATDVT FLCCVFPFTA LLYPLPGWVL GDFMCKFVNY 120
 IQQVSVQATC ATLTAHSVDR WYVTVFPLRA LHRRTPLRAL AVSLSIWVGS AAVSAFVLAL 180
 HRLSPGPRAY CSEAPPFRAL ERAFALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAP 240
 ADSALGGQVL AERAGAVRAK VSRVAAVVL LFAACWGIQI LFLVLQALGP AGSWHPRSYA 300
 AYALKTWAKC MSYNSALNP LLYAFLGSHF RQAFRRVPCP AFRPRRRPRR PGPSDPAAPH 360
 AELHRLGSHF APARAQKPGS SGLAARGLCV LGEDNAPL

A31 DNA SEQUENCE

Gene name: CH22_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog (CELSR1)

Unigene number: Hs.252387

Probeset Accession #: NM_014246

Nucleic Acid Accession #: NM_014246

Coding sequence: 1-9045 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
 | | | | |
 ATGGCGCGGC CGCGCGCGGC CGTGTGCTGC GTGCTGCTGC TCCTGGCGGC GCGCGCGGCC 60
 CTGCGCGCGA TGGGGCTGCG AGCGGCGGCC TGGGAGCGGC GCGTACCGCG GCGGACCGGC 120
 GCGTTCGCCC TCGCGCCCGG CTGTACCTAC GCGGTGGGCG CCGCTTGACG GCGCGCGGCC 180
 CCGCGGAGCG TGCTGGAGCT GGGCGCGGAT GGGCGGCTGG CAGGACGTGC GCGCGTCTCG 240
 GGCGCGGGGC GCGCGCTGCC GCTGCAAGTC CGCTTGGTGG CCGCGAGTGC CCGGACGCGG 300
 CTGAGCGCGC GCGTGGCGGC GCGCAACGAC CTTCGCGGCT GCGGAGCGCG TGCGCGGCTC 360
 TGCGGAACCG GTGCGCGGCT CTGCGGGGCG CTCTGCTTCC CGTCCCCGCG CGGCTGCGCG 420
 GCGCGCGCAG ATTGCGCGCT CGCAGCTCCG ACCACCTTAC CCGCTGCGCG CTGCGCGCGG 480
 CGCGCCAGCG CCGCGCTGCC CCGCGCTCCC ATCTGCCTGC CCGCGGGCGG CTCGCTCCGC 540
 CTGCGCTTGC TGTGCGCGCT GCGCGCGCGG GCTGCGCGCG TCGGGTGGGG ACTGCGCGTG 600
 GAGGCGCGCA CCGCGGGGAC GCGCTCCGCG TCGCATCCCG CATCGCGGCC CCGCGCGCGG 660
 AACTTGCCTG AAGCGCGGCG GGGCGCGGCG CGACGGGCCC GCGCGGGCAC GAGCGGCGAG 720
 GCGAGCTTGA AGTTTCCGAT GCCCAACTAC CAGGTGGCGT TGTTTGAGAA CGAACCGCGG 780
 GGCACCTTCA TCCTCCAGCT GCACGCGCAC TACACCATCG AGGGCGAGGA GGAGCGCGTG 840
 AGCTATTACA TGGAGGGGCT GTTCGACGAG CGTCCCGGCG GCTACTTCCG AATCGACTCT 900
 CCGACGCGCG CCGTGAGCAC GGCACGCGTA CTGAGCGCGG AGACCAAGGA GAGCGACGTC 960
 GTCAGGTGGA AAGCGGTGGA CTACAGTACG CCGCGCGGCT CGGCCACAC CTACATCACT 1020
 GTCTTGTGTA AAGACACCAA CGACCAACAG CCGGTCTTCC AGCAGTCCGA GTACCGCGAG 1080
 CGCGTGGCGG AGAACCTGGA GGTGGGCTAC GAGGTGCTGA CCATCCGCGC CAGCGACCGC 1140

	GACTCGCCCA	TCAACGCCAA	CTTGCGTTAC	CGCGTGTGG	GGGGCGCGTG	GGACGTCTTC	1200
	CAGCTCAAG	AGAGCTCTGG	CGTGGTGAGC	ACACGGGCGG	TGCTTGACCG	GGAGGAGGCG	1260
	GCCAGGTACC	AGCTCTCTGG	GGAGGCCAAC	GACCAGGGGC	GCAATCCGGG	CCCGCTCAGT	1320
5	GCCACGGCCA	CCGTGTACAT	CGAGGTGAG	GACGAGAACG	ACAATACCC	CCAGTTCAGC	1380
	GAGCAGAACT	ACGTGGTCCA	GGTGCCCGAG	GACGTGGGGC	TCAACACGGC	TGTGCTGCGA	1440
	GTGCAGGCCA	CGGACCCGGG	CCAGGGCCAG	AACGCGGCCA	TTCACCTACG	CATCCTCAGC	1500
	GGGAAOCTGG	CGGCCAGATT	CTACCTGCAC	TCGCTGAGCG	GGATCCTGGA	TGTGATCAAC	1560
	CCCTTGAGTT	TGAGGATGT	CCAGAAATAC	TCGCTGAGCA	TTAAGGCCCA	GGATGGGGGC	1620
10	CGGCCCCCGC	TCATCAATTC	TTGAGGGTG	GTGTCTGTGC	AGGTGCTGGA	TGTCAACGAC	1680
	AACGAGCCTA	TCTTTGTGAG	CAGCCCCCTC	CAGGCCACGG	TGCTGGAGAA	TGTGCCCTTG	1740
	GGCTACCCCG	TGGTGCACAT	TCAGGCGGTG	GACGCGGACT	CTGGAGAGAA	CGCCCGGCTG	1800
	CACATATGCC	TGGTGGACAC	GGCCTCCACC	TTTCTGGGGG	GCGGCAGCGC	TGGGCTTAAG	1860
	AATCCTCGCC	CCACCCCTGA	CTTCCCTTC	CAGATCCACA	ACAGCTCOGG	TGGATCACA	1920
15	GTGTGTCCCG	AGCTGGACCG	CGAGGAGGTG	GAGCACTACA	GCTTCGGGGT	GGAGGCGGTG	1980
	GACCAOGGCT	CGCCCCCATC	GAGCTCCTCC	ACCAGCGTGT	CCATCACGGT	GCTGGACGTG	2040
	AATGACAAGC	ACCCGGTGT	CACGCAGCCC	ACCTACGAGC	TTCTGCTGAA	TGAGGATGCG	2100
	CGCGTGGGGA	GCAGCGTGCT	GACCTTCGAC	GCCCCGGACC	GTGACGCCAA	CAGTGTGATT	2160
	ACCTACCAAG	CCAGCCCGGG	CAACACCCGG	AACCGCTTTG	CACCTACGAG	CCAGAGAGGG	2220
20	GGCGGCTCTA	TCACCTCGGC	GCTACCTCTG	GACTACAAGC	AGGAGCAGCA	GTACGTGCTG	2280
	CGCGTGACAG	CATCCGACGG	CACACGGTCG	CACACTGCGC	ATGTCTTAAT	CAACGTCACT	2340
	GATGCCAACA	CCCAAGAGCG	TGTCTTTTCA	AGCTCCCAT	ACACAGTGAG	TGTGAGTGAG	2400
	GACAGGCGTG	TGGGCACTTC	CATTGCTACC	CTCAGTGCCA	ACGATGAGGA	CACAGGAGAG	2460
	AATGCCCGCA	TACCTTACGT	GATTGAGGAC	CCCGTGCCGC	AGTTCCGCAT	TGACCCCGAC	2520
25	AGTGGCAGCA	TGTACACCAT	GATGGAGCTG	GACTATGAGA	ACCAGGTCCG	CTACACGCTG	2580
	ACCATCATGG	CCCAGGACAA	CGCATCCCG	CAGAAATCAG	ACACACCCAC	CCTAGAGATC	2640
	CTCATCCTCG	ATGCCAATGA	CAATGCACCC	CAGTCTCTGT	GGGATTCTTA	CCAGGGTTCC	2700
	ATCTTTGAGG	ATGCTCCACC	CTGACACAGC	ATCCTCCAGG	TCTCTGCCAC	GGACCGGGAC	2760
	TCAGGTCCCA	ATGGGGGTCT	GCTGTACACC	TTCCAGGGTG	GGGACGACGG	CGATGGGGAC	2820
30	TTCTACATCG	AGCCCACTGC	CGGTGTGATT	CGCACCCAGC	GCCGCTGGA	CCGGGAGAA	2880
	GTGGCGGTGT	ACAACCTTTG	GGCTCTGGCT	GTGGATCCGG	GCACTCCAC	TCCCTTAGC	2940
	GCCTCGGTAG	AAATCCAGGT	GACCATCTTG	GACATTAATG	ACAATGCCCC	CATGTTTGAG	3000
	AAGGAGCAAC	TGGAGCTGTT	TGTTGAGGAG	AACAACCCAG	TGGGGTCCGT	GGTGGCAAG	3060
	ATTCTGTGTA	ACGACCTCGA	TGAAGGCCCT	AATGCCACGA	TCATGTATCA	GATTGTGGAA	3120
35	GGGAGATGCG	GGCATTTCTT	CCAGCTGGAC	CTGCTCAACG	GGGACCTGCG	TGCCATGCTG	3180
	GAGCTGGACT	TTGAGTCCG	CGGGAGTAT	GTGCTGGTGG	TGCAGGCCAC	GTCCGCTCCG	3240
	CTGGTGAGCC	GAGCCACCGT	GCACATCCTT	CTCGTGGACC	AGAATGACAA	CCCGCTCTGT	3300
	CTGCCCGACT	TCCAGATCTC	CTTCAACAAC	TATGTACCCA	ACAAGTCCAA	CAGTTTCCCC	3360
40	ACCGGCGTGA	TCGGCTGCAT	CCCGGCCCAT	GACCCCGACG	TGTCAGACAG	CCTCAACTAC	3420
	ACCTTCTGCT	AGGGCAACGA	GCTGCGCCTG	TGCTGTCTGG	ACCCCGCCAC	GGGCGAAGCT	3480
	CAGCTACGCC	CGACCTCTGA	CAACAACCGG	CCGCTGGAGG	CGCTCATGGA	GCTGTCTGTG	3540
	TCTGATGGCA	TCCACAGCGT	CACGGCCTTC	TGCACCTGCG	GTGTACCAT	CATCACGGAC	3600
	GACATGTCTG	CCACAGCAT	CACGTGCCGC	CTGGAGAACA	TGTCCACGGA	GAAGTCTCTG	3660
45	TCCCGCTGCG	TGGCCCTCTT	CGTGGAGGGG	GTGGCCGCGG	TGCTGTCCAC	CACCAAGGAC	3720
	GAOCTGTCTG	TCTTCAAGCT	CAGAAAGGAC	ACCGACGCTA	GCTCCACAT	CCTGAACGCT	3780
	ACCTTCTCGG	CGCTGCTGCC	TGGCGGCGTC	CGCGGCCAGT	TCTTCCCGTC	GGAGGACGCT	3840
	CAGGAGCAGA	TCTACCTGAA	TCGGACGCTG	CTGACCACCA	TCTCCACGCA	CGCGTGTCTG	3900
	CCCTTCGACG	ACAACATCTG	CCTGCGCGAG	CCCTGCGAGA	ACTACATGAA	GTGCGTGTCC	3960
50	GTCTCTGCGAT	TGACAGCTC	CGCGCCCTTC	CTCAGCTCCA	CCACCGTCT	CTTCCGCCCC	4020
	ATCCACCCCA	TCAACGGGCT	GCGCTGCCGC	TGCCCGCCCG	GCTTCACCGG	CGACTACTGC	4080
	GAGACGGAGA	TGACCTCTG	CTACTCCGAC	CGGTGGGGCG	CCAACGGCGG	CTGCCGACG	4140
	CGCGAGGGCG	GCTACACCTG	CGAGTGCTTC	GAGGACTTCA	CTGGAGAGCA	CTGTGAGGTG	4200
	GATGCCCGCT	CAGGCGCGTG	TGCCAACGGG	GTGTGCAAGA	ACGGGGGCAC	CTGGTGAAC	4260
	CTGCTCATCG	GCGGCTTCCA	CTGCGTGTGT	CCTCTCGGCG	AGTATGAGAG	GCCCTACTGT	4320
55	GAGGTGACCA	CCAGGAGCTT	CCCGCCCCAG	TCTTCTGTCA	CCTTCCGGGG	CCTGAGACAG	4380
	CGCTTCCACT	TACCATCTC	CCTCACGTTT	GCCACTCAGG	AAAGGAACGG	CTTGTCTTCT	4440
	TACACGGGCC	GCTTCAATGA	GAAGCAGGAC	TTCACTCGCC	TGGAGATCGT	GGACGAGCAG	4500
	GTGCAGCTCA	CCTTCTCTGC	AOGGAGAGCA	ACAACGACCG	TGGCACCGAA	GGTTCACAGT	4560
	GGTGTGAGTG	ACGGGGGGTG	GCACTCTGTG	CAGGTGCACT	ACTACAACAA	GCCCCAATAT	4620
60	GGCCACCTGG	GCCTGCCCCA	TGGGCGGTCC	GGGGAAAAGA	TGGCCGTGGT	GACAGTGGAT	4680
	GATTGTGACA	CAACCATGGC	TGTGCGCTTT	GGAAAGGACA	TCGGGAACCT	CAGCTGCGCT	4740
	GCCACGGGCA	CTCAGACCGG	CTCCAAGAAG	TCCCTGGATC	TGACCGGCCG	TCTACTCTCT	4800
	GGGGGTGTCC	CCAACCTGCC	AGAAGACTTC	CCAGTGACAC	ACCGGCAGTT	CGTGGGCTGC	4860
	ATGCGGAACC	TGTCAGTCCA	CGGCAAAAAT	GTGGACATGG	CCGGATTCTA	CGCCAACAAT	4920
65	GGCACCCGCG	AAGGCTGCGC	TGCTCGGAGG	AACTTCTGCG	ATGGGAGGCG	GTGTCAGAAT	4980
	GGAGGCAACT	GTGTCAACAG	GTGGAATATG	TATCTGTGTG	AGTGTCCACT	CCGATTCCGC	5040
	GGGAAGAAGT	GTGAGCAAGC	CATGCCCTAC	CCCCAGCTCT	TCAGCGGTGA	GAGCGTCTGT	5100
	TCTTGAGTGT	ACCTGAACAT	CATCATCTCT	GTGCCCTGGT	ACCTGGGGCT	CATGTTCCGG	5160
	ACCCGGAAGG	AGGACAGCGT	TCTGATGAG	GCCACCACTG	GTGGGCCCCA	CAGCTTTCGC	5220
70	CTCCAGATCC	TGAACAACTA	CCTCCAGTTT	GAGGTGTCCC	ACGGCCCCCT	CGATGTGGAG	5280
	TCCGTGATGC	TGTCGGGTTT	GCGGGTGACC	GACGGGGAGT	GGCACCACTT	GCTGATGGAG	5340
	CTGAGAAGTC	TTAAGGAGGA	CAGTGAGATG	AAGCACTGGT	TACCAATGAC	CTTGGACTAT	5400
	GGGATGGACC	AGAACAAGGC	AGATATCGGG	GGCATGCTTC	CCGGGCTGAC	GGTAAGGAGC	5460
	GTGGTGTGCG	GAGGCGCCTC	TGAAGACAAG	GTCTCGGTGC	GCCGTGGATT	CCGAGGCTGC	5520
75	ATGCAGGGAG	TGAGGATGGG	GGGGACGCCC	ACCACGTCG	CCACCCGTAA	CATGAACAAC	5580
	GCACTCAAGG	TCAGGCTGAA	GGACGCGTGT	GATGTGGAAG	ACCCCTGTAC	CTCGAGCCCC	5640
	TGTCCCCCA	ATAGCCGCTG	CCAAGACGCG	TGGGAGGACT	ACAGCTCGGT	CTGTGACAAA	5700
	GGGTACCTTG	AGATAAATG	TGTGGATGCC	TGTCACTGTA	ACCCCTGOGA	GAACATGGGG	5760
	GCCTGCTGCG	GCTCCCCCGG	CTCCCCGCG	GGTACGTTGT	GCGAGTGTGG	GCCCCGTCAC	5820
80	TAGGGGCGGT	ACTGTGAGAA	CAAACTCGAC	CTTCCGTGCC	CCAGAGGCTG	GTGGGGGAAC	5880
	CCCGTCTGTG	GACCCGTGCA	CTGTGCCGTC	AGCAAGGCTT	TTGATCCCGA	CTGTAATAAG	5940
	ACCAACGGCC	AGTGCCAAAT	CAAGGAGAA	TACTACAGC	TCCTAGCCCA	GGCCACCGGG	6000
	CTGCCCTGCG	ACTGCTTCCC	CCATGGCTCC	CACAGCCGCA	CTTGCGACAT	GGCCACCGGG	6060
	CAGTGTGCTT	GCAAGCCCGG	CGTCACTGGC	CGCCAGTGCA	ACCGCTCGGA	CAACCCGTTT	6120
	GCGGAGGTCA	CCAAGCTCGG	CTGTGAAGTG	ATCTACAAATG	GCTGTCCCAA	AGCATTTGAG	6180

	GCCGGCATCT	GGTGGCCACA	GACCAAGTTC	GGGCGCCGG	CTGCGGTGCC	ATGCCCTAAG	6240
	GGATCCGGTG	GAAATGCGGT	CCGACACTGC	AGCGGGGAGA	AGGGCTGGCT	GCCCCCAGAG	6300
	CTCTTTAACT	GTACCAACCAT	CTCCTTCGTG	GACCTCAGGG	CCATGAATGA	GAAGCTGAGC	6360
5	CGCAATGAGA	CGCAGGTGGA	CGGCGCCAGG	GCCCTGCAGC	TGGTGAGGGC	GCTGCGCAGT	6420
	GCTACACAGC	ACACGGGCAC	GCTCTTTGGC	AATGACGTGC	GCACGGCCTA	CCAGCTGCTG	6480
	GGCCACGTCC	TTGAGCAGGA	GAGCTGGCAG	CAGGGCTTGG	ACCTGGCAGC	CACGAGGAGC	6540
	GCCGACTTTC	ACGAGGACGT	CATCCACTCG	GGCAGGCGCC	TCCTGGCCCC	AGCCACCAGG	6600
	GCGGCGTGGG	AGCAGATCCA	GCGGAGCGAG	GGCGGCAOAG	CACAGCTGCT	CGGCGGCTTC	6660
	GAGGGCTACT	TCAGCAACGT	GGCAGCGAAC	GTGCGGCGGA	CGTACCTGCG	GCCTTTCGTG	6720
10	ATCGTCAOCC	AGTGACAGTA	TCTTGCTGTG	GACATCTTTG	ACAAGTTCAA	CTTTACGGGA	6780
	GCCAGGGTCC	CGCGATTGGA	CACCATCCAT	GAAGAGTTCC	CCAGGGAGCT	GGAGTCTCTC	6840
	GTCTCCTTCC	CAGCGGACTT	CTTCAGACCA	CCTGAAGAAA	AAGAAGGCCC	CCTGCTGAGG	6900
	CCGGCTGGCC	GGAGGACCAC	CCCGCAGACC	ACGCGCCCGG	GGCTTGGCAC	CGAGAGGGAG	6960
	GCCCCGATCA	GCAGGCGGAG	GCGACACCTT	GATGACGCTG	GCCAGTTCCG	CGTGCCTCTG	7020
15	GTATCATTTT	AGTGACACCT	GGGGCAGCTC	CTGCCCGAGC	GCTACGACCC	CGACCGTCCG	7080
	AGCCCTCCGT	TGCCTCACCG	GCCCATCATT	AATACCCCGA	TGGTGAGCAC	GCTGGTGTAC	7140
	AGCGAGGGGG	CTCGGCTCCC	GAGACCCCTG	GAGAGGCCCG	TCCTGGTGGG	GTTCGCCCTG	7200
	CTGAGAGTGG	AGGAGCGAAC	CAAGCCTGTC	TGCGTGTCTT	GGAACTACTC	CCTGGCCGTT	7260
20	GGTGGGACGG	GAGGGTGGTC	TGCCCGGGGG	TGCGAGCTCC	TGTCCAGGAA	CGGACACAT	7320
	GTGCGCTGCC	AGTGACAGCA	CACAGCCAGC	TTTGCGGTGC	TCATGGATAT	CTCCAGCGGT	7380
	GAGAACGGGG	AGGTCTCTGC	TCTGAAGATT	GTCACTATG	CCGCTGTGTC	CTTGTCACTG	7440
	GCAGCCCTGC	TGGTGGCTCC	GTCTCTCTG	AGCCTGGTCC	GCATGTCTGG	CTCCAACTCT	7500
	CACAGCATTC	ACAAGCACCT	CGCCGTGGCG	CTCTTCTCTT	CTCAGCTGGT	GTTCGTGATT	7560
25	GGGATCAACC	AGACGGGAAA	CCGTTTCTTG	TGCACAGTGG	TGCTCATCTC	CCTCCACTAC	7620
	ATCTACATGA	GCACCTTTGC	CTGGAACCTC	GTGGAGAGCC	TGATGTCTTA	CGCATGCTG	7680
	ACCGAGGTGC	GCAACATCGA	CACGGGGCCC	ATGCGGTCTT	ACTACGTCTG	GGGTGGGGGC	7740
	ATCCCGGGCC	TTGTCAAGAG	ACTGGGGTTC	GGCTTGGACC	CCGAGGGCTA	CGGGAACCCC	7800
	GACTTCTGCT	GGCTGTGCTG	TCAAGACACC	CTGATTGGA	GCTTTGCGGG	GCCCATCGGA	7860
30	GCTGTATTAA	TCAATCAACAC	AGTCATTTCT	GTCTTATCTG	CAAGGTTTTC	CTGCCAAAGA	7920
	AAGCACCAAT	ATTATGGGAA	AAAAGGGATC	GTCTCCCTGC	TGAGGACCGC	ATTCTCTTGA	7980
	CTGCTGTCTA	TCAGCGCCAC	CTGGCTGTCT	GGGCTGCTGG	CTGTGAACCG	CGATGCACTG	8040
	AGCTTTCACT	AGCTCTTTCG	CATCTTCAGC	GGCTTACAGG	GCCCTTCTGT	CCTCTTTTTC	8100
	CACCTGCGTC	TCAACACAGA	GGTCCGGAAG	CACCTGAAGG	GCGTGTCTCG	CGGAGGGAAG	8160
35	CTGCACTTGG	AGGACTTCCG	CACCACCAGG	GCCACCTCTG	TGACGCGCTC	CCTCAACTGC	8220
	AACACCAACT	TCGGTGACGG	GCCTGACATG	CTGCGCACAG	ACTTGGGGCA	GTCCACCGCC	8280
	TCGCTGGACA	GCAATGTCAG	GGATGAAGGG	ATCCAGAAGC	TCGGCGTGTG	CTCTGGGCTG	8340
	GTGAGGGGCA	GCCACGGAGA	GCCAGACGCG	TCCCTCATGC	CCAGGAGCTG	CAAGGATCCC	8400
	CCTGGCCACG	ATTCCGACTC	AGATAGCGAG	CTGTCCCTGG	ATGAGCAGAG	CAGCTCTTAC	8460
40	GCCTCTCTAC	ACTCGTCAGA	CAGCGAGGAC	GATGGGGTGG	GAGCTGAGGA	AAAATGGGAC	8520
	CCGGCCAGGG	GCGCGGTCGA	CAGCACCCCC	AAAGGGGACG	CTGTGGCCAA	CCAGCTTCCG	8580
	GCGCGCTGGC	CCGACAGGAG	CCTGGCTGAG	AGTGACAGTG	AGGACCCACG	CGGCAAGCCC	8640
	CGCTCAAGGG	TGGAGACCAA	GGTCAGCGTG	GAGCTGCACC	GCGAGGAGCA	GGGCAGTCA	8700
	CGTGGAGAGT	ATCCCCCGGA	CCAGGAGAGC	GGGGGCGCAG	CCAGGCTTGC	TAGCAGCCAG	8760
45	CCCCCAGAGC	AGAGGAAAGG	CATCTTGAAG	AATAAAGTCA	CCTACCCGCG	GCGGCTGAGG	8820
	CTGACGGAGC	AGACGCTGAA	GGGCCGGCTC	CGGGAGAAAG	TGGCCGAGTG	TGAGCAGAGC	8880
	CCCACTCACT	CGCGCAGCTG	TTCCCTGGGC	TCTGGCGGCC	CCGACTGCGC	CATCAGAGTC	8940
	AAGAGCCCTG	GGAGGGAGCC	GGGGCGTGAC	CACCTCAAGG	GGGTGGCCAT	GAATGTGGGC	9000
	ACTGGGAGCG	CCCAGGCCGA	TGGCTCCGAC	TCTGAGAAAC	CGTGAGGCAA	GCCCGTCACC	9060
50	CCACACAGCG	TGCGGATCA	CCCTCAGACC	TTGGAGCCCA	AGGGGCCACT	GCCCTTGAAG	9120
	TGGAGTGGGC	CCAGAGTGTG	GCGGTCCCCA	TGGTGGCAGG	CCCCCGACTG	ATCATCCAGA	9180
	CACAAAGTGT	TTGGTTCTCC	CAGGAGCTCA	GCGGCTGTCA	GACCTGTGTA	CAAGTGCCAA	9240
	AGGCCACAGG	GCCAGGGGAG	GCGTGGACCA	CTGGGCCAGC	ACCGCTGAGT	CCTAAGACTG	9300
	CAGTCAAGGC	CAGAAGTGTG	AGGGGAGCCC	AGACTGGGCC	CAGAGGCTGG	CCAGAGTTCA	9360
55	GGAAACCGCG	GCAACAGACA	AAGACCGCGG	TCCAGCCCGG	CCCAGGCGGG	CATCTCATGG	9420
	CAGTGGGAGC	CCGTGGCTGG	CAGCCCGGGC	AGTCTCTTTC	AAAGGCACCC	CTTGTCTTAA	9480
	AATCACTTCG	CTATGTGGGA	AAGGTGGAGA	TACTTTTATA	TATTTGTATG	GGACTCTGAG	9540
	GAGGTCAAC	CTGTATATAT	ATTGCACTCG	TGCTGACTTT	GTTATCCCGA	GAGATCCATG	9600
	CAATGATCTC	TGCTGTCTTT	CTCTGTCAAG	ATTGCACAGT	TGTACTTGAA	TCTGGCATGT	9660
60	GTGAGCAAAA	CTGTGTCCCC	AGCAGATCAA	AGGTGGGAAA	TACGTACGCA	GTGGGGCTAA	9720
	AAACCAAGCG	CTAGAAGCCC	TACAGCTGCC	TTCCGCGCAG	AAGTGAGGAT	GGTGTGGGCC	9780
	CTCCCGCGCG	GCCCGCTGGG	TCCCGAGTGT	TGCGTGTGTG	TGCGTTTGTG	CTCTGCTGCC	9840
	ATCTGCCCCG	CTGTGTGAAA	TTCAAGACAG	GGCAGTGCAG	CACATAGGAG	GTGTGAGGAG	9900
	CCCTGCTGAG	GTCACTGTGG	GGCACGGTTG	CCACACGGCT	GTCAATTTTC	ACCTGGTCAT	9960
65	TCTGTGACCA	CCACCCCTTC	CCCTCACCGC	CTCCAGGTTG	GCCCGGGAGC	TGCAAGTGGG	10020
	GATGGCTTTG	TCCTTTTGCTC	CTGCTCCCGG	TGGGACCTGG	GACCTTAAAG	CGTTGCAAGT	10080
	TCCTGATTGG	GACAGAGGTG	TGGGCGCTTC	CAGGCGGTTA	CATACCTCTT	GCCATTTCTC	10140
	TAACCTCTTG	AGACTGCGAG	GATCTCCAAG	CAGGTTTCTC	CCCTCTGGAG	TCTGAACCAAT	10200
	TACTTCAATT	TGCTTCAAAAT	GGCCAAATGT	GCAGAGGGAC	AAAGCCACAG	CCACACTCTT	10260
70	CAACGGTTAC	CAAACTGTTT	TTGGAAATTC	ACACCAAGGT	CGGGCCCACT	GCAGGACAGT	10320
	GGCACAGGCT	GGCCCGAGGG	GCTGTGGAAC	GGGTCCCGGA	ACTGTACAGC	ATGTTTGATT	10380
	TTAGCGTTTC	CTTTGTCTCT	CAAAATCAGG	GCCCAAAATA	GTGATCAGCA	CAGCTGCTTC	10440
	CAAAATAGGAG	AAACCATATA	ATAGGATGAA	AATCAAGTAA	AATGCAAGCA	TGTCCACACT	10500
	GTTTTAAACT	TGACCCCTGAT	GAAAATGTGA	GCACTGTTAG	CAGATGCCCTA	TGGGAGAGGA	10560
75	AAAGCGTATC	TGAAAATGGT	CCAGGACAGG	AGGATGAAAT	GAGATCCAGG	AGTCTCTACA	10620
	CCTGAATGAA	TATATACATG	GCCCTAACAG	GTGAGTGGTC	TTTCCGAAGT	AAAAAACTCT	10680
	AGTCCCTTTA	AACGTTTGCC	CCTGGCGTTT	CCTAAGTACG	AAAAGGTTTT	TAAAGTCTTG	10740
	AACAGTCTCC	TTTCACTGAT	TTAACAGGAT	TCTGCCCTCT	GAGGTGTAAT	TTTTTTGTTT	10800
	TATTTTTTTC	CACGTACTCC	ACAGCCAACA	TCAAGAGGTG	TAAATTTTAA	TTTTGATCAG	10860
80	ACTGTTACCA	AAAAACAACCT	GTCACTTTTA	TTGAGATGGG	AAAAATGTAA	ACCTATTTTT	10920
	ATTACTTAAG	ACTTTATGGG	AGAGATTAGA	CACGTGAGGT	TTTTAACAGA	ACGTGTATTT	10980
	ATTAATGTTC	AAAAACACTGG	AATTACAAAT	GAGAAAGATC	TACAAATAAT	TAAAGTTTTT	11040
	GAATTTGTAT	TTCTGGGGTG	CTGGTTTCTC	TCCACAAACA	CCCCCGCCCC	TCCCATGCCC	11100
	CAGGGTGGCC	GTGGAAGGGA	CGGTTTACGG	ACGTGCAGCT	GAGCTGTCCG	TGTCCCATGC	11160
	TCCCTCAGCC	AGTGGAACTG	GCCGAACTT	TTTGTCCATT	CCCTAGTAGG	CCTGCCACAG	11220

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CCTAGATGGG CAGTTTTTGT CTTTCACCAA ATTGAGGAC TTTTTTTTTT TGCCATTATT 11280
 TCTTCAGTTT TCTTTCTCTG CACTGATCTT TCTCTCTCC TTCTGTGACT CCAGTGACTC 11340
 AGACGTTAGA CTTCTTGATG TTTTCCCACT GGTCCCTGAG GCTCTGTTT

5 **A32 Protein Sequence**
 Gene name: CH22_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo
 (Drosophila) homolog (CELSR1),
 Hs.252387
 Unigene number:
 Protein Accession #: NP_055061
 10 Signal sequence: 1-20
 Cadherin domains: 250-344, 358-449, 464-556, 570-678, 692-780, 794-883, 897-990, 1004-1092,
 1110-1199
 Pfam domains: Laminin_EGF [2003-2048], 7tm_2 [2465-2708]
 Latrophilin/GPS domains: 2407-2460
 15 Transmembrane domains: 1219-1238, 2473-2492, 2507-2522, 2529-2547, 2616-2634, 2659-2675, 2687-2704
 Cellular Localization: plasma membrane

20 1 11 21 31 41 51
 MAPPPPPVLP VLLLLAAAA LPAMGLRAAA WEPRVPGGTR AFALRPGCTY AVGAACFPRA 60
 PRELLDVGRD GRLAGRRRVV GAGRPLPLQV RLVARSAFTA LSRRLRARTH LPGCGARARL 120
 CGTGARLCA LCFPVPGGCA AAQHSALAAP TTLPACRCPP RPRPCRCPP ICLPPGGSVR 180
 25 LRLLCALRA AGAVRVGLAL EAATAGTPSA SPSPPPLPP NLPEARAGPA RRARRGTSGR 240
 GSKFPMFNY QVALFENEP GTLILQLHAH YTIEGEEERV SYMEGLFDE RSRGYFRIDS 300
 ATGAVTDSV LDRETKETHV LRVKAVDYST PPRSATTYIT VLVKDTNDHS PVFEQSEYRE 360
 RVRENLEVG EVLITIRASDR DSPINANLRY RVLGGAWDVF QLNSSSGVVS TRAVLDREEA 420
 AEYQLLVEN LQGRNPGPLS ATATVYIEVE DENDNYPQPS EQNYVVQVPE DVGLNTAVLR 480
 VQATDRDQQQ NAAIHYSILS GNVAGQFYLE SLSGILDVIN PLDFEDVQKY SLSIKAQDGG 540
 30 RPPLINSSGV VSVQVLVDND NEPIFVSSPF QATVLENVPL GYPVHHQAV DADSGENARL 600
 HYRLVDAST FLGGGSAGPK NPAPTDFDFP QIHNSSGMIT VCAELDREEV EHYSPGVEAV 660
 DHGSPPMSS TSVSITVLVD NDNDPVFTQP TYELRLNEDA AVGSVSLTLQ ARDRDANSVI 720
 TYQLTGNTN NRPALSSQSG GGLITLALPL DYKQEQYVAV AVTASDGTSS HTAHVLINVT 780
 DANTRHPVQ SSHYTVSVSE DRPVGTISIAT LSANDEDTGE NARITYVIQD PVPQFRIDPD 840
 35 SGTMYTMEL DYENQVAYTL TIMAQDNGIP QKSDTTTLEI LILDANDNAP QFLWDFYQGS 900
 IFEDAPPSTS ILQVSATDRD SGPNRLLYT FQGGDDGDGD FYIEPTSGVI RTQRRLDREN 960
 VAVYNWALA VDRGSPTPLS ASVEIQVTIL DINDNAPMPE KDELLEFVEE NNPVGSVVAK 1020
 IRANDPDEG NAQIMYQIVE GDMRHFQQLD LLNGDLRAMV ELDFEVRREY VLVVQATSAP 1080
 LVSRAVHIL LVQDNDNPFV LPDFQILFNN VYTNKNSNFP TGVIGCIPAH DPVDSDSLNY 1140
 40 TFVQGNELRL LLLDPATGEL QLSRDLDNMR PLEALMEVSV SDGIHVSATF CTRLVITITD 1200
 DMLTNSITVR LENNSQEKFL SPILLALFVSG VAAVLSTTKD DVFFVFNQND TDVSSNILAV 1260
 TFSALLPGGV RQGFPPSEDL QEIQYLNRNL LTTISTQRVL PFDDNICLRE PCENYMKCVS 1320
 VLRFDSSAPP LSSTTVLFRP IHPINGLRCR CPPGFTGDYC ETEIDLCSYD PCGANGRCRS 1380
 45 RBGGYTCRCF EDOFTGERCEV DARSGRCAAG VCKNGGTCVN LLIGGFHCVC PPGEYERFYC 1440
 EVTTRSPFPQ SPVTFRGLRQ RFHFTISLTF ATQERNGLLL YNGRFNEKHD FIALEIVDEQ 1500
 VQLTFSAGET TTTVAPKVPS GVSQGRWHSV QVQYNNKPI GHILGLPHGS GEMMAVTVTD 1560
 DCDTMAVRF GKIDIGNYSCA AQGTQTSKSK SLDLTGPLLL GGVNPLPDPF PVHRNQFVGC 1620
 MRLNSVDGKN VDMAGFIANN GTREGCAARR NFGDGRCCQN GGTVCNRRNM YLCECLPRFG 1680
 50 GKNCQAMPH PQLFSGESVV SWSDLNIIIS VPWYGLMFR TRKEDSVLME ATSGGPTSF 1740
 LQILNNYLQF EVSHGFSQVE SVMLSQLRVT DGEWHELLIE LKNVKEDSEM KHLVTMTLDY 1800
 GMDQNKADIG GMLPGLTVRS VVVGASEDK VSVRGFRGC MQGVRMGSTP TNVATLAMNN 1860
 ALKVRVKDGC DVDDPCTSSP CPFNRSCHDA WEDYSCVCDK GYLGINCVDA CHLNPENMG 1920
 55 ACVRSPGSPQ GYVCEGSPSH YGPYCENKLD LPCPRGWGN PVCGPCHCAV SKGFPDPCNK 1980
 TNQCQCKEN YYKLLAQDTC LPCDCPPHGS HSRTCMMATG QCACKPGVIG RQCNRCNPF 2040
 AEVTTLGCEV IYNGCPKAFE AGIWWPQTKF GQPAAVPCPK GSVGNVAVRH SGEKGLPFPE 2100
 LFNCTTISPV DLRAMNEKLS RNETOVDGAR ALQLVRLRSL ATQHTGTFLFG NDVRTAYQLL 2160
 GHVLQESWQ QGFDLAATQD ADFHEDVIHS GSALLAPATR AAWEQIQRSE GGTAQLLERL 2220
 EGYPSNVARN VRTYLRFPV IVTANMILAV DIFDKENPTG ARVPRFTDIH EEPFRELSS 2280
 VSPFADFPFP PEEKGGLLR PAGRRTTPQT TRPGPGETER APISRRRRHP DDAGQFAVAL 2340
 60 VIIYRTLGQL LPERYDFDRR SLRLPHRPII NTPMVSTLVY SEGAPLPRPL ERFVLVEFAL 2400
 LEVEERTKPV CVFVNHSLAV GGTGGWSARG CELLSNRNTH VACQCSHTAS FAVLMDISRR 2460
 ENGEVLPKLI VTYAAVSLSL AALLVAFVLL SLVRMLRSNL HSIHKHLAVA LPLSQLVFVI 2520
 GINQTNPFPL CTVVAILLHY IYMSTPAWTL VESLHVYRML TEVRNIDTGP MRFYTVVWG 2580
 65 IPAIVTGLAV GLDPQGYGNP DFCNLSLQDT LIWSFAGPIG AVIIINTVTS VLSAKVSCQR 2640
 KHYYTGKGI VSLRLTAFL LLLISATWLL GLLAVNRDAL SFHYLFAIPS GLQGFVLLF 2700
 HCVLNQEVK HLKGVLGGRK LHLSDSATR ATLLTRSLNC NTFPGDGPDM LRTDLGESTA 2760
 SLDSIVRDEG IQKLGVSGL VRSGHGEPDA SLMPRSCKDP PGHDSDSSE LSLDEQSSSY 2820
 ASSHSSDSED DGVGAZEKWD PARGAVHSTP KGDVAVNHVP AGWPDQSLAE SDEDPGSKP 2880
 70 RLKVTKVSV ELHREEQGSH RGEYPPDQSS GGAARLASSQ PFEQRKGLK NKVTYPPPLT 2940
 LFEQTLKGR LREKLADCEQS PTSSRTSSLG SGGPDCAITV KSPGREPGRD HINGVAMNVR 3000
 TGSQAQDQSD SEKP

75 **A33 DNA SEQUENCE**
 Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3
 Hs.198252
 Unigene number:
 Probeset Accession #: X95876
 Nucleic Acid Accession #: X95876
 80 Coding sequence: 69-1175 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CCAACCAAA GCACCAAAAGC AGAGGGGCGAG GCAGCACACC ACCCAGCAGC CAGAGCACCA 60
 GCCCAGCCAT GTCTCTTGAG GTGAGTGACC ACCAAGTGCT AAATGACGCC GAGGTGCGG 120

CCTCTCTGGA GAACCTCAGC TCTTCTCATG ACTATGGGAA AACAGAGAGT GACTGTGCTC 180
 GTACCTCCCC GCGCTGCCCA CAGGACTTCA GCGTGAACCT CGACCGGGCC TTCTGTCGAG 240
 CCTCTACAG CCGCTCTTTT CTGCTGGGCG TGCTGGGCAA CGCGCGGCTG GCAGCGCTGC 300
 TCGTGAAGCG GCGGACAGCC CTGAGCAGCA CCGACACCTT CCGCTGCCAC CTAGCTGTAG 360
 CAGACACGCT GCTGTGTCTG ACTGTCGCGC TCTGGGCACT GGACGCTGCC GTCCAGTGGG 420
 TCTTTGGCTC TGGCCTCTGC AAAGTGGCAG GTGCCCTCTT CAACATCAAC TTCTACGCGAG 480
 GAGCCCTCTC GCTGCGCTGC ATCAGCTTTG ACCGCTACCT GAACATAGTT CATGCCACCC 540
 AGCTCTACAG CCGGGGCGCC CGGCGCGCGG TGACCTCTAC CTGCGTGGCT GTCTGGGGGC 600
 TCTGCTGCTT TTTCGCGCTC CCAGACTTCA TCTTCTGTCT GGCCCAACCAC GACGAGCGCC 660
 TCAACGCCAC CCACTGCCAA TACAACCTCC CACAGGTGGG CGCAGCGGCT CTGCGGCTGC 720
 TGCAGCTGGT GCGTGGCTTT CTGCTGCCCC TGCTGGTCAT GGCTTACTGC TATGCCACCA 780
 TCGTGGCGGT GCTGTCTGTT TCCAGGGGCC AGCGGCGGCT GCGGGCCATG CGGCTGGTGG 840
 TGGTGGTGGT GGTGGGCTTT GCGCTCTGCT GGACCCCTTA TCACCTGGTG GTGCTGGTGG 900
 ACATCTCAT GGAACCTGGG GCTTTGGGCC GCAACTGTGG CCGAGAAAGC AGGGTAGACG 960
 TGGCCAACTG GGTCACTCA GCGCTGGGCT ACATGCACTG CTGCGCTCAAC CCGCTGCTCT 1020
 ATGCCCTTGT AGGGGTCAAG TTCCGGGAGC GGATGTGGAT GGTGCTCTTG CGCTTGGGCT 1080
 GCGCCAAACA GAGAGGGGCT CAGAGGCAGC CATCGTCTTC CCGCGGGAT TCATCTCTGT 1140
 CTGAGACTCT AGAGGCTCTC TACTGGGCT TGTGAGGCG GAATCGGGG TCCCTCTTCT 1200
 CCCACAGTCT GACTTCCCGG CATTCAGGCG TCTTCCCTCC CTCTGCCGCG TCTGGCTCTC 1260
 CCCAATATCC TCGCTCCCGG GACTCACTGG CAGCCCGAGC ACCACCAAGT CTCCCGGGAA 1320
 GCCACCCCTC CAGCTCTGAG GACTGCACCA TTGCTGCTCC TTAGCTGCCA AGCCCATATC 1380
 TCGCCCGCGA GGTGGCTGCC TGGAGGCCCA CTGCGCTTCT CATTTGGAAA CTAACACTTC 1440
 ATCTTCCCA AGTGCGGGGA GTACAAGGA TGGGTAGAG GGTGCTGCC CATGAAGCCA 1500
 CAGCCAGGCG CTCAGCTCA GCACTGACTG TGGCCATGGT CCCCAGACC TCTATATTG 1560
 CTCTTTTATT TTTATGTCTA AAATCTGCTT TAAACTTTT CAATAACAA GATCGTCAGG 1620
 ACCAAAAAAA AAAAAA AAAA AAAAAA AAAAAA AAAAAA BHCLITERAT 1680
 UREBHCBLAS TPBHCORTHO LOGUESMOUS ECXCRMYLEV SERQVLDAVD PAFLEENST 1740
 PVDGENESD FSDSPCPQD FSLNFDRTFL PALYSLFLLL GLLGNAGAVA VLLSQRALS 1800
 STDFTLLHLA VADVLLVLT PLWAVDAVQ WVFGPLCKV AGALFNINPY AGAFLLACIS 1860
 FDRYLSIVHA TQIYRRDPRV RVALTCIVVM GLCLLPALPD FIYLSANYDQ RLNATHCQYN 1920
 FPQVGRTRAL VLQLVAGFLL PLLVMAYCYA HILAVLLVSR GQRRFRAMBL VVVVVAFAV 1980
 CWTPLYHLVL VDILMDVGV LARNCGRESHV DVAKSVTSGM GYMHCCLNPL LYAPVGVKFR 2040
 EQNMMLFTRL GRSDQRGPQR QPSSSRRESS WSETTEASYL GL

A34 Protein sequence
 Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3
 Unigene number: Hs.198252
 Protein Accession #: P49682
 Signal sequence: none found
 Pfam domains: 7tm_1 [70-318]
 Transmembrane domains: 57-78, 92-113, 129-147, 169-190, 222-243, 257-275, 307-323
 DRY box: 148-149
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MVLEVS DHQV LNDAEVAALL ENFSSSYDYG ENESDSCTCS PPCPDPSLN PDRAFLPALY 60
 SLFLFLGLLG NGAVAAVLLS RRTALSSTDT FLLHLAVADT LLVLTLPLWA VDAAVQWVFG 120
 SGGLCKVAGAL FNINFYAGAL LLACISFDRY LNIHVATQLY RRGFPARVTL TCLAVWGLCL 180
 LFALPDVIFPL SAHNDERLNA THOQYNFPQV GRTALRVLQL VAGFLLPLLV MAYCYAHILA 240
 VLLVSRGQMR LRAMRLVVVV VVAFALCWTP YHLVVLVDIL MDLQALARNC GRESRVDAK 300
 SVTSGLLGYMH CCLNPLLYAF VGKFRERMW MLLRLGCPN QRGLQRQPS SRSDSSWSET 360
 SEASYSGL

A35 DNA SEQUENCE
 Gene name: Differentially expressed CO16 gene (clone MGC:5257)
 Unigene number: Hs.69517
 Probeset Accession #: AA447522
 Nucleic Acid Accession #: BC001291
 Coding sequence: 44-541 (start and stop codons are underlined)

1 11 21 31 41 51
 GGGGGCGCGG CGCGCTGACC CTCCTTGGGC ACCGCTGGGG AGGATGGGCG TGTCTGCCTT 60
 GCTGCTGGTG GTGGCCCTAC GCGGGGTGTG GACAGACGCC AACCTGACTC CGAGACAACG 120
 AGATCCAGAG GACTCCGCTG GACGCGACGA GGGTGACAAT AGAGTGTGGT GTCATGTTTG 180
 TGAGAGAGAA AACACTTTGG AGTGCCAGAA CCGAGGAGGG TGCAAAATGA CAGAGCCATA 240
 CTGCGTTATA GCGGCGGTGA AAATATTTC ACCTTTTTTC ATGGTTTGGC AGCAGTGCTC 300
 CGCTGTTTGT GCAGCGATGG AGAGACCCAA GCGCAGGAGG AAGCGGTTTC TCTCGGAAGA 360
 GCGCATGCCC TCTTTTATAC TCAAGTGTG TAAATTCGCT TACTGCAATT TAGAGGGGCG 420
 ACCTATCAGT TCATCAGTGT TCAAGAAATA TGCTGGGAGC ATGGGTGAGA CTAATGGTGG 480
 GCTGTGGCTG GCCATCTCTC TGCTGCTGGC CTCCATTGCA GCGGCGCTCA GCGTGTCTTG 540
 AGCCACGGGA CTGCCACAGA CTGAGCCTTC CGGAGCATGG ACTCGCTCCA GACCGTTGTC 600
 ACCGTGTGCA TTAACATTGT TTCTGTGTGA TTACCTCTTG GTTTGACTTC CCAGGGTCTT 660
 GGGATGGGAG AGTGGGGATC AGGTGCAATT GGCTCTTAAC CCTCAAGGGT TCTTTAACTC 720
 ACATTACAGG GAAGTCCAGA TCTCTGAGT AGTGATTTTG GTGACAAGTT TTCTCTTTTG 780
 AAATCAAACC TTGTAACATA TTTATTGCTG ATGGCCACTC TTTTCTTGA CTCCCTCTG 840
 CCTCTAGGG CTTCAGTATT GATGGGGAGG GAGGCCAAG TACCCTCAT GGAGAGTATG 900
 TGCTGAGATG TCTCGAGCTT GCAGGAAACAC TGGGGGAGTC TGAATGATTG 960
 GGGTGAAGAC ATCCCTCGAG TGAAGGACTC CTCAGCATGG GGGGCAAGTG GGCACACGTT 1020
 AGGGCTGCC CCATTCAGT GGTGGAGGCG CTGTGGATGG CTGCTTTTTC TCAACCTTTC 1080

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CTACCAGATT CCAGGAGGCA GAAGATAACT AATTGTGTTG AAGAACTTA GACTTCACCC 1140
 ACCAGCTGGC ACAGGTGCAC AGATTCTATA ATCCCCACAC GTGTGTGTTT AACATCTGAA 1200
 ACTTAGGCCA AGTAGAGAGC ATCAGGGTAA ATGGCGTTCA TTTCTCTGTT AAGATGCAGC 1260
 CATCCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCCACC AAAACCAAT ACAAGGGGAC 1320
 TCAAAAGTT CACGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA

A36 Protein sequence:

Gene name:

Differentially expressed CO16 gene (clone MGC:5257)

Unigene number:

Hs.69517

Probeset Accession #:

AA447522

Protein Accession #:

AAH01291

Signal sequence:

1-17 (first underlined sequence)

Transmembrane domain:

146 - 162

Cellular localization:

plasma membrane

1 11 21 31 41 51
 MALLALLLVV ALPRVWTDAN LTARQRDPED SORTDEGDNR VWCHVCEREN TPBCQNPRRC 60
 KWTEPYCVIA AVKIFPPPFM VAKQCSAGCA AMERPKPEEK RFLLEPMFPF FYLKCKKIRY 120
 CNLEGPFIN SVFKYVAGSM GESCGGLWLA ILLLLASIAA GLSL

A37 DNA SEQUENCE

Gene name:

ESTs

Unigene number:

Hs.293616

Probeset Accession #:

AW043782

Nucleic Acid Accession #:

none found

Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
 AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGGCCCATG TGGCTGCTGG GGCCGCTGTG 60
 CCTGCTGCTG AGCAGCGCGG CGGAGAGCCA GCTGCTCCCC GGGAAACACT TCACCAATGA 120
 GTGCAACATA CCAGGCAACT GCTGCTGACT GATGATGAG AAGGAGTGCC CCAAGGCTAA 180
 GTGTGACGGG CTGCTGACT GCTTCGACAA GAGTGTGAG AAGGAGTGCC CCAAGGCTAA 240
 GTGCAAAATG GGGCCAACTT TCTTCCCTCG TGCCAGCGCG ATCCATTGCA TCATTGGTGG 300
 CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
 AAACCCCTCG CTTTGTCTCA CCGCCCGCTA CCACTGCAAG AACGGCCTCT GTATTGACAA 420
 GAGCTTCATC TGCGATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
 AAGTTCTCAA GAACCCGGCA GTGGGCGAGT GTTTGTGACT TCAGAGAACC AACTGTGTGA 540
 TTACCCGAGC ATCACCATTG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600
 CCTGCTGGCA CTGGTCTTGG ACCACCAGCG GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660
 GCACCGGCTG CAGCACCTGT TGCTGCTGTC CCGCTGCTGG GTCTTGGAGC ACCCCACCA 720
 CTGCAACCTC ACCTACAAAG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780
 GAATGGCTCG GAAGTAGGCT CCCCACTCTC CTACTCCGAG GCCTTGTCTG ACCAGAGGCC 840
 TGCGTGGTAT GACCTTCTCT CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900
 CGACCTGCCC CCCTACCGCT CCGGCTCCGG GAGTGCCAAAC AGTGCCAGCT CCCAGGCAGC 960
 CAGCAGCCTG CTGAGCGTGG AAGACACCAG CCACAGCCCG GGGCAGCCTG GCCCCAGGA 1020
 GGGCACTGCT GAGCCGAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080
 AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACT GTTGCCATTC TAACAATTG 1140
 TGCTCATGGG AAGCTCTTTA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200
 AACTATCTCT GCATTCOCCT CCTCCCCAG ACTTCAGAGA TGTTTTCTG GGTCTCTAGT 1260
 TGACATCTCT TGTGTGGGT CTTTCTGTC AGGTCACCTT TCCCTTGGGA CCCGAGATCA 1320
 CACCCCTATT TTTACATTA TTCTGTTTCT GTTGGAGAGA CAGCATATAA AACAGTATTG 1380
 AAATAGGCTG GAGAGAGACA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440
 CGCTGGACCC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTGGGGA TTTGGGTTAG 1500
 ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCCCC CAATAAAATT CCAATTGAGC 1560
 ATCAAAACCT GCTTGCACA ATCCTATTGG ATGCCCCAG TTCAGCAGAG TCAGTGGCCA 1620
 AAGAAACCTT TGGACGTGAG TAACACCCCT CAGCAGTCGC AACGTTATTT TGGTTTGTG 1680
 AAGGACTCTG AAACCATCTA CCTGTATATA ATTCTGGCTT TAGAAATTG CCAAGAAATG 1740
 CTCATTCTGA GAGCTTCTCT CAGCAGCATA TATCATCAGC CTCATCCTAA AATAGGCAGG 1800
 GAGCCCTCC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC 1860
 TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCCAC CTCCAGCTG 1920
 ACCTGCCCGT AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAGATC TGACCTGGCT 1980
 GTATGTCCCT GTGGCCACA CCGACCTGT CTGCTCATTT CATGCAGCCT CRACACTGGC 2040
 CTCCAAGATT CCTTAAACAC TTGCAAAGTC CTTTTTACCT GTGCATTGG ACTTGAGGAC 2100
 ACTGGTTTCT ATCAGAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160
 CTGCACTGTG CAGCTCTCTC TTCCCAAGGT CCCAATACCA GACCTCTAG TTAGAGTTAG 2220
 GGTGAGGCTC AGGCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280
 AGACAATTG GAGTCAAGAT TTCCATTGTT GATCTATTTT AAATCTTTTA GAAATGCATT 2340
 TGAATACAGT TGTTTGTTT TTCCCTTCTA GTTAAGGAC TATTATATG TGTATAGGAA 2400
 AGCTGTCTCT TTTTGTGTTT TTCCCTTAAAC AAGTCCAAA GAAAGATGCA AAAGGAGATC 2460
 ACACCTTGGC CCGCTGAGC CCGGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520
 ACATTGTGTC ATTGTGCAC TTTGAGGTTA TTATTATCA AGTCTCTGAA GGAAGCAGAA 2580
 AGAGGGACTC CTCTCTCCTC CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTT 2640
 TTCTCTGTGT CAGCTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAAAGTT 2700
 AGGTGTTGTT TGGCAGAGAA CCACACTGAC TGATGAGGGG TAAATGGA CCAGGTAGAG 2760
 CCATCCCGGG CAGCTGTGAC CCATTGAGAA CTCTTTCCG CAGCTGAAGA AATGTTCACT 2820
 AACCTGTTTG AGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAG TGGCATTCAG 2880
 TGATCCTGTT CTGTAGACTT TTCTTTCTTT TTTTAAACCA ATCCAAAGGA TGTACAGAA 2940
 AAGCTAGCCA CTGGTATTTT GTTTGTTTAA AAAAAAAAAA GAAGAGAGA AAGAAAGAAA 3000

AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
 CTGAGTAATC CAATAAAGAA CTTTGTATGA CAGCCAGAAAT GTGTAGAAC TCTGGCTGAA 3120
 CATTTCATCT CCTGTGAGTC AGAAGGGCTT TATTTCTCCC TTGTATGGGG CCCCTCTCTC 3180
 5 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTATGT 3300
 AGATAAGGGA TGCCCTACTAA TGCTTTTITA AAACAAACAG GGACATTTT ATTATAGATT 3360
 TGATTTTITT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT 3420
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480
 10 TTTTAACTC ATTTCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAAACAG 3540
 AAAATAGTCT CATCTCTTTT TTTCTCAAT GAGATCCGTG TTTTATTTA GCATTAAAT 3600
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTGA ATGTAAACTG 3720
 GAAAGGTTGT GTGTGCTTGC TTTTGTGTTT TTGGTTAGGC TTGGTTTGT TTTTAAATT 3780
 15 TTATCTTTC TAATAAATTT GCAGTTTCAT TCTTCTGTTT TGTGCAAANG GWNCTAMARM 3840
 AAMMAAAAC AWYWTGCGG GGGCTTGGGC CTCGGAATAA GTTTTAAACA CCACTTCGGG 3900
 TGGGGCGGGG GGGCCACGCT AGGTACGGGG ACCACGCGGG CCCAAACGGG ACCCCAGAGG 3960
 GAAACCCCTG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAAA ACGCGCGGG 4020
 20 GGAACCGCA GAGTGTTCG TAAACACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

A38 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293616
 25 Probeset Accession #: AW043782
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: 169-191
 30 LDL domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 35 MWLLGPLCLL LSSAAESQLL PGNNPTNECN IPGNFMCNNG RCIPGAWQCD GLPDCFDKSD 60
 EKECFKAKSK CGPTFFPCAS GIHCLIGRFR CNQFEDCPDG SDEENCTANP LLCSTARYHC 120
 KNGLCIDKSF ICDQNNQCD NSDEBSCSS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180
 VIFVLVALL ALVLHQRKR NNLMTLPVHR LQEPVLLSRL VVLDHPHRCN VTYNVMNGIQ 240
 YVASQABQNA SEVGSPSPYS EALLDQRPW YDLPPFPYSS DTESLNQADL PPYRSRSGSA 300
 40 NSASSQAASS LLSVEDTSHS PQQPQPGQBT ABPRDSEPSQ GTEEV

A39 DNA sequence

Gene name: ESTs
 45 Unigene number: Hs.128899
 Probeset Accession #: AA983251
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)
 1 11 21 31 41 51
 50 ATGCTGCTG GCTTCTTGAT GAGTCCCACT ACCCAGCACA GAGCAGAGTA CACTCCCGGA 60
 GGAAGAAAC TTCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCGAGG GCGAGGCAGC 120
 GACCGGGAGA GCGAGAGCGG GCGGAGGCT GCGGGCTCC TGTGGGACG CGCTGCAGCC 180
 GGGGAGGCGG AGAAGGGGAA CCGGGCGGAG CCGCCCGCCT GGATCCGCG CAGCAGCAG 240
 55 CGCGCGCGCG CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC CAGGAGCCCT 300
 CGCTGCTGTC CTGGACGTTT CCGGGGGAGG GTCCGTTTGC CAGTGAACCC TCCAGAGGCT 360
 TCCGAGCAGC AGCCCCGGGG GCCTTCTGAC TGATCCCGA GATTTCATC AGCAGTGA 420
 ACTCATAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGA TGGCTTAGA 480
 GCTCTGGAC CTAGGGCCCG GGTGTGTGCG CTCTGCGCG TCGCGGAGA GGGGAGTGGC 540
 60 CCGCGCGGAA AGCGCGCGCG GACAGTCAGT GACGAGGCC GGGGGTGCCT GGGGCCACGA 600
 CTCTCGGAG ACCGTCTGTC GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTGCCA 660
 TGTGGGGCGC TCGCGCTCG TCGTCTCTCT CATCTGGAA CGCGCTTGG CTCTGCAGC 720
 TGTGCTGGC TCGCTGCTG GCGGCGGGGG CGAGGGCCCA GCGCGAGTA CTGCCACGGC 780
 TGGCTGGAG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGG CTTCCAGCGC 840
 65 GCGGACGCCA CCATCTGCTG CGGCACTGCG GGTGTGCGCT ACTGCTGCTC CAGCGCCGAG 900
 GCGCGCTGT ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 960
 CGGGCGGACA AAGACGGGCC CGGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020
 GGAGACCGCG AGGGTGGCGC CCCACCGTGG AGGGCTGGC AGCGGTGCTC CCTGAAGGC 1080
 70 TCCCGAAG GAAGGAGCT CCTCAGGGCT TTCCCGGGG TGCTGCCCG TGCCAGAGC 1140
 CGCGGATTC CATCTTCTCC ACGCGGGCG CCTCTCCCC TGCGAGGGC CGCTTGGCC 1200
 ATCTACGTG CGTTCCTCAT TGTGGCTCC GTGTTGTGG CCTTATCAT CTTGGGGTCC 1260
 CTGGTGGCAG CCTGTTGCTG CAGATGTCTC CGGCTAAGC AGGATCCCCA CAGAGCCGA 1320
 GCGCCAGGGG GTAAACGCTT GATGGAGACC ATCCCCATGA TCCCCAGTGC CAGCACCTCC 1380
 CGGGGTGCT CCTACGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACTCC 1440
 75 GGGGCGCGGG CGCCCCAAC AAGGTACAG ACCAAGTGT GTTTCGCGA AGGGACCAT 1500
 AACAAAGTGT ATGTCAACAT GCCCAAGAA TTCTCTGTGC TGAACCTGCA CGAGGCCAAC 1560
 CAGATTGTGC CACATCAAGG CAGATATCTG CATCCCCAT ACGTGGGGTA CAGCGTGCAG 1620
 CACGACGCT TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCTGCA GCTGGCTAC 1680
 AGGCAGATTC AGTCCCCCTT CCTTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740
 80 ACTGTATAAC CGAGAGTAC TGGTGGGTTT CTTTACTGAA GGGAGAGCAA GGCAGGGGTG 1800
 GATTCTCGAG GTGGAACTCC GCACATGTGG GTGGTATTTA TGGCAGATT CTTTGGATG 1860
 GCTTCATTGG CCCCCAGACT GTATGAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920
 CATCCAGGCT ATCATTGATT TATGATGAA AACCGGCTC AGCTGGAGAT GAGTGTGATG 1980
 TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040
 AAGAATTTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCTTTT 2100

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5 TTGTTGTGA CTGCACAGSA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTTT 2160
 TTTTITTTTT TTTTITTTAA TCAGACAGGG TCTTGCTCTG TTGCCAGGC TGGAGTGCAG 2220
 TGGTGGGATC TCGGCTCACT GCAACTTCAG CCTCCTGGAT TCAGGCAACA CTCCTGCCTC 2280
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCAT GGCTAATTTT TGTATTTTT 2340
 TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGTGGGTCTC ACTCTCCTGA CCTCAAGCAA 2400
 TCTGCCTGTC TCAGCCTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460
 TGAGCCTTTT TTTTITTTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAAA TAACAGGACT 2520
 ATTTCTAAAG GAAACCTGTT TGAACCTGTT GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580
 GGCACACCTT AATTTCAATT TAAAAAGATA TATATATTTT GTCTATTTTT GTGCTTTTGG 2640
 10 GGGCCTATTT TGTGCTTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTCTACA 2700
 TTAATAAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAATCT 2760
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCCATT CATCCCTTC 2820
 TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTTCTTTT 2880
 TATATTGAAA TCATAAATA TCACCCGCTG CTTCTCTGAG TTACTTTTAA TTTTGCTTGG 2940
 15 TGGTTATGGT TTGGCGTTTC CTTCTGTTG GTTTTCAGAG CCCCATGTCT ATATAGTCTC 3000
 GAGTGCAAGT AATTACTATA CTTGTAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA 3060
 AAAAATTTTC TTGCTTAGT TATAAAATT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120
 TAGCTCTCA GCCATAACCT GAGACTTGGG ATGAAATTA AACCAGATAC GATTTACTTT 3180
 GCAGATCATA AGGCTTTTTA TACTCTGTT ATCAAATGG CTTATTTTC AGGCACCTAG 3240
 20 GATTGTAAAG AGAAAGCTT TTCAACGAAG GATTGCTTT CTTCTCCAC ACTGTTCTTG 3300
 AITTTCTCTC TCTTTCAGGC CTCACAGGC ACTGTATTCA TTGCCAATGT TCCAAATTAT 3360
 CAAATTCAG TGAATTTATT TGTGTGTTCT TTACTTATAT AAAAAAGAT AACTTTAAG 3420
 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAATATT TTGTAATTAA ACAAATCGCT 3480
 GTATGGTATG GTCTTCTACA CATTATATG TATAGATATC TATCGATCAT CTTTCTATT 3540
 25 TGTTCATGA CTGAATAATG TAAACCAAG GTTGGCAATT GGTATCATCA ATGATACTCA 3600
 TTTTITAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAATA TTTTATGATG 3660
 TGAATAAAAA AAAAAAATA AAAAAAATA

30 A40 Protein sequence
 Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 35 Transmembrane domains: 402-424
 Cellular localization: not determined

40 1 11 21 31 41 51
 MLGFLMSPS TQRAQYTPG GKLEWEASI GAHSRGRGS DRERESRPEA AGLWDRAAA 60
 GEAEKNGRGE PPWIRAQQQ PRPPFAGQAP GTAAGGAQDP RLRPGRSRGR VRLEVKPPEA 120
 SGRQPRGPSD CIPRFPSSASA TEKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAEGSG 180
 45 PRGKRRTVTS DEARGSPGPR LLGDRPALSG DALSAFRRVP CGALAARPSF HPGTPLRSCS 240
 CCMWRCHRRG RGPSGEYCHG WLDAQGVWRI GFQCFERFDG GDATICCGSG ALRYCCSSAE 300
 ARLDQGGCDN DRQQGAGEPG RADKDGPRRL GRASCLRGTO GDGEGAPPFV RAWQRCSPEG 360
 SPKGRQLLRA FPGLLFRARR RGFPSSPRGG PSPLQRPALP IYVFLIVGS VFVAFIILGS 420
 LVAACCCRL RPKQDFQQR APGNRLMET IPMIPSASTS RGSSSRQSST AASSSSANS 480
 50 GARAPPTRSQ TNCCLPEGTM NNYYVMPTN FSVLNCQAT QIVFHQGYL HPYVGYTVQ 540
 HDSVPMTAVP PFMDGLQPGY RQIQSFPFHT NSEQMYPV TV

A41 DNA SEQUENCE:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 55 Probeset Accession #: AA487468
 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
 CTACACTCAG CTTTGGGTCT CTGCTCTTA CTGTCACAG TTTCTTCCA CCTTGCCATT 120
 GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGG AGATGACATC 180
 65 ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
 ATGGTTATTC ATCAGCTGGA GGATGTGCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300
 CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
 GAAACCACTG ATAAGAAATT ATCAGCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
 GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
 70 TATGAGCCTC GGGATTACCT CCTATTGATA GAAACATGA AGAAAGCAAT AAGACTTATT 540
 CAGTCAGAGC TATAAGAGAT GATAGAAAA AGCCTTCACT TCAAGCAAGT CAAATTTTAT 600
 CAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAA 660
 75 TTAATTTTAA GTTTTITTTA TGTGTTTGA ATAGTCTTAT TAAATAAAT GTTTTITTTA 720
 TCTGAAAAAA AAAAAAATA AAAAAAATA

80 A42 Protein sequence:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Protein Accession #: none found
 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted

5
1 11 21 31 41 51
MMIHSALGLC LLLVTSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK 60
PLMVIHLED CQYSQALKKV PAQNEEIQEM AQNKFIMLNL MHETTDKNLS PDGQYVPRIM 120
FVDPSTLVRA DIAGRYSNRL YTYEPRDLPL LIENMKALR LIQSEL

10 A43 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1
Unigene number: Hs.106778
Probeset Accession #: N51919
Nucleic Acid Accession #: AF189723
15 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

20
1 11 21 31 41 51
ATGATTCCTG TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60
ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120
TTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180
TCTCAGTTTA AAAATCCOCT TATTATGCTG CTTCTGGCTT CTGCAGTCAT CAGTGTITTA 240
ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTTCAGTTC 300
GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360
CCAGAAATGCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGCCCG AGACTTGGTT 420
CCAGGTGATA CAGTTTGCTT TCTGTGGGG GATAGAGTTC CTGCTGACTT AGCTTGTITT 480
GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTCCT 540
AAGGTGACAG CTCTCAGACC AGCTGCAACT AATGAGATC TTGCATCGAG AAGTAACATT 600
GCCTTTATGC GAAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTCTT TGGAACAGGA 660
GAAATATTCTG AATTGGGGGA GGTTTTTTAA ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720
CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACITT CCTTTACTC CTTTGGTATA 780
ATAGGAATCA TCACTGTGGT TGGCTGGTTA CTGGGAAAAG ATATCCTGGA AATGTTTACT 840
ATTAGTGTA A GTTTGGCTGT AGCAGCAATT CCTGAGGTTC TCCCATTTGT GGTTCACAGT 900
ACGCTAGCTC TTGGTGTAT GAGAATGGTG AAGAAAAGGG CCATTGTGAA AAAGCTGCCT 960
ATTGTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAACTG AGACATGACG 1020
AAGAATGAAA TGACTGTATC TCACATATT ACTTCAGATG GTCTGCATCG TGAGGTACT 1080
GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATT 1140
TATAACCCAG CTGTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAAAT 1200
40 AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAATTGCTCT TGCAATGAAG 1260
ATGGGCTCTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT 1320
GAGCAAAAGT GATGGCTGT TAAGTGTGTA CACCAACAC AGCAGGACAG ACCAGAGATT 1380
TGTTTTATGA AAGGTGCTTA CGAACAAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440
GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAGA GAAGGCACGC 1500
45 ATGGGCTCAG CCGGACTCAG AGTTCTTGCT TTGGCTCTG GTCCCTGAAT GGGACAGCTG 1560
ACATTCTCTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620
ACACACTCA TTGCTCTCAG AGTATCAATA AAAATGATTA CTGAGATTTC ACAGGAGACT 1680
GCAAGTGCAA TCGCCAGCTG TCTGGGATTG TATCCAAAA CTTCAGCTC AGTCTCAGGA 1740
50 GAAGAAATAG ATGCAATGGA TGTTACAGCAG CTTCACAAA TAGTACCAAA GGTTCAGTA 1800
TTTTACAGAG CTAGCCCAAG GCACAAGATG AAAATTATTA AGTCGTACA GAAGAACGGT 1860
TCAGTTGAG CCATGACAGG AGATGGAGTA AATGATGAGC TTGCTCTGAA GGCTGCAGAC 1920
ATTGAGTTG OGATGGGCCA GACTGGTACA GATGTTTGA AAGAGGCAGC AGACATGATC 1980
CTAGTGGATG ATGATTTTCA AACCAATATG TCTGCAATG AAGAGGGTAA AGGGATTAT 2040
AATAACATTA AAAATTTCTG TAGATTCCAG CTGAGCAGCA GTATAGCAGC ATTAACCTTA 2100
55 ATCTCATTGG CTACATTAAAT GAACTTTCTT AATCCTCTCA ATGCCATGCA GATTTTGTGG 2160
ATCAATATTA TTATGGATGG ACCCCAGCT CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220
GATGTCTTC GTAAACCTCC TCGCAACTGG AAGACAGCA TTTTGACTAA AAACCTTGATA 2280
CTTAAAAATC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTGTTG CTTCTGGCT 2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400
60 TTTTGTGACA TGTTCATGTC ACTAAGTTCC AGATCCGAGA CCAAGTCTGT GTTTGAGATT 2460
GGACTCTGCA GTAATAGAAAT GTTTGCTAT GCAGTTCTTG GATCCATCAT GGGACAATTA 2520
CTAGTTAATT ACTTTCTCTC GCCTCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
GATCTGTTGT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700
65 CTTGAAGTAT GA

A44 Protein sequence:

Gene name: ATPase, Ca++ transporting, type 2C, member 1
Unigene number: Hs.106778
Probeset Accession #: N51919
Protein Accession #: AAF27813
Signal sequence: none found
Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
75 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
Cellular Localization: not determined

80
1 11 21 31 41 51
MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHERRA PRGWNEFDIS EDEPLWKIYI 60
SQFNPLIML LLASAVISVL MEQFDDAVSI TVAILIVVTV APVQSYRSEK SLEELSKLVP 120
PECHVREBK LEHTLARDLV PGDTVCLSVG DRVPADLRLE EAVDLSDIES SLTGETTPCS 180
KVTAPOPAAT NGDLASRSNI APMGTLVROG KAKGVVIGTG ENSPEGEVFK MMQAEAPKT 240
PLQKSMDDLG RQLSPYSPGI IGIIMLVGWL LGKDILEMPT ISVSLAVAAI PEGLEIVVTV 300

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5 TLALGVMRMV KKRAIVKKLP IVETLGCCNV ICSDKTGLT KNEMIVTHIF TSDGLHAEVT 360
 GVGYNQFGEV IVGDVVHGF YNPAVSRIVE AGVCNDNAVI RNTLMGKPT EGALIALAMK 420
 MGLDGLQDY IRKAEYPPSS BQKMAVKCV HRTQDRPEI CFMKGAYEQV IKYCTTYQSK 480
 GQTLTLTQQ RDVYQEKAR MGSAGLRVLA LASGPGLQL TFLGLVGIID PPRTGVKEAV 540
 TTLIASGVSI KMITGDSQET AVAIASRLGL YSKTSQSVSG EEDAMDVOQ LSQIVPKVAV 600
 FYRASPRHKM KIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMQGTGT DVCKEADMI 660
 LVDDDFQTIM SAIEEGKGIY NNKNFVRFP LSTSLAALT ISLATLMNFP NPLNAMQILW 720
 INIIMGPPA QSLGVEFVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFW 780
 10 ELRDNVITPR DTTMTFTCFV FDFMFLSS RSQTSVFEI GLCSNRMFCY AVLGSIMQQL 840
 LVIVFPPLQK VFQTESLSIL DLLFLGLTS SVCIVAEIHK KVERREKIQ KHVSTSSSF 900
 LEV

A45 DNA sequence

15 Gene name: ESTs
 Unigene number: Hs.157601
 Probeset Accession #: W07459
 Nucleic Acid Accession #: AC005383
 Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51
 GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT 60
 TTTTATTGCG AGACCTGGGC CGATGCCGCT TTAATAAACG CGAGGGGCTC TATGCACCTC 120
 25 CTTGGCGGTA GTTCTCCGGA CCTCAGCCGG GTCCGGTCTG GCCGCCCTCT CCCAGGAGAG 180
 ACAAAACAGT GTCCACAGTG GCAGCCGCGC CCGGGGCGCC CCTCCTGTGA TCCCGTAGCG 240
 TCGCCGCTCT CCTCCGTTA TATCAACATG CCCCCTTTCC TGTGTGTGGA GGCCTCTGT 300
 GTTTTCTCTG TTTCCAGAGT GCCCCATCTC CTCCCTCTCC AGGAAGTCCA TGTAAGCAAA 420
 30 GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480
 ATCATGTTC TGTAGATCG GTCTAACAGC GTCCGGAAAG GAGAGCTTGA AAGSTCCAAG 540
 CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600
 GCATTCCAGT TCAAGTCCAC TCCTCATCTG GAATTCCTCT TGGATTCAAT TTCAACCCAA 660
 CAGGAAGTGA AGGCAAGAAAT CAAGAGGATG GTTTTCAAG GAGGGCGCAC GGAGACGGAA 720
 35 CTGTCTCTGA AATACCTTCT GCACAGAGGG TTGCCTGGAG GCAGAAATGC TTCTGTGCCC 780
 CAGATCCTCA TCATGTCAC TGATGGGAAG TCCAGGGGGG ATGTGCACT GCCATCCAAG 840
 CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGGG TCAGGTTTCC CAGGTGGGAG 900
 GAGCTGCATG CACTGCCAGC CGAGCCTAGA GGGCAGCAGG TGCTGTGGCC TGAGCAGGTG 960
 40 GAGGATGCCA CCAAGCGCCT CTTCAGCACC CTCAGCAGCT CGGCCATCTG CTCAGCGGCC 1020
 ACGCCAGCTG GCAAGGTGGA GGTCAACCCC TGTGAGCACA GAGCGCTGGA GATGGTCGG 1080
 GAGTTCGCTG GCATGCCCCC ATGCTGAGGA GGATCGCGGC GGACCTTTCG GGTGCTGGCT 1140
 GCACACTGTC CTTTCTACAG CTGGAAGAGA GTGTTCTTAA CCCACCTGTC CACTGCTAC 1200
 AGGACCACTT GCCCAGGCCCT CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1260
 45 CCAGAGGAGC TGGACGGCTA CCAAGTGCCTC TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC 1320
 TGTGCTCTGA AGCTGAGCGT GGAATGCAGG GTGACCTCC TCTTCTGTCT GCACAGCTCT 1380
 GCGGGCACCA CTCGAGCAGG CTTCCTGCGG GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG 1440
 GCCGTGCTCA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG 1500
 CTGGTGGCGG TGCTGTGGG GAGTACCCAG GATGTGCTCG ACCTGGTCTG GAGCCTCGAT 1560
 50 GGCATTCCCT TCGCTGGTGG CCCCACCTTG ACGGGCAGTG CCTTGGCGCA GGCGGCAGAG 1620
 CGTGGCTTGG GGAAGCCGAC CAGGACAGGC CAGGACCGGC CAGTAGAGT GGTGTTTGTG 1680
 CTCAGTGTG CACTCTCCGA GGATGAGGTT GCGGGCCAGC CGCTCAGCG AAGGGCGCGA 1740
 GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG GCGGTGCGGG CAGAGCTGGA GGAGATCACA 1800
 GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAATCCCT 1860
 55 GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG CGGCCAGGCT GCGGACACA AGCCCTGGAC 1920
 CTGTCTTCA GTTGGACAC CTCTGCCTCA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980
 AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTGCGC 2040
 CTGTGTGTGT ATGCGACCCA GGTGCAGACT GCCTTCGGGC TGGACACCAA ACCCACCCTG 2100
 GCTGCGATGC TCGGGCCAT TAGCCAGGCC CCTACCTAG GTGGGTGGG CTCAGCCGGC 2160
 60 ACCGCCCTGC TGACATCTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCTGGT 2220
 GTCCCAAAG CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCCGTCTCT 2280
 GCGCAAGAGC TGAAGAACAA TGGCATCTCT GTCTTGTGTG TGGCGTGGG GCCTGTCTTA 2340
 AGTGAGGCTC TCGGAGGCT TGCAGTCCC CGGATTTCCC TGATCCACGT GGCAGCTTAC 2400
 GCGCACTGCG GGTACCAACA GGCAGTCTC ATTGATGGC TGTGTGAGA AGCCAGCAG 2460
 65 CCAAGTCAAC TCTGCAAAAC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CCTGCAGAA 2520
 GGGAGCTACC GCTGCAAGTG TOGGATGGC TGGGAGGGCC CCCACTGCGA GAACCGTGAG 2580
 TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GATGAGATTC TTGAGAGGCC CCTGAGGCGC 2640
 ATGGCTCCCG TCGGAGGAGG CAGCAGCGGT ACCCCTCCCA GCAACTACAG AGAAGGCGCT 2700
 GGCAGTGAAT TGGTGCCTAC CTCTGGAAT GTCTGTGCC CAGGTCTTCA GAATGTCTGC 2760
 70 TTCCCGCGGT GGCCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2820
 ATGCTGCTTA GAGACAGAAA AGCAGCTGAT GTCAACCCAA AACGATGTTG TTGAAAAGTT 2880
 TTGATGTGTA AGTAATATCC CACTTTCTGT ACCTGCTGTG CCTTGTGTAG GCTATGTCTA 2940
 CTGCGCTTCC TCCCTTGAGG ATAAACAAGG GGTCTGTAAG ACTTAAATTT AGCGGCTGTA 3000
 CGTTCTCTTG CACACAATCA ATGCTCGCCA GAATGTGTT GACACAGTAA TGCCAGCAGC 3060
 75 AGGCCTTTAC TAGACATCC TTTGGAAGGC GAAGGCCAAG GCCTTTCAAG ATGGAAGACA 3120
 GCAGCTTTTC CACTTCCCCA GAGACATCTT GGATGCATTT GCATTGATC TGAAAGGGGG 3180
 CTTGAGGGAC GTTGTGACT TCTTGGCGAC TGCCCTTTGT GTGTGGAAGA GACTTGGAAA 3240
 GGTCTCAGC TGAATGTGAC CAATTAACA GCTTGGTTGA TGATGGGGA GGGGCTGAGT 3300
 TGTGCTAGG CCCAGTCTG GAGGGCCAG TAAATCGTT CTGAGTCTG AGCAGTGTCC 3360
 80 ACCTGAAGG TCTTC

A46 Protein sequence

Gene name: ESTs

Unigene number: Hs.157601
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: none found
 VGM domains: 49-223; 341-518; 529-706
 EGF domains: 298-333; 715-748
 Cellular Localization: secreted

10 1 11 21 31 41 51
 | | | | |
 MPPFLLLEAV CVFLFSRVFP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
 SVGKGSFERS KHPAITVCDG LDISPERVRV GAFQF6STPH LEPPLDSPST QOEVKARIKR 120
 15 MVFKGGRRET ELALKVLLHR GLPGGRNASV PQILIIIVTDG KSQCDVALPS KQLKRGVTV 180
 FAVGVPRPFW EELHALASEP RGQHVLLAQ VEDATNGLPS TLSSSAICSS ATPDCRVEAH 240
 PCEHRTLEMV RFPAGNAPCW RGSRRTLAVL AAHCFFPYSWK RVFLTHPATC YRTTCPCGCD 300
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGBA NCALKLSLEC RVDLLFLDLS SAGTTLGDFL 360
 RAKVVFVRKV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT 420
 20 LTGSAIRQAA ERGFGSATRT GQDRPRRVVV LLETSHSEDE VAGPARHARA RELLLLGVGS 480
 EAVRAELEBI TGSPKHMVMY SDPQDLFNQI PELQGLCSR QRPGRCTQAL DLVFMLDISA 540
 SVGPENFAQM QSFVRSCALQ FEVNPVDTQV GLVVYGSQVQ TAPGLDTKPT RAAMLRAISQ 600
 APYLGVGSA TALLHIYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQKLNNNGI 660
 SVLVVGVGFV LSEGLRRLAG PRDSLIVHAA YADLRVHQDV LIENLCGEAK QPVNLCKPSP 720
 25 QNNEGSCVLQ NGSYRCCKRD GWBOPHCENR EWSSCSVCVS QGWILEBPLR HMAPVQEGSS 780
 RTPPSNYREG LGTEMVPTFW NVCAFGP

COLON

30 A47 DNA SEQUENCE:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Nucleic Acid Accession #: AA487468
 35 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 40 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
 CTACACTCAG CTTTGGGTCT CTGCTCTTA CTGCTCACAG TTTCTTCCAA CCTTGCCAT 120
 GCAATAAATA AGGAAAGAGG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
 ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
 45 ATGTTTATTC ATCACTTGA GGAATTGTCA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300
 CAAATGAAG AATAACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
 GAAACCACTG ATAAGAATTT ATCACTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
 GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
 TATGAGCTTC GGGATTATCC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540
 50 CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAGAGAT CAAATTTTAT 600
 GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660
 TTACTATTTA GTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTAAATA 720
 TCTGAAAAAA AAAAAA AAAAAA

55 A48 Protein sequence:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Protein Accession #: none found
 60 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted

65 1 11 21 31 41 51
 | | | | |
 MMLHSAIGLC LLLVTVSSNL AIAIKKEKRP PQTLRSGWGD DITWQTYEE GLFYAQKSKK 60
 PLMVIHLED QYQSALKKV FAQNEBIQEM AQNKPIMLNL MHETTDKNLS PDGQYVPRIM 120
 70 FVDPSTLVRA DIAGRYSNRL YTYEPRDLPL LIENMKALR LIQSEL

A49 DNA SEQUENCE
 Gene name: G protein-coupled receptor 56
 Unigene number: Hs.6527
 75 Probeset Accession #: AA478599
 Nucleic Acid Accession #: NM_005682
 Coding sequence: 163-2244 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
 | | | | |
 CGGCAGCAGG GTCTCGCTCT GTCACACAGS CTGGAGTGCA GTGGTGTGAT CTTGGCTCAT 60
 CGTAACTCC ACCTCCCGGG TTCAAGTGAT TCTCATGCTC CAGCTCCCG AGTAGCTGGG 120
 ATTACAGGTG GTGACTTCCA AGAGTGACTC CGTGGAGGA AAATGACTCC CCAOTCGCTG 180

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CTGCAGACGA CACTGTTCTT GCTGAGTCTG CTCTTCTCTG TCCAAGGTGC CCAOCCGAGG 240
 GGCCACAGGG AAGACTTTCG CTTCTGCAGC CAGCGGAACC AGACACACAG GAGCAGCCTC 300
 CACTACAAAC CCACACACGA CTTGCGCATC TCCATCGAGA ACTCCGAAGA GGCCCTCACA 360
 GTCCATGCCC CTTTCCCTGC AGCCCAACCT GCTTCCCGAT CCTTCCCTGA CCCACGGGGC 420
 CTCTACCACT TCTGCCTCTA CTGGAACCGA CATGCTGGGA GATTACATCT TCTCTATGGC 480
 AAGCGTGACT TCTTGCTGAG TGACAAAGCC TCTAGCCTCC TCTGCTTCCA GCACCAGGAG 540
 GAGAGCCTGG CTCAGGGCCC CCGCTGTGTA GCCACTTCTT CCTTCCACAG TCCTCCCCAC 600
 CAGAACATCA GCCTGCCGAG TGCCGCGCAG TTCACCTTCT CCTTCCACAG TCCTCCCCAC 660
 ACGGCGGCTC ACAATGCCCT GGTGGACATG TCGGAGCTCA AAAGGGACCT CCAGCTGCTC 720
 AGCCAGTTTC TGAAGCATCC CCAGAAGGCC TCAAGGAGGC CTTCGGCTGC CCCCGCCAGC 780
 CAGCAGTTGC AGAGCCTGGA GTGGAACCTG ACCTCTGTGA GATTATGGG GGACATGGTG 840
 TCCTTCGAGG AGGACCGGAT CAACGCCAGG GTATGGAAGC TCCAGCCAC AGCCGCGCTC 900
 CAGGACCTGC ACATCCACTC CCGGCAGGAG GAGGAGCAGA GCGAGATCAT GGAGTACTCG 960
 GTGCTGCTGC CTTCCAGAGG ACGAAAGGCC GGAGCGGGGA GGCTGAGAAG 1020
 AGACTCTCTC TGGTGGACTT CAGCAGCCAA GCCCTGTTCG AGGACAAGAA TTCCAGCCAA 1080
 GTCTGCTGCG AGAGGCTTGA GGGGATTGTG GTACAGAAAC CCAAGTAGC CAACCTCAGG 1140
 GAGCCCGTGG TGCTCACTTT CCAGCACCAG CTACAGCCGA AGAATGTGAC TCTGCAATGT 1200
 GTGTCTGCGG TTGAAGACCC CACATTGAGC AGCCCGGGGC ATTGGAGCAG TGCTGGGTGT 1260
 GAGACCGTCA GGAGAGAAAC CCAAACTTCC TGCTTCTGCA ACCACTTACG GAGCTTCTCA 1320
 GTGCTGATGG TCTCTCGGT GAGGTGGAC GCGGTGCACA AGCACTACCT GAGCTTCTCA 1380
 TCTTACGTGG GCTGTGCTGT CTTGCCCCTG GCCTGCCCTG TCACCATTCG CGCCTACCTC 1440
 TGCTCCAGGG TGCCCTCTCC GTGCAGGAGG AAACCTGGGG ACTACACCAT CAAGGTGCAC 1500
 ATGAACCTGC TGCTGGCGGT CTTCTGCTG GACAGAGCT TCTTGTCTCA CTTCTCCCTG 1560
 GCCCTGACAG GCTCTGAGGG TGGCTGCCGA GCCAGTGCCA TCTTCTGCA CTTCTCCCTG 1620
 CTCACCTGCC TTTCTGTGAT GGGCCTCGAG GGGTACAACC TCTACCGACT CGTGGTGGAG 1680
 GTCTTGTGCA CCTATGTGCC TGGCTACCTA CTCAGCTGA GCGCCATGGG CTGGGCTTTC 1740
 CCATCTCTTC TGGTGAACCT GGTGGCGCTG GTGGATGTGG ACAACTATGG CCCCATCATC 1800
 TTGGCTGTGC ATAGACTTCC AGAGGGCGTC ATCTACCCCT CCATGTGCTG GATCCGGGAC 1860
 TCCTTGTGCA GCTACATCAC CAACCTGGGC CTCTTACGCC TGGTGTCTTC GTTCAACATG 1920
 GCCATGCTAG CCACCATGGT GGTGCAGATC CTGCGGCTGC GCCCCACAC CCAAAAGTGG 1980
 TCACATGTGC TGACATGCTG GGGCCTCAGC CTGGTCTCTG GCCTGCCCTG GGCCTTGATC 2040
 TTCTTCTCTC TTGCTTCTGG CACCTTCCAG CTGTGTCTCC TCTACCTTTC CAGCATCATC 2100
 ACCTCTCTCC AAGGCTTCTC CATCTTCATC TGGTACTGGT CCATGCGGCT GCAGGCCGCG 2160
 GGTGGCGGCT CCCCTCTGAA GAGCAACTCA GACTGGGCCA GGCTCCCATC CAGCTCGGGC 2220
 AGCACCTGCT CCAGCCGATC CTAGGCGCTC AGCCCACTG CCATGTGAT GAAGCAGAGA 2280
 TGCGGCGCTG TCGCACATG CCGTGGGCC CCGAGCCAGG CCCAGCCCCA GGCCAGTCCA 2340
 CCGCAGACTT TGGAAAGCCC AACGACCATG GAGAGATGGG CCGTGGCAT GGTGGACGGA 2400
 CTCCCGGGGC TGGGGCTTTT GAATTGGCCT TGGGGACTAC TCGGCTCTCA CTGAGCTCCC 2460
 ACGGGACTCA GAAGTGGGCC GCCATGTGTC CTAGGGTACT GTCCCCACAT CTGTCCCAAC 2520
 CCAGCTGGAG GCCTGTGCTC TCCTTACAC CCCTGGGGCC AGCCTCATTG CTGGGGGCCA 2580
 GGCCCTGGAT CTTGAGGGTC TGGCACATCC TTAATCTGT GCCCTGCTG GGGACAGAAA 2640
 TGTGCTCCA GTTCTCTGT CTCTCGTGGT CACCTGAGG GCACTCTGCA TCCTCTGTCA 2700
 TTTTAACTC AGGTGGCACC CAGGGCGAAT GGGGCCAGG CAGACCTTC AGGGCCAGAG 2760
 CCCTGGCGGA GGAGAGGCC TTTGCCAGGA GCACAGCAGC AGCTCGCTA CCTCTGAGCC 2820

A50 Protein sequence

50 Gene name: G protein-coupled receptor 56
 Unigene number: Hs.6527
 Protein Accession #: NM_005682.1
 Signal sequence: 1-26
 GPS domain: 342-394
 Pfam domain: 7tm_2[400-665]
 55 Transmembrane domains: 410-432, 446-468, 482-504, 517-539, 575-597, 608-630, 638-659
 Cellular Localization: plasma membrane

60
 65
 70

1 11 21 31 41 51
 MTPQSLQTT LFLLSLLPLV QGAGHGRGHE DFRFCSQRNQ THRSSLHYKP TPDLRISIEN 60
 SEEALTVPAP FPAAPASRS FPDPRGLYHF CLYWRHAGR LHLVYGRDF LLSDKASSLL 120
 CFQHQEBESLA QGPPLLATSV TSWNSPQNIS LPSAASFTFS FHSPPHTAAH NASVDMCELK 180
 RDLQLLSQFL KHPQKASRRP SAAPASQQLQ SLESKLTSSR FMGDMVSFE DRINATVWKL 240
 OPTAGLDLH IHSRQEBEQS EIMEYSVLLF RTLFQRTKGR SGAEKRLLL VDFSSQALFQ 300
 DKNSSQVLGB KVLGIVVQNT KVANLTFPVV LTFQHQLPK NVTLQCVFVW EDPFLSSPGH 360
 WSSAGCBTVR RETQTSFCFN HLTYFAVLWV SSVEVDVAVK HYLSSLXYVG CVVSALACLIV 420
 TIAAYLCSRVR PLPCRKRPRD YTIKVMNLL LAVFLDTSF LLSEFVALTG SEAGCRASAI 480
 FLHFSLTCL SWMGLEGYNL YRLVVEVFGT YVPGYLLKLS AMGWGFFIFL VTLVALVDVD 540
 NYGPILAVH RTPBGVIYPS MCWIRDSLVS YITNLGLFSL VPLFNAMLA TMVVQILRLR 600
 PHTQKSHVL TLLGLSLVLG LFWALIFFSF ASGTFQLVVL YLFSIITSFQ GPLFIWYWS 660
 MRLQARGGPS PLKSNSDCAR LPISSGSTSS SRI

A51 DNA SEQUENCE

75 Gene name: Hypothetical protein FLJ20063
 Unigene number: Hs.5940
 Probeset Accession #: AA053660
 Nucleic Acid Accession #: AA053660
 80 Coding sequence: 218-1360 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CCCCCATGAC TTTGTACAGC TACTTCACTG CTTCCCCCCA ATTAGTACAC ATAGTTCCTC 60

5	CACAATTCTT	ACACCTGCTC	CCCCATAAT	CAGTACACAT	AGTTCCTCCA	CAATTCCTAT	120
	ACCTACTGCT	GCAGACAGTG	AGTCAACCAC	AAATGTAAAT	TCATTAGCTA	CCTCTGACAT	180
	AATCACCCTG	TCATCTCCAA	ATGATGGATT	AATCACAATG	GTTCCTTCTG	AAACACAAAG	240
	TAACAAATGAA	ATGTCCCCCA	CCACAGAAGA	CAATCAATCA	TCAGGGCCTC	CCACTGGCAC	300
	CGCTTTATTT	GAGACCAGCA	CCCTAAACAG	CACAGGTCCC	AGCAATCCTT	GCCAAAGATGA	360
	TCCTGTGCA	GATAATTCGT	TATGTGTTAA	GCTGCATAAT	ACAAGTTTTT	GCCTGTGTTT	420
	AGAAGGGTAT	TACTACAAC	CTTCTACATG	TAAGAAAGGA	AAGGTATTCC	CTGGGAAGAT	480
	TTCACTGACA	GTATCAGAAA	CATTTGACCC	AGAAGAGAAA	CATTCCATGG	CCTATCAAGA	540
10	CTTGATAGT	GAAATTACTA	GCTTGTTTAA	AGATGTATTT	GGCACAATCT	TTTATGGACA	600
	GACTGTAATT	CTTACTGTAA	GCACATCTCT	GTCACCAAGA	TCTGAAATGC	GTGCTGATGA	660
	CAAGTTTGT	GATGTAACAA	TAGTAACAAT	TTTGGCAGAA	ACCACAAGTG	ACAATGAGAA	720
	GACTGTGACT	GAGAAAATTA	ATAAAGCAAT	TAGAAGTAGC	TCAAGCAACT	TTCTAAACTA	780
	TGATTTGACC	CTTCGGTGTG	ATTATTTATG	CTGTAAACAG	ACTGCGGATG	ACTGCCCTCA	840
	TGGTTTAGCA	TGCGATTGCA	AATCTGAOCT	GCAAAGGCCT	AACCCACAGA	GCCCTTCTCG	900
15	CGTTGCTTCC	AGTCTCAAGT	GTCTGTATGC	CTGCAACGCA	CAGCACAAGC	AATGCTTAAT	960
	AAAGAAGAGT	GGTGGGGCCC	CTGAGTGTGC	GTGCGTGCCC	GGCTACCAAG	AAGATGCTAA	1020
	TGGGAACATG	CACAAAGTGT	CATTGGGCTA	CAGTGGACTC	GACTGTAAGG	ACAAATTTCA	1080
	GCTGATCTCT	ACTATTTGTG	GCACCATCGC	TGGCATTGTC	ATTCTCAGCA	TGATAATTGC	1140
20	ATTGATTGAT	ACAGCAAGAT	CAAATAACAA	AACGAAGCAT	ATTGAAGAAG	AGAACTTGAT	1200
	TGACGAAGAC	TTTCAAAATC	TAAACTGCG	GTGACACAGC	TTCAACCAAT	TTGGAGCAGA	1260
	AGGAGCGCTC	TTTCTAAGG	TCAGGATAAC	GGCTCCAGAG	GACAGCCAGA	TGCAAAATCC	1320
	CTATTCAAGA	CACAGCAGCA	TGCCCCGCC	TGACTATTAG	AATCATAAGA	ATGTGGAAAC	1380
	CGCCATGACC	CCCAACCAAT	GTACAGCTA	TTATTTAGAG	TGTTTAGAAA	GACTGATGGA	1440
25	GAAATGAGCA	CCAGTAAAGA	TCTGGCCTCC	GGGTTTTC	TTCCATCTGA	CATCTGCCAG	1500
	CCTCTCTGAA	TGGAAGTTGT	GAATGTTTGC	AACGAATCCA	GCTCACTGTC	TAAATAAGAA	1560
	TCTATGACAT	TAAATGTAGT	AGATGCTATT	AGCGCTTGTC	AGAGAGGTGG	TTTCTCTCAA	1620
	TCAGTACAAA	GTACTGAGAC	AATGGTTAGG	GTTGTTTTCT	TAATTTCTTT	CTGGTAGGGG	1680
	CAACAGAAC	CATTTCCTAT	CTAGAGGAAA	GCTCCCGAGC	ATTGCTTGCT	CCTGGGCAAA	1740
30	CATTGCTCTT	GAGTTAAGTG	ACCTAATTCC	CCTGGGAGAC	ATACGCATCA	ACTGTGGAGG	1800
	TCGAGGGGGA	TGAGAAGGGA	TACCCACCAT	CTTTCAGAGG	TCACAAGCTC	ACTCTCTGAC	1860
	AAGTCAGAA	AGGGACACTG	CTTCTATCCC	TCCAATGGAG	AGATTCTGGC	AACCTTTGAA	1920
	CAGCCACAGG	CTTGCAACCT	AGCCTCACCC	AAGAAGACTG	GAAAGAGACA	TATCTCTCAG	1980
	CTTTTTTCAG	AGGCGTGCTT	GGGAATCCAG	GAACTTTTTG	ATGCTAATTA	GAAGGCCTGG	2040
35	ACTAAAATG	TCCACTATGG	GCTGCACTCT	ACAGTTTTTG	AAATGCTAGG	AGGCAGAAAG	2100
	GGCAGAGAGT	AAAAACATG	ACCTGCTAGA	AGGAAGAGAG	GCAAGGAAA	CTGGGTGGGG	2160
	AGGATCAATT	AGAGAGGAGG	CACCTGGGAT	CCACCTTCTT	CCTTAGGTCC	CCTCCTCCAT	2220
	CAGCAAGAGA	GCACCTCTCT	AATCATGCCC	TCCCGAAGAC	TGGCTGGGAG	AAGGTTTAAA	2280
	AACAAAAAT	CCAGAGTAA	GAGCCTTAGG	TCAGTTTGA	ATTGGAGACA	AACGTCTCGG	2340
40	CAAAGGCTGC	GAGAGGGAGC	TTGTGCTCAG	GAGTCCAGCC	GTCCAGCCTC	GGGGGTGATG	2400
	TTTCTGAGGT	GTGCCATTGG	GGCCTCAGCC	TTCTCTGGTG	ACAGAGGCTC	AGCTGTGGCC	2460
	ACCAACACAC	AACCAACAC	ACACAACCAC	ACACAACAT	GGGGGCAACC	ACATCCAGTA	2520
	CAAGCTTTTA	CAAAATGTTAT	TAGTGTCCCT	TTTTATTTC	AATGCCCTGT	CCTCTTAAAA	2580
45	GTTATTTTAT	TTGTTATTAT	TATTGTCTCT	TGACTGTTAA	TTGTGAATGG	TAATGCAATA	2640
	AAGTGCCCTT	GTTAGATGGT	GAIAIAIAIA	AAAAIAIAIA	AAAAIAIAIA	A	

A52 Protein sequence:

50	Gene name:	Hypothetical protein FLJ20063
	Unigene number:	Hs.5940
	Probeset Accession #:	AA053660
	Protein Accession #:	none found
	Signal sequence:	none found
	Transmembrane domains:	289-311
55	EGF domain:	45-74
	SEA domain:	80-196
	Cellular Localization:	plasma membrane

60	1	11	21	31	41	51	
	MVPSETQSN	EMSPPTEDNQ	SSGPPTGTAL	LETSTLNSIG	PSNPOQDDPC	ADNSLCVKLH	60
	NTSFCLCLEG	YYNNSSTCKK	GKVPFGKISV	TVSETFDPEE	KHSMAYQDLH	SEITSLFKDV	120
	FGTSVYQTV	ILTVSTSLSP	RSEMRADDKF	VDVTIVTILA	ETTSNNEKIV	TEKINKAIRS	180
65	SSSNFLNYDL	TLRCDYYGCN	QTADDCLNGL	ACDCKSDLQR	PNPQSPFCVA	SSLKCPDAON	240
	AQHKQCLIKK	SGGAPEACAV	PGYQEDANGN	CQKCAFPGYS	LDCCKDKFQLI	LTIVGTIAGI	300
	VILSMIALI	VTARSNNKTK	HIEEENLIDE	DFQNLKLRST	GFTNLGAEBS	VFPKVRITAS	360
	RDSQMNPYS	RHSSMPRPDY					

A53 DNA SEQUENCE

70	Gene name:	TMPRSS3a
	Unigene number:	Hs.298241
	Probeset Accession #:	A1538613
	Nucleic Acid Accession #:	AB038157
75	Coding sequence:	202-1566 (underlined sequences correspond to start and stop codons)

80	1	11	21	31	41	51	
	ACCGGSCACC	GGACGGCTCG	GGTACTTTCC	TTCTTAATTA	GGTCATGCC	GTGTGAGCCA	60
	GGAAAGGGCT	GTGTTTATGG	GAAGCCAGTA	ACACTGTGGC	CTACTATCTC	TTCCGTGGTG	120
	CCATCTACAT	TTTGGGACT	CGGGAATTAT	GAGGTAGAGG	TGGAGGCGGA	CGCGGATGTC	180
	AGAGGTCCTG	AAATAGTCAC	CATGGGGGAA	AATGATCCGC	CTGCTGTTGA	AGCCCCCTTC	240

WO 03/042661

5 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCCTGTGTC ACCAGATGCA 300
 GATGCTGTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTC AATCATCGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
 TCAGGGAAGT ACAGATGTGC CTATCCCTTT AAGTGTATGC AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600
 AAGGGTCACT ACGCAATGTG TGCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT 720
 10 CACCTCTGTC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 TGTGCTCTGT GCCAGGTGGT TACCTTGCAG TGCACAGCCT GTGGTCATAG AAGGGGCTAC 840
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGSC AGTGGCCCTG GCAGGCCAGC 900
 CTTCAGTTCC AGGGCTACCA CTGTGCGGG GGCTCTGTCA TCACGCCCTT GTGGATCATC 960
 ACTGCTGCAC ACTGTGTTTA TGACTTGTA CCCCCAAGT CATGGACCAT CCAGTGGGT 1020
 CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC 1080
 15 AGCAAGTCA AGCCAAAGAG GCTGGCAAT GACATCGCCC TTATGAAGCT GGCCTGGCCA 1140
 CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACTTCCCC 1200
 GATGGAAAAG TGTGCTGGAC GTCCAGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260
 TCCCCTGTCC TGAACACGCG GGCCTGCTT TGTATTCCA ACAAGATCTG CAACCCACAG 1320
 GAGCTGTAGC GTGGCATCAT CTCCCCTCC ATGCTCTGGG CGGGCTACCT GACGGGTGGC 1380
 20 GTGGAGTCA AGCCAAAGAG CAGCGGGGGG CCCTGTGTGT GTCAAGAGAG GAGGCTGTGG 1440
 AAGTTAGTGG GAGCGACCA CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
 TACACCCGTG TCACCTCTCT CTTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
 ACTGAAGAG GAGGGGACA AGTAGCCACC TGAGTTCTGT AGGTGATGAA GACAGCCCGA 1620
 TCCTCCCTGG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680
 25 TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCCCTTCA TCTGATTCCA GCACAACTT 1740
 CAGCTGCTT TTTGTTTTTT GTTTTTTGA GGTGGAGTCT CGCTCTGTGG CCCAGGCTGG 1800
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCGCTT CCCTGGTTCA AGCGATTCTC 1860
 TTGCTCAGC TTCCCGAGTA GCTGGGACCA CAGGTGCCCG CCACCAACCC CAACTAATTT 1920
 TTTGATTTTT AGTAGAGACA GGGTTTCACT ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
 30 CTTCAAAATG TGTGCTGCTC TCAGCCTCCC ACAGTGTCTG GATTACAGCG ATGGGCCACC 2040
 AGCCTAGGCC TCACGCTCCT TTTGATCTT CACTAAGAAC AAAAAGAGCA GCAACTTGCA 2100
 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCTGT 2160
 ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
 GCACACGCC AGAAGTGCAG AACTGCAGTC ACTGCAGCTT TTCTATCTTA GGGACCAGAA 2280
 35 CCAAAACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
 ATGACTGCTT TAAGGCTCAT TTTCATGATT TCTTTGTAGC ATTTGTGTCT TGACGTATTA 2400
 TTGTCTTTTG ATTCAATA ATATGTTTCC TTCCCTCAA AAAAAAAAAA AAAAAAAAAA 2460
 AAAAAA

40 A54 Protein sequence:
 Gene name: TMPS33a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Protein Accession #: BAB20077
 45 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 Tryp_SPC domain: 216-444
 Cellular Localization: plasma membrane

50 1 11 21 31 41 51
 | | | | |
 MGENDPFAVE APFSFRSLFG LDDLKISFVA PDADAVAAQI LSLLEPLKFPF IIVIGIILI 60
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGONAVLQVF 120
 55 TAASWTKMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREBFV SIDHLLPDDR 180
 VTALHSHSVV REGCAGSHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPF QASLQFQGYH 240
 LCGSGATVPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QPVCLFNSSE NFPDGKVCWT SGWGATEDGA GDASFVLNHA 360
 60 AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVDSQGD SGGPLVQGER RLWKLVGATS 420
 FGIGCAEVNK PGVYTRVTSF LDWIHEQMER DLRT

A55 DNA SEQUENCE
 Gene name: Putative G protein-coupled receptor GPCR150
 Unigene number: Hs.97101
 65 Probeset Accession #: AA215333
 Nucleic Acid Accession #: NM_014373
 Coding sequence: 322-1338 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51
 | | | | |
 GTGGCCTCGA GGTGGTGGCA GGGCGGCCCC CTGCAGTCOG GAGACGAACG CACGGACCGG 60
 GCCTCCGGAG GCAGGTTCGG CTGGAAGGAA CGCTCTCTCG TTGCTCTTAC ACTTGGGCAA 120
 75 ATGTCTCCGA GCTTACTCAC ATAGCATATT GGTATATCAA AATGAAATGC AAGGAACCAA 180
 AAATAACATA ATTGAAGGCA GTAAAGTGA AATTAATAG GAAGATCATC AGTCAAGGAA 240
 GACCACTGCG AGAGACAGA AATGAAGCA GTGTTTATC ATGTGTATT CAGCAGGTCT 300
 TCTTGAAATT TAACTAAAAA TATGACTGCT CTCTCTTCMG AGAACTGCTC TTTTCACTAC 360
 CAGTTACGTC AAACAAACCA GCCCTAGAC GTTAACTATC TGCTATTCTT GATCATACTT 420
 80 GGGAAAATAT TATTAAATAT CCTTACACTA GGAATGAGAA GAAAAACAC CTGTCAAAAT 480
 TTTATGGAAT ATTTTTCAT TTTACTAGCA TTTGTTGATC TTTTACTTTT GGTAAACATT 540
 TCCATTATAT TGTATTTTCA GGATTTTGTG CTTTAAAGCA TTAGGTTTCA TAAATACCA 600
 ATCTGCCTAT TTACTCAAAAT TATTTCTTTT ACTTATGGCT TTTTGCAAT TCCAGTTTTC 660
 CTGACAGCTT GTATAGATTA TTGCTGAAT TTCTCTAAAA CAACCAAGCT TTTATTTAAG 720
 TGTCAAAAAA TATTTTATTT CTTTACAGTA ATTTTAAATT GGATTTTCACT CTTTGTCTAT 780

5 GTTTTGGGAG ACCCAGCCAT CTACCAAAGC CTGAAGGCAC AGAATGCTTA TTCTCGTCAC 840
 TGTCTTCT ATGTCAGCAT TCAGAGTTAC TGGCTGTCTAT TTTTCATGGT GATGATTTTA 900
 TTTGTAGCTT TCATAACCTG TTGGGAAGAA GTTACTACTT TGGTACAGGC TATCAGGATA 960
 ACTTCTCTA TGAAATGAAC TATCTTATAT TTTCTTTTTC CATCCCACTC CAGTTATACT 1020
 GTGAGATCTA AAAAAATATT CTTATCCAG CTGATGTCT GTTTTCTCAG TACCTGGTTA 1080
 CCATTGTGAC TACTTCAGGT AATCATTTGT TTTACTTAAAG TTCAGATGCC AGCATATATT 1140
 GAGATGAATA TTCCCTGGTT ATACTTTGTC AATAGTTTTT TCATTGCTAC AGTGATTTGG 1200
 TTTAATTGTC ACAAGCTTAA TTTAAAAGAC ATTGGATTAC CTTTGGATCC ATTTGTCAAC 1260
 10 TGAAGTGTCT GCTTCATTCC ACTTACAATT CCTAATCTTG AGCAAAITGA AAAGCCTATA 1320
 TCAATAATGA TTTGTTAATA TTATTAATTA AAGTTACAG CTGTCTAAG ATCATAATT 1380
 TATGAACAGA AAGAACTCAG GACATATTAA AAAATAAACT GAACATAAAC AACTTTTGCC 1440
 CCTGACTGA TAGCATTTCA GAATGTGTCT TTTGAAGGGC TATACCAAGT ATTAAATAGT 1500
 GTTTTATTTT AAAAAACAAA TAATCCCAAG AAGTTTTTAT AGTTATTCAG GGACACTATA 1560
 15 TTACAAATAT TACTTTGTTA TTAACACAAA AAGTGATAAG AGTTAACTT TGGCTATACT 1620
 GATGTTTGTG TTACTCAAAA AAACACTCTG ATGCAAACTG TTATGTAAAT CTGAGATTTC 1680
 ACTGACAACT TTAAGATATC AACCTAAACA TTTTATTAA ATGTTCAAAT GTAAGCAAGA 1740
 AAAAAAAA

20 A56 Protein sequence
 Gene name: Putative G protein-coupled receptor GPCR150
 Unigene number: Hs.97101
 Protein Accession #: NP_055188
 Signal sequence: none found
 25 Transmembrane domains: 23-45, 59-81, 97-119, 138-160, 184-206, 241-263, 276-297
 Cellular Localization: plasma membrane

30 1 11 21 31 41 51
 MTALSSSENC FQYQLRQTNQ PLDVNYLLFL IILGKILLNI LTLGMRKNT QQNFMEYFCI 60
 SLAPVDLLLL VNISIILYFR DVLLSIRFT KYHICLFTQI ISFTYGLFHY FVPLTACIDY 120
 CLNFSKTKL SPKCKQLFYF FTVILWISV LAYVLGDPAL YQSLKAQNAV SRHCPFYVSI 180
 QSWLSFPMV MILEVAFITC WEEVTLVQA IRITSYMNFT ILYFPSSHS SYTVRSKKIF 240
 35 LSKLIVCFSL TWLPFVLLQV IIVLLKVQIP AYIEMNIPWL YFVNSFLIAT VYWFNCHKLN 300
 LKDIGLPLDP FVNWKCCFIP LTIPNLEQIE KPISIMIC

40 A57 DNA SEQUENCE
 Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
 Unigene number: Hs.19322
 Probeset Accession #: AA088458
 Nucleic Acid Accession #: AA088458
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
 GCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60
 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120
 50 GCGCGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180
 CTGGGCCAGA GCAGAGCCAG CCGCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCTGCG GGGAGCTGCT GGCTGCAGCC 300
 TGTGCCAGCC GGGCCCTGCC CCGTCTCTCC TCCGGGCCCC CCGTCCCTGC CCTGAOGTCC 360
 55 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCCTCATGC TGAAGGAGCA GAACCGACTC 420
 CTACCCACAG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAGTTCG 480
 GCGCTCATTA AGCAGCTGTT TGAGGCCCGC GCGCTGAGCC AGCAGGACGG GGGAGCTCTG 540
 GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGCCC CCAGGGCCAG CCTGGCACTC 600
 AGCCCTTCGA GGGTGGGGCC CCGATCGCAC CCACCTCTC TGGCTGGAGA CCCCAGGAG 660
 60 GCCCAGGCAC AGTCCCGGAG TGGGCGCCTT CCTGCGCCCC TTGCCAGATG GGCTCCCCAG 720
 GCTGCCCCC GGTGTGTCCC CGCACCGAGC GCTTGACTCC GTTTGGGCTC CTGGTTGTTG 780
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGCG CTACTACTGG CGCTGTTCAG 840
 TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCG TTTCAGAGGG TGCGGCCCTG 900
 GGTCCCATCT TCAGGGAAAG GCACTGCCCA CGCCAGGCTG CACTTCCAC AACGGGCAGC 960
 65 AGAGGGCGCG GGGGGGCTCC GACGCGGGTC CRAAGGCAGC TTCCCGCTCA ACCAGGGCAC 1020
 CAGGACGAGG TGGCTGTAGC TGGGACGGAC GGAAGTAGAT GGAGGGGGTG GGAAGGGCCT 1080
 GTAAGCGGGG GGTGCTGCCC TGGCTGGGGA GCCCCAGGGA TAGCGGTCCG ACTTCAGGTT 1140
 CTGGCCAGG CTGAGGGACC CTGGCTGCAG GCGATCGGCA CGCGGGGTGG GCGAGAGCTT 1200
 GGCTCTGATG TGCTCCCCAC AGACCCCTGG GTGATGGCCT TCCCTCTCTT GGCGGGGACG 1260
 70 TTGCCCCAGG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCCAGG AGGGCCCCCA 1320
 GACAGCTCCC AGGCAOGTCA TAGGCAAAAG CTGTTTCCCC CGACTCAGGA TTTCCAAGGC 1380
 CTGGGGTCCG GCTCACCCCC CTTTGTCTCT ACGCCAGGCC TGTCCCCAGG TTTTCTGCTG 1440
 GAGAGGCCAC CTCCTCAGC CAAGGAAAC GAGAACCCCC AGGGTACAGG AGGAGGCTGG 1500
 GGCAGGTCCC CTTGGGTGTC ACTCCCTCAG CCGCTGCCCA GGCCCACTCC CGCTGGTGCT 1560
 75 GGAGTACGCA CTGTGGGGGG GGCCCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTACCA 1620
 GAAACAGGG CACCGCAACA GCATOGATGG GTTCTGAGC CCAGGGCCCC CGATGGGGGG 1680
 TCAGTGTGTG TGGGGGCGAG GGCCCTCGAT GGGGGGTGAG TGGTGGGGGG GGCAGGGGCC 1740
 CCGATGCGG GGTGAGTGG TGGGGGGGCG AGGGCCCCCT CGTGTCCAGG GCACCTTGGT 1800
 ACACCTGTCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCACTC 1860
 80 CCTTCCGAG CCCAGCTCCA TGCTAACCTG CCCACAGCAA CCCACAGAG CCACATTCCC 1920
 TGCTGCACCT GGTCTGCAGG GGTGTCCCAG GACAGGCCCA AGTCAGGCCA GCATGACACT 1980
 GCGCTCTTAC CCTGAAGATG GGAGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCCTGG 2040
 ACCTCTCTGG CAGGAAGGGG TGCAGTCTCT GAGGGCCTGT GCCCCACAGC CCCAGCACCC 2100
 AGGTGAGCTG CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCGCTCAGCA 2160
 GGCTGGGGTC TGCCACCACG GGCCCTCCCA CGTCTGCTT TGAGGGTGCC TGCCATGCC 2220

5 TGGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG 2280
 GGTGACTTCA TCAGGAGACC GCCACATAG AGCTGGACCC CGCAGCTGAA GCGGAAATGT 2340
 GAGACAGGCT GGCACCTCCG GAAAACTGC CTTTCAGCCT TGGTGTCCG TGCAAGGTGA 2400
 AAAGAAATAG GTCTCCCGAG TTTCAGCTT GAAATCAGG TAGTGAGTGG CCTCGGAGAC 2460
 CACGAGGGGA GAATTTAAG GCCCCGGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT 2520
 GCAGACCCTG CCTGGAGCCT GCCCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAGGATGT 2580
 GAGCAGCGTC CCTGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAGGT ACATACACGT 2640
 GCGTGACAC TGTGATGACA CCGGAAATG TCTCAGGATG TTGAAATGTG TCCTTGGGGG 2700
 10 CAGAAGTGTG CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACACCA GGCTCAGGA 2760
 TTTTGTGTG ATCAAGTTCC AAGGAAAGG AACATCTCAG CCGGCGTGG TGGTTCAAGC 2820
 CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAAGCAGC CTGGGCAACG CAGTGAGAGA 2880
 CCCCATCTCT ACAAAAAA AAAAAAGAA AAGAAAAATG AGAGATCCAG GTTTAAAAAT 2940
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000
 15 TAGACCCAGA TACTAGAAAT ATCAGAGAGA ATATAAAGTA ACAGTGTITT ATATATCTAA 3060
 AGAAATAAAA GAGATTCTCG GAAACATGAA AAAAAA

A58 DNA sequence

Gene name: ESTs
 Unigene number: Hs.157601
 20 Probeset Accession #: W07459
 Nucleic Acid Accession #: AC005383
 Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
 GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCTAGAAG TGAAGTACTT 60
 TTTTATTTGC AGACCTGGGC CGATGCCGCT TTAATAAACG CGAGGGGCTC TATGCACCTC 120
 CCTGGGCGTA GTTCTCTCGA CCTCAGCCGG GTCCGGTCTG GCGCCCTCT CCCAGGAGAG 180
 30 ACATAACAGT GTCCACCGTG GCAGCCCGCG CCGGGCGGCC CCTCTCTGTA TCCCCTAGCG 240
 CCCCTTGCCC CGAGCCGCGC CCGGGTCTGT GAGTAGAGCC GCGCGGGCAC CGAGCGCTGG 300
 TCGCGCTCT CCTTCGTTA TATCAACATG CCCCCTTTCC TGTGTCTGGA GGCGGTCTGT 360
 GTTTCTCTGT TTTCCAGAGT GCGCCCATCT CTCCCTTCC AGGAAGTCCA TGTAAGCAAA 420
 GAAACGATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGCG TGCAGTGGAC 480
 ATCATGTTTC TGTAGATGG GTCTAACAGC GTCCGGAAGG GGAGCTTTGA AAGGTCCAAAG 540
 35 CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600
 GCATTTCCAGT TCAGTTCCAC TCCTCATCTG GAATTCCTCT TGGATTCTAT TTCAACCCAA 660
 CAGGAAGTGA AGGCAAGAAAT CAAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720
 CTGCTCTGA AATACCTTCT GCACAGAGGG TTGCTGGAG GCAGAAATGC TTCTGTGCCC 780
 CAGATCTCTA TCATCGTAC TGAATGGGAG TCCAGGGGGG ATGTGGCACT GCCATCCAAAG 840
 40 CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGGG TCAGTGTTC CAGGTGGGAG 900
 GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGCAGCAGG TGCTGTGGC TGAGCAGGTG 960
 GAGGATGCCA CCAACGGGCT CTTCAGCACC CTCAGCAGCT CGGCCATCTG CTCACGGGCC 1020
 ACGCCAGACT GCAGGGTCTG GGCTCACCCC TGTGAGCACA GGACGCTGGA GATGGTCCGG 1080
 GAGTTGCGTG GCAATGCCCC ATGCTGGAGA GGAATGCGGG GGACCTTGC GGTGTGCGG 1140
 45 GCACACTGTC CTTCTACAG CTGGAAGAGA GTGTTCTTAA CCCACCTGCG CACTGTCTAC 1200
 AGGACCACT GCCCAGGCCC CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1260
 CCAGAAAGAG TGAAGCGCTA CCAGTGCTCT TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC 1320
 TGTGCGCTGA AGCTGAGCCT GGAATGCAGG GTCCAGCTCC TCTTCTGTCT GGACAGCTCT 1380
 GCGGGCACCA CTCTGAGCG CTTCCTGCGG GCCAAGTCT TCGTGAAGCG GTTTGTGCGG 1440
 50 GCGGTCTGA GCGAGGACTC TGGGGCCGGA GTGGGTGTGG CCACATACAG CAGGAGGTG 1500
 CTGGTGGCGG TGCCGTGTGG GAGTACACAG GATGTGCTG ACCTGGTCTG GAGCTCTGAT 1560
 GGCATTCCTT TCGGTGTGG CCCACCTCTG ACGGGCAGTG CCTTGCAGCA GGCGGCAGAG 1620
 CGTGCTCTCG GGAGCGCCAC CAGGACAGGC CAGGACCGGC CACGTAGAGT GGTGGTTTGG 1680
 CTCACCTGAG CACACTCCGA GGATGAGGTT GCGGGCCAG CCGCTACAGC AAGGGCGCGA 1740
 55 GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG GCGGTGCGGG CAGAGCTGGA GGAGATCACA 1800
 GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTCAA CCAATCCCT 1860
 GAGCTGCAGG GGAAGCTGTG CAGCGCGCAG CGGCCAGGT GCGGACACA AGCCCTGGAC 1920
 CTCGTCTTCA TGTGGACAC CTCTGCCTCA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980
 AGCTTTGTA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGAGGTGAC ACAGGTCCGC 2040
 60 CTGGTGTGT ATGGCAGCCA GGTGCAGACT GCGTTGGGC TGGACACCAA ACCCACCCTG 2100
 GCTGCGATGC TCGGGCCATC TAGCCAGGCC CCTACCTAG GTGGGGTGGG CTCAGCCGGC 2160
 ACCGCGCTGC TGCACATCTA TGACRAAGTG ATGACCGTCC AGAGGGGTGC CCGCCTGGT 2220
 GTCCCCAAAG CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCCGTCTCT 2280
 GCGCAGAAAG TGAGGAACAA TGGCATCTCT GTCTTGGTGG TGGGGTGGG GCGTGTCTTA 2340
 65 AGTGAGGGTC TGCGGAGGCT TGCAAGTCCC CGGATTCCC TGATCCAGT GGCAGCTTAC 2400
 GCGACCTGCG GGTACACCA GAGCGTCTCT ATTGAGTGGC TGTGTGAGGA AGCCAGCAG 2460
 CCAGTCAACC TCTGCAAGTG TCGGATGGC TGGGAGGGCC CCCACTGCGA GAACCGTGAG 2520
 GGGAGCTACC GCTGCAAGTG TGTGAGCCAG GATGGAATC TTGAGAGGCC CCTGAGGCAC 2580
 70 ATGGCTCCCG TGCGAGGGG CAGCAGCGT ACCCTCCCA GCAACTACAG AGAAGGCCCTG 2640
 GGCACGTAAA TGTGTCTTAC CTCTCTGGAAT GTCTGTGCC CAGGTCTTAA GAATGTCTGC 2700
 TTCCCGCGGT GGCCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2760
 ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTCAACCCACA AACGATGTTG TTTAAAAGTT 2820
 75 TTGATGTGTA AGTAATATAC CACTTTCTGT ACCTGTCTGT CCTTGTGTAG GCTATGTCTAT 2880
 CTGCCACCTT TCCCTTGAGG ATAAACAAGG GGTCTGAAG ACTTAAATTT AGCGGCCCTGA 2940
 CGTTCCTTTG CACACATCA ATGCTCGCCA GAATGTGTGT GACACAGTAA TGCCAGCAG 3000
 AGGCTTTTAC TAGAGCATCC TTTGGAAGGC GAAGGCCAAG GCTTTTCAAG ATGGAAGCA 3060
 GCAGCTTTTC CACTTCCCA GAGACATTCT GGATGCAATTT GCATTGATC TGAAGGGGGG 3120
 80 CTGAGGGAGC GTTTGTGACT TCTTGGCGAC TGCCTTTTGT GTGTGGAGA GACTTGGAAA 3180
 GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTTGA TGAATGGGGA GGGGCTGAGT 3240
 TGTGATGGG CCCAGTCTG GAGGGCCAG TAAATCGTT CTGAGTGTG AGCAGTGTCC 3300
 ACCTTGAAGG TCTTC

A59 Protein sequence

Gene name: ESTs
 Unigene number: Hs.157601
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: none found
 VGM domains: 49-223; 341-518; 529-706
 EGF domains: 298-333; 715-748
 Cellular Localization: secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
15  MPPFLLEAV CVFLPSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLDGSN 60
    SVKGGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QOEVKARIKR 120
    MVFKGGRTET ELALKVLLHR GLPGGRNASV PQILIIVTDG KSQGDVALPS KQLKERGVTV 180
    FAVGVRRPFR EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
    PCEHRTLEMV REPAGNAPCW RGSRRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCGPGCD 300
    SQPCQNGGTC VPBOLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDDGFL 360
    RAKVFKRFV RAVLSBDSRA RVGVATYSRE LLVAVPVGEY QDVDPDLVWSL DGIPFRGGPT 420
    LTGSLRQAA ERGGSATRT QDRPRRVVV LITESHSEDE VAGPARHARA RELLLGVGS 480
    EAVRAELEBI TGSPKHYVMV SDPQDLFNQI PELQGLCSR QRPGRCTQAL DLVFMLDTS 540
    SVGPENFAQM QSFVRSALQ FEVNPDTVQV GLVVYGSQVQ TAPGLDTKPT RAAMLRAISQ 600
    APYLGVGVS APTALLHIYDK VMTVQRGARP GVPKAVVLT GARGAEDAAV PAQKLKNGI 660
    SVLVVGVGV LSEGLRRLAG PRDSLHVA AADLRYHODV LIEWLCGEAK QFVNLCKPSP 720
    CMNEGSCVLQ NGSVRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETFLR HMAPVQBSGS 780
    RTPPSNYREG LGTEMVPTFW NVCAPGP
  
```

A60 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Nucleic Acid Accession #: NM_016425
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
40  ATGTTACAG ATCTGACAG TGATCAACCT CTGAACAGCC TOGATGTCAA ACCCTGCGC 60
    AAACCCCGTA TCCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
    CTGAGCCTGT CGAGTATCAT CATTGTGGTT GTCTTCATCA AGGTGATTCT GGATAAATAC 180
    TACTTCTCTT GGGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
    CTGAGCTGTC CCTTGGGGGA GGAACGAGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
    GCAGTGGCAG TCCTGCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA 360
    GGAACCTGGT TCTCTGCTGT TTTCAGAAC TTACAGAAAG CTCTCGCTGA GACAGCCTGT 420
    AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
    GATCTGGATG TTGTTGAAAT CACAGAAAC AGCCAGGAGC TTCGATGCG GAACTCAAGT 540
    GGGCCCTCTT TCTCAGGCTC CTGTGCTTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
    AAGACCCCTC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
    AGCATCCAGT ACGACAAACA GCAOGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC 720
    CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCACTGGAA GGTGCGGGCA 780
    GGCCTCAGCA AACTGGGCAG CTTCCTATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840
    TTCAACCCCA TGTAACCCAA AGACAATGAC ATGCGCCTCA TGAAGTGCA GTTCCCACTC 900
    ACTTCTTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
    GCCACCCAC TCTGATCAT TGGATGGGGC TTACGAAGC AGAATGGAGG GAAGATGTCT 1020
    GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGCTGCA TGCAGACGAT 1080
    GCGTACCAGG GGGAGATGAC CGAGAAGATG ATGTGTGAGC GCATCCCGGA AGGGGGTGTG 1140
    GACACCTGCC AGGGTGACAG TGTGGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
    GTGGGCATG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCACAG AGTATACACC 1260
    AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA
  
```

A61 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Protein Accession #: NP_057509
 Signal sequence: none found
 Transmembrane domains: 31-53
 LDLa domain: 54-94
 Tryp_SPC domain: 204-429
 Cellular Localization: plasma membrane/ER

```

1      11      21      31      41      51
|      |      |      |      |      |
75  MLQDPDSDQF LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY 60
    YFLCQQLRHF IPRKQLCDGE LDCPLGEDEB HCVKSPFEGP AVAVRLSKDR STLQVLDSAT 120
    GWNFSACPDN FTEALAEATC RQMGYSKPT FRAVEIGPDQ DLDVVBITEV SQELRMNRNS 180
    GPCLSGSLVS LKCLACGKSL KTRPVVGGEE ASVDSWFWQV SIQYDRQHVC GGSILDPRHV 240
    LTAHCFPRKH TDVFNWKKVRA GSKLGSPPS LAVAKIIIE FNPMPKNDND IALMKLQFPL 300
    TFSQTVRPIK LPFFDEELTP ATPLNIIWNG FTKQNGGKMS DILLQASVQV IDSTRCNADD 360
    AYQGEVTEKM MCAGIEPGGV DTCQDSGGP LMYQSDQMHV VGIVSWGYGC GGPSTPGVYT 420
    KVSAYLNWIV NVWKAEI
  
```


A62 DNA SEQUENCE

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Nucleic Acid Accession #: none found
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

```

10      1      11      21      31      41      51
      |      |      |      |      |      |
      CCAAACAGAT TTGCAGATCA AGGAGAACCCT AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60
      CTGAGATCCT TGCCTAGCT ACATCCTCAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120
15      CGGCTGCTCC TATTGCTGAG CTGCCTGGCC AAAACAGGAG TCCTGGGTGA TATCATCATG 180
      AGACCCAGCT GTGCTCCTGG ATGGTTTAC CACAAGTCCA ATTGCTATGG TTACTTCAGG 240
      AAGCTGAGGA ACTGCTCTGA TGCCGAGCTC GAGTGTCACT CTTACGGAAG CGGAGCCAC 300
      CTGGCATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360
      CAGAGAAGCC AGCCGATATG GATTGGCCTG CACGACCAC AGAAGAGGCA GCAGTGGCAG 420
20      TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGGTCTG GCAAGTCCAT GGTGGGAAC 480
      AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTAA CTGGAGCAG CAACGAATGC 540
      AACAGCCGCC AACACTTCTT GTGCAAGTAC CGACCATAGA GCAAGAATCA AGATTCTGCT 600
      AACTCTCTCA CCAGCCCGCT CCTCTCCTT TCTGCTAGCC TGGCTAAATC TGCTCATTAT 660
      TTCAGAGGGG AAACCTAGCA AACTAAGAGT GATAAGGCC CTACTACACT GGCTTTTAA 720
25      GGCTTAGAGA CAGAACTTT AGCATTTGGC CCAGTAGTGG CTCTAGCTC TAAATGTTG 780
      CCGCGCCATC CCTTTCCACA GTATCCTTCT TCCTCTCTCC CTGTCTCTG GCTGTCTCGA 840
      GCAGTCTAGA AGAGTGCATG TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAGT 900
      AAAGATTGA AGACAGAAGG AAGAACTCA GGAGTAAGCT TCTAGACCCC TTCAGCTTCT 960
      ACACCTCTCT GCGCTCTCTC CATTCCTGCG ACCCAACCCC AGCCACTCAA CTCTGCTTG 1020
30      TTTTCTCTT GGCCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGGTTG ATGTGGGCCA 1080
      TACATTCCTT TAATAAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA
  
```

A63 Protein sequence:

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Protein Accession #: none found
 Signal sequence: 1-22
 Transmembrane domains: none found
 C-type lectin domain: 47-156
 Cellular Localization: secreted

```

45      1      11      21      31      41      51
      |      |      |      |      |      |
      MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGNFYHKSN CYGYFRILRN WSDAELECSQ 60
      YGNARHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQQWQWIDG AMYLYRSWSG 120
      KSMGGNKHCA EMSSNNNPLT WSSNECNKRQ HFLCKYRP
  
```

A64 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

```

60      1      11      21      31      41      51
      |      |      |      |      |      |
      GCGGAACACC GCGCGCGCGT CGGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
      TCCCTCGTGG ACCTCTCGCG TCTCTCTCC TTCTCCAGGT TTGCTGGCTG CAGTGCCGGG 120
      CCTCCGAGCC GTGCGCGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180
      CGGAGCAGGA GCGCGGCCAG GCGCTGGGGA AAGTATTCTT GGGCTGCCCT GGGCAGAGCC 240
      CAGCTCTGTT TAGCACTGAT AATGATGACT TCAGTGTGCG GAATGGCGAG ACAGTCCAGG 300
65      AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCATCCAAA CGTATCTTAC 360
      GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAT GGCAGGGTTC 420
      CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
      ACAGCATCAC GGGGCGGGGG GCAGACAGCC CCGCTGAGGG TGTCTTGGCT GTAGAGAAGG 540
      AGACAGGCTG GTTGTGTTG AATAAGCCAC TGGACCGGGA GGAGATTGCG AAGTATGAGC 600
70      TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGG GSAACCCATG AACATCTCCA 660
      TCATGTGTAC CGACCAAGAT GACCACAGC CCAAGTTTAC CCAGGACACC TTCGAGGGA 720
      GTGTCTTAGA GGGAGTCTTA CAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
      ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840
      AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCCACCTC AGCCTCATCT 900
75      CCAGTGGCCT GGACCGGGAA AAAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
      TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCCT GATGCCAATG 1020
      ACAATGCTCC CATGTTTGAC CCCCAGAAGT ACGAGGCCCA TGTGCTGAG AATGCACTGG 1080
      GCGATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGACGC CCCCACCTCA CCAGCGTGGC 1140
      GTGCCACTTA CCTTATCATG GCGGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
80      CTGAGAGCAA CCAGGGCATC CTGACAACCA GGAAGGGTTT GGATTTTGGG GCCAAAAACC 1260
      AGCACACCTT GTACGTTGAA GTGACCAACG AGGCCCCCTT TGTGCTGAAG CTCCCAACCT 1320
      CCTCAGCCAC CATAGTGGTC CAGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCCAT 1380
      CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCACTGG GAGCCTCTGT TGTGTCTACA 1440
      CTGCAGAAGA CCTTGACAAG GAGAATCAA AGATCAGCTA CCGCATCCTG AGAGACCCAG 1500
  
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CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTCGACC 1560
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 ACCATGGCCC AGTCCCTGAG CCCCCTCAGA TCACCATCTG CAACCAAGC CCTGTGGGCC 1740
 ACGTGCTGAA CATCACGGAC AAGGAOCTGT CTCCCCACAC CTCCCTTTC CAGGCCACG 1800
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAG CGAGGAAGGT GACACAGTGG 1860
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACTT TCTCTGTCTG 1920
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 TCAAGGAGCC CCTCTACTC CCAGAAGATG ACACCOGTGA CAACGTCTTC TACTATGGCG 2160
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 CACAGAGCAT CTCCAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTCA 2640
 GGAAGTGGCC GTAGCAACTT GCGGAGAGCA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700
 TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCAAGTTGAC TTCAGCAGTG AAAACCTCTC 2760
 CACCTGGGCC AGGGTTGCTT CAGAGGCCAA GTTCCAGAA GCCTCTTACC TGCCTAAGA 2820
 TGCTCAACCC TGTGTCTGCG GCCTGGGCTT GCTGTGACTG ACCTACAGTG GACTTCTCT 2880
 CTGGAATGGA ACCTTCTTAG GCCTCTGTGT GCAACTTAAT TTTTITTTT AATGCTATCT 2940
 TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCGAGA GCTGCTGGGC CCACTGGCCG 3000
 TCCTGCATTT CTGGTTTCCA GACCCCAATG CCTCCCATTC GGAATGGATCT CTGCGTTTIT 3060
 ATACTGATG TGCCTAGGTT GCCCTTATT TTTTATTTT CCGTTGTGCT TGTATAGAT 3120
 GAAGGGTGAG GACAACTCTG TATATGTACT AGAATTTTT TATTAAGAA A

A65 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675 (second underlined sequence)
 Cellular localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVPFGCPG 60
 QEPALPSTDN DDFTVRNGET VQERRSLKER NPLKIPPSKR ILRRHKRDWV VAPISVPENG 120
 KGFPFQRINQ LKSNKDRDTC IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREBIK 180
 YELFGHAYSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTP RGSVLEGVLP GTSVMQVTAT 240
 DEDDAIYTYN GVVAYSIHQS EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TMDGDGSGTT TAVAVVEILD ANDNAPMDFP QKYEAVHPEN AVGHEVQRLT VTDLDAFNSP 360
 AWRATYLIMG GDDGDHFTIT THPESNQGIL TTRKGLDPEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVV VEDVNEAPVF VPPSKVVEVQ BGIPTEGPVC VYTAEDPKE NQKISYRILR 480
 DPAGWLAMPD DSQQTAVTCT LDREDBQFVR NNIYEVMLA MDNGSPPTTG TGTLLLTLD 540
 VNDHGVPEFP RQITICNQSP VRHVLNITDK DLSFHTSPFQ AQLTDDSDIY WTAEVNEEGD 600
 TVVLSLKFL KQDTVDVHLS LSDHGNKEQL TVIRATVCDK RGHVETCPGP WKGGFILPVL 660
 GAVLALLFL LVLLLVLRK RKIKPFLLP EDDTRDNVVF YGEBGGSEED QDYDITQLHR 720
 GLEARPEVVL RNDVAPTII TPMYRPRPAN PDEIGNFIIE NLKAANTDPT APPYDTLLVF 780
 DYEGBSGDAA SLSSLTSSAS DQDQDYDYLW EWGSRFKKLA DMVGGGEDD

A66 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 Probeset Accession #: N51919
 Nucleic Acid Accession #: AF189723
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 ATGATTCCTG TATTGACATC AAAAAAGCA AGTGAATTAC CAGTCAAGTA AGTTGCAAGC 60
 ATTCTCCAG CATGACTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120
 TTTATGCTCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180
 TCTCATGTTA AAAATCCCTT TATTATGCTG CTTCTGGCTT CTGCAGTCAT CAGTGTITTA 240
 ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300
 GCCTTTGTTT AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360
 CCAGAAATGCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGCCCG AGACTTGGTT 420
 CCAGGTGATA CAGTTTGGCT TCTGTGTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTCT 480
 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTCTT 540
 AAGGTGACAG CTCTCAGGCC AGCTGCAACT AATGAGATC TTGCATCGAG AAGTAACATT 600
 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAAG GTGTTGTCTAT TGGAAACAGGA 660
 GAAAATTTCTG AATTGTGGGA GGTTTTAAAG ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720
 CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGTGATA 780
 ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAG ATATCTCTGA AATGTTTACT 840

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ATTAGTGTAA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCATTTGT GGTACAGTG 900
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AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTTACT 1080
GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATTG 1140
TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200
AGAAACATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAAATTGCTCT TGCAATGAAG 1260
ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT 1320
GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380
TGTTTTATGA AAGGTGCTTA CGAACAAAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440
GGCAGAGCTT TGACCTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAAG GAAGGCACGC 1500
ATGGGCTCAG CCGGACTCAG AGTCTTGTCT TTGGCTTCTG GTCCGTGAAT GGCAGAGCTG 1560
ACATTTCTTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620
ACCAACTCCA TTGCCTCAGG AGTATCAATA AAAATGATTA CTGGAGATTC ACAGGAGACT 1680
GCAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTCACAAA CTTCACAAA TAGTACCAA GGTTCAGTA 1740
GAAGAAATAG ATGCAATGGA TGTTCAGCAG CTTCACAAA TAGTACCAA GGTTCAGTA 1800
TTTTACAGAG CTAGCCCAAG GCACCAAGATG AAAATTATTA AGTCGTACAA GAAGAACGGT 1860
TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920
ATTGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980
CTAGTGGATG ATGATTTTCA AACCATAATG TCTGCAATCG AAGAGGCAGC AGACATGATC 2040
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ATCAATATTA TTATGGATGG ACCCCAGCTC CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220
GATGTCATTG GTAAACCTCC TCGCACTGGG AAGACAGAGA TTTTGACTAA AACTTTGATA 2280
CTTAAATATC TTGTTTCATC AATAATCATT GTTTGTGGGA CTCTGTTTGT CTCTGGGCT 2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACACAAA TGACCTTCAC ATGCTTTGTG 2400
TTTTTTGACA TGTTCATGTC ACTAAGTCC AGATCCCGA CCAAGTCTGT GTTTGAGATT 2460
GGACTCTGCA GTAATAGAAT GTTTTGTCTAT GCAGTTCTTG GATCCATCAT GGCACAATTA 2520
CTAGTTATTT ACTTTCCTCC GCTTCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
GATCTGTTGT TTCTTTTGGG TCTCACCTCA TCAAGTGTGCA TAGTGGCAGA AATTATAAG 2640
AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTGA GTTCGACATC ATCATCTTTT 2700
CTTGAAGTAT GA
  
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A67 Protein sequence:

35 Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 ProbeSet Accession #: N51919
 Protein Accession #: AAF27813
 40 Signal sequence: none found
 Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
 Cellular Localization: not determined

45
 50
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 60

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1 11 21 31 41 51
MIPVLTSKKA SELPVSEVAS ILQADLQNGI NKCEVSHRRA FHGWNEFDIS EDEPLNKKYI 60
SQFKNPLIML LLASAVISVL HQFDDAVSI TVAILIVTV APVQEYRSEK SLEELSKLVP 120
PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLE EAVDLSDIES SLTGETTPCS 180
KVTAQPAAAT NGDLASRSNI AFMGTLVROG KAGGVVIGTG ENSEFGEVFK MMQAEAPKT 240
PLQKSMILLG KQLSFYSPGI IGIIMLVGML LQKIDLEMT ISVSLAVAAI PEGELIVTV 300
TLALGVMRMV KKRAIVKKLP IVETLGCNV ICSDKTGTLT KNEMTVTHIF TSDGLHAETV 360
GVGYNQFGEV IVDGDVVGHF YNPVSRIVE AGVCNDAVI RNNILMGKPT SCALIALAMK 420
MGLDGLQDQY IRKAEYFPSS EQKMAVKCV HRTQDRPEI CFMKGAYEQV IKYCTTYQSK 480
GQTLTLTQQQ RMYVQEKAR MGSAGLRVLA LASGPELQQL TFLGLVGIID PRTGVKEAV 540
TTLIASGVSI KMTIGDSQET AVAIALRLGL YSKTSQSVSG BEIDAMDVOQ LSQIVPKVAV 600
FYRASPRHM KIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVMGQTGT DVCKEADMI 660
LVDDDFQTIM SAIBEGKIY NNKPNFVRFO LSTSLAALTL ISLATIMNFP NPLNAMQILN 720
INIIMDPPA QSLGVEFVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VOGTLFVFWR 780
ELRDNVITPR DTMFTPTCFV PFDMPNALSS RSQTKSVFBI GLCSNRMPCY AVLGSIHQQL 840
LVIFYFPPLQK VFQTESLSIL DLLFLLGLTS SVCIVAEIHK KVERSRKIQI KHVSTSSSF 900
LEV
  
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A68 DNA SEQUENCE

65 Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 ProbeSet Accession #: BE616633
 Nucleic Acid Accession #: NM_001719
 70 Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

75
 80

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1 11 21 31 41 51
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CGGAGCGCGT GGTAGCGCGT AGAGCCGCGC 120
CGATGCACGT GGGCTCACTG CGAGCTGCGG CGCGCAGCAG CTTCGTGGCG CTCTGGGCAC 180
CCCTGTTCTT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAAAGAG GTGCACTCGA 240
GCTTCATCCA CGGGCGCTCC CGCAGCCAGG AGGGCGGGGA GATGACGCGC GAGATCCTCT 300
CCATTTTGGG CTTCGCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCGCGCG 420
GCCAGGGCTT CTCTACCCC TACAAGGCGG TCTTCAGTAC CCAGGGCCCC CTCTGGGACA 480
GCCTGCAAGA TAGCCATTTC CTCACGACG CGACATGGT CATGAGCTTC GTCAACCTCG 540
TGAACATGA CAAGGAATTC TTCCACCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
TTTCCAGAT CCCAGAGGG GAAGCTGTCA CGGCGCGCA ATTCCGATC TACAAGGACT 660
  
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5 ACATCCGGGA ACGCTTGGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
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 AGGAGGGCTG GCTGGTGTTC GACATCAGAG CCACAGAGCAA CCACTGGGTG GTCAATCCGC 840
 GGCACAACCT GGGGCTGCAG CTCTCGGTGG AGACGCTGGA TGGGAGAGC ATCAACCCCA 900
 AGTTGGCGGG CCGATTGGG CGGCAAGGGC CCCAGAACA GACAGCCCTC ATGGTGGCTT 960
 TCTTCAAGGC CACGAGGTGC CACTTCCGCA GCATCCGCTC CACGGGGAGC AACAGCGCA 1020
 GCCAGAACCG CTCCAAGACG CCCAAGAAC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
 AGAACAGCAG CAGGACCCAG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
 10 GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCCGCC TACTACTGTG 1200
 AGGGGAGTGT TGCCCTTCCCT CTGAACCTCT ACATGAAAGC CACCAACCAC GCCATCGTGC 1260
 AGACGCTGGT CCACCTTATC AACCCGGAAG CCGTGCCCAA GCGCTGTGTG GCGCCCAAGC 1320
 AGCTCAATGC CATCTCCGTC CTCTACTTGG ATGACAGCTC CAACGTATC CTGAAGAAAT 1380
 ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CTCCGAGAA TTCAGACCT 1440
 15 TTGGGGCCAA GTTTTCTGAG ATCTCCATT GCTCGCTTGG GCCAGGAACC AGCAGACCAA 1500
 CTGCTTTTGT TGAGACCTTC CCCTCCCTAT CCCCAACTT AAAGGTGTGA GAGTATTAG 1560
 AAACATAGAG AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
 TCCTCAAGC TGTGCAGGCA AAACCTAGCA GGAAGAAAA ACAACGCATA AAGAAAAATG 1680
 GCCGGGCCAG GTCATTTGGT GGAAGTCTC AGCCATGCAC GGAAGTGTG CCAGAGGTAA 1740
 20 TTATGAGCGC CTACAGGACA GGCCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
 GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCTGTGA ATAAATGTCA 1860
 CAATAAAACG AATGAATG

25 A69 Protein sequence:
 Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Protein Accession #: NP_001710.1
 30 Signal sequence: 1-30
 Pfam domains: TGF β propeptide [37-281]
 Transmembrane domains: none found
 Cellular Localization: secreted

35 1 11 21 31 41 51
 | | | | |
 MHVRSRLRAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRLRSQRE RREMQREILS 60
 ILGLPFRPRP HLQCKENSAP MFMLDLINAM AVEBGGGPGG QGFSYPYKAV PSTQSPPLAS 120
 40 LQDSHFLIDA DMVMSFVNLV EHDKEFFHPR YHREFRFDL SKIPEGEAVT AAEFRIYKDY 180
 IRERFDNRTF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGMVLVFDIT TSNEHVVNPR 240
 HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300
 QNRSKTFPNQ EALRMANVAE NSSSDQRQAC KKHLYVVSFR DLGWQDWIIA PEGYAAYCE 360
 GECAPFLNSY MNATNHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLYPD DSSNVILKKY 420
 45 RNMVVRACGC H

Cervical

50 A70 DNA sequence
 Gene name: bone morphogenetic protein receptor IB (ALK-6)
 Unigene number: Hs.87223
 Probeset Accession #: AA250737
 Nucleic Acid Accession #: NM_001203
 Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
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 GCGGGGGCGC GAGATCGGGC GGGGCTCGCG GAGCGCGGGC AGTGCGGAGA CCGCGGCGCT 60
 GAGGACGCGG GAGCGCGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT 120
 60 GTGAAAGGAA AGGAAGATCA TTTCATGCCT TGTGATAAAA GGTTCAGACT TCTGCTGATT 180
 CATAACCATT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240
 TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAAATTA 300
 AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCCCG TCCAAAGGTC 360
 TTGGTGTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420
 65 GACGGATATT GTTTCAGAT GATAGAAGAG GATGACTCTG GGTTCGCTGT GGTCACTTCT 480
 GGTTCGCTAG GACTAGAAGG CTCAGATTTT CAGTGTGGGG ACACTCCCAT TCCTCATCAA 540
 AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCCCTACA 600
 CTGCTCCAT TGAAAAACAG AGATTTTGTT GATGGACCTA TACACCACAG GGTCTTACTT 660
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 70 TATAAAGAC AAGAAACCAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAAACTTAC 780
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 75 ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGACAC 1080
 GGGTCTCTGA CCAAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140
 TATCTGAAGT CCACACCCCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC 1200
 AGTGGCTTAT GTCAATTACA CACAGAAATC TTAGTACTC AAGGCNAACC AGCAATTGCC 1260
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 ACTCGAGTGT GCACCAAAAG CTATATGCCT CCAGAAAGTGT TGGACGAGAG CTTGAACAGA 1440
 AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG 1500
 GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAA ACCAGCTTCC TTATCATGAC 1560
 CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAAGTTA 1620

CGCCCTCAT TCCCAACCG GTGGAGCAGT GATGAGTGC TAAGGCAGAT GGGAAACTC 1680
ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTAAAGAAA 1740
ACACTTGCCA AAATGTGAGA GTCCAGGAC ATTAACTCT GATAGGAGAG GAAAAGTAAG 1800
CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAAA 1860
TAAGCATCCA CAGTACAAGC CTGAACATC GTCCTGCTTC CCAGTGGGTT CAGACCTCAC 1920
CTTTGAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980
TCTGTTTGTG GCGGAGAAA CCGTGGGTA ACTTGTTCAT GATATGATGC AT

A71 Protein sequence
Gene name: bone morphogenetic protein receptor IB (ALK-6)
Unigene number: Hs.72472 / Hs.87223
Probeset Accession #: AA250737 / U89326
Protein Accession #: NP_001194
Signal sequence: 1-13
Transmembrane domains: 128-144
PFAM domains: activin_receptor [30-111], protein kinase [204-491]
Cellular Localization: plasma membrane

1 11 21 31 41 51
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DSGLPVVTSGL CLGLEGSDFQ CRDTPIPHQ RSI ECCTERN ECNKDLHPTL PPLKNRDFVD 120
GPIHRRALLI SVTVCSLLLV LILFCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180
BQSQSSSGSGS GLPFLVQRTI AKQIQMWKQI GKGRYGEVVM GKWRGEKVAV KVFFTTTEAS 240
WPRETEIYQT VLMRHNILG FIAADIKGTG SWTQLYLITD XHENGSLYDY LKSTTLDAKS 300
MLKLAYSSVS GLCHLHTBIF STQGKPAIAH RDLKSKNILV KKNGTCCCIAD LGLAVKFI SD 360
TNEVDIPFNT RVGTRKRYMPP EVLDESLNRN HFQSYIMADM YSFGILILEV ARRCVSGGIV 420
EEYQLFVHDL VPSDFSYEDM REIVCIKCLR PSFPNRWSSD ECLRQMGKLM TECWAHNPAS 480
RLTALRVKKT LAKMSQSQDI KL

Bladder

A72 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA
Unigene number: Hs.63325
Probeset Accession #: AA411502
Nucleic Acid Accession #: NM_016425
Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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CTGAGCCTGG CGAGTATCAT CATTTGGTGT GTCTCATCA AGGTGATTCT GGATAAATAC 180
TACTTCTCT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
CTGACTGTG CCTTGGGGGA GGAAGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
GCAGTGGCAG TCCGCTCTC TTCGACAAC TTCACAGAAG CTCTCGCTGA CAGAGCCTGT 360
GGGAAGTGGT TCTTCGCTG TTTGACAAC TTCACAGAAG CTCTCGCTGA CAGAGCCTGT 420
AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGATGCG GAATCAAGT 540
GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
AGCATCCAGT AGCAACAACA GCAGTCTGT GGAAGGAGCA TCCTGGAGCC CCACTGGGTC 720
CTCACGGCAG CCCACTGCTT CAGGAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
GGCTCAGACA AACTGGGCGC CTTCCTATCC CTGGCTGTGG CCAAGATCAT CATCATGAA 840
TTCAACCCCA GTATCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
GCCACCCAC TCTGGATCAT TGGATGGGGC TTACGAAGC AGAATGGAGG GAAGATGTCT 1020
GCATACCTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
GCGTACCAGG GGAAGTCAAC CGAGAAGATG ATGTGTGTCG GCATCCCGGA AGGGGGTGTG 1140
GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

A73 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA
Unigene number: Hs.63325
Probeset Accession #: AA411502
Protein Accession #: NP_057509
Signal sequence: none found
Transmembrane domains: 31-53
LDLa domain: 54-94
Tryp_SPC domain: 204-429
Cellular Localization: plasma membrane/ER

1 11 21 31 41 51
MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIV VLIKVILDY 60
YFLCGQLPHF IPRQLCDGE LDCPLGEDEB HCVKSFPFEG AVAVRLSKDR STLQVLDSAT 120

5
GNWFSACFDN FTBALASTAC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
GPCISSGLVS LHCLACGKSL KTRPVVGEE ASVDSWPHQV SIQYDKQHV C GGSILDPHV 240
LTAHCFRKH TDVFNWKVRA GSKLGSFPPS LAVAKIIIE FNFMYPKND IALMKLQFPL 300
TFSGTVRPIC LPFFDBELTP ATPLWIIGWG FTKQNGGKMS DILLQASQV IDSTRCNADD 360
AYQGEVTERK MCAGIPBGV DTCQGDGGP LMYQSDQWVH VGIVSNGYGC GGPSTPGVYT 420
KVSAYLWYI NVWKAEI

A74 DNA SEQUENCE

10 Gene name: ESTs, Weakly similar to OGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
Unigene number: Hs.19322
Probeset Accession #: AA088458
Nucleic Acid Accession #: AA088458
Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

15
1 11 21 31 41 51
GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60
CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGTGTC TGCAGGGTTT GAGATGATG 120
GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180
CTGGGCGAGA GCAGAGCCAG CGCCGACTTT GGGGTGTCAG GGAGCCCCCG CCCACTGGGG 240
CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCTGG GGGAGCTGCT GGTGTCAGCC 300
TGTGCCAGCC GGGCCCTGCC CCCGTCTCTC TCGGGGCCCC CCTGCCCTGC CTGACGTCTC 360
ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC 420
CTCACCCAGG AGGTGACGGA GAAGAGTGAG CGCATCAGC AGCTGGAGCA GGAGAACTG 480
GCGCTACATTA AGCAGCTGTT TGAGGCCCGC GCCTGAGCC AGCAGGAAGG GGGACCTCTG 540
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AGCCCTTCGA GGGTGGGCGC CCCATGCGAC CCACCTCTTC TGGCTGGAGA CCCCCTGGAG 660
GCCAGGACAC AGTCCCGGAG TGGGCGCCTT CCTGCCGCC TTGCCAGATG GGTCTCCCGAG 720
GCGTCCCCCG GGTCTGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGTTGTGTC 780
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CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080
GTAAGCGGGG GGTGCTCTGC TGGCTGGGGA GCCCCAGGGA TAGCGGTGCG ACTTCAGGTT 1140
CTGGCCAAGG CTGAGGGACG CTGGCTGCG CGGATCGGCA CGCCGGGTGG GCGAGAGCTT 1200
GGCTGTCATG TGCTCTCCAC AGACCTTGGG GTGATGGCCT TCCCCCTCTT GGCCTGGAGC 1260
TTGCCCAACG TTGATGCCCA CACAACATCC TGTGAGCCTG GCTCCCGAGG AGGGCCCCCA 1320
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CTGGGTCTCT GCTCACCCCC CTTTGTCTCT AOGCCAGCC TGTCCCGAGG TTTGAGCTGG 1440
GAGAGGCCAC CTCCTTCAGC CAAGGAAAAA GAGAACCCCC AGGGTACAGG AGGAGGCTGG 1500
GGCAGGTCCC CTTGGGTGTC ACTCCCTCAG CCCCTGCCCA GGCCCACTCC CGCTGGTGCT 1560
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GAAACAGGGG CACGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG 1680
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CCCGATGCGG GGTCACTGCG TGGGGGGGCG AGGGCCCCCT CGTGTCCAGG GCACCTTGGT 1800
ACACTGTCCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAACTC 1860
CCTTCCGGAG CCCAGCTCCA TGCTAACCTG CCCACAGCAA CCCACAGAG CCACATTCCC 1920
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TGGGGGATCC TGCCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG 2280
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CAGAGGGGGA GAATTTAAAG GCCCGGGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT 2520
GCAGACCCCT CCGTGAGGCT GCCCTAGGAC GCTGGGGCGG TCAGTCTCCG TGCAGGATGT 2580
GAGCAGCGTC CCGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAAGT ACATACAGT 2640
GCGTGCAAC TGTGATGACA CCCGGAATG TCTCAGGATG TTGAATGTG TCCTTGGGGG 2700
CAGAAGTGTG CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACACCA GGCTCAGGA 2760
TTTTGTGTG ATCAAGTTCC AAGGAAAGG AACATCTCAG CCGGGCGTGG TGTTTCAAGC 2820
CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880
CCCCATCTCT ACAAARAAAA AAAAGAAAG AAAAGAAATG AGAGATCCAG GTTTAAAAAT 2940
TCATAAACAC CACAGGAA CAATACACTA TGAGACCCAG CAGAAACAAC AGATTGACTC 3000
TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAGTA ACAGTGTTTT ATATATCTAA 3060
AGAAATAAAA GAGATTCTG GAAACATGAA AAAAAA

A75 DNA SEQUENCE

75 Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor
Unigene number: Hs.227948
Probeset Accession #: AB035089
Nucleic Acid Accession #: AB035089
Coding sequence: 9845-10219 (underlined sequences correspond to start and stop codons)

80
1 11 21 31 41 51
GGGCATGCAG CCATCGGGGA AAATCCATAG TGCAGATAAA GCAAGGAGGA AGAAGAAGGA 60
CAGTTCTAGT AAAAGGGAGA ACATCAATAT AGGATGTTTC TTAGCAATAG AAAAAGAAGG 120
CCAAGAGGAA TAGGGAGAG AGTTATAAGA GATCAGCAGG GGCACAGGGT TAGATTGGT 180
TTGGTTTGAA AGCATACAGT AAATATGATG TCTGTCCCTG GCAGTGTGGG CAGAGTAGGA 240

	AGGAGGAAGG	GAGGCAAGAG	ATAATATCAT	TTTCTCTGTG	CTCCAACGTG	ACTTACATAT	300
	GAGACTATTT	CCCTCTCTGC	TTTTCAAACC	TTACTGGAGT	TGTTTTCCCT	CATGAAAACC	360
	AAGAAAGGAA	AGCTAGTTAG	TCTTGTCTCG	AGGTGTGTCA	ATGTATACAT	ATCTATATCT	420
5	GTAGACAGAA	TCCTTGGGAA	TACAGTAATT	GACATATATT	CTGTATTITG	ATGCTTGAAA	480
	AATCTCTCC	ACTAACAGT	TTCCCTATAG	ATTGCCACAA	GCACATAATA	AGAAACATA	540
	AATAAAATGT	TCTCTTGACT	TTGTTACTTA	ACAATGCTGA	GAAAACITTA	CAGCCTTCAT	600
	AAGGAAGTGA	GSTCCAGGAA	AATCTAGGAG	ATATTTCTTA	ACCAATCTAT	AAAGGCATT	660
	GTAATGACAG	GATATTTCTT	GAAAGTGTAA	TTTCCCATTG	AGGATTGTGT	TTTAATTTCT	720
10	GGATTCTCG	AGCCAATGAA	GTGGGTGTAT	GTTTATGAAA	TATCAAGAGA	CATAAGTTGG	780
	CAAGTGTTC	TATGCAAAAA	CTTCTTGGAA	TTTCTGAGTT	CTCTGTGGCA	ATATATGACA	840
	TCAGGATATG	TCCAGTCTCA	CACACCAGGA	TATGTCTTTT	CTAGCCTGTC	TATCACATGC	900
	TAGGAGAAGT	ATTTAGGAAC	AGAAAAAAT	GCCTGAAATG	ATTTCTCAAT	TGAACCTATC	960
	CAAGCTTTCT	CTAAATTTAA	GCAAACTCCT	GGTCATTTTC	AGTTAGTACC	TTTCTTAAAG	1020
15	TTCAACCTTC	AGGGCAAACT	TCCGTGCCTC	AGACGTTTAG	CCATAGTCTG	AAATCTCTCT	1080
	CCATAGATGT	GTCCCTCTGT	ACCCCGGTTC	GTCTCAGCTT	GTATCTCTGT	TTTTTCTTTC	1140
	CCTCCATTCC	CAGGATGAGC	TGTGTGCTTC	TGTCTATGTA	GACATTAGAT	TCCTTTTCTT	1200
	TGGTACCCGA	GTAAATCCAT	CCTACTCCAA	TAGAGGAAGG	TCCATTTTGT	TCTTATAGCG	1260
	CTGGATGCG	ACTCAGCTGA	GAAGACCAT	ATTCATTTT	GGAATCTTTT	ATCTCAGATA	1320
20	TTTCTCTTTC	TTTCTTTTTC	TTCTATCTTT	GGATTTTITG	TCCATCAACG	CCCCATTAGT	1380
	CTATTCCCG	ACTTCAATCA	GGGAACITAT	ACCTCTTAAA	CTCATCAGA	GACTCAAAAC	1440
	ATATATATTG	ATACAGGAGA	CCTAAGAAGA	GCATGTCTTG	GGGGTTGAGG	AAACAGGCAG	1500
	GTGAGAAAT	TCCAGATTGG	AAACACAGCT	TCCTTTCTCC	CATCCAGCCC	CTACTTTTTC	1560
25	CCTATGTGTT	TCTGGCACC	TGTTGTAGAT	AAATCTCCCT	TGACTTTGTG	ATGTGCTGAG	1620
	AAAACAAACT	CACGGCTGGT	GTAAAAAAGG	GCCCATGACA	ATACCAAGTG	TTGGGGAGAA	1680
	TGTGGAGAAA	TCAGAAGTCT	ATTCAGGTC	GGTTGSAATG	CACACTGTGT	CAGAATTCTA	1740
	TGGAGAAGAG	TCTGGCATT	CCTCAAAATG	TTAACCTGGA	TTTACCATAT	GAOCCAGCGA	1800
	TTTCATTCTAT	AGGTTTATAC	TCAAAAGAAA	TGAAGAAATA	TGCCATGCAA	AAAAATGTAC	1860
	ATGAAAGGTC	ACACATCAT	TATTCATAAT	AGTAAAGGA	TGGAAACAAC	ACAAATGTCC	1920
30	ATCAACTTAT	GATTAAGAA	AATCTGGTCT	ATTCATAGAA	TGGAAATATTA	TTGAGCCACA	1980
	AAAAGGAATG	ATGTACTGAT	CCATGCAATG	ATGTGGACAA	ACCATGAAAA	TAACTAGATA	2040
	TTAAAGAAAG	CAGTCAACAA	AGGACTTACT	GTATGATTCC	ATTTACCTGA	AATGTTTGGG	2100
	ATAGGCAAT	CCATAGAAAC	AGGAGGTAGA	TTCTGGTTT	CCAGGGTCTC	CAGGAAGGGA	2160
	AGAATGAAGT	ACAAGATTTC	TTTTGGAGGT	AGTGAATTTG	TTGTGGAAATG	AGATCATGAT	2220
35	GATGATAGCA	CAACTTTGTG	AATATAATAA	AATCATTGAA	TTGTACAGTT	GAATTTATGG	2280
	TATATAAAT	ATATGTTAAT	AAAAAGGGGG	TCCACAAAAC	AAACAGCCCC	CCACTCTGGT	2340
	TGTCAGGGAG	ATATTGGATT	AAATGGCCTT	GGACAACAAC	CCCTCTCCCT	GGCCACAGAC	2400
	ATTCTTCAGA	TTACAAGATA	TTCCAGGGGA	AAACATGGAA	TGAGTCTGAA	CCAGGTGCT	2460
	AAACAGAAAG	ACCATTTGGA	AATGTTGTGA	TCCTGACAGG	TCAAGCAATT	TATTTTTCGG	2520
40	CTTCATTTT	AAATGTAAAA	TTAGAAAGCT	GCCATTAAAA	ATGGCCCGTC	TGTTTCAATT	2580
	GCTCTTCTCA	GTGTCAGCTT	GTAACTCAA	TGTGTTAGTC	TGTTTTCATG	CTGCTGATAA	2640
	AAACATACCT	GAGACTGGCA	AGAAAAAGAG	GTTTAATITG	GCTTAGAGTT	CCACGTGATT	2700
	GGGGAGGCC	CAGAATCACA	GTAGGAGGCA	AAAGTTATTC	TTACATGTTG	CTGCTGAGAG	2760
	AAGATGAGGA	AGAAGCAAAA	GAAGAAACCC	CTGATAAAC	CATCGGAATC	CCTGAGGCTT	2820
45	ATTAACATAT	ATGAGAATAG	CACAAGAAAG	ACCGGCCCCC	ATGATTCAAT	TACCTCTACC	2880
	TGGGTCCTCT	CAATAACATG	TGAAATTTCT	GGTAGATACA	ATTCAAGTTG	AGATTGGGT	2940
	GGGAACACAG	CCAAACACATA	TCACTCAGCA	AGGCAGATAA	CTTTCTCACT	GAGCCTATGC	3000
	AACAGAAAC	CATCTGGGAT	GGTTGTAAGG	GGCAGAGGAA	GTGACTGGTA	GGATCACTGC	3060
	CAAGCTGAG	CACCTCAGGAG	AAGGCAATAG	AATCTTATTC	TCCATAGTAT	GCTATAGAT	3120
50	ACTGAAGTAC	ACTTCTTAC	TATCTCTTTC	GACTTAGAAT	TAGCACTACA	TTCTTGTGTA	3180
	TACAGAAAA	TTACTAAGGA	AATTCATAGG	ATGACAAAA	CTTTCAGAG	TGAAAAACAG	3240
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	CAAGAAAAAG	ATGGTGGGTT	TTTTGTTTGT	TTGTTTGTGT	TTTGTGTTTA	CAGCTGGAGT	3360
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55	CNTTGCATT	AGAAAGGCAC	CTACATGTAT	TTCAATGAG	CCGGTGAAGT	CTGACTTGCA	3480
	TTCTTATTTT	TTCCCTATAG	ATTAAAAAGG	AGGTACAATG	GTAGAACTGT	AATCCTGTCC	3540
	TTTGTATATA	ATTTTCATAT	TCATAAAGGT	GAGTGTITAG	COGCTTGTA	AATCTGAAGT	3600
	TGAGTAACTT	CAATACTATA	CCACAGAGGG	AAAGGCAGCA	AGAGGAGAGG	CATAAATTTA	3660
	GGATCTCACC	CTTCATTCCA	CAGACACACA	CAGCCTCTCT	GCCCACCTCT	GCTTCTCTTA	3720
60	GGACACAGG	TAGAGCTTTC	AAGCCTCTCC	AGCTTAATAA	CATGAATTAT	TTTTGAGAA	3780
	AATAATGATA	CTGTGTTCTA	TATCATGCAT	CTCCTGCATT	CTGTCTGATT	ATATTTTACT	3840
	TATTTCTGCC	GAGCAAAAT	AAAATACCTA	TTTCTCTGTA	TTTGTCTTTT	ATCTAAATTT	3900
	CTTAGTTCCA	AGTAAACCAA	GGCACTTTTA	GGACACAGA	GGGAGAGTGC	CTTGACGCCA	3960
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65	AGGTCTCCTG	TTAGCATTCA	TTGTAAAGCC	ATCCTACCTA	GCTCTAGTGT	AACCAGCAAT	4080
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	TAAAGCTTCT	AATTAGGACA	TTAATATATT	TAAATATATG	ACATTGTAGA	AAGATTGAAG	4200
	CGTTAAAAAT	AAGAGAAAAA	CTTTAAATGT	CAAAATCTCA	CAACCCAGAT	ATATCATTTT	4260
	TTTAAGAAAA	TTGTACTACA	AAATACCAAT	CCATTATTAT	AAGTCAATCT	GACAGGAATC	4320
70	TGATGCTTTT	CCAGGAGTTC	CAGATCAAT	CGAGTTCAAC	ATGAATTCAC	TCAGTGAAGC	4380
	CAACACCAAG	TTATGTTTCG	ATCTGTTCCA	ACAGTTTACA	AAATCAAAAG	AGAACACAT	4440
	CTTCTATTTT	CTATCAGCA	TCACATCAGC	ATTAGGGATG	GTCCCTCTAG	GAGCCAAAGA	4500
	CAACACTGCA	CAACAAATTA	GCAAGGTAGC	TATCAGCATC	ATTACGTTGT	CCTGTTGCG	4560
	TTTTTCTCTG	GTTCCTGTGG	CTAGCAAGCA	GATGTTAATA	GATGTTGTTG	TCTGATGGGT	4620
75	AGCACAGGGG	GCTGTGACGG	AATTTCCATA	ACTGTGAGAC	CACCTGACTTA	AACAGATCTT	4680
	TTGAGTAAAG	TTTTCTGTTC	COGCTTCATG	TCTCTTCCAG	GTCTTCTACT	TTGATCAAGT	4740
	CACAGAGAAC	ACCACAGAAA	AAGCTGCAAC	ATATCATGTG	AGTCACAGAG	CACCTGTGAT	4800
	CAGCTTTAGA	TCCCTGAACA	GGTCATAGTT	TAAACCTGGA	ACTTCACAAA	AACTAAGAAA	4860
	AGGCCAGTTT	TAGGGAATAA	CTTGGACACA	AAGATTGAGA	CATACAGAGT	GGGTTGGCAT	4920
80	TTCAATGGAC	ATAATTTATTA	TTCTCTATTT	CTGGGTTACT	AAAAGACAGT	CAGCACTGTA	4980
	CCTCAGACCA	TAGGCTCTGA	TCAGGATAGG	CTGGGTTTCA	ACTTCCAGCTT	TGCTCTTTC	5040
	AAATGATGAA	TAAAGCAGG	ACACACTGCT	TCCGAGTCCC	AGTGACCTCA	TCCAGAAAA	5100
	CTAAGGGTAA	GAAAAAATCT	GACTCAATAC	ATGCAAAATC	ATGCAAAATG	TTACACAGAT	5160
	GCCTTGCCCA	TAAAGTCAT	AATAAATGTT	ATTATTTATTA	TAAAGTAGCT	ATAATTATAC	5220
	TAATCATAAT	AATGTGAAAA	TAATTTAATT	TTCAATGAGT	CATTAATGAG	ATTCAGAGGA	5280

	ATAAGCACAA	GTCCAAGTAT	ATTTTGGAAA	ATGATTGCTA	TGGAATATAT	TGTTTAGAG	5340
	CCTTAATAGT	GCAAAATGCT	TTGCTGGAAG	GTAGAAAGTT	CTAGATTTAA	ACAGGCTTAG	5400
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5	TGAGCTTTCT	TGTGTTTCATC	TGAATTGAAC	TAAAGACTTA	GAGTTACCCA	TGTAAAGTCC	5520
	TTAGCCATGG	ACCTGGCATA	CACCTTCTTT	ACGTGCAGAG	AATGACCATC	ATGAGGAAAG	5580
	AGCCACAGAT	CAGTCAATGT	GTCTTACAAG	ATAATAGCAC	CAACAGGTAT	AACAGGGCTT	5640
	CCTGGCATAA	TCTATTTAAA	ATATCCAACC	TTCAACATAC	TCGTATCCTT	GATGACTGTT	5700
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10	AACCCCTTAA	ACCAACAAGG	AGAAATCTA	CTGGTAGACA	GCGCTGCATC	TTTAGTTTCA	5820
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	GGTGAGTTTT	GAAGGGTATT	TGAGGTGAAA	TACACCAATT	ATCAGGGAAT	AACATCAAAG	5940
	GTCTCAATG	AGACTACCGA	CATTTAGGGA	CTGATCTAAC	AGACTTAGCA	TGGGTTTAGT	6000
	ATTTACATTG	ATACAGCAAT	TGAATGATCT	CCTTTTTTGA	TGTTTGAAGG	TTGATAGGTC	6060
	AGGAAATGTT	CATCAACAGT	TTCAAAAGCT	TCTGACTGAA	TTCAACAAAT	CCACTGATGC	6120
15	ATATGAGTAG	AAGATGCGCA	ACAAGCTCTT	CGGAGAAAAG	ACGTATCAAT	TTTTACAGGT	6180
	AAATTCACCT	GGCTTACCCA	CATTTCAATT	GCATCTGTAT	GTCTGTGTCT	CTGAGTGGCC	6240
	AAATGGAAGA	AGCAAGGCA	GATGAGCCTG	GCGGACCCAG	GTGGAGAGCA	TTTACTCAGA	6300
	GTGCATTAGC	TCCATTTCOA	CAACTCTCCC	CCACTGGAGT	GTCCCAGACC	CCAAACGATC	6360
20	ATCAGTGAAG	TGTGATTATA	GGGATAATCT	TGTGATAAAA	GAGGAGGTTG	TGTAATAGAG	6420
	TGAGTAAGAG	TAAATAAGTAA	TAAAGATACCA	TCGATAAACT	GGCACTGACT	CAGTCACATA	6480
	CGATACATCT	TGTTGGGAAA	TGTATGACTA	ATGGGATATT	ATTGGAATGG	GCAGGCTTGG	6540
	GTGAGTTTCT	GAGAATAGTT	GAGGAAGTAC	CAGGAAATAT	TGAATGCACA	GGATGAAAGA	6600
	CAAAAACAAA	GATCAGAAAT	ATCATGGTTA	AAATTAAGTG	AGAGAAGTCT	GAGAAGCAAT	6660
25	GAATCTCTCT	CAGGGAAGCC	TGCTCTGCAG	TTTGCAAAAC	ACAGGCTCTT	CTGCTTCTGC	6720
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	TTTTTGCATTG	CCTACATGAC	ACCTGTATAA	AAATATCCAT	GGACAGGAGA	TACTGTCATCT	6840
	ATTCAAGGTC	TGGATTTCAG	TTACTGTTGT	TACAAATAAG	TAAGTTTGGT	AATATATAGT	6900
	TACATAAATT	ACTCCTAATT	CCTACTTCTT	CCTTCATATC	TCAAAGGAAT	ATTTAGATGC	6960
30	CATCAAGAAA	TTTTTACCAGA	CCAGTGTGGA	ATCTACTGAT	TTTGCAAAATG	CTCCAGAAGA	7020
	AAGTGAAGA	AAGATTAACT	CTGGGTGGA	AAGTCAAAAG	AATGGTAGGA	GAGCCACCCA	7080
	TTATAGAAAC	ACCTTTGAGA	AACCTATGCC	AGTGAGCCTT	GTGCTTGACA	CTGCATGGGG	7140
	GAACAGGTGT	GGGATTGTAG	ATGGSTTTCG	AGGGAGGGCT	GAAGAGGGCA	CTCCAGATGA	7200
	AGGATTGTGC	CAATGAATA	TGAAGAGAGC	CTAGGGGAGC	CAAGGAGGAA	ATCACAGGAA	7260
35	GCCAAATAGA	TGGAAACACA	TCTGGAGAAT	TATTTGCTTA	TGGCCCTGCA	TGACAAATAGC	7320
	TTTGTGGATC	CCCTGTCTCC	GCTCAGACCT	ATTTTGAGAT	CATATCTCTT	ACTTTAAATC	7380
	AGACTCAAAT	TTTTATGATG	AATATTTAAT	AGAAAACATT	AGAAAAGCTC	TCTGCTCTCC	7440
	TTTACTAATT	GGGAAACAAG	CAGCTCTCTG	GTAAATCAC	CTTTGTCTCT	TGAGCTGGAG	7500
	CTGCCTGGAT	CACATCTGTA	GCCAAATGTT	TCTGCAGGGA	TTATCACAGC	TCTCTTCCCC	7560
40	ATCAAGGGCA	AAGAGCTTGA	CAAAGTCTCC	ATTTCTACAGA	CATCTTTCTT	ACCTCCCACC	7620
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	GAAGTAGTGT	CTGACAGCAC	AGGACATGCG	TTTCATATTA	CAGAGCTCAA	GTCACTCATC	7740
	CTAAAAATGCA	ATCAGGGCCT	CCTTCTCTCT	AATGGGGACC	CCGTAGTTAA	AAAAAATAA	7800
	AAGTAGGAAG	AGGAGGGAGG	GAGAAAGGAA	AGACACATGT	TGGAAGAGTA	GACAAAAATCA	7860
45	GTTTATCAGT	ATTCAAAATT	AGATGATTGG	AGACATTCAT	ACACAGAGAA	CGTGAATCTC	7920
	TTCTCTATCA	CAAGAAGTGA	TGTCTCCATC	AAGGGTAACT	TTATACGACT	GGAGCCTTGA	7980
	AGAAAGCTGC	ATCTGGTGAA	CCACTGTGTA	GTGAGTCTAA	CAATTCAAAG	ATCAAAGTCA	8040
	GTGAGTCTCA	AGCAGGGATT	TGGTCAATA	ATTAAAGATC	AGTCAAGAAC	ATTTGCAAG	8100
	CATCTTCCAG	ACAAGCCATT	TGTAGCTTGT	GTAAAGACT	CTTTTATTCT	TTCCCTTGCA	8160
50	GAAAAAATTA	AAAACTTATT	TCTGATGGG	ACTATTGGCA	ATGATACGAC	ACTGTTCTCT	8220
	GTGAACGCAA	TCTATTTCAA	AGGGCAGTGG	GAGATAAAT	TTAAAAAGAA	AAACACTAAA	8280
	GAGGAAAAAT	TTTGCCCAAA	CAAGGTATTG	TCTATATTTT	ATTTATATAG	TGTAATATGT	8340
	TAATACATGT	AATGTTAAAC	ATTTCTGATG	GAATGTAAAC	TGATAAGTAA	AAAAATAAAA	8400
	TGTTTATGTT	CTGTTATTTT	GTTGTTTTAC	TCTTATAACT	TTATTTAGTT	AGGAATACCT	8460
55	GAAAAACTAT	TGTTTCTAAC	TCATGGAATT	CCTGGGTTAT	TTCTTAGAAG	AAGAAGGATG	8520
	TGTTGCTATC	TCAATAATAT	TATCTTTTTT	GTCTTGTTGT	TCAAGTGTTA	TTTGTGGAC	8580
	ACATTTGATT	ATTGACAGAT	ACATACAAAT	CTGTACAGAT	GATGAGGCAA	TACAATCTCT	8640
	TTAATTTTGC	CTTGCTGGAG	GATGTACAGG	CCAAGGCTCT	GGAAATACCA	TACAAAGGCA	8700
60	AGATCTAAG	CATGATTGTG	CTGCTGCCAA	ATGAAATOGA	TGGTCTGCAG	AAGGTAAAGAA	8760
	CTTGCACTTA	CAACTCTTCC	TTCTACTGCC	GGACATTTTT	CCAAAGATAC	CAAGTTTAAA	8820
	CAAGGTAATA	GCTTATGACC	GAGTTGCCCT	AAAATGATGA	AAAATTCTAA	ATGAGGAATG	8880
	ATGACTCACC	TTCATATTAC	AAATATTGTA	GCATAGGGCC	TGACACAAAC	TGAAAGCTTA	8940
	GTTTTTGTGT	GTTTGTGTGT	TTTTATTATT	ATTATTATAA	TACTTTAAGC	TTTAGGGTAC	9000
	ATGTGCACAA	TGTGCAGGTT	AGTTACATAT	GTATACATGT	GCCATGCTGG	TGTGCTGCAC	9060
65	CCATTAACTC	ATCATTTAGC	GTTAGGTATA	TCTCCTAATG	CTATCCCTCC	CCCTTCCCCC	9120
	CACCCCAACA	CAGTCTCCAG	AGTGTGATGT	TACCTTCTCG	TGTCCAAGTG	TTCTCAATGT	9180
	TCAATTTCCA	TCTATGATTT	AATTCATCT	ATGGCTTAGT	TAATGATTAA	TTTATTAGAG	9240
	TTACATGCAT	TGGATATCAA	TTTGTATGTA	TTATTATGCA	GCAATTTAAA	CTTGACTGGG	9300
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70	ATTTAGGAAT	TTAGGGAATT	ACAATTTAAT	AATTGCAATG	TGTACTAAAT	AATGTATACA	9420
	GAAAAAATATG	ATGAGCCTAT	TAAAAATTGA	CACATGTAGT	AGGCTGTTGG	CACAAGAAAT	9480
	AGTGAATCAT	ACAGTTCATT	GTGTACAAAA	TAATGTAATC	ATATTTTACA	TGTGTATCAT	9540
	ACAATTTGAT	ACATACATAT	GTACACATAT	ACATATACGT	AAAAACATGA	TTCTGTTTTT	9600
	ACATACATGT	ATATACATAT	ACACATATAA	CCCAATGTAT	TTATATATTC	AGGACTCATA	9660
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	CCAAATAAAC	GAAATCTCAC	ATAGTCAATT	CATTGTTAAG	GTGTATTAGA	GATOGACAGT	9780
	TAGTCATATC	AGTTTCTTTT	TTCCATTGTT	ATAGCTTGAA	GAGAACTCA	CTGCTGAGAA	9840
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	TGCCACCCCT	GTAGTAGTAG	TGGAATTATC	ATCTCTCTCA	ACTAATGAAG	AGTTCTGTTG	10140
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	CAGATTCTCA	TCCCATAGTA	TGCAATTAGT	CTGTCACTCC	ATTTAGAAAA	TGTTCACTTA	10260
	GAGGTGTTCT	GGTAAACTGA	TTGCTGGCAA	CAACAGATTC	TCTTGCTCA	TATTTCTTTT	10320

5 CTATCTCATC TTGATGATGA TAGTCATCAT CAAGAATTTA ATGATTAAAA TAGCATGCCT 10380
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 15 AGAAGACAT CTAAGTTGCT GACCTATCTG ACTGGATGGA TGGAGAGATA TCTTGTCTCT 11160
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 20 AAAGAAGAA CTAGAAATGA CCTGGAAGTA TATCAGCATG TGTAAAGATC AGGAATTGAT 11460
 CATTTTATT TTCCAGAAAG TAGCTTTTCT TAGGGTTCCA TATTACTCTC CATAGATTCT 11520
 TCCC

25 A76 Protein sequence:
 Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor
 Unigene number: Hs.227948
 Probeset Accession #: AB035089
 Protein Accession #: BAB21525
 30 Signal sequence: none found
 Transmembrane domains: none found 13-390
 Serine Proteinase Inhibitor domain:
 Cellular Localization: secreted

35 1 11 21 31 41 51
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 QVTENTTEKA ATYHVDKSGN VHHQFQKLLT EFNKSTDAYE LKIANKLFG E KTYQFLQEVYL 120
 40 DAIKKFPQTS VESTDFANAP EESRKKINSW VESQTNKIK NLFPDGTIGN DTLVLVNAI 180
 YPKQWENKF KKENYKKEKF WFNKNTYKSV QMMRQYNSEF FALLEVDQAK VLEIPYKGD 240
 LSMIVLLPNE IDGLQKLEEK LTAEKIMEWT SLQNMRETCV DLHLFRFKME ESYDLKDTLR 300
 TMGMVNIENG DADLSGMTWS HGLSVSKVLH KAFVEVTEEG VEAAAAATVV VVELSSPSTN 360
 EEFCCNHFFL FPIRQNKINS ILFYGRFPSSP

45 A77 DNA SEQUENCE
 Gene name: hypothetical protein FLJ13459
 Unigene number: none found
 Probeset Accession #: XM_047266
 Nucleic Acid Accession #: XM_047266
 50 Coding sequence: 485-1471 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 CATAAATGAG GACTAACCTG TCTCCCGTTG GGAGTTTGA ACCTAGACCT CATGCTTCA 240
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 GTCAAGGTGG GCAGCAAGT CTTCTGACA CCACCGGAGA COCTGCCCCC AGGGATCTCT 480
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 65 GGTGAAGGGG TTGAGCATG ACAAGCAGGA GACAGAGTT CACTTCAACT CCCTGACTGG 720
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 70 ATCCCTGGAG TTGCGCTAC CAGACATGTT GCGTGGGGCC CGGGCCCCCG AGCTCTGCTC 960
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A78 Protein sequence:
 Gene name: hypothetical protein FLJ13459

Unigene number: none found
 Probeset Accession #: XM_047266
 Protein Accession #: XP_047266
 Signal sequence: none found
 Transmembrane domains: 291-313
 C2 domain: 27-86
 Cellular Localization: plasma membrane / ER

1 11 21 31 41 51
 MWIDIFPDQV PAPPVVDIKP RQPISYELRV VIWNTEDVVL DDENPLTGEM SSDIYVKSVM 60
 KGLEHDKQET DVHFNLSLTGE GNFNWRPFVFR FDYLPTRERE SVWRRSOPFA LEEABFRQPA 120
 VLVQLQVMDYD RISANDPLGS LELQLPDMVR GARGPELCSV QLARNAGGPR CNLFRCRRLR 180
 GWNPFVVKLE AEDVEREAQE AQAGKKKQKQ RRRKGRPEDL EPTDMGGNVY ILTGKVEAEF 240
 ELLTVEBAEK RFGVGRKQF BPLEKPSRPF TSFNWFWNPL KTFVFFIWR YWRTLVLVLL 300
 VLLTVFLLLV FYTIPGQISQ VIFRPLHK

20 A79 DNA SEQUENCE
 Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)
 Unigene number: Hs.161031
 Probeset Accession #: AL137708
 Nucleic Acid Accession #: AL137708
 Coding sequence: 1315-1791 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 55 CCAGGGCCCC GCTGGGCTCT CATTGCGGGC GCGCTTGGCG CGGGCGTCTT CCGCTCTCC 1560
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 70 GTGGGCTGGA GGCAGGCAGC GCACTGAGG CCGGGGGCA CGGTGGAACC CTATGCCCGG 2400
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 TACGTGCCCA GCTGAGCCCG GCTGACCGTG GTGGGTCTGG AGGCTCGAGG CCGCTGCCA 3060
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CCCTGTCAGC ACTGGGCAGA CATGCTGGCC CACGCCGGC GGGCCATTGC CCAGCGGCAC 3360
 CCCTGCGGC CAGCGAGGGA GGTGGACCGC ATGCTGGCC TGCAGCCCCG CCTTCGCTG 3420
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 GCACTTGCCC AGGCCGCCCT GCAGGACCAC TGCAATAAAC GCCTTCTCCT GCC

A80 Protein sequence:

Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)
 Unigene number: Hs.161031
 Probeset Accession #: AL137708
 Protein Accession #: CAB70885
 Signal sequence: none found
 Transmembrane domains: 69-85
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MGHPPVSPSA PAPAGTTAIP GLIPDLVAGT PCELWDSQEG CGDNPAKWGL QLSTDALSLA 60
 STFGFRWALI AGALAAGVLL VSCLLCAACC CCRHRKPKPR DKESVGLGSA RGTITTHLVR 120
 SGSLLTQSRG GLKSRLQSPG QRGEFSFRDG LTPTEAGR

A81 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

1 11 21 31 41 51
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 CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240
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 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCTGAAAAA GGCAAGGGTC 420
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 ACAGCATCAC GGGCCCGGGG GCAGACAGCC CCCCTGAGGG TGCTTGTGCT GTAGAGAAGG 540
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 ATACTGAGTG TGCCTAGGTT GCGCCCTTAT TTTTATTTTC CCGTGTGCGT TGCTATAGAT 3120
 GAAGGCTGAG GACAACTGCT TATATGTACT AGAACTTTT TATTAAAGAA A

A82 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675 (second underlined sequence)
 Cellular localization: plasma membrane

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15  MGLPRGPLAS LLLQLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVPNGCPG 60
    QEPALPSTDN DDPFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
    KGPPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREBIAK 180
    YELPGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
    DEDDAIYTYN QVAVYSIHSQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
    TDMGDGSGTT TAVAVVEILD ANDNAPMFDP QKYBAHVPEV AVGHEVQRLT VTDLDAFNPS 360
    AWRATYLMG GDDGDHFTIT THPESNQIIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
    PTSTATIVKH VEDVNEAPVF VPPSKVVEVQ EGIPTGEFVC VYTAEDPOKE NQKISYRILR 480
    DPAGWLMDF DSGQVTAVGT LDREDEQFVR NNIYEVMLVA MDNGSPPTTG TGTLLLTLLID 540
    VNDHGFVPEP RQITICNQSP VRHVLNITDK DLSPTSPFPQ AQLTDDSDIY WTAENVNEGD 600
    TVVLSLKKPL KQDTYDVHLS LSDHGNKEQL TVIRATVCDK HGHVETCPGP WKGGFILPVL 660
    GAVLALLFL LVLVLLVRKK RKIKEPLLLP EDDTRDNVYF YGEGGGGSED QDYDITQLHR 720
    GLEARPEVVL RNDVAPTIIIP TPMYRPRPAN FDEIGNFIE NLKAANTDPT APPYDTLLVF 780
    DYEQSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKCLA DMYGGGEDD
  
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A83 DNA SEQUENCE

Gene name: putative G-protein coupled receptor
 Unigene number: Hs.16085
 Probeset Accession #: F07953
 Nucleic Acid Accession #: NM_016334
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
40  AGCACCTGGG AAAAGGCAGA CCGTGTGAGG GGGCCTGTGG CCCAGCGGTG CTGTGGCCTC 60
    GGGGAGTGGG AAGTGGAGGC AGGAGCCTTC CTTACACTTC GCCATGAGTT TCCTGATCGA 120
    CTCCAGCATC ATGATTACCT CCCAAATACT ATTTTITGGA TTTGGGTGGC TTTTCTTCAT 180
    GGGCCAAATT TTTAAAGACT ATGAGATACG TCAGTATGTT GTACAGGTGA TCTTCTCGGT 240
    GACGTTTGCA TTTTCTTGCA CCATGTTTGA GTCATCATC TTTGAAATCT TAGGAGTATT 300
    GAATAGCAGC TCCCGTTATT TTCACGTGAA AATGAACCTG TGGTAAATTC TGCTGATCCT 360
    GGTTTTCTAT GTGCCCTTTT ACATTGGCTA TTTTATTGTG AGCAATATCC GACTACTGCA 420
    TAAACAACGA CTGCTTTTTT CCTGTCTCTT ATGGCTGACC TTTATGATT TCTTCTGAAA 480
    ACTAGAGAT CCCTTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGCT 540
    CATCAGCCGG GTTGGTGTGA TTGGAGTGAC TCTCATGGCT CTCTTTCTG GATTTGGTGC 600
    TGTCACCTGC CCATACACTT ACATGTCTTA CTTCCTCAGG AATGTGACTG ACACAGATAT 660
    TCTAGCCCTG GAACGGCGAC TGCTGCAAA CAGGATATG ATCATAAGCA AAAAGAAAAG 720
    GATGGCAATG GCACGGAGAA CAATGTTCGA GAAGGGGGAA GTGCATAACA AACCATCAGG 780
    TTTCTGGGGA ATGATAAAAA GTGTTACCA TTCAGCATCA GGAAGTGAAG ATCTTACTCT 840
    TATTCAACAG GAAGTGCATG CTTTGAAGA ATTAAGCAGG CAGCTTTTT TGGAAACAGC 900
    TGATCTATAT GCTACCAAGG AGAGAATAGA ATACTCCAAA ACCTTCAAGG GGAATATTT 960
    TAATTTTCTT GTTACTTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGGCTACCAT 1020
    CAATATTGTT TTTGATCGAG TTGGGAAAAC GGATCTCTGC ACAAGAGGCA TTGAGATCAC 1080
    TGTGAATTAT CTGGGAATCC AATTGATGT GAAGTTTGG TCCCAACACA TTTCTTCAT 1140
    TCTTGTGGA ATAATCATCG TCACATCCAT CAGAGGATTG CTGATCACTC TTACCAAGTT 1200
    CTTTATGCC ATCTCTAGCA GTAAGTCCTC CAATGTCATT GTCCTGCTAT TAGCAGAGAT 1260
    AATGGGCATG TACTTTGTCT CCTCTGTGCT GCTGATCCGA ATGAGTATGC CTTTAGAATA 1320
    CCGCACATA ATCACTGAAG TCCTTGGA GA CTGCAGTTC AACTTCTATC ACCGTGGTT 1380
    TGATGTGATC TTCTTGTTCA GCGCTCTCTC TAGCATACTC TTCCTCTATT TGGCTCACAA 1440
    ACAGGCACCA GAGAAGCAAA TGGCACCTTG AACTTAAGCC TACTACAGAC TGTTAGAGGC 1500
    CAGTGGTTTC AAAATTAGA TATAAGAGGG GGGAAAAATG GAACCAAGGC CTGACATTTT 1560
    ATAAACAAC AAAATGCTAT GGTAGCATT TACCTTCA TAGCATACTC CTTCCCTC 1620
    AGGTGATACT ATGACCATGA GTAGCATCAG CCAACAATG AGAGGGAGAA CTAACCTCAG 1680
    ACATACTCA GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CGGAGAGGAG 1740
    CCAAGAACT AAAGGTGAAA AATACACTGG AACTCTGGGG CAAGACATGT CTATGTTAGC 1800
    TGAGCCAAAC ACGTAGGATT TCCGTTTAA GTTTCACATG GAAAAGGTTA TAGCTTTGCC 1860
    TTGAGATTGA CTCATTAAAA TCAGAGACTG T
  
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A84 Protein sequence

Gene name: putative G-protein coupled receptor
 Unigene number: Hs.16085
 Protein Accession #: NP_057418.1
 Signal sequence: none found
 Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402.
 Cellular Localization: plasma membrane

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1      11      21      31      41      51

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5
10
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60
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70
75
80

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MSPLIDSSIM ITSQILFFGF GNLFFMRQLF KDYEIRQYVV QVIPSVTFAF SCTMFELIIF 60
EILGLVNSSS RYFHWKMLC VILLILVEMV PFYIGYFIVS NIRLLHKQRL LFSCLLMLTF 120
MYFFWKLGGP PFILSPKHGI LSIEQLISRV GUGIVTLMAL LSGFGAVNCP YTYMSYFLRN 180
VTDITDILALE RRLILQTMDMI ISKKKRMAMA RRTMPQKGEV HNKPSGFWGM IKSVTTSASG 240
SENLTLIQOE VDLEELSRQ LPLETADLYA TKERIEYSKT PKGKYFNPLG YPFSIYCVWK 300
IFMATINIVF DRVGKTDPTV RGLIETVNYL GIQFDVKFWS QHISFILVGI IIVTSIRGLL 360
ITLTKEFFYAI SSSKSSNVIV LLLAQIMGMY FVSSVLLIRM SMPLEYRTII TEVLGELQFN 420
FYHRWEDVIF LVSALSSILF LYLAHQKQPE KQMAP

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A85 DNA SEQUENCE:

Gene name: TTK protein kinase

Unigene number: Hs.169840

Probeset Accession #: M86699

Nucleic Acid Accession #: NM_003318

Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

```

20 GGAATTCCTT TTTTITTTT TTTGAGATGG AGTTTCACTC TTGTTGGCCA GGCTGGAGTG 60
CAATGGCACA ATCTCAGCTT ACTGCAACCT CCGCTCCCG GGTTCAGCG ATTCTCCTGC 120
CTCAGCTCTT CAAGTAGCTG GGATTACAGG CATGTGCCAC CACCCTGGC TAACTAATTT 180
CTTTTCTATT TAGTAGAGAT GGGGTTTCAC CATGTTGGTC AGGCTGGTCT TGAATCCTTG 240
ACCTCAGGTG ATCCACTTGC CTTGGCCTCC CAAAGTGCTA GGATTACAGC CGTGAAGCTG 300
TGCTGGCTG ATTCTTTTT TGTGTGGGA TTTTGAAGC AGGGTCTCCC TTGTCGCC 360
AGCTGGAGT GCAGTGGTGC GATCTTGGCT CACTATAACC TCCACTCTCT GGTTCAGT 420
GATCTCCCA CTTTAGCCTC CTGAGTAGCT GTGATTACAG GGTGCAACA CCACACCCGG 480
CTAATTTTGT TATTTTATT AGAGACAGGG TTTCACCATG TTGCCAGGC TGTCTCAAA 540
CTCTGGACT CAAGGATCC GCCTGCCCTC ACTTCCCAA GTCCGAGAT TACAGGTGTG 600
AGTCACCATG CCTGACCTTA TAATCTTAA GTCAATTTT CTGTCCATT TCTTCTTAG 660
GGTCCCTACA ACAAATCTGC ATTAGCCGGT ACAATAATCC TTAACCTCAT GATTACAAA 720
AGGAAGATGA AGTGATTAT GATTAGAAA GGGGAAGTAG TAAGCCACT GCACACTCCT 780
GGATGATGAT CCTAAATCCA GATACAGTAA AAATGGGGTA TGGGAAGGTA GAATACAAA 840
TTTGGTTTAA ATTAATTATC TAAATATCTA AAAACATTTT TGGATACATT GTTGATGTGA 900
ATGTAAGACT GTACAGACTT CCTAGAAAAC AGTTTGGGTT CCATCTTTTC ATTTCCCGAG 960
TGCAATTTTC TGTAGAAATG GAATCCGAGG ATTTAAGTGG CAGAGAATTG ACAATGATT 1020
CCATAATGAA CAAAGTGAGA GACATTAAAA ATAAGTTTAA AAATGAAGAC CTTACTGATG 1080
AACTAAGCTT GAATAAAAT TCTGCTGATA CTACAGATAA CTCGGGAATC GTTAACCAAA 1140
TTATGATGAT GCRAACAAC GCTCTTTTAA ATAAATTGAT TGGTCGTTAC AGTCAAGCAA 1200
ACAGTGTTC CCTAAGTAT GCTCTTTTAA ATAAATTGAT TGGTCGTTAC AGTCAAGCAA 1260
TTGAAGCGCT TCCCCAGAT AAATATGGCC AAATAGAGAG TTTTGCTAGA ATTCAGTGA 1320
GATTTGTCTA ATTAAGAGCT ATTCAAGAGC CAGATGATGC ACGTGACTAC TTTCAAATGG 1380
CCAGAGCAA CTGCAAGAAA TTTGCTTTT TTTATATATC TTTTGCAAAA TTTGAATCTG 1440
CACAAGGTA TGTCAAAAA AGTAAACAAC TTTTCAAAA AGCTGTAGAA CTGGAGCAG 1500
TACCACTAGA AATGCTGGAA ATTGCCCTGC GGAATTTAAA CCTCAAAAA AAGCAGCTGC 1560
TTTCAGAGGA GGAAGAAGAG AATTATCAG CATCTACGGT ATTAACCTGC CAAGAATCAT 1620
TTTCCGGTTC ACTTGGGCAT TTACAGATA GGAACAACAG TTGTGATTCC AGAGGACAGA 1680
CTACTAAGC CAGTTTTTA TATGGAGAGA ACATGCCACC ACAAGATGCA GAAATAGGTT 1740
ACCGGAATC ATTAGACAA ACTAACAAA CTAACACGTC ATGCCCATTT GGAAGAGTCC 1800
CAGTTAACTT CTAAATAGC CCAGATTGTG ATGTGAAGAC AGATGATTCA GTTGATCCTT 1860
GTTTATGAA AAGACAAACC TCTAGATCAG AATGCCGAGA TTTGGTGTG CTGGATCTA 1920
AACCAAGTGG AAATGATTCC TGTGAATTAA GAAATTTAAA GTCTGTTCAA AATAGTCATT 1980
TCAAGGAACC TCTGGTGTCA GATGAAAAGA GTTCTGAACT TATTATTACT GATTCAATAA 2040
CCCTGAAGCA TAAACGGAA TCAAGTCTTC TAGCTAAAT AGAAGAAATC AAAGAGTATC 2100
AAGAACCGA GGTTCAGAG AGTAACCGA AACAGTGCCA AGCTAAGAGA AAGTCAGAGT 2160
GTATTAACCA GAATCTGCT GCATCTTCAA ATCACTGGCA GATTCCGGAG TTAGCCCGAA 2220
AAGTTAATAC AGAGCAGAAA CATACCCTTT TTGAGCAACC TGCTTTTCA GTTCAAAAC 2280
AGTCACCACC AATATCAACA TCTAAATGTT TTGACCCAAA ATCTATTGTT AAGACACCAA 2340
GCAGCAATAC CTTGGATGAT TACATGAGCT GTTTTAGAAC TCCAGTTGTA AAGATGACT 2400
TTCCACCTGC TTGTCAGTTG TCAACACCTT ATGGCCAAAC TGCTGTTTC CAGCAGCAAC 2460
AGCATCAAT ACTTGCCACT CCACTTCAAA ATTTACAGGT TTTAGCATCT TCTTCAGCAA 2520
ATGAATGCAT TCGGTTAAA GGAAGAATTT ATTCCATATT AAAGCAGATA GGAAGTGGAG 2580
GTTCAAGCAA GGTATTTCAG GTGTTAAATG AAAAGAAACA GATATATGCT ATAAATATG 2640
TGAACCTTGA AGAAGCAGAT AACCAACTC TTGATAGTTA CCGGAACGAA ATAGCTTATT 2700
TGAATAAATC ACAACAACAC AGTGATAAGA TCATCCGACT TTATGATTAT GAAATCAGGG 2760
ACCAATACAT CTACATGGTA ATGGAGTGTG GAAATATTGA TCTTAATAGT TGGCTTAAA 2820
AGAAAAAATC CATTGATCCA TGGGAACGCA AGAGTTACTG GAAAAATATG TTAGAGGCAG 2880
TTCAACAAT CCATCAACAT GGCATTGTTT ACAGTGATCT TAAACCACT AACTTTCTGA 2940
TAGTTGATGG AATGCTAAAG CTAATTGATT TTGGGATTGC AAACCAATG CAACCAAGATA 3000
CAACAAGTGT TGTAAAGAT TCTCAGTTG GCACAGTTAA TTATATGCCA CCAGAAGCAA 3060
TCAAGATAT GTCTTCTCC CAGAGAGATG GGAATCTAA GTCAAGATA AGCCCCAAA 3120
GTGATGTTG GTCTTAGGA TGTATTTTGT ACTATATGAC TTACGGGAAA ACACCATTTT 3180
AGCAGATAAT TAATCAGATT TCTAAATATC ATGCCATAAT TGATCTTAAT CATGAATTG 3240
AATTTCCCGA TATTCAGAG AAAGATCTTC AAGATGTGTT AAGTGTGTT TTAAGAGGG 3300
ACCCAAAACA GAGGATATCC ATTCTGAGC TCCTGGCTCA TCCATATGTT CAAATTCAAA 3360
CTCATCCAGT TAACCAATG GCCAAGGGA CCACTGAAGA AATGAATAT GTTCTGGGCC 3420
AACTTGTGG TCTGAATCT CTAATCTCCA TTTTGAAGC TGCTAAACT TTATATGAAC 3480
ACTATAGTGG TGGTGAAGT CATATTTCTT CATCTCCCAA GACTTTTGA AAAAAAGGG 3540
GAAAAAATG ATTTGAGTT ATTCTGATG TCAGATAGGA GGTATAAAT ATATTGGACT 3600
GTATATCTCT TGAATCCCTG TGGAAATCTA CATTTGAAGA CAACATCACT CTGAAGTGT 3660
ATCAGCAAAA AAATTCAGT GAGATTATCT TTAAGAGAAA ACTGTAAAA TAGCAACCAC 3720
TTATGCCACT GTATATATTG TAGACTTGT TTCTCTGTT TATGCTCTG TGAATCTAC 3780
TTGACATCAT TTACTCTTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAACTTG 3840

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TAAATAAAGT TTTGTGGCTA AAATGA

A86 Protein sequence:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Protein Accession #: NP_003309
 Signal sequence: none found
 Transmembrane domains: none found
 Protein Kinase Domain: 510-775
 Cellular Localization: cytoplasmic and nuclear

1 11 21 31 41 51
 MNKYRDIKNN FKNEEDLTDEL SLANKISADTT DNSGTVNQIM MMANNPEDWL SLLKLKLEKNS 60
 VPLSDALLNK LIGRYSQAIE ALPPDKYQON ESPARIQVRF AELKAIQEPD DARDYFQMAR 120
 ANCKKPAFVH ISPAQPELSQ GNVKKSQQLL QKAVERGAVP LEMLEIALRN LNLQKKQLLS 180
 EEEKKNLSAS TVLTAQESFS GSLGHLQNRN NSCDNRGQTT KARPLYGENM PFQDAEIGYR 240
 NSLRQTNKTK QSCPFGRVPV NLLNSPDCDV KTDSDVVPFP MKRQTSRSEC RDLVVPVPSKP 300
 SGNDSCBLRN LKSNVQNSHPK EPLVSDKSS ELIITDSITL NKRTESLLA KLEETKEYQE 360
 PEVPESNQKQ WQAKRKSECI NQNPAASSNH WQIPELARKV NTEQKHTTPE QPVFVSQKQS 420
 PFISTSKWFD PKSICKTPSS NTLDDYMSCF RTPVVKNDFP PACQLSTPYG QPACFQQQHH 480
 QILATPLQNL QVLASSANE CISVKGRIYS ILKQIGSGGS SKVPQVLNEK KQIYAIKYVN 540
 LEEADNQTLN SYRNEIAYLN XLQQRSDKII RLYDYEITDQ YIYMVMCEGN IDLNSWLKKK 600
 KSIDPWERKS YWKNMLEAVH TIHQHGIVHS DLKPANFLIV DGMLKLLIDFG IANQMPPDFT 660
 SVVKDSQVGT VYNYMPEAK DMSSSRENGK SKSKISPKSD VNSLGCILYY MTYKGTFFPQQ 720
 IINQISKLHA IIDFNHEIEF PDIEPKDQD VLKCCCLKRDP KQRISIPELL AHPYVQIQTH 780
 PVNQMAKGTI EEMKYVLQQL VGLNSPNSIL KAAKTLYEHY SGGESHNSSS SKTPEKRGK 840
 K

A87 DNA SEQUENCE

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BB616633
 Nucleic Acid Accession #: NM_001719
 Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GGGGCGAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
 CTGCCACCTG GGGCCGTCGCG GGGCCCGAGC CGGAGGCCCG GGTAGCGCGT AGAGCCGGCG 120
 CGATGCACGT GCGCTCAGTG CGAGCTGCGG GCGCCGACAG CTTCGTGGCG CTCTGGGCAC 180
 CCTCTTCTCT GCTGGGCTCC GCGCTGGCCG ACTTCAGCCT GGCAACGAG GTGCACCTGA 240
 GCTTCATCCA CGGCGGCGCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
 CCATTTTGGG CTGCCCCAC GCGCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
 CCATGTTTCT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG 420
 GCGAGGGGCTT CTCTTACCCC TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
 GCGTCGAAGA TAGCCATTTC CTCACCGAG CGACATGTGT CATGAGCTTC GTCAACCTCG 540
 TGGAAACATGA CAAGGAATTTC TTCCACCCAC GCTACCAACA TOGAGAGTTC CGGTTTGATC 600
 TTTCACAGAT CCAGAAAGGG GAAGCTGTCA CGGCAGCCGA ATTCGGGATC TACAAGGACT 660
 ACATCCGGGA ACCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
 AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTOGACAG CGTACCCCTC TGGGCTTCGG 780
 AGGAGGGCTG GCTGGGTGTT GACATCACAG CCACAGCAG CACTGGGTG GTCAATCCGC 840
 GGCACAACCT GGGCCTGCAG CTCTCGGTGG AGAAGCTGGA TGGGCAGAGC ATCAACCCCA 900
 AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT 960
 TCTTCAGGCG CACGGAGGTC CACTTCCGCA GCATCCGCTC CACGGGAGC AAACAGCGCA 1020
 GCGAGAACCG CTCCAAGAG CCCAAGAAC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
 AGAACAGCAG CAGCGACCG AGGCAAGCCT GTAAGAGCA CGAGCTGTAT GTCAAGCTTC 1140
 GAGACCTGGG CTGCGAGGAC TGGATCATCG CGCCTGAAGS CTACGCGCGC TACTACTGTG 1200
 AGGGGGAGTG TGCTTCCCT CTGAACCTCT ACATGAACGC CACCAACAC GGCATCGTGC 1260
 AGACGCTGCT CCACTTCATC AACCCGAAA CGGTGCCCAA GCGCTGCTGT GCGCCACGC 1320
 AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAAGCTCATC CTGAAGAAAT 1380
 ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCAGAA TTCAGACCTC 1440
 TTGGGGCCAA GTTTTCTGCG ATCCTCCATT GCTCGCCTTG GCGAGGAACC AGCAGACCAA 1500
 CTGCTTTTGT TGAGACCTTC CCTCCCTAT CCCCAACTTT AAGGTGTGA GAGTATTAGG 1560
 AAACATGAGC AGCATATGCG TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
 TCCTACAAGC TGTGAGGCA AAACCTAGCA GGAAAAAAA ACAACGCATA AAGAAAAATG 1680
 GCGGGGCCAG GTCAATTGGCT GGGAACTCT AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
 TTATGAGCGC CTACCAAGCA GGGCAACCG CGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
 GGGCATTG GTGTCTGTGC GAAAGGAAA TTGACCCGGA AGTTCCGTGA ATAAATGTCA 1860
 CAATAAACG AATGAATG

A88 Protein sequence:

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BB616633
 Protein Accession #: NP_001710.1
 Signal sequence: 1-30
 Pfam domains: TGF β propeptide [37-281]
 Transmembrane domains: none found
 Cellular Localization: secreted


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1      11      21      31      41      51
|      |      |      |      |      |
5  MHVRSRLRAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRLRSQE RREMQREILS 60
   ILGLPHRPRP HLQGHKINSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV PSTQGPPLAS 120
   LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHRFRPFDL SKIPEGEAVT AAEFRIYKDY 180
   IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVDITA TSNNHVVNPR 240
   HNLGLQLSVB TLDGQSINPK LAGLIGRHGP QNKQPFMVAE FKATEVHPRS IRSTGSKQRS 300
   QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KHHELYVSFR DLGWQDWIIA PEGYAAYYCE 360
10  GCAFLPLNSY MNATNHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLVFD DSSNVILKKY 420
   RNMVVRACGC H

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A89 DNA SEQUENCE:
 Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
 Unigene number: Hs.27373
 Probeset Accession #: F13036
 Nucleic Acid Accession #: AC012478
 Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

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20  1      11      21      31      41      51
   |      |      |      |      |      |
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   GCTCCCGCGG CCCGCGCCAG CAGAGCCGAG TCCGTCTCCG CGCCGTGGCC CGAACCCGAG 120
25  CGCGAGTGGC GGCCACCGCC CGGCCCGGGG CCGGGGAACA CCACCGGTTT TGGGTCTGGG 180
   GCGGCGGGCG GCAGCGGCGG CTCCAGCTCC AACAGCAGTG GCGACGCTT GGTGACCCGC 240
   ATTTCCATCC TCCTCCGCGA CCTACCCACC CTCAGGCAG CCGTGATCGT GCGGTTGCGC 300
   TTTACCAACC TCCTCATGCG CTGCGTCTGC CTGCGGCTGT TCAGGTGGGG AAAGAGGTTA 360
   AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGG AATGGCGCCA 420
   CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
   TCCTTGCGGG CTGCACGTAG ACCTCAGCTG CCAGGCTGCC AGACGCTACT GACAGTTCTT 540
   GTGCCCCCA CCTTCATCCT CGACATTGAC CTTCAGCAA GATGCAGTGG AAGGCTGAT 600
   GGTGGAATCA GACCTGTTAA AACCTGTTTC CCAGCTGGT GGCATCTGT GGAAGTTGG 660
   TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTTGTGT CGGAGGTGTT 720
35  GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT GTGCGTGTTC AGGCATCTGC 780
   TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCACCAAAA TGGAGTTGCT TCTGCCACCC 840
   TTTGGGCATC CCTTTAAAGT GCCCCTTACT TCTACTCCCC ATGTTTTCG ACAACTGCAG 900
   CTGAATCTCA TGGAAAAGCT GGATTCTCTT GCCTTAAGCA GAAACACCCG GGCTCCATCT 960
   GCCAGGTGCT TGCCACTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
   CCTTGCTGGC ACTTCAGGCG CACAGGCTCT CCAATAAAAA CCCTTTACAC ACAACCCATG 1080
40  AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCGGCGCAGC GGGGCACCTT TTGTGAAGAC 1140
   AGAGCAGTGA CTAAGGTTCT CCAGGCTAGC TCTTCTTCCA AACAGCTGCG CTGGAAGCCA 1200
   GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260
   ACCCATCTCT TCAGGTTGGC TGGTTCAGAT GCCCGGGGAC AAGCCAGCCT GAGCGGGAGG 1320
   AGGGTGTTTC GGGCTCCGCG GCAGTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCAACT 1380
45  TGCCTTTTGG TCTTGAAGAT TCTGTTGAGG CGCCATCTCT ACCTTGACCT CTCTACAAA 1440
   ATCTGTCTCC CCGTCTGTGC CGTGAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500
   GTCTTGTGCT CATTTGAGCA GAGCCCAAAA AAGGCAGCTG CTGCCCACGG GGAGCCTGTC 1560
   AAACGAGGGC CCAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620
50  GCGAACCTGC AGACAATTCC AGATACCCAA GGCCAGGAAG GCCACAGTGA GGATGTCACT 1680
   CACCCCTGAG GAGACTTGGA TGGGTTGGCA AATTCTTATT TGGAGGAAGA GGGTTTCCAG 1740
   GATGGCAGAT GCCAGAAGAT GGTCTGTATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800
   TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCTTCTCTT 1860
   TCCCCCGAC AGCCCTGTGT TCTGTCCAGG CCTTGA

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A90 Protein sequence:
 Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
 Unigene number: Hs.27373
 Probeset Accession #: F13036
 Protein Accession #: FGENSEH predicted
 Signal sequence: 1-27
 Transmembrane domains: 94-115, 448-469
 Cellular Localization: not determined

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65  1      11      21      31      41      51
   |      |      |      |      |      |
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   AAGSGSSSSS NSSGDALVTR ISILLRLDPT LKAADVIVAPA PTTLLIACLL LRVRSGKRL 120
70  KTRKYDIIT TPAERVEMAP LNEEDDEDED STVFDIKYRV SLPAALRRQL PGQQTLLTVP 180
   VPPPIILDID LPARCSGRPD GGIRPGKTCF PAWWHPVESW SAATWGVKDW TWKPCVGGV 240
   ETKNVMYKT PAPSCVSGIC SDCHWQARFH VITMELLPP FGHPPKVPPT STPEGFRQLQ 300
   LNLMEKLDSS ALRNRTRAPS ARCLFLVLAE MAAESDLFN PWWHFSATGS PIKTLTYTQM 360
   STLGLDVPFG AGQGTGFCED RAVTKVLQGS SPSKQLRWKP ALLVLKILLR RPHLDLFLYK 420
75  THPVRLARSD ARGQASLTGR RVFRRPRQSL HGGGSAGTAT CLLVLKILLR RPHLDLFLYK 480
   ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAAGPEPV KRGPSSQLTR HTCPGNGITH 540
   ANLQITPDQD GQGGPREDDV HPGGDLGVA NFYLEEGGFQ DGRQCKMVLN SEEGPPSLTG 600
   CERLTGSHRF SSSKSWSFSL SPRQPLFLSR P

```

EWING

A91 DNA SEQUENCE
 Gene name: G protein-coupled receptor 64
 Unigene number: Hs.184942

Probeset Accession #: AA435577
 Nucleic Acid Accession #: NM_005756
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55
 60
 65
 70
 75
 80

1 11 21 31 41 51
 AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTTCTGAA 60
 CTCGCGGTCA GGATGGTTTT CTCTGTCAAG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA 120
 GTTTTACTGA CGTTCAAGAT ATTCTTGTG ATCATTGTG TTCATGCGT TCTGGTAACA 180
 TCCCTGGAAG AAGATACTGA TAATCCAGT TTGTACCAC CACCTGTCAA ATTATCTGTT 240
 GTCAGTTTTG CCCCTCTCT CAATGAGGTT GAAACAACAA GCCTCAATGA TGTTACTTTA 300
 AGCTTACTCC CTTCAAACGA AACAGAAAAA ACTAAAATCA CTATAGTAAA AACCTTCAAT 360
 GCTTCAGGCG TCAAAACCCA GAGAAATATC TGCAATTTGT CATCTATTG CAATGACTCA 420
 GCATTTTITA AAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCCAGAAT 480
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 GAGCTCAACA AAACCTTGCA AACCTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600
 GAGGCCCAAA GCACATTAAA TTGTACATT ACATAAAAC TGAATAATAC AATGAATGCA 660
 TGTGTGCAA TAGCCGCTTT GGAAGAGTA AAGATTGAC CAATGGAACA CTGCTGCTGT 720
 TCTGTCAAGT TACCCTGCC TTCTCCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780
 CAGGATCCCA TTGTCTGTCT TGCTGACCAT CCAGCTGGCC CACCATTTC TTCCAGCCAA 840
 TCCATCCAG TGCTGCTCTG GGCCACTGTG CTTTCCAGG TCCCCAAAG TACCTCTTT 900
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 CAACCCCTTT CACCCAGGCC TTCAGTCCC ATAGCTTCCA GCCCTGCCAT TGACATGCC 1020
 CCACAGTCTG AAGCATCTC TTCCCTATG CCCCACACCC ATGTCTCCG CACCCACCT 1080
 CCTGTGAAG CCTCATTTTC CTCTCCACC GTGTCTGCC CTGGAATGT CAACACTACC 1140
 AGCGCACCTC CTGTCCAGAC AGACATCGTC AACACCAGCA GTATTTCTGA TCTTGAGAAC 1200
 CAAGTGTGCG AGATGGAGAA GGCTCTGTCC TTGGGCGACC TGGAGCCTAA CCTGCGAGGA 1260
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 GCTCAAGAT TCCCTGAAGT AGTGGATGAC ATTGGCTAC AGCTGAACCT TCAACACAG 1380
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 ATGGCTCTCA GAAGGACTTC AAAGCGGGA AGCTTACACT TTATTGAGCA AATGTGATTG 3120
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 CTCTCTTAAA AAAGGTACAT ATATATGGAA AAAAATCATA TTGCGTTCT TTAAGAGGCA 4200
 ACTGACAGCC ACATTGTTGA TTGTTATGAC TGGTACACTC TGGCCAGGCC AGAGCTATAA 4260
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 GGGAACTGTC CACACTGCT ATTGTGCTA CATGTATGGA GCCTTGATTG CTCTAGTTA 4380
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 TTATTAGGAA CATTTCAAAC CCTTTTAGT TAAGTCTTTC ACTAAGGTTT TCTTGACATAT 4500
 ATTTCAAGT ATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG 4560
 CTGACTGTG TTTGCAATAT TTCCTTCTG ATTTATTAA TTTTCTGTA TTTATAGTT 4620

AAAAACAAAA ATGTTAAAAAT CAATGAAATA AATTGTCAGT TAAGA

A92 Protein sequence

Gene name: G protein-coupled receptor 64
 Unigene number: Hs.184942
 Protein Accession #: NP_005747.1
 Signal sequence: 1-38
 GPS domain: 564-615
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 15 MVFSVRQCGH VGRTEEVLLT FKIFLVIICL HVVLVTSLEE DTDNSSLSPK PAKLSVVSPA 60
 PSSNEVETTS LNDVTLSELL SNETERKIT IVKTFNAGV KPQRNICNL SINDSAFFR 120
 GEIMFQYDKE STVPQNHIT NGTLTGVLSL SELKRSELNK TLQTLSETYF IMCATAEAQS 180
 TLNCTFTIKL NNTMNAACAI AALERVKIRP MEKCCSVRI PCPSSPEELG KLQCDLQDPI 240
 VCLADHPRGP PPSSSQIPV VPRATVLSQV PKATSPAEPP DYSPVTHNVP SPIGEIQPLS 300
 PQPSAPIASS PAIDMPQSE TISSPMPQTH VSGTPPFVKA SPSSPTVSAP ANVNTTSAPP 360
 20 VQTIDIVNTSS ISDLENQVLQ MEKALSLGSL EPNLAGEMIN QVSRLLHSFP DMLAPLAQRL 420
 LKVVDDIGLQ LNFSTNTISL TSPSLALAVI RVNASSPNTT TFVAQDPANL QVSLAQPE 480
 NSIGTITLPS SLMMNLPAHD MELASRVQFN PFETPALFQD PSLENLSLIS YVSISSVANL 540
 TVRNLTRNVT VTLKHINFSQ DELTVRCVFW DLGRNGGRGG WSDNGCSVKD RRLNETICTC 600
 25 SHLTSFGVLL DLSTRTSVLPA QMMALTFTY IGCGLLSIFL SVTLVTYIAF EKIRRDYPSK 660
 ILIQLCAALL LLNLVFLDLS WIALYKMQGL CISVAVFLHY FLLVSFTWNG LEAFHMYLAL 720
 VKVFNTYIRK YILKFCIVGW GVPVVVVTTI LTISPNDYGL GSYGKFPNGS PDDFCWNNN 780
 AVFYITVGVY FCVIFLLNVS MFIVVLVQLC RIKKKKQLGA QRKTSIQDLR SIAGLTFLG 840
 ITWGFAPPAW GPVNVTFMYL FALFNTLQGF FIFIFYCVAK ENVRKQWRRY LCCGKLRLAE 900
 30 NSDWKSTATN GLKKQTNNQG VSSSSNSLQS SSNSTNSTTL LVNNDCSVHA SGNGNASTER 960
 NGVSFSVQNG DVCLHDFTGK QHMFNEKEDS CNGKGRMALR RTSKRGLSHF IEQM

Fibrosis

A93 DNA SEQUENCE

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

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 CGCGAGAGGA GCCTCGGCCA GCCTAGCCAG GCGGCCCCCA GCGCCTCCCC AGGCGCGGAG 60
 CGCCCTCGCC GCGGTGCTCG GCCTCCCTCC CCAGACTGCA GGGACAGCAC CCGGTAACTG 120
 CGAGTGGAGC GGAGGACCGG AGCGGCTGAG GAGAGAGGAG GCGCGCGCTT AGCTGTCTAG 180
 45 GGGTCCGGCC GCGCGCTCCG CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGCAGAG 240
 ATGCTCTGCG CCGTGGAGCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC 300
 GGGACGCGCG CCAGTGCAAG GCATCAGCGG TTGTAGCAT CGGCACGTCA GCCTGGGGTC 360
 TGTCACTATG GAACATAACT GGCCTGCTGC TACGCTGGA GAAGAAACAG CAAGGGAGTC 420
 50 AGATGCTTTC CAGGATACAC CGGAAACACC TGCAGTCAAG ATGTGAATGA GTGTGGAATG 480
 AAACCCCGGC CATGCAACAC CAGATGTGTG AATACACAG GAAGCTACAA GTGTCTTTGC 540
 CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 600
 ATAACTGTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 660
 TCAGGACTCC GCGTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCTCT 720
 55 GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTGGAAG CTACTACTGC 840
 AATGTGCACA TTGGTTTTCG ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
 AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
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 60 ATCCCTGAAA ATTCTGTGAA GGAAGTCCCT AGAGCACCTG GTACCATCAA AGACAGAATC 1080
 AAGAAGTTCG TTGCTACCAA AAACAGCATG AAAAAGAAGG CAAAATTAAT AAATGTTACC 1140
 CCAGAACCCA CCGAGACTCC TACCCCTAAG GTGAACCTTC AGCCCTCAA CTATGAAGAG 1200
 ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAAATGAAA 1260
 GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA 1320
 AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCTGTGAT 1380
 65 CTGCTCCAAA GGAAGCGCT AACTTCCAAA CTGGAACATA AAGATTAAA TATCTGGTT 1440
 GACTGCGAGT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTGAC 1500
 TGGAATCCTG CTGATCGAGA TAATGCTATT GGCCTCTATA TGGCAGTTCC GGCCTGGCA 1560
 GGTACACAGA AAGACATTGG CCGATTGAAA CTCTCTCTAC CTGACCTGCA ACCCAAAGC 1620
 70 AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCCCGAGACA AAGTCCGGAA ACTTCGAGTG 1680
 TTTGTGAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGATGAAAAG 1740
 TGGAAAGCAG GGAATAATCA GTTGTATCAA GGAAGTATG CTACCAAAG CATCATTTT 1800
 GAAGCAGAAC GTGGCAAGGG CAAAACCGGC GAAATGCGAG TGGATGGCGT CTGCTGTGTT 1860
 TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
 75 TTGACTTTGT ATGTCACTTC CTGTTTCTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
 TTAGATTATC TAGCTGAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT 2040
 TCTTGATATA GATATGCCAA TATTGCTTT AAATATCATA TCACGTATC TTCTCAGTCA 2100
 TTTCTGAATC TTTCCACATT ATATTATAAA ATATGGAAAT GTCACTTTAT CTCCCTCTCT 2160
 CAGTATATCT GATTGTGATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TCTTAGAAAA 2220
 TAGAAAAAAA AGCAGAGAGA AATGTTTAACT TGTTTGACTC TTATGATACT TCTTGGAAAC 2280
 80 TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGTCTTTCA TAGCCAAACT 2340
 TGTATATTTA AATTCCTTGT AATAATAATA TCCAAATCAT CAAAAAATAA AAAAAAAA

A94 Protein sequence:

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Protein Accession #: NP_056322.2
 Signal sequence: 1-21
 Transmembrane domains: none found
 MAM domain: 402-546
 EGF domain: 80-259
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
15  MPLPWSLALP LLLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRNRNSKGV 60
    CEATCEPGCK FGECVGFNKC RCFPGYTGKT CSQDVNECGM KPRPCQHRV NTHGSYKCPK 120
    LSGHMLMPDA TCVNSRTCAM INQYSCEDT EGGPQCLCPG SGLRLAFNRC DCLDIDECAS 180
    GKVICPYNRR CVNTFGSYIC KCHIGFELQY ISGRYDCIDI NECTMDSHSC SHHANCFTNQ 240
    GSFKCKCKQG YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KKLLAHKNSM KKKAKIKQVT 300
20  PEPTRTFPFK VNLQPPNYEE IVSRGQNSHO GKKGNEEKMK EGLEDEKREE KALKNDIEER 360
    SLRGDVFPPK VNEAGBFGLI LVQRKALTSK LEHKDLNISV DCSFNHGICD WKQDREDDPD 420
    MNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLFDLPQPS NFCLLPDYRL AGDKVKGKLRV 480
    FVKNSNNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF EAERGKGTG BIAVDGVLLV 540
    SGLCPDLSLS VDD
  
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GLIOBLASTOMAA95 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Nucleic Acid Accession #: none found
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

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1      11      21      31      41      51
|      |      |      |      |      |
35  AGCAACGACG CGCGGCGCGG GGAGCGGCGG CGCGGCCATG TGGCTGCTGG GGCGGCTGTG 60
    CCTGCTGCTG AGCAGGCGCG CGGAGAGCCA GCTGCTCCCC GGAACAACCT TCACCAATGA 120
    GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCAATCCGG GCGCCTGGCA 180
    GTGTGACGGG CTGCCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
40  GTGAAATGT GGCCTCAACT TCTTCCCTG TGCCAGCGGC ATCCATTGCA TCATTGCTCG 300
    CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
    AAACCTCTCG CTTTGTCTCA CGGCCCGCTA CCATGCAAG AACCGCCTCT GTATTGACAA 420
    GAGCTTCATC TGCAGTAGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
    AAGTTCCTCA GAACCCGCGC GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACCTGTGTA 540
45  TTACCCGAGC ATCACTATG CCATCATCGG CAGCTCGTCT ATTTTGTGTC TGGTGGTGGC 600
    CCTGCTGGCA CTGCTCTTGC ACCACGAGCG GAAGCGGAAC AACCTCATGA CGCTGCCCCG 660
    GCACCGGCTG CAGCACCGCT TGCTGTCTGC CGCCTGGTGT GTCCCTGAGC ACCCCCAACA 720
    CTGCAACGTC TGCAGTAGAC TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780
    GAATGCGTGG GAATGAGGCT CCCCAACCTC CTACTCGAG GCCTTGCTGG ACCAGAGGCC 840
50  TGCCTGGTAT GACCTTCTCT CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900
    CGACCTGCCC CCTTACCGCT CCCGGTCCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC 960
    CAGCAGCCTC CTGAGCGTGG AAGACACCG CCACAGCCCG GGGCAGCCTG GCCCCCAAGA 1020
    GGGCAGCCTC TGCAGCGTGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080
    AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTC TAACTATTG 1140
55  TGCTCATGGG AAGCTCTTTA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATAIT 1200
    AACTATCTCT GCATTCCCTT CCTCCCCAG ACTTCAGAGA TGTTTTCTG GCGTCTCAGT 1260
    TGACATGATC TGTGTGCGT CTTTCTGTCT AGGTCACTCT TCCCTTGGGA CCGGAGATCA 1320
    CACCCTCAT TTTCACTATA TTCTGTTTCT GTTGAGAGA CAGCATATAA AACAGTATTG 1380
    AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440
60  CGCTGGACCC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTTAG 1500
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    ATCAAAACCT GCTTTGCACA ATCTTATTG ATGCCCCAG TTGAGCAGAG TCAGTGGCCA 1620
    AAGAAACCTT TGGACGTGAG TAACACCCCT CAGCAGTGGC AACGTTATTT TGGTTTGTG 1680
    AAGGACTCTG AAACCATCTA CCCTGTATAA ATTCTGGCTT TAGAAATTTG CCAAGAATG 1740
65  CTCACTCGA GAGCTTTCCT CAGCAGCATA TATCATCAGC CTCATCTTAA AATAGGCAGG 1800
    GAGCCCCCTC CATGAGTTTA TCCAAGTTCT CAGCTCTTAA AATGCAGGCT GCCAAGACCC 1860
    TACACCTGCC CTGCTCTTAC AGCCACTTAC CTGGTTTCTG GACTGTCAAC CTCCAGCTG 1920
    ACCTGCCCCG AGGCCAAGGA ACTTGAGTTG GCCCAAGGTC TGACCTGGCT 1980
    GTATGTCCCT GTGGCCCA CAACAGCCTG CTGTCTCAT CATGCAGCCT CAACACTGGC 2040
70  CTCCAAAGTT CCTTAAAC TTGCAAGTC CTTTTTACCT GTGCATTGG ACTTGAGGAC 2100
    ACTGGTTTCT ATCAGAGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCGTGGCTCC 2160
    CTGCATCTGG CAOGCTCTCT TTCCCAAGGT CCAATACCA GCACCTCTAG TTAGGTTAG 2220
    GGTGAGGCTC AGGCCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280
    AGACAAATTT GAGTCAAGAT TTTCCATTG GATCTATTTT AAATCTTTTA GAAATGCATT 2340
75  TGAAACAGTG TGTTTGTTT TTCCCTTCTA GTTAAGGAC TATTTATATG TGTATAGGAA 2400
    AGCTGTCTCT TTTTGTGTT TTCTTTAAC AAGGTCCAAG GAAAGATGCA AAAGGAGATC 2460
    ACACCCCTGC CCGCTGAGC CCGGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520
    ACATTTGTGC ATTTGTGCAC TTTGAGGTTA TTAITTAATC AGTCTCTGAA GGAAGCAGAA 2580
    AGAGGAGACT CTCTCTCCCT COGRTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTT 2640
80  TTCTCTGTGT CCAGTCAAGC ACAGGCGCCG CCTCCCTGCA GGAATAAGGG GTAAAAAGTT 2700
    AGGTGTGTGT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATGGA CCAGGTAGAG 2760
    CCCTCCGGG CAGCTGTGAC CCATTGAGAA CTCTTTCCG CAGCTGAAGA AATGTTCAAT 2820
    AACCTGTTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAAG TGCATTCAAG 2880
  
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WO 03/042661

5 TGATCCTGTT CTGTAGACTT TTCTTTCTTT TTTTAACCAA ATCCAAAGGA TGTTACAGAA 2940
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 CATTTTCATCT CCTGTGAGTC AGAAGGGCTT TATTTCTCCC TTGATGGGG CCCCTTCTTC 3180
 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATCTTA ATTTTAATTA ATTGCGCAGT 3240
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TCGTTTGTAGT 3300
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 10 TGATTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAGC GGCAGGGTTT 3420
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 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACAG 3540
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 15 TTTTAAAAA ATGCAACTAA GTGGTAATA GTGTGTAGC CTCAAAGTTA ATGTAACCTG 3720
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 AAMMAAAAC ANYTTTGGGG GGGCTTGGGC CTCGGAAAAA GTTTTAAACA CCACTTCGGG 3900
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 GAAACCTCG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACGCCCGGG 4020
 20 GGAACCGCA GAGTGTGCG TAAACCAAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

25 A96 Protein sequence:
 Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AN043782
 Protein Accession #: none found
 Signal sequence: 1-17
 30 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

35 1 11 21 31 41 51
 MWLLGLPLCLL LSSAABESQLL PGNFTNECN IPGNFMCNSG RCIPGAWQCD GLPDCFDKSD 60
 EKECPKAKSK CGPTFFPCAS GIHCLIGRFR CNPFEDCPDG SDEENCTANP LLCSTARYHC 120
 40 KNGLCLDKSF ICDGQNNQD NSDEESCESS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180
 VIFVLVALL ALVLHHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ 240
 YVASQAEQNA SEVGSPPSYS EALLDQRPAN YDLPPPPYS DTESLNQADL PFYRSRSGSA 300
 NSASSQAASS LLSVEDTSHS PQQPGPQEGT AEPRDSEFSQ GTEEV

45 LUNG

50 A97 DNA SEQUENCE
 Gene name: putative GPCR, Weakly similar to dJ365012.1
 Unigene number: Hs.256897
 Probeset Accession #: BE001836
 Nucleic Acid Accession #: BE001836
 Coding sequence: 1-2955 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
 ATGGCCGCTA AATCTTTTTC CTTCAACACT GGAATGATG GGCTAGACCC AGACCCAATC 60
 ATGTTAAGTA TGATAGGAT CAGTGGCCCA GCTGGTGTGG AAGACAAGTG GGTCACTACTG 120
 GGTTAGGCC CACATAGCAC TAAAGTCTT CAACATGCAA TTAGAAGCTC AAATGTTGAC 180
 60 GGAATATTG TCACTCTAA AAAAGATGTT TCTATTAGAA TTTACTACT CTTTCATGAA 240
 AACATAGATG CTTCTCTTT CTGATTAGT GATGGCCATC AGTTAACCCA AGTGCACTCA 300
 GAGAAGTCAA ATTCGACAC AATCCAGCAA GTAACATAAA AAAGTATGAG CCCAGTCGAA 360
 GAATATCAGC TGCTGCTTCA GGTGACCTAT AGAGATTCCA AGGAGAAAAG AGATTTGAGA 420
 AATTTTCGA AGCTCTTGAA GCTCCATTA TTATGGTCAC ATGGGCTAAT TAGAATTATC 480
 65 AGAGCAAAGG CTACACAGA CTGCAACAGC CTGAATGGAG TCCTGCAGTG TACCTGTGAA 540
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 70 AAAGCATATG AAGAATTCA AGGTTTGGAG TCGGTTGAG TCACCCAAT TCAGAAATGGA 840
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 75 TGTGAGTCTT CTGGGTGACA GGTGATCAGG GAGACTTGTG TGCTCTCTCT GCTTGAAGAA 1140
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 80 GTAACCACTT GGACAGTCTT ACTGCGGAA GAAAGTATG CCAGCTCACG GTTACTAGAG 1440
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TCCACGGTTA TTCAAACTA TTCCATAAAT GAAGTTTTCC TATTTTTTTC CAAGATAGAG 1800
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ATCCGCGTGG GGAAGAGCCT CCTCATTCTG ACCCTCTGTC TAGGGCTCAC CTGGGGCTTT 2640
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CAACTTCTGT TCAACAAGTT GTCTGCCTTA AGTTCTTGGG AGCAACACAGA AAAGCAAAAC 2820
TCATCAGCTG TATCTGCGAA ACCCAAATTC TCAAAGCCTT TCAACCCACT GCAAAACAAA 2880
GGCCATTATG CATTTTCTCA TACTGGAGAT TCCTCCGACA ACATCATGCT AACTCAGTTT 2940
GTCTCAAATG AATAA

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A98 PROTEIN SEQUENCE

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30

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Gene name: putative GPCR, Weakly similar to dJ365012.1
Unigene number: Hs.256897
Protein Accession #: none found
Signal sequence: 1-17
Pfam domain: 7tm_2 [561-820]
Transmembrane domains: 545-567, 571-593, 605-627, 641-663, 677-699, 721-743, 767-789
Cellular Localization: plasma membrane

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1 11 21 31 41 51
| | | | |
MHALLLCFSV LNASGLSL QSPVEEYQLL LQVTYRDSKE KRDLRNFLKL LKPPLLWSHG 60
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QSVNFCERTK IWGTGFKINER FTNDLLN88S AIYSKYANGI EIQLKKAYER IQGFESVQVT 180
QFRNGSIVAG YEVVGSSSAS ELLSAIEHVA EKAKTALHKL FPLEDGSPRV FGKAQCNDIV 240
PFGSGKDEY TLPCSSGVRG NITAKCESSG WQVIRETCVL SLLEBLNKNF SMIVGNATEA 300
AVSSEVQMLS VIIRNPSTT VGNLASVSVI LSNISLSLSL SHPRVSNSTM EDVISIADNI 360
LNSASVTNWT VLLREEKYAS SRLLETLENI STLVPPTALP LNPFRKFDWM KGIPVNSQL 420
KRGYSYQIKM CPQNTSIPR GRVLIGSDQF QRSLETTIIS MASLTGLNLL PVSKNGNAQV 480
NGPVISTVIQ NVSINEVFLF FSKIESNLSC PHCVFWDPSH LQWNDAGCHL VNETQDIIVTC 540
QCTHLTSFSI LMSPPVPSTI FPPVKNITYV GLGISIGSLI LCLIEALEFW KQIKKSQTS 600
TRRICMNVIA LSLLIADVMF IVGATVDITV NP8GVCTAAV FPTHFFYLSL FFWMLMLGIL 660
LAYRIILVPH HMAQHLMMAV GPCLGYGCPL IISVITIAVT QPSNTYKRRD VCNLWNSNGS 720
KELLAFVPPA LAIVAVNFPV VLLVLTKLWR PTVGERLSRD DKATIIRVGK SLLILTPLLG 780
LTWGPFGICT VDSQNLAWHV IPALLNAFQV RTVTITYCIV K

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A99 DNA SEQUENCE

55

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Gene name: putative G-protein coupled receptor
Unigene number: Hs.16085
Probeset Accession #: F07953
Nucleic Acid Accession #: NM_016334
Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
| | | | |
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CTCCAGCATC ATGATTAACT CCCAAATACT AITTTTGGGA TTTGGGTGGC TTTTCTTCAT 180
GGGCCAATTG TTTAAAGACT ATGAGATACG TCAGTATGTT GTACAGGTGA TCTTCTCGGT 240
GACGTTTGCA TTTTCTTGCA CCATGTTTGA GCTCATCATC TTTGAAATCT TAGGAGTATT 300
GAATAGCAGC TCCCGTTATT TTCAGTGAA AATGAACCTG TCGTAATTC TGCTGATCCT 360
GGTTTTCATG GTGCCTTTTT ACAITGGCTA TTTTATTGTG AGCAATATCC GACTACTGCA 420
TAAACAACGA CTGCTTTTTT CCTGTCTCTT ATGGCTGACC TTTATGTATT TCTTCTGGAA 480
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CATCAGCGGG GTTGGTGTGA TTGGAGTGAC TCTCATGGCT CTCTTCTCTG GATTTGGTGC 600
TGTCAACTGC CCATACACTT ACATGTCTTA CTCTCTCAGG AATGTGACTG ACACAGATAT 660
TCTAGCCCTG GAACGGCGAC TGCTGCAAAAC CATGGATATG ATCATAAGCA AAAAGAAAAG 720
GATGGCAATG GCACGGAGAA CAATGTTCCA GAAGGGGGAA GTGCATAACA AACCATCAGG 780
TTCTGGGGGA ATGATAAAAA GTGTTACCAC TTCAGCATCA GGAAGTGAAA ATCTTACTCT 840
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TGATCTATAT GCTACCAAGG AGAGAATAGA ATACTCCAAA ACCTTCAAGG GGAATATTAT 960
TAATTTCTCT GTGTTACTTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGGTACCAT 1020
CAATATTGTT TTTGATCGAG TTGGGAAAAC GGATCCTGTC ACAAGAGGCA TTGAGATCAC 1080
TGTGAATTAT CTGGGAATCC AATTGATGT GAAGTTTTGG TCCCAACACA TTTCTTCTAT 1140
TCTTGTGGA ATAATCATCG TCACATCCAT CAGAGGATTO CTGATCACTC TTACCAAGTT 1200
CTTTTATGCC ATCTCTAGCA GTAAAGTCTC CAATGTCTAT GTCTGCTATC TAGCAGAGAT 1260
AATGGGCATG TACTTTGTCT CCTCTGTGCT GCTGATCCGA ATGAGTATGC CTTTGAAGA 1320
CGCACCATAT ATCACTGAAG TCCTTGGAGA ACTGCAGTTC AACTTCTATC ACGTGTGGTT 1380
TGATGTGATC TTCCTGGTCA GGGCTCTCTC TAGCATATCT TTCTCTATT TGGCTACAAA 1440

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	ACAGGCACCA GAGAAGCAAA TGGCACCTTG AACTTAAGCC TACTACAGAC TGTTAGAGGC 1500
	CAGTGGTTTC AAAATTTAGA TATAAGAGGG GGGAAAAATG GAACCAAGGC CTGACATTTT 1560
	ATAAACAAAC AAAATGCTAT GGTAGCATTT TTCACCTTCA TAGCATACTC CTTCCCCCTC 1620
	AGGTGATACT ATGACCATGA GTAGCATCAG CCAGAACATG AGAGGGAGAA CTAACCTCAG 1680
5	ACAATACTCA GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CGGAGAGGAG 1740
	CCAAGAAACT AAAGGTGAAA AATACACTGG AACTCTGGGG CAAGACATGT CTATGGTAGC 1800
	TGAGCCAAAC ACGTAGGATT TCCGTTTAA GGTTCACATG GAAAAGGTTA TAGCTTTGCC 1860
	TTGAGATTGA CTCATTAAAA TCAGAGACTG T
10	<u>A100 Protein sequence</u>
	Gene name: putative G-protein coupled receptor
	Unigene number: Hs.16085
	Protein Accession #: NP_057418.1
	Signal sequence: none found
15	Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402, 424-446
	Cellular Localization: plasma membrane
20	1 11 21 31 41 51
	MSFLIDSSIM ITSQILFFFG GWLFFMRQLF KDYEIRQYVV QVIFSVTFAF SCTMPELIIF 60
	EILQVINSSS RYFHWKMLC VILLILVFMV PFYIGYFIVS NIRLLHKQRL LFSCLLWLTF 120
	MYFFWKLQDP PFILSPKHGI LSIEQLISRV GVIGVTLMAL LSGFGAVNCP YTYMSYFLRN 180
	VTDITLALAE RRLQTMDMI ISKKRMMAMA RRTMFQKGEV HNKPSGFWMG IKSVTTSASG 240
	SENLTLLQOE VDLEELSRQ LPLETADLYA TKERIEYSKT PKGKYFNFLG YFFSIYCVWK 300
25	IFMATINIVF DRVGKTDPTV RGIETVNYL GIQFDVKFWS QHISFILVGI IIVTSIRGLL 360
	ITLTKPFYAI SSSKSSNVIV LLLAQIMGY FVSSVLLIRM SMPLEYRTII TEVLGELQFN 420
	FYHRWFDVIF LVLSLSSILF LYLAKQAPB KQMAP
30	<u>A101 DNA SEQUENCE</u>
	Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
	Unigene number: Hs.19322
	Probeset Accession #: AA088458
	Nucleic Acid Accession #: AA088458
35	Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)
40	1 11 21 31 41 51
	GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60
	CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120
	CGCGGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180
	CTGGGCCAGA GCAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240
	CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCTGG GGGAGCTGCT GGCTGCAGCC 300
	TGTGCCAGCC GGGCCCTGCC CCCGTCTCC TCCGGGCCCC CCTGCCCCGC CCTGACGTCC 360
	ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCCTCATG TGAAGGAGCA GAACCGACTC 420
45	CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCAAGC AGCTGGAGCA GGAGAAGTCG 480
	CGGCTCATTA AGCAGCTGTT TGAGGCCCGC GCCCTGAGCC AGCAGGACGG GGGACCTCTG 540
	GATTCACCTT TCATCTAGTC CTTGTGGGCC GGGTGGGCC CCAGGGCCAG CCTGGCACTC 600
	AGCCCTTCGA GGGTGGGCGC CCCATCGCAC CCACCTCTC TGGCTGGAGA CCCCAGGAG 660
	GCCAGGCGAC AGTCCGCGAG TGGGCGCCTT CTTGCCGCC TTGCCAGATG GGCTCCCCAG 720
50	GCCCTGCCCC GCGTGGTCCC CGCACCGAGC GCTTACTTCC GTTTGGCTC CTGGTTGYTG 780
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55	CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080
	GTAAGCGGGG GGTGCTCTGC TGGCTGGGGA GCCCCAGGGA TAGCGGTGG ACTTCAGGTT 1140
	CTGGCCAGGG CTGAGGGACC CTGGCTGCAG CGGATCGGCA CGCGGGGTGG GCGAGAGCTT 1200
	GGCTGCTATG TGCTCCCCAG AGACCTCGGG GTGATGGCCT TCCCCCTCTT GCGCGGGAAG 1260
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	GAGAGGCCAC CTCCTCAGC CAAGGAAAAA GAGAACCCCC AGGGTACAGG AGGAGGCTGG 1500
	GGCAGGTCCC CTGGGTGTC ACTCCCTCAG CCCCTGCCCA GGCCCACTCC CGCTGGTGCT 1560
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	CCCGATCGGG GGTCAAGTGG TGGGGGGGCG AGGGCCCCCT CGTGTCCAGG GCACCTTGGT 1800
	ACACTGTCCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCC GGCAGGCAGC GTGGCACTC 1860
	CCTTCCGGAG CCCAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCC 1920
70	TGCTGCACCT GGTCTGCAGG GGTGTCCAG GACAGGCCCA AGTCAGCCA GCATGCAGCT 1980
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	GGCTGGGGTC TGCCACCCAG GGCCTCCCCA CGTCTGCCCT TGAGGGTGCC TGCCATGCC 2220
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5 CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880
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A102 DNA SEQUENCE

10 Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Nucleic Acid Accession #: AB038157
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

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 CCATCTACAT TTTTGGGACT OGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCGGATGTGC 180
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 AAAAAAA

A103 Protein sequence:

65 Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Protein Accession #: BAB20077
 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 70 Tryp_Spc domain: 216-444
 Cellular Localization: plasma membrane

75 1 11 21 31 41 51
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 MGENDPPAVE APFSFRSLFG LDDLKISFVA PDADAVAAQI LSLPLKFPF IIVIGIIALI 60
 LALAIGLGIH FDCSGKYRRC SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLPQV 120
 TAASHKTMCS DDMKHYANV ACAQLGPPSY VSSDNLRVSS LEGQFRESEFV SIDHLLPDDK 180
 VTALHHSYVY REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWFW QASLQFQGYH 240
 80 LCGGSVITPL WITTAHCVY DLYLPKSWTI QVGLVSLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QPVCLPNSBB NFFDGRVCWT SGWGATEDGA GDASPVLAHA 360
 AVFLISNKKIC NHRDVGIGII SPSMLCAGYL TGGVDSQCGD SGGPLVQGER RLWKLVGATS 420
 FGIGCAEVNK PGVYTRVTSF LDWIEQMER DLKT

A104 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (H077175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM_032551.1

Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

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GACGCTTGCG TCGTGCCGCT CTCTTCGCG GCGCTGATGC TGTGGGCGCT GGTGGGGAAC 180
TCGCTGGTCA TCTACGTCA CTGCGCCAC AAGCGATGC GGACCGTGAC CAACTTCTAC 240
ATCGCCAACC TGGCGGCCAC GGACGTGACC TTCTCTCTGT GCTGCGTCCC CTTCACGGCC 300
CTGCTGTACC CGCTGCCCGG CTGGGTGCTG GCGGACTTCA TGTGCAAGTT CGTCAACTAC 360
ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCCATGAG TGTGGACCGC 420
TGGTACGTGA CGGTGTTCCC GTTGCGCGCC CTGCACCGCC GCAAGCCCGC CTTGGCGCTG 480
GCTGTACGCC TCAGCATCTG GTTAGGCTCT GCGGCGGTGT CTGCGCCGCT GCTGCGCCCTG 540
CACGCGCTGT CACCCGCGCC GCGCGCTTAC TGCACTGAGG CCTTCCCCAG CCGCGCCCTG 600
GAGCGCGCTT TCGCACTGTA CAACCTGCTG GCGCTGTACC TGCTGCCGCT GCTCGCCACC 660
TGCGCCTGCT ATGCGGCCAT GCTGCGCCAC CTGGGCGCGG TCGCGGTGCG CCGCGCGCCC 720
GCCGATAGCG CCGTGCAGGG GCAGGTGCTG GCAGAGCGCG CAGGCGCCGT GCGGGCCAA 780
GTCTCGCGCC TGGTGGCGGC GTGGTCTCT CTCTTCGCGC CTGCTGCGGG CCCATCCAG 840
CTGTCTCTGG TGCTGCAGGC GCTGGGCCCC GCGGGCTCCT GGCAACCCAG CAGCTAGGCC 900
GCCTACGCGC TTAAGACCTG GGCTCACTGC ATGTCTTACA GCAACTCCGC GCTGAACCCG 960
CTGCTCTAGC CTTTCTCTGG CTGCACTTTC CGACAGGCGT TCCGCGCGCT CTGCCCCCTG 1020
GCGCGCGCGC CCGCCCGCGG CCGCGGACCT CGGACCCCGC AGCCCCACAC 1080
GCGGAGCTGC ACCGCTTGG GTCCACCCCG GCGCCCGCCA GGGCGCAGAA GCCAGGGAGC 1140
AGTGGGTGCG CCGCGCGCGG GCTGTGCGTC CTGGGGGAGG ACAACGCCCC TCTCTGA

```

A105 Protein sequence

Gene name:

Homo sapiens G protein-coupled receptor (H077175), mRNA

Unigene number:

Hs.208229

Protein Accession #:

AI819198

Signal sequence:

none found

Pfam domains:

7tm_1 [59-323]

Transmembrane domains:

43-65, 86-108, 122-144, 159-181, 203-225, 260-282

Cellular Localization:

plasma membrane

40

45
50

```

1      11      21      31      41      51
|      |      |      |      |      |
MHTVATSGFN ASWGAPANAS GCPGCGANAS DGEVPSPRAV DAWLVPLFFA ALMLLGLVGN 60
SLVIYVICRH KPMRTVTNFI IANLAATDVT FLCCVPEPFA LLYPLFGWVL GDFMCKFVNY 120
IQQVSVQATC ATLTAMSVDR WYTVFPLRA LHRRTPLRAL AVSLSIWVGS AAVSAPVLAL 180
HRLSPGPRAY CSEAFPSRAL ERAFALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAP 240
ADSALGGVQL AERAGAVRAK VSRLLVAAVLV LFAACWGPQI LFLVLQALGP AGSWHPRSYA 300
AYALKTWAKH MSYNSALNPL LLYAFILGSHF RQAFRRVCPC APRRRRRPRR PGPSDPAAAPH 360
AELHRLGSHF APARAQKPGS SGLAARGLCV LGEDNAPL

```

A106 DNA SEQUENCE

Gene name:

integrin, beta 8

Unigene number:

Hs.52620

Probeset Accession #:

AA479726

Nucleic Acid Accession #:

NM_002214

Coding sequence:

680-2990 (underlined sequences correspond to start and stop codons)

60
65
70
75
80

```

1      11      21      31      41      51
|      |      |      |      |      |
CCCAGAGCGG CCTCCCCCTG TTGCTGGCAT CCCGAGCTTC CTCCCTTGCC AGCCAGGAGG 60
CTGCGGACTT GTCTTTGCCC GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT 120
GTTGGCTCCG CTGCGCACTT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTT 180
TCCCTCGTAC CTGCGCGGCG TACCCTCCCA CAGATCCAGC ATCACCCAGT GAATGTACAT 240
TAGGGTGGTT TCCCGCCGAG CTTCGGGCTT TGTTTGGGTT TGATTGTGTT TGCTCTTCG 300
CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCTTTCTTT 360
TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCCGC GCGCGGCCCT 420
TGGCGGTGGA AGGAGGTGCT TCTCGCGGAG ACCGCGGGAC CCGCGGTGCC GAGCGGGGAG 480
GGCGGTAGGG GCCTTGAGAT GCGGAGCGGT GCGCGGGGCC GCTTACCTGC ACCGCTTGCT 540
CGGAGCGCGG GGGTCCGCTT GCTAGGCTTG CGGAAAACGT CCTAGCGACA CTGCGCCGCG 600
GCGCCCGAGG TCGCCCGGGA GCGCGAGCCC GCGTCCGGAA GGCAGCCAGG CCGCGGGCGC 660
GGGGCGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCCGGC TTTTTTTACC GCTGCAATTG 720
TCTGCTTGCA AAACGACCGG CGAGGTCCCG CCTGTTCTC CTGGGCAGCC TGGGTGTTTT 780
CACTGTGTTT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCACTTTCA AATGCAGCAT 840
CTGTGCGCAG GTGCTTGGG CTGGGTCCAG AATGTGGATG GTGTGTTCAG GAGGATTTC 900
TTTCAGTGGG ATCAAGAGT GAACGTTGTG ATATTGTTT CAATTTAATA AGCAAGGCT 960
GCTCAGTTGA TTCAATAGAA TACCATCTG TGCAATGTTT AATACCCACT GAAATGAAA 1020
TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA 1080
ATTTTATGCT GAAGTTTCAT CCTCTGAAGA AATATCTCTG GGATCTTTAT TATCTGTTG 1140
ATGCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAT TTCCGTGGA AACGATTAT 1200
CTAGAAAATG GGCAATTTTC TCCGCTGACT TTGCTCTTGG ATTGGCTCA TACGTTGATA 1260
AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCAGTGACT 1320
ACAATTAGAA CTGCATGCCT CCCATGGAT ACATCCATGT GCTGTCTTGG ACAGAGAACA 1380
TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACCCAG 1440

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5 AAGGAGGTTT TGACGCCATG CTTGAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA 1500
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560
 GCATAATGGC AGGCATAGTG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACAACTGCT 1620
 ACGTCAAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG 1680
 ACAACAACAT TAATGTGATC TTTGAGTTC AAGGAAACA ATTTCAATGG TATAAGGATC 1740
 TTCTACCCCT CTGCGCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACTCA 1800
 ATAATTTGGT AGTGGAGGCC TATCAGAAGC TCATTTTCTG AGTGAAAGTT CAGGTGGAAA 1860
 ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC 1920
 CAGGCATGGA AGGATGACGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG 1980
 10 TTACAATGAA AAAATGTGAT GTCAACAGGAG GAAAAAATA TGCAATAATC AAACCTATTG 2040
 GTTTTAATGA AACCGCTAAA AITTCATATC ACAGAACTG CAGCTGTGAG TGTGAGGACA 2100
 ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACCTTTCT AGATTCCAAG TGTTCACAGT 2160
 GTGATGAGAA TAAATGTCAT TTTGATGAAG ATCAGTTTTC TTCTGAGAGT TGCAAGTCAC 2220
 ACAGGATCA GCCTGTTTGC AGTGGTCGAG GAGTTTGTGT TTGTGGGAAA TGTTCATGTC 2280
 15 ACATAATGAA AAGATGAGAA GTGTATGGA AACTACTGTGA AAAGGATGAC TTTTCTGTG 2340
 CATATCACC ACGGAACTCT GTGTCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400
 GCCTCAGTGT CTGGGAAGGT GATCGATGCC AGTGCCTTTC AGCAGCAGCC CAGCACTGTG 2460
 TCAATTCAAA GGGCCAAAGT TGCACTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520
 GCACGATCC CAGGAGCATC GCGCGCTTCT GTGAACACTG CCCCACCTGT TATACAGCCT 2580
 20 GCAAGGAAA CTGGAATTGT ATGCAATGCC TTCACCTCA CAATTTGTCT CAGGCTATAC 2640
 TTGATCAGTG CAAACCTCA TGTGCTCTCA TGGAACAACA GCATTATGTC GACCAAACTT 2700
 CAGATGTTT CTCCAGCCCA AGCTACTTGA GAATATTTT CATCATTTTC ATAGTTACAT 2760
 TCTTGATTGG GTTGCTTAAA GTCTGTATCA TTAGACAGGT GATACTACAA TGGAAATAGTA 2820
 25 ATAAATTAAT GTCTCATCA GATTACAGAG TGTGAGCCTC AAAAAAGGAT AAGTTGATTC 2880
 TGCAAAAGT GTGCAAGA GCACTCACCT ACGGACGTGA GAAGCCTGAA GAAATAAAAA 2940
 TGGATATCAG CAAATTAAT GCTCATGAAA CTTTCAGGTG CAACTTCTAA AAAAAGATT 3000
 TTAAACACTT AATGGGAAAC TGGAAATTGT AATAATTGCT CCTAAAGATT ATAATTTAA 3060
 AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGTTTGT ACATCGAAC 3120
 30 GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180
 AAAATGTGTC TTACTACTGT TTGAGACTAG TGTGCTGTGA GCACCTTACT GTAATATATA 3240
 ACTTATTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTACAGG 3300
 TACCTGTTT CCTACGCTT CCGAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATTTGT 3360
 CACTACAAGG GTACAGTAAT CCGTGCCTG GACATGTGAG GAAAAAATA ATCTGGCAAG 3420
 35 TATATTCTAA GGTGCGCAA CACTTCAACA GTTGGTGGT GAATAGACAA GAACAGCTAG 3480
 ATGAATAAAT GATTCTGTGT TCACTCTTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA 3540
 AAAGATTATT GCTTTTAAA GTGTGTAGTT TTATGCAATG GTGTTTATGG TTTGCTTATT 3600
 TTTGCAAGAT GGATACTAAT TCCAGCATTC TCTCCTCTTT GCCTTTATGT TTTGTTTCT 3660
 TTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720
 40 TACTGCCATA AAAAATAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAGCT 3780
 GAATGTAA

A107 Protein sequence:

45 Gene name: Integrin, beta 8
 Unigene number: Hs.52620
 Probeset Accession #: AA479726
 Protein Accession #: NP_002205.1
 Signal sequence: 1-39
 50 Transmembrane domains: 682-704
 EGF domain: 552-584
 INB domain: 54-469
 Cellular Localization: plasma membrane

55 1 11 21 31 41 51
 MCGSALAFFT AAFVCLQND RGPASFLWAA WFPSLVGLG QGEDNRCASS NAASCARCLA 60
 LGPECGWCVQ EDFISGSSRS ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP 120
 60 GEVSIQLRPG AEANFMLKVH PLKKYPVDLY YLVDVSASME NNIEKLNSVG NDLSRKMAFF 180
 SRDFRLGFGS YVDKTVSPYI SIHPERIHQ CSDYNLDOMP RHGYIHVLSL TENITEPEKA 240
 VHRQKISGNI DTPEGGFDM LQAACVESHQ GWRKEAKRLL LVMTDQTSHL ALDSKLAGIV 300
 VPNDGNCHLK NNIVVKSTTH EHPSLGQLSE KLIDNNINVI FAVQKQFHW YKDLLP LLPG 360
 65 TIAGEIESKA ANLNNLVREA YQKLISEVKV QVENQVQGIY PNITAIKPDG SRKPGMEGCR 420
 NVTNDEVLV NVTVTMKCD VTGGRNYALI KPIGFNETAK IHIHRNCSCQ CEDNRGPKGK 480
 CVDETFLDSK CFQCDENKCH FDEQPFSSBS CKSHKDPVC SGRGVCVCGK CSCHKIKLKG 540
 VYGRYCEKDD FPCPYHHGNL CAGHGECEAG RQCPGSGWEG DRQCPSAAA QHCVNSKQV 600
 CSRGRTCVCG RCECTDPRSI GRPCEHCPTC YTACKENWNC MQCLHPNLS QAILDQCKTS 660
 70 CALMEQGHYV DQTECFSSP SYLRIFPIIF IVTFLIGLLK VLIIRQVILQ WNSNRIKSSS 720
 DYRVSASKKD KLILQSVCTR AVTYRREKPB EIKMDISKLN AHSTFRCNF

A108 DNA sequence

75 Gene name: ESTs
 Unigene number: Hs.128899
 Probeset Accession #: AA983251
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
 ATGCTGTCG GCTTCTTGAT GAGTCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60
 GGAAGAAGAC TTCGTGGGA GGCTTCCATC GGTGCGCACA OCTCCGAGG GCGAGGCAGC 120
 GACCGGAGAG GCGAGAGCCG GCGGAGGCT GCGGGCTCC TGTGGGACCG CGCTGCAGCC 180
 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCTT GGATCCGGC CCAGCAGCAG 240

5 CCGCGGCGCG CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCTT 300
 CGCTCGCTGC CTGGAGCTTC CCGGGGGAGG GTCCGGTTGC CAGTGAAACC TCCAGAGGCT 360
 TCCGGACGAC AGCCCGGGGG GCTTCTGAC TGATCCCGA GATTTCCATC AGCGAGTGCA 420
 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480
 GCTCCTGGAG CTAGGGCCCG GCGTCGTGCG CTCTGCGCG TOGCGGCAGA GGGAGTGGC 540
 CCGCGCGGAA AGCGCGCGGG GACAGTCAGT GACGAGGCCG GGGGGTCGCC GGGGCCACGA 600
 CTTCTCGGAG ACCGTCTGCG GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTGCCA 660
 TGTGCGGCGC TCGCGCTGCG TCCGTCTCCT CATCTGGAA CCGCGCTTCG CTCTGCGAGC 720
 TGCTGCTGGC TGCGCTGCTG GCGCGCGGGG CGAGGGCCCA GCGCGAGTA CTGCCACGGC 780
 10 TGCTGGAAG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 840
 GGGGACGCCA CCACTCTGCT GCGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900
 GCGCGCTGCG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 960
 CCGCGCGACA AAGACGGGCC CCGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020
 GGAGACGGCG AGGGTGCGCC CCCACCGGTG AGGGCTGGC AGCGGTGCTC CCTGAAGGC 1080
 15 TCCCGGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGG TGCTGCCCGG TGCCAGAAGC 1140
 CGCGGATTCC CATCTCTCC ACGCGCGCGC CCCTCTCCCC TGACGCGGCC CGCTTGCCCC 1200
 ATCTACGTGC CGTTCCTCAT TGTGTGCTCC GTGTTTGTG CTTTATCAT CTGGGGTTC 1260
 CTGCTGGCAG CCGCTTGTCT CAGATGTCTC CGGCCTAAGC AGGATCCCCA CGAGAGCCGA 1320
 20 GCGCCAGGGG GTAACCGCTT GATGAGACCC ATCCCATGA TCCCGAGTGC CAGCAGCTCC 1380
 CCGGGGTGCT CCTCAGGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAGCTCC 1440
 GGGGCGCGGG CGCCCCCAAC AAGGTCACAG ACCAACTGTT GCTTCCCGGA AGGGACCATG 1500
 AACACCGTGT ATGTCAACAT GCCACGAAAT TTCTCTGTGC TGAAGTGTCA GCAGGCCACC 1560
 CAGATTGTGC CAGATCAAGG GCAGTATCTG CATCCCCAT ACCTGGGGTA CACGGTGCAG 1620
 25 CACGACTCTG TCGCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCTGCA GCCTGGCTAC 1680
 AGGCGAGTTC AGTCCCCCTT CCTCACACC AACAGTGAAC AGAAGATGTA CCGACGGGTG 1740
 ACTGTATAAC CGAGAGTTCAC TGGTGGGTTT CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800
 GATTCCTGAG GTGCAAGTCC GCACATGTG GTGGTAITTA TGGCAGGATT CCTTTGGATG 1860
 GCTTCATTGG CCCCCAGACT GTATGAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920
 30 CATCCAGGGT ATCATTTGAT TATGATGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980
 TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CTTGAGATA TGGTTGACGA 2040
 AAGAATTTTA TAACTGATA AATTAAGGAT TTTTATTATG TTGTATTAT TATTCTTTT 2100
 TTGTTGTGA CTGACAGGA TCAAATGCC TGTATCTCC CTTTACTGG GACTTTTTT 2160
 TTTTTTTTT TTTTTTTTA TCAGACAGGG TCTTGCTCTG TTGCCCAGGC TGGAGTGCAG 2220
 35 TGGTGGATC TCGGCTCACT GCAACTCAG CCTCTGGAT TCAGGCAACA CTCTGCTC 2280
 AGCCTOCCAC GTGGCTGGGA TTACAGGTGC CTGCCOCCAT GGCTAATTTT TTGTATTTT 2340
 TGTAGAGATG GGGTTTCAAC ATGTTGGCTG GSGTGGTCTC ACTCTCCTGA CCTCAAGCAA 2400
 TCTGCTGTC TCAGCCTCCC AAGTGTCTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460
 TGAGCCTTTT TTTTCTCTA ATGCAATCCAA GGTAAAGGGG AAGACGCAAA TAACAGGACT 2520
 40 ATTCTAAAAG GAAACCTGTT TGAATCTGT GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580
 GGCACACCTT AATTTCTATG TAAAAAGATA TATATATTTT GTCTATTTT GTGCTTTGG 2640
 GGGCTTATTT TGTGCTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTCTTACA 2700
 TTAAGAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCAATT CATCCOCTTC 2820
 45 TTGATGTAT CTAATTTTC TGGCTTAAAG GTGACATCTG AGAGGTAATG CATCTTTT 2880
 TATATTGAAA TCATAAATA TCACCGCTG CTTCTCTGAG TTACTTTTAA TTTTGCTT 2940
 TGGTTATGGT TTGGCGTTTC CTTCTGTTG GTTTTCAGAG CCCCAGTCT ATATAGTCTC 3000
 GAGTGCAAGT AATTACTATA CTGTAAATG AAGATCAGTA TTTCTGCTA GATCTGATAA 3060
 50 AAAAATTTTC TGTCTTAGT TATAAAAT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120
 TAGCTCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACAGATAC GATTTACTTT 3180
 GCAGATCATC AGGCTTTTTA TACTCTGTT ATCAAAATG CTTATTTTC AGGCACTAAG 3240
 GATTGTAAAG AGAAAGCTT TTCAACGAAG GATTGCTTT CTTCTCCAC ACTGTCTTG 3300
 ATTTCTCTC TCTTTCAGGC CTCAACAGGC ACTGTATCTA TTGCCAATG TCCAAATTAT 3360
 CAAATTCAG TGAATTTAT TGTGTGTTT TACTTATAT AAAAAAGAT AACTTTAAG 3420
 55 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAATAT TTGTAATTA ACAATCGCT 3480
 GTATGGTATG GTCTCTACA CATTATGTC TATAGATATC TATCGATCAT CTTCTATT 3540
 TGTTCATGA CTGAATAAGT TAAACCAAGT GTTGCAATT GGTATCATCA ATGATATCA 3600
 TTTTAAATA ACCAAGGCA GGGGAAATC ATTTTACTTA TTAATAATA TTTTATGATG 3660
 TGAATAATAA AAAAAAATA AAAAAAATA

A109 Protein sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 Transmembrane domains: 402-424
 Cellular Localization: not determined

70 1 11 21 31 41 51
 1 MLSGFLMSPS QHRAQYTPG GKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60
 75 GAEKGNRGE PPAMIRAQQQ PRPPAGQAP GTAAGQAQDP RLPRGRSRGR VRLPVKPEEA 120
 PRGQPRQPSD CIPFPSSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAAEGSG 180
 PRGRRRTVS DEARGSPGPR LLGDRPALSG DALSAFVRVP OGALAAPRSP HPPTPLRSCS 240
 CMLRCMRRG RGPSSGECHE WLDAGQVMRI GFQCFERFDG GDATICCGSC ALRYCCSSAE 300
 ARLDQGGCDN DRQQAGGEPG RADKDGPRRL GRASCLRGTO GDGEGAPPPV RAMQRCSPG 360
 SPKGRQLLRA FPGLLPRARR RGFPSSPRGG PSPLQRPALP IYVPLIVGS VFVAFILGS 420
 80 LVAACCCRCI RPKQDPQQR APGNGRLMET IPMPSASTS RGSSSRQSGT AASSSSSANS 480
 GARAPPTRSQ TNCCLPEGTM NNVTNNMPTN FSVLNCQQAT QIVPHQGYL HPPYVGYTVQ 540
 HDSVPMATVP PFMDGLQPGY RQIQSPFPHT NSEQKMPAV TV

A110 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JB0350 Anterior gradient-2 (H.sapiens)

Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

5

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1      11      21      31      41      51
|      |      |      |      |      |
10  CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
    CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTGTCACAG TTCTCTCCAA CCTTGCCATT 120
    GCAATAAAAA AGGAAAAGAG GCCTCTCTAG ACACTCTCAA GAGGATGGGG AGATGACATC 180
    ACTTGGGTAC AAACCTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
    ATGGTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGGCC 300
    CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
15  GAAACCACTG ATAAGAATTT ATCACTGATG GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
    GACCCCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
    TATGAGCCTC GGGATTTACC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540
    CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTTCAT 600
    GAAGAAAACC TCTGGCAGAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTATA 660
20  TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAAA 720
    TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA
  
```

25 All1 Protein sequence:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Protein Accession #: none found
 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted

```

35  1      11      21      31      41      51
    |      |      |      |      |      |
    MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEB GLFYAQKSKK 60
    PLMVIHLELD QYQSALKKVV FAQNBEIQEM AQNKPIMLNL MHETTDKNLS PDGQYVFRIM 120
    FVDPISLTVRA DIAGRYSNRL YTYEPRDLFL LIENMKKALR LIQSEL
  
```

40 All12 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Nucleic Acid Accession #: NM_016425
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

```

50  1      11      21      31      41      51
    |      |      |      |      |      |
    ATGTTACAGG ATCTGACAGC TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60
    AAAACCCGTA TCCCATGAGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
    CTGAGCCTGG CGAGTATCAT CATTTGTGGT GTCCCTCATCA AGGTGATTCT GGATAAATAC 180
    TACTTCTCTC GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
    CTGACTGTGC CCTTGGGGGA GGAAGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
55  GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCCACTGCG AGGTGCTGGA CTGGGCCACA 360
    GGGAACTGGT TCTCTGCGTG TTTGACAAC TTCACAGAAG CTCTGCTGA GACAGCCTGT 420
    AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
    GATCTGGATG TTGTTGAAT CACAGAAAAC AGCCAGGAGC TTGCGATGCG GAACTCAAGT 540
    GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
60  AAGACCCCCC GTGTGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
    AGCATCCAGT ACACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGAGCC CCACTGGGTC 720
    CTCACGGCAG CCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
    GGCTCAGACA AACTGGGCAG CTTCOCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840
    TTCAACCCCA TGTAACCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
65  ACTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
    GCCACCCAC TCTGGATCAT TGGATGGGGC TTACGAAAGC AGAATGGAGG GAAGATGTCT 1020
    GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGCTGCAA TGCAGACGAT 1080
    GCGTACCAGG GGGGAAGTAC CGAGAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG 1140
    GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
70  GTGGGCATGC TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
    AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA
  
```

75 All13 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Protein Accession #: NP_057509
 Signal sequence: none found
 Transmembrane domains: 31-53
 LDLa domain: 54-94
 Tryp_SPc domain: 204-429
 Cellular Localization: plasma membrane/ER


```

1      11      21      31      41      51
5      |      |      |      |      |      |
      MLQDPDSQDP  LNSLDVVKPLR  KPRIPMETFR  KVGIPILIAL  LSLASIIIVV  VLIKVILDKY  60
      YFLCQQLPHF  IPRKQLCDGE  LDCPLGEDBE  HCVKSPFEPG  AVAVRLSKDR  STLQVLDSAT  120
      GWNFSACFDN  FTEALAEAC  RQMGYSSKPT  FRAVEIGPDQ  DLDVVEITEN  SQELRMNRSS  180
      GPCLSGSLVS  LHCLACGKSL  KTRPVVGEE  ASVDSWFWQV  SIQYDKQHV  GGSILDPHWV  240
      LTAACHFRKH  TDVFNWVRA  GSKLGSFPS  LAVAKIIIE  FNPMPKOND  IALMKLQFPL  300
      TFSGTVRPI  LPFFDEELTP  ATPLWIIGWG  FTKQNGGKMS  DILLQASQV  IDSTRCNADD  360
10     AYQGEVTEK  MCAGIPGEGV  DTCQDSSGSP  LMYQSDQWHV  VGIVSWGYGC  GGPSTPGVYT  420
      KVSAYLNWIY  NVWKAEAL

```

A114 DNA SEQUENCE:

Gene name: TTK protein kinase

Unigene number: Hs.169840

Probeset Accession #: M86699

Nucleic Acid Accession #: NM_003318

Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

```

20      1      11      21      31      41      51
      GGAATTCCTT  TTTTITTTTT  TTTGAGATGG  AGTTTCACCTC  TTGTTGGCCA  GGCTGGAGTG  60
25      CAATGGCACA  ATCTCAGCTT  ACTGCAACCT  CCGCCTCCCG  GGTTCAAGCG  ATTCTCCTGC  120
      CTCAGCCTCT  CAAGTAGCTG  GGATTACAGG  CATGTGCCAC  CACCCCTGGC  TAACTAATTT  180
      CTTTCTTATT  TAGTAGAGAT  GGGGTTTCAC  CATGTTGGTC  AGGCTGGTCT  TGAATCCTCG  240
      ACCTCAGGTG  ATCCACTTGC  CTGGGCTCC  CAAAGTGCTA  GGATTACAGC  CGTGAAGACTG  300
      TGCCTGGCTG  ATTCTTTTTT  TGTGTTGGA  TTTTGAAGAC  AGGGTCTCCC  TTGGTCGCCC  360
30      AGGCTGGAGT  CGAGTGGTGC  GATCTGGCT  CACTATAACC  TCCACCTCCT  GGTTCAGT  420
      GATCTCCCA  CTTAGCTCT  CTGAGTAGCT  GTGATTACAG  CGGTGCACCA  CCACACCCGG  480
      CTAATTTTGG  TATTTTATT  AGAGACAGGG  TTTCAACATG  TTGCCAGCG  TGTCTCAAAA  540
      CTCTCGGACT  CAAGGGATCC  GCTGCTCTC  ACTTCCCAA  GTCCCGAGAT  TACAGGTGTG  600
      AGTCACCATG  CCTGACCTTA  TAATCTTAA  GTCAATTTTT  CTGCTCCATT  TCTTCTCTAG  660
      GGTCTCTACA  ACAATCTCG  ATTAGGCGGT  ACAATAATCC  TTAATTCAT  GATTACAAAA  720
35      AGGAAGATGA  AGTGATTCAT  GATTAGAAA  GGGGAAGTAG  TAAGCCCACT  GCACACTCCT  780
      GGATGATGAT  CCTAAATCCA  GATACAGTAA  AAATGGGGTA  TGGGAAGGTA  GAATACAAAA  840
      TTTGGTTTAA  ATTAATATC  TAAATATCTA  AAAACATTTT  TGGATACATT  GTTGATGTGA  900
      ATGTAAGACT  GTACAGACTT  CCTAGAAAAC  AGTTTGGGTT  CCATCTTTTC  ATTTCCCCAG  960
40      TGCAGTTTTC  TGTAGAAATG  GAATCCGAGG  ATTTAAGTGG  CAGAGAATTG  ACAATTGATT  1020
      CCATAATGAA  CAAAGTGAGA  GACATTAATA  ATAAGTTTAA  AAATGAAGAC  CTTACTGATG  1080
      AACTAAGCTT  GAATAAAATT  TCTGCTGATA  CTACAGATAA  CTCGGGAAT  GTTAAACAAA  1140
      TTAATGATGAT  GGCAACACAC  CCAGAGGACT  GGTGAGTTT  GTTGCTCAA  CTAGAGAAAA  1200
45      ACAGTGTCC  GCTAAGTGT  GCTCTTTTAA  ATAAATGAT  TGGTCTGAT  AGTCAAGCAA  1260
      TTTGAAGCGT  TCCCCAGAT  AAATATGGCC  AAAATGAGAG  TTTTGCTAGA  ATTCAAGTGA  1320
      GATTGCTGA  AITAAAGCT  ATTCAAGAGC  CAGATGATGC  ACGTGACTAC  TTTCAATGG  1380
      CCAGAGCAAA  CTGCAAGAAA  TTTGCTTTT  TTCTATATAT  TTTTGCAAAA  TTTGAATGTT  1440
      CACAAGGTAA  TGTCAAAAA  AGTAACCAAC  TTCTTCAAAA  AGCTGTAGAA  CGTGGAGCAG  1500
      TACCCTAGAA  AATGCTGGAA  ATTGCCCTGC  GGAATTTAAA  CCTCCAAAA  AAGCAGCTGC  1560
50      TTTCAAGAGA  GGAAGAAGAA  AATTATCAG  CATCTACGGT  ATTAAGTCCC  CAAGAATCAT  1620
      TTTCCGGTTC  ACTTGGGCT  TTACAGAATA  GGAACAACAG  TTGTGATTCC  AGAGGACAGA  1680
      CTACTAAAGC  CAGGTTTTTA  TATGGAGAGA  ACATGCCACC  ACAAGATGCA  GAAATAGGTT  1740
      ACCGGAATTC  ATTGAGACAA  ACTAACAAAA  CTAAACAGTC  ATGCCCATTT  GGAAGAGTCC  1800
      CAGTTAACCT  CTAAATAGC  CCAGATTGTG  ATGTGAAGAC  AGATGATTCA  GTTGTACCTT  1860
55      GTTTATGAA  AAGACAAACC  TCTAGATCAG  AATGCCGAGA  TTTGGTTGTG  CTTGGATCTA  1920
      AACCAGATGG  AATGATTTCC  TGTGAATTAA  GAAATTTAAA  GTCTGTTCAA  AATAGTCATT  1980
      TCAAGGAACC  TCTGTTGCTA  GATGAAAAGA  GTTCTGAACT  TATTATTACT  GATTCAATAA  2040
      CCTGAAGAA  TAAAACGGAA  TCAAGTCTTC  TAGCTAAATT  AGAAGAACT  AAGAGATATC  2100
      AAGAACCAGA  GGTTCAGAG  AGTAACCAAG  AACAGTGGCA  AGCTAAGAGA  AAGTCAGAGT  2160
      GTATTAAACA  GAATCCCTGC  GCATCTTCAA  ATCACTGGCA  GATTCCGGAG  TTAGCCCGAA  2220
60      AAGTTAATAC  AGAGCAGAAA  CATACCACCT  TTGAGCAACC  TGCTTTTCA  GTTTCAAAAC  2280
      AGTCACCAAC  AATATCAACA  TCTAAATGTT  TTGACCCAAA  ATCTATTGTT  AAGACACCAA  2340
      GCAGCAATAC  CTTGGATGAT  TACATGAGCT  GTTTTAGAAC  TCCAGTTGTA  AAGAATGACT  2400
      TTCCACCTGC  TTGTCAGTTG  TCAACACCTT  ATGGCCAAAC  TGCTGTTTC  CAGCAGCAAC  2460
      AGCATCAAA  ACTTGCCACT  CCACTTCAAA  AITTACAGGT  TTTAGCATCT  TCTTCAGCAA  2520
65      ATGAATGCAT  TTCGTTAAA  GGAAGAATTT  ATTCCATATT  AAAGCAGATA  GGAAGTGGAG  2580
      GTTCAAGCAA  GGTATTTTCA  GTGTTAAATG  AAAAGAAACA  GATATATGCT  ATAAAAATG  2640
      TGAATTTAGA  AGAAGCAGAT  AACCAAACTC  TTGATAGTTA  CCGGAACGAA  ATAGCTTATT  2700
      TGAATAAAT  ACAACAACAC  AGTGATAAGA  TCAATCCGACT  TTATGATTAT  GAAATCACGG  2760
      ACCAGTACAT  CTACATGGTA  ATGGAGTGTG  GAAATATTGA  TCTTAATAGT  TGGCTTAAAA  2820
70      AGAAAAAATC  CATTGATCCA  TGGGAACGCA  AGAGTTACTG  GAAAAATATG  TTAGAGGCAG  2880
      TTCACACAA  CCATCAACAT  GGCATTGTT  ACAGTATCT  TAAACCACT  AACTTTCTGA  2940
      TAGTGTATGG  AATGCTAAAG  CTAATTGATT  TTGGGATTGC  AAACCAATG  CAACAGATA  3000
      CAACAAGTGT  TGTAAAGAT  TCTCAGTTG  GCACAGTTAA  TTATATGCCA  CCAGAAGCAA  3060
      TCAAGATAT  GTCTTCTTCC  AGAGAGAAATG  GGAAATCTAA  GTCAAGATA  AGCCCCAAAA  3120
75      GTGATGTTG  GTCTTAGGA  TGTATTTTGT  ACTATATGAC  TTACGGGAAA  ACACCATTTG  3180
      AGCAGATAAT  TAATCAGATT  TCTAAATTAC  ATGCCATAAT  TGATCTTAAT  CATGAAATTG  3240
      AATTTCOCGA  TATTCAGAG  AAAGATCTTC  AAGATGTGTT  AAAGTGTGTT  TTAAGAGGG  3300
      ACCCAAAACA  GAGGATATCC  ATTCTGAGC  TCCTGGCTCA  TCCATATGTT  CAAATTCAAA  3360
80      CTCATCCAGT  TAACCAAAATG  GCCAAGGGAA  CCACTGAAGA  AATGAAATAT  GTTCTGGGCC  3420
      AACTTGTGG  TCTGAATCT  CCTAATCCA  TTTTGAAGC  TGCTAAACT  TTATATGAAC  3480
      ACTATAGTGG  TGTGAAAGT  CATAATCTT  CATCTCCAA  GACTTTTGAA  AAAAAAGGG  3540
      GAAAAAATG  ATTTGAGTT  ATTCTAATG  TCAGATAGGA  GGTATAAAAT  ATATTGGACT  3600
      GTTATACTCT  TGAATCCCTG  TGGAAATCTA  CATTGAAGA  CAACATCACT  CTGAAGTGT  3660
      ATCAGCAAAA  AAAATTCAGT  GAGATATTCT  TTAAGAGAAA  ACTGTAAAAA  TAGCAACCA  3720

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TTATGGCACT GTATATAITG TAGACTTGTT TTCTCTGTTT TATGCTCTTG TGTAATCTAC 3780
 TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATCTTA AAAAATTG 3840
 TAAATAAAGT TTTGTGGCTA AAATGA

A115 Protein sequence:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Protein Accession #: NP_003309
 Signal sequence: none found
 Transmembrane domains: none found
 Protein Kinase Domain: 510-775
 Cellular Localization: cytoplasmic and nuclear

1	11	21	31	41	51	
MNKVRDIKKN	PKNEDLTDEL	SLNKISADTT	DNSGTVNQIM	MMANNPEDWL	LLLLKLEKNS	60
VPLSDALLNK	LIGRYSQAIK	ALPPDKYQGN	ESFARIQVRF	AELKAIQEPD	DARDYFQMAR	120
ANCKKFAFVH	ISPAQFELSQ	GNVKKSKQLL	QKAVERGAVP	LEMLEIALRN	LNLOKKQLLS	180
EEKKNLSEAS	TVLTQESFSS	GSLGHLQNRN	NSCDSRGQTT	KARFLYGENM	PPQDASIGYR	240
NSLRQTNKTK	QSCPFGRVPV	NLLNSPDCDV	KTDDSVVPCF	MKRQTSRSEC	RDLVVPGRKP	300
SGNDSCELRN	LKSVQNSHPK	EPLVSDEKSS	ELIITDSITL	KNKTESSLLA	KLEETKEYQE	360
PEVPESNQKQ	WQAKRKSECI	NQNPAAASNN	WQIPELARKV	MTBQKHTTFE	QPVFSVSKQS	420
PPISTSKWFD	PKSICKTPSS	NTLDDYMSCF	RTPVVQKDFP	PACQLSTPYG	QPACFQQQQH	480
QILATPLQNL	QVLASSSSANE	CISVKGRIYS	ILKQIGSGGS	SKVPQVLNEK	KQIYAIKYVN	540
LEEADNQTLT	SYRNEIAYLN	KLQQHSKII	RLYDYBITDQ	YIYVMMECGN	IDLNSWLKKK	600
KSIDPWERKS	YWKNNLEAVH	TIHQHGIVHS	DLKPFANFLV	DGMLKLIDFG	IANKMQPDTT	660
SVVKDSQVGT	VNYMPEALIK	DMSSSRENGK	SKSKI SPKSD	VWSLGCILYY	MTYGTTPFQQ	720
INQISKLHA	IIDPNHEIEF	FDIPEKDLQD	VLKCKLKRDP	QKRISIPELL	AHPYVQIQTH	780
FVNQMAKGTG	BEKMYVLGQL	VGLNSPNSIL	KAAKTLIEHY	SGGSEHNSSS	SKTPEKGRGK	840
K						

OVARIAN**A116 DNA SEQUENCE**

Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Nucleic Acid Accession #: NM_001508
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
ATGGCTTCAC	CCAGCCTCCC	GGGCAGTGAC	TGCTCCCAA	TCATTGATCA	CAGTCATGTC	60
CCCGAGTTTG	AGGTGGCCAC	CTGGATCAAA	ATCACCCTTA	TTCTGGTGTG	CCTGATCATC	120
TTCTGTATGG	GCTTCTCTGG	GAACAGCGCC	ACCATTGCGG	TCACCCAGGT	GCTGCAGGAG	180
AAAGGATACT	TGCAGAAAGG	GGTGACGAGC	CACATGGTGA	GTTTGGCTTG	CTCGGACATC	240
TTGGTGTTC	TCATGCGCAT	GCCCATGGAG	TTCTACAGCA	TCATCTGGAA	TCCCTGACCC	300
ACGTCCAGCT	ACACCCTGTC	CTGCAAGCTG	CACACTTTCC	TCTTCGAGGC	CTGCAGCTAC	360
GCTACGCTGC	TGCAGTGTCT	GACACTCAGC	TTTGAGCGCT	ACATCGCCAT	CTGTCACCCC	420
TTCAAGTACA	AGGCTGTGTC	GCGACCTTGC	CAGGTGAAGC	TGCTGATTGG	CTTCGCTCTG	480
GTCACTCTCG	CCTCGGTGGC	ACTGCCCTTG	CTGTTTGCCA	TGGGTACTGA	GTACCCCTCT	540
GTGAACGTGC	CCAGCCACCG	GGGTCTCACT	TGCAACCGCT	CCAGCACCCG	CCACCACGAG	600
CAGCCCGAGA	CCTCCAATAT	GTCCATCTGT	ACCAACCTCT	CCAGCCGCTG	GACCGTGTTC	660
CAGTCCAGCA	TCTTCGGGCG	CTTCGTGGTC	TACCTCGTGG	TCTGCTCTCT	CCTAGCCTTC	720
ATGTGCTGGA	ACATGATGCA	GGTGCTCATG	AAAAGCCAGA	AGGGCTCGCT	GCGCGGGGGC	780
ACGCGGCTCT	CGCAGCTGAG	GAAGTCCGAG	AGCGAAGAGA	GCAGGACCGC	CAGGAGCCAG	840
ACCATCATCT	TCTGAGGCT	GATTGTGTG	ACATTGGCGG	TATGCTGQAT	GCCCAACCCG	900
ATTCGGAGGA	TCATGGCTGC	GGCCAAACCC	AAGCACGACT	GGACGAGGTC	CTACTTCGGG	960
GGTACATGA	TCTCTCTCCC	CTTCTCGGAG	ACGTTTTTCT	ACCTCAGCTC	GGTCATCAAC	1020
CGCTCTCTGT	ACAAGGTGTC	CTCGCAGCAG	TTTGGCGGGG	TGTTGCTGCA	GGTGTGTGTC	1080
TGCGCGCTGT	CGCTGAGCA	CGCCAAACCC	GAGAAGCGCG	TGCGCGTACA	TGCGCACTCC	1140
ACCACCGACA	GCGCCGCTTT	TGTGACGCGC	CCGTTGCTCT	TGCGGTCCCG	GCGCCAGTCC	1200
TCTGCAAGGA	GAAGTGAAGA	GATTTTCTTA	AGCACTTTTC	AGAGCGAGGC	CGAGCCCCAG	1260
TCTAAGTCCC	AGTCATTGAG	TCTCGAGTCA	CTAGAGCCCA	ACTCAGCGCG	GAAACCGACC	1320
AATTCTGCTG	CAGAGAATGG	TTTTCAGGAG	CATGAAGTTT	GA		

A117 Protein sequence:

Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Protein Accession #: NM_001508, NP_001409
 Signal sequence: none found
 Pfam domains: 7tm_1 [72-172, 224-344]
 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342
 Cellular Localization: plasma membrane

1	11	21	31	41	51	
MASPSLPGSD	CSQIIDHSHV	PEFEVATWIK	ITLILVYLII	FVMGLLGNSA	TIRVTQVLQK	60

5
 KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTPLFEACSY 120
 ATLLHVLTLF FERYIAICHP FRYKAVSGPC QVKLLIGFVN VTSALVALPL LFMGTETPL 180
 VNPVSHRGLT CNRSSTRHHE QPETSNSIC TNLSSRWTFV QSSIFGAFVV YLVVLLSVAF 240
 MCWNMMQVLM KSQKSLAGG TRPPQLRKSE SEESRTARRQ TIIFLRLIVV TLAVCHMPNQ 300
 IRRIMAAKP KHDWTRSYFR AYMILLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFQVLC 360
 CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARTEKIFL STPQSEAEFQ 420
 SKSQSLLES LEPNSGAKPA NSAAENGFEQ HEV

10
A118 DNA sequence
 Gene name: bone morphogenetic protein receptor IB (ALK-6)
 Unigene number: Hs.87223
 Probeset Accession #: AA250737
 Nucleic Acid Accession #: NM_001203
 Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

15
 1 11 21 31 41 51
 CGCGGGGCGG GGAGTCGGCG GGGCCTCGCG GGACGCGGCG AGTGC GGAGA CGCGGGGCT 60
 GAGGACGCGG GAGCGGGGAG CGCAGCGCGG GGTGGAGTT CAGCCTACTC TTTCTTAGAT 120
 20 GTGAAGAGAA AGGAAGATCA TTTCATGCCT TGTGATAAA GGTTCAGACT TCTGCTGATT 180
 CATAACCAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTCACAGCC 240
 TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TCGGAAGTGC AGGAAAATTA 300
 AATGTGGGCA CCAAGAAAGA GATGCTGAG AGTACAGCCC CCACCCCGG TCCAAAGGTC 360
 25 TTGCGTTGTA AATGCCACCA CCATGTGCCA GAAGACTCAG TCAACAAATAT TTGCAGCACA 420
 GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTGCGCTGT GGTCACTTCT 480
 GGTTCGCTAG GACTAGAAGG CTCAGATTTT CAGTGTCCGG ACACCTCCAT TCCTCATCAA 540
 AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCTACA 600
 CTGCTCCAT TGAAAACACG AGATTTTGTG GATGGACCTA TACACCACAG GGTCTTACTT 660
 30 ATATCTGTGA CTGTCTGTAG TTGTCTCTTG GTCTTATCA TATTATTTTG TTACTTCCGG 720
 TATAAAGAC AAGAAACGAC ACCTCGATAC AGCAITGGGT TAGAACAGGA TGAACCTTAC 780
 ATTCTCTCTG GAGAAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGG 840
 TCAGGCTCC CTCTGCTGCT CCAAGGAGCT ATAGCTAAGC AGATTCAGAT GGTGAAACAG 900
 ATTGGAAAAG GTGCTATGCG GGAAGTTTGG ATGGGAAAGT GCGCTGGCGA AAAGGTAGCT 960
 35 GTGAAAGTGT TCTTCACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020
 ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGGAGA 1080
 GGTTCCTGGA GCGAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140
 TATCTGAAGT CCACCAACCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTCTGTCT 1200
 AGTGGCTTAT GTCATTTTACA CACAGAAATC TTTAGTACTC AAGGCAAAAC AGCAATTGCC 1260
 40 CATCGAGATC TGAAAAGTAA AAACATTCTG GTGAAGAAA ATGGAACCTG CTGTATTGCT 1320
 GACCTGGGCC TGGCTGTATA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380
 ACTCGAGTTG GCACCAAAAG CTATATGCCT CCAAGAGTGT TGGACGAGAG CTTGAACAGA 1440
 AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGSCCTCAT CCTTTGGGAG 1500
 GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC 1560
 45 CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620
 CGCCCTCAT TCCCAACCG GTGAGCAGT GATGAGTGT TAAGGCAGAT GGGAAAACCT 1680
 ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTTAAGAAA 1740
 ACACCTGCCA AAATGTGAGA GTCCAGGAC ATTAACCTCT GATAGGAGAG GAAAAGTAAG 1800
 CATCTCTGCA GAAAGCCAAAC AGGTACTCTT CTGTTGTGG GCAGAGCAGG AGACATCAA 1860
 50 TAAGCATCCA CAGTACAAGC CTTGAACATC GTCTGTCTC CAGTGGGTT CAGACCTCAC 1920
 CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980
 TCTGTTTGTG GCGGAGAAA CCGTTGGGTA ACITGTITCA GATATGATGC AT

55
A119 Protein sequence
 Gene name: bone morphogenetic protein receptor IB (ALK-6)
 Unigene number: Hs.72472 / Hs.87223
 Probeset Accession #: AA250737 / U89326
 Protein Accession #: NP_001194
 Signal sequence: 1-13
 Transmembrane domains: 128-144
 60 PFAM domains: activin_receptor [30-111], protein kinase [204-491]
 Cellular Localization: plasma membrane

65
 1 11 21 31 41 51
 MLLRSAGKLN VGTKEKEDGES TAPTPRPKVL RCKCHHCPE DSVNNICSTD GYCFTMIEED 60
 DSGLEPVVTS GIGLEGSDPQ CRDTPIPHQ RSIECCTERN ECKDLHPTL PPLKNRDFVD 120
 GPIHRRALLI SVTVCSLLLV LIILFCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180
 70 EQSQSSGSGS GLPLLVQRTI AKQIQMVKQI GKGRYGEVVM GWRGGEKVV KVPFTTEAS 240
 WPRETEIYQT VLMRHNILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300
 MLKLYSSVS GLCHLHTEIF STQGKPAIAH RDLKSKNLLV KNGTCCIAID LGLAVKPID 360
 TNEVDIPNT RVGTIKRYMPP EVLDESINRN HFQSYIMADM YSFGILILWEV ARRCVSGGIV 420
 ERYQLPYHDL VPSDPSYEDM REIVCIKCLR PSFPNRWSSD ECLRMGKLM TECWAPNPAS 480
 75 RLTLRVKKT LAKMESQDI KL

80
A120 DNA SEQUENCE
 Gene name: LIV-1 protein, estrogen regulated
 Unigene number: Hs.79136
 Probeset Accession #: U41060
 Nucleic Acid Accession #: NM_012319.2
 Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

5	CTCGTGGCGA	ATTGGGCACG	AGACCCGCTG	TTGCGCCTG	GTAGAGATT	CTGGAAGACA	60
	CCAGTGGGCC	CGTGTGGAAC	CAAACCTGCG	CGCGTGGCCG	GGCGTGGGA	CAACGAGGCC	120
	GCGGAGACGA	AGGCGCAATG	GCGAGGAAGT	TATCTGTAAT	CTTGATCCCTG	ACCTTTGCC	180
	TCTCTGTAC	AAATCCCTT	CATGAACATA	AAGCAGCTGC	TTTCCCCAG	ACCACTGAGA	240
	AAATTAGTCC	GAATTGGGAA	TCTGGCATT	ATGTTGACTT	GGCAATTTCC	ACACGGCAAT	300
	ATCATCTACA	ACAGCTTTTC	TACCGCTATG	GAGAAAATAA	TTCTTTGTCA	GTTGAAGGGT	360
	TCAGAAAATT	ACTTCAAAAT	ATAGGCATAG	ATAAGATTAA	AAGAATCCAT	ATACACCATG	420
	ACCACGACCA	TCACCTCAGC	CACGAGCATC	ACTCAGACCA	TGAGGCTCAC	TCAGACCATG	480
10	AGCATCACTC	AGACCAACGAG	CATCACTCTG	ACCATGATCA	TCACCTCTAC	CATAATCATG	540
	CTGCTTCTGG	TAAAAATAG	CGAAAAGCTC	TTTGCCCGA	CCATGACTCA	GATAGTTTCA	600
	GTAAGATCC	TAGAAACAGC	CAGGGGAAAG	GAGCTCACCG	ACCAGAACAT	GCCAGTGGTA	660
	GAAGGAATGT	CAAGGACAGT	GTTAGTGCTA	GTGAAGTGAC	CTCAACTGTG	TACAACACTG	720
	TCTCTGAAGG	AACTCACTTT	CTAGAGACAA	TAGAGACTCC	AAGACCTGGA	AAACTCTTCC	780
15	CCAAAGATGT	AACTCACTCC	ACTCCACCCA	GTGTCAATC	AAAGAGCCCG	GTGAGCCGCG	840
	TGGCTGGTAG	GAACAACAAAT	GAATCTGTGA	GTGAGCCCGG	AAAGGCTTTT	ATGTATTCCA	900
	GAACACAAA	TGAAAATCCT	CAGGAGTGT	TCAATGCATC	AAAGCTACTG	ACATCTCATG	960
	GCATGGGCAT	CCAGGTTCGG	CTGAATGCAA	CAGAGTTCAA	CTATCTCTGT	CCAGCCATCA	1020
20	TCAACCAAT	TGATGCTAGA	TCTTGTCTGA	TTTATACAAG	TGAAAAGAAG	GCTGAATCC	1080
	CTCCAAAGAC	CTATTCAATTA	CAAAATAGCCT	GGGTGGTGG	TTTTATAGCC	ATTTCATGC	1140
	TCAGTTTCT	GTCTCTGCTG	GGGTTATCT	TAGTGCTCT	CATGAATCCG	GTGTTTTTCA	1200
	AATTTCTCT	GAGTTTCTCT	GTGGCACTGG	CGTTGGGAC	TTTGAGTGGT	GATGCTTTT	1260
	TACACCTTCT	TCACATCTT	CATGCAAGTC	ACCACCATAG	TCATAGCCAT	GAAGAACCAG	1320
25	CAATGGAAT	GAAGAAGAGA	CCACTTTTCA	GTCTCTGTCT	TTCTCAAAAC	ATAGAAGAAA	1380
	GTGCGTATTT	TGATTCACG	TGGAAGGGTC	TAACAGCTCT	AGGAGGCGTG	TAITTCATGT	1440
	TTCTTGTGA	ACATGCTCT	ACATTGATCA	AACAATTTAA	AGATAAGAAG	AAAAAGAATC	1500
	AGAAAGAAC	TGAAAATGAT	GATGATGTGG	AGATTAAAG	GCAGTGTGTC	AAGTATGAAT	1560
	CTCAACTTTC	AACAATGAG	GAGAAAGTAG	ATACAGATGA	TCGAAGTGA	GGCTATTATC	1620
	GAGCAGACTC	ACAGAGCCG	TCCCACTTTG	ATTCTCAGCA	GCCTGCAGTC	TTGGAAGAAG	1680
30	AAGAGTCTAT	GATAGCTCAT	GCTCATCCAC	AGGAAGTCTA	CAATGAATAT	GTACCCAGAG	1740
	GGTGCAAGAA	TAAATGCCAT	TCACATTTCC	ACGATACACT	CGGCCAGTCA	GACGATCTCA	1800
	TTCAACACCA	TCATGACTAC	CATCATATTC	TCCATCATCA	CCACCACCAA	AACCACATC	1860
	CTCACAGTCA	CAGCCAGCGC	TACTCTCGGG	AGGAGCTGAA	AGATGCCGGC	GTGCCCACTT	1920
35	TGGCCTGGAT	GGTGATAATG	GCTGATGGCC	TGCACAATTT	CAGCGATGGC	CTAGCAATTG	1980
	GTGCTGCTTT	TACTGAAGGC	TTATCAAGTG	GTTTAAGTAC	TTCTGTGTCT	GTGTTCTGTC	2040
	ATGAGTTGCC	TCATGAATTA	GCTGACTTTG	CTGTCTACT	AAAGGCTGGC	ATGACCGTTA	2100
	AGCAGGCTGT	CTTTTATAAT	GCAATGTCTAG	CCATGCTGGC	GTATCTTGGA	ATGGCAACAG	2160
	GAATTTTCAT	TGTCATTAT	GCTGAAAATG	TTTCTATGTG	GATATTTGCA	CTTACTGCTG	2220
	GCTTATTCAT	GTATGTTGCT	CTGGTTGATA	TGGTACCTGA	AATGCTGCAC	AATGATGCTA	2280
40	GTGACCAATG	ATGATGCGCG	TGGGGGTATT	TCCTTTTACA	GAATGCTGGG	ATGCTTTTGG	2340
	GTTTGTGAAT	TATGTTACTT	ATTCCATAT	TTGAACATAA	AATGATGTTT	CGTATAAATT	2400
	TCATGTTAAG	GTTTAAATGC	TAGAGTAGCT	TAAAAAGTTG	TCATAGTTTC	AGTAGGTCAT	2460
	AGGGAGATGA	GTTTGTATGC	TGTACTATGC	AGCGTTTAAA	GTTAGTGGGT	TTTGTGATTT	2520
45	TTGTATTGAA	TATGCTGTCT	TGTTACAAAG	TCAGTTTAAAG	GTACGTTTAA	ATATTTAAGT	2580
	TATTTATCT	TGGAGATAAA	ATCTGTATGT	GCAATTCACC	GGTATTACCA	GTTTATTATG	2640
	TAAACAAAG	ATTGCGCATG	ACATGTTCTG	TATGTTTCAG	GGAAAAATGT	CTTTAATGCT	2700
	TTTTCAAGAA	CTAACACAGT	TATTCCTATA	CTGGATTTTA	GGTCTCTGAA	GAACTGCTGG	2760
	TGTTTAGGAA	TAAGAATGTG	CATGAAGCCT	AAAATACCAA	GAAAGCTTAT	ACTGAATTTA	2820
50	AGCAAGAGAA	TAAAGGAGAA	AAGAGAAGAA	TCTGAGAAAT	GGGAGGCGAT	AGATTCTTAT	2880
	AAAAATCACA	AAATTTGTTG	TAAATTAGAG	GGGAGAAATT	TAGAATTAA	TATAAAAAAG	2940
	CAGAAATAGT	ATAGAGTACA	TTCAATTAAC	ATTTTGTCA	GGATTATTTC	CGTAAAAAAC	3000
	GTAGTGAGCA	CTCTCATATA	CTAATTAGTG	TACATTTAAC	TTTGTATAAT	ACAGAAATCT	3060
	AAATATATTT	AATGAATTCA	AGCAATATAC	ACTTGACCAA	GAAATTTGAA	TTTCAAAATG	3120
	TTGCTGCGGG	TTATATACCA	GATGAGTACA	GTGAGTAGTT	TATGATTCAC	CAGACTGGGT	3180
55	TATTGCCAAG	TTATATATCA	CCAAAAGCTG	TATGACTGGA	TGTTCTGTGT	ACCTGGTTTA	3240
	CAAAATATATC	AGAGTAGTAA	AACTTTGATA	TATATGAGGA	TATTAAACT	ACACTAAGTA	3300
	TCATTTGATT	CGATTACGAA	AGTACTTTGA	TATCTCTCAG	TGCTTCAGTG	CTATCATGT	3360
60	GAGCAATTGT	CTTTATATAC	GGTACTGTAG	CCATCTAGG	CCTGCTCTGT	GCAATCTCTA	3420
	GATGTTTCTT	TTTTACACAA	TAAATTCCTT	ATATCAGCTT	G		

A121 PROTEIN SEQUENCE

Gene name: LIV-1 protein, estrogen regulated
 Unigene number: Hs.79136
 Protein Accession #: NP_036451
 Signal sequence: 1-21
 Pfam domain: Zip[591-743]
 Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745
 Cellular Localization: plasma membrane

70	1	11	21	31	41	51	
	MARKLSVILI	LTPALSVTNP	LHELKAAAF	QTTEKISPFW	ESGINVDLAI	STRQYHLQQL	60
	FYRYGNNLS	SVGGFRKLLQ	NIGIDKIKRI	HIHHDHDS	DHEHSDHER	HSDHEHSDH	120
75	EHHSDDHDS	HHHHAASGN	KRKALCPDHD	SDSSGKDPN	SQKGAHRPE	HASGRNRVKD	180
	SVSASEVTST	VYNTVSEGT	PLETIETPRP	GKLFPRKDVSS	STPPSVTSKS	RVSRLAGRKT	240
	NESVSEPRKO	FMYSRNTNEN	PQECFNASKL	LTSHGMIQV	PLNATEFNVL	CPALINQIDA	300
	RSCLHTSEK	KABIPPKTYS	LQIAWVGFI	AISIISFLSL	LGVLVPLMN	RVFPKFLSLP	360
80	LVALAVGTL	GDAPLHLLPH	SHASHHSHS	HEEPAMEMKR	GPLPSHLSQ	NIESAYFDS	420
	TKKGLTALGG	LYPMFLVEHV	LTLLKQPKDK	KKKQKKPEN	DDVRIKKQL	SKYESQLSTN	480
	EEKVDVDDRT	EGYLRADSQ	PSHFDSSQPA	VLEEBEVMIA	HAHPQBYNE	VYPRGCKNKC	540
	BSHFHDTLQ	SDDLHHRHD	YHHILEHHRH	QNHHPHSHSQ	RYSRBELKDA	GVATLAWMVI	600
	MGDGLHNP	GLAIGAAPTE	GLSSGLSTSV	AVPCHLPHE	LGDFAVILLKA	GMTVKQAVLY	660
	NALSAMLA	GMATGIFIGH	YAENVSMWIP	ALTAGLFMYV	ALVDMVPEML	HNDASDHGCS	720

RWGYFFLQNA GMLLGFGLML LISIFEHKIV FRINF

5 A122 DNA SEQUENCE

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

10
 15
 20
 25
 30
 35
 40
 45
 50

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CGCCAGAGGA GCCTCGGCCA GGCTAGCCAG GGCGCCCCCA GCCCCTCCCC AGGCCGCGAG 60
CGCCCTTGCC GCGGTGCTCT GCCTCCCTCT CCAGACTGCA GGGACAGCAC CCGTAACTG 120
CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
GGGTCCGGCC GGCGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGCAGAG 240
ATGCTCTGCG CTGGAGCCTT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC 300
GGGAACGCGG CCAGTGCAAG GCATCACGGG TTGTTAGCAT CGGCACGTCA GCCTGGGGTC 360
TGTCACTATG GAACTAAACT GGCTGTCTGC TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
TGTGAAGCTA CATGCGAACC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAAATGC 480
AGATGCTTTC CAGGATACAC CGGAAAAACC TGCACTCAAG ATGTGAATGA GTGTGGAATG 540
AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACACG GAAGCTACAA GTGCTTTTGC 600
CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
ATAAACTGTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 720
TCAGGACTCC GCGTGGCCCG AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCCTCT 780
GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTTGGAAG CTACTACTGC 840
AAATGTCACA TTGGTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
GGGTCCCTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTTCTGCT 1020
ATCCCTGAAA TGCTGTGTGA GGAAGTCTCT AGAGCACCTG GTACCATCAA AGACAGAAATC 1080
AAGAAGTTGC TTGCTCACA AAACAGCATG AAAAAGAAGG CAAAATTAAT AAATGTTACC 1140
CCAGAACCCA CCAGGACTCC TACCCCTAAG GTGAACCTGC AGCCCTTCAA CTATGAAGAG 1200
ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAATGAAA 1260
GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA 1320
AGCCTCGAGG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCTGATT 1380
CTGGTCCAAA GGAAGCGCTT AACTTCCAAA CTGGAACATA AAGATTAAAA TATCTCGGTT 1440
GACTGCACTT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTGAC 1500
TGGAACTCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCC GGCCTTGGCA 1560
GGTCACAAGA AAGACATTGG CCGATTGAAA CTCTCTCTAC CTGACCTGCA ACCCCAAAGC 1620
AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCGGAGAGCA AAGTCGGGAA ACTTCGAGTG 1680
TTTGTGAAAA ACAGTAAACA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGATGAAAAG 1740
TGGAAGACAG GGAATAATCA GTTGTATCAA GGAACCTGAT CTACCAAAG CATCATTTT 1800
GAAGCAGAAC GTGGCAGGGG CAAAACCGGC GAAATGCGAG TGGATGGCGT CTGCTTGTG 1860
TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
TTGACTTTGT ATGTCTGTTT CCGGTTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
TTAGAAATAC TAGCTGAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT 2040
TCTTGATATA GATATGCCAA TATTGCTTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100
TTTCTGAATC TTTCCACATT ATATTATAAA ATATGGAATG GTCAGTTTAT CTCCCCTCT 2160
CAGTATATCT GATTGTGATA AGTAAGTTGA TGAGCTTCTC TCTACAACTT TTCTAGAAAA 2220
TAGAAAAAAA AGCACAGAGA AATGTTTAAC TGTTTGACTC TTATGATACT TCTTGGAAAC 2280
TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGTCTTTCA TAGCCAAACT 2340
TGTATATTTA AATCTTTTGT AATAATAATA TCCAAATCAT CAAAAAATAA AAAAAAAA

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55 A123 Protein sequence:

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Protein Accession #: NP_056322.2
 Signal sequence: 1-21
 Transmembrane domains: none found
 MAM domain: 402-546
 EGF domain: 80-259
 Cellular Localization: secreted

65
 70
 75

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1      11      21      31      41      51
MPLFWSLALP LLLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRNRNSKGV 60
CEATCEPGCK FGECVGFNKC RCPFGYTGKT CSQDVNECGM KPRPCQHERV NTHGSYKFC 120
LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EEGPQCLCPG SGLRLAPNGR DCLDIDECAS 180
GKVICFPYNR CVNTFGSYYC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFTNQ 240
GSFKCKCKQG YKNGLRCSA IPENSVKEVL RAPGTIKDRI KLLAHKNSM KKKAKIKNTV 300
PEPTRTPTPK VNLQPFNYEE IVSRGGSNSHG GKKGNKEEMK EGLEDEKREE KALKNDIEER 360
SLRGDVFFPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHGICD WKQDREDDFD 420
WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLFDLQPPS NFCLLFYRL AGDKVGKLRV 480
FVKNSNNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF EAERGGKKTG EIAVDGVLLV 540
SGLCPDLSLS VDD

```

80 A124 DNA SEQUENCE

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Nucleic Acid Accession #: NM_001719

Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

5 1 11 21 31 41 51
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
CTGCCACCTG GGGCGGTGCG GGGCCGGAGC CGCGAGCCCG GGTAGCGCGT AGAGCCGGCG 120
CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCGGCACAG CTTCGTGGCG CTCTGGGCAC 180
CCCTGTTCCT GCTGCGCTCC GCGCTGGCGG ACTTCAGCCT GGACAAACGAG GTGCACTCGA 240
10 GCTTCATCCA CGGCGGCTC CGCAGCCAGG AGCGGCGGGA GATGCAGGCG GAGATCCCTCT 300
CCATTTCGGG CTGCCCCAC CGCCCGCGCC CGCACTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTCA CTGGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGGCGC GGGCCCGCGC 420
GCCAGGGCTT CTCTACCCCG TACAAGGCGG TCTTCAGTAC CAGGGGCGCC CTCTGGCCA 480
GCCTGCAAGA TAGCCATTTC CTCACCGAGC CCGACATGGT CATGAGCTTC GTCAACCTCG 540
15 TGAACATGA CAAGGAATTC TTCCACCCAC GCTACCAACA TCGAGAGTTC CGGTTTGATC 600
TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCCGA ATTCGGGATC TACAAGGACT 660
ACATCCGGGA CGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CGTACCCCTC TGGGCTCGG 780
AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACCGAGCA CCACTGGGTG GTCATCCGC 840
20 GGCACAACCT GGGCCCTGCG CTCTCGTGG AGACGCTGGA TGGGAGAGC ATCAACCCCA 900
AGTTGGGGGG CCTGATTGGG CGGCAGCGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT 960
TCTTCAAGGC CACGGAGGCT CACTTCCGCA GCATCCGGTC CACGGGAGAG AACACAGCGA 1020
GCCAGAACCG CTCCAAGACG CCCAAGAAC AGGAAGCCCT CGCGATGGCC AACGTGGCAG 1080
AGAACAGCAG CAGCGACCCG AGGCAGGCGT GTAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
25 GAGAACCTGG CTGGCAGGAC TGGATCATCG CGCTGAAGG CTACGCCGCC TACTACTGTG 1200
AGGGGGAGTG TGCCCTTCCT CTGAATCCTT ACATGAACGC CACCAACCA CCGCTCGTGC 1260
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AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTATC CTGAAGAAAT 1380
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30 TTGGGGCCAA GTTTTCTGG ATCTCTCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
CTGCCCTTTG TGAACCTTTC CCTTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG 1560
AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
TCCTACAAGC TGTGACGGCA AAACCTAGCA GGAACAAAAA ACAACGCATA AAGAAAAATG 1680
GCCGGGCCAG GTCATTGGCT GGGAACTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
35 TTATGAGCGC CTACCAAGCA GGCACCCAG CGTGGGAGG AAGGGGGCGT GGCAGGGGT 1800
GGGCACATTG GTGTCGTGTC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
CAATAAACG AATGAATG

40 A125 Protein sequence:
Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
Unigene number: Hs.170195
Probeset Accession #: BE616633
Protein Accession #: NP_001710.1
45 Signal sequence: 1-30
Pfam domains: TGFb_propeptide [37-281]
Transmembrane domains: none found
Cellular Localization: secreted

50 1 11 21 31 41 51
MHVRSRLRAAA PHSFVALWAP LFLRLSALAD PSLDNEVHSS FIHRRRLRSQF REMOREILS 60
ILGLPHRPRP HLQGHNSAP MFMLDLYNAM AVBGGGPGG QQPSYPYKAV PSTQGPPLAS 120
55 LQDSHPLTDA DMVMSFVNLV EHDKEFPFHR YHREPRFDL SKIPEGEAVT AAEFRITYNDY 180
IRERFQNETF RISVYQLQE HLGRESDLFL LDSRTLNAE EGWLVPDITA TSNHVVNFR 240
HNGLGLQLSV TLDQSNINPK LAGLIGRHGP QNKQPFMVAF FKATVHFHRS IRSTGSKQRS 300
QNRSKTPKQI BALRMANVAE NSSSDQRCAC KKHLYVSVR DLGWQDNIIA PEGYAAAYCE 360
60 GECAFFLNSY MNATNHAIVQ TLVHFINFET VPKPCCAPTQ LNAISVLYPD DSNVILKKY 420
RNMVVRACGC H

A126 DNA SEQUENCE
Gene name: integrin, beta 8
Unigene number: Hs.52620
Probeset Accession #: AA479726
65 Nucleic Acid Accession #: NM_002214
Coding sequence: 680-2990 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51
CCCAGAGCCG CCTCCCCCTG TTGCTGGCAT CCGAGGCTTC CTCCCTTGCC AGCCAGGACG 60
CTGCCAGCTT GTCTTTGCCG GCTGCTCCGC AGACGGGGCT GCAAGAGTGC AACTAATGGT 120
GTGTGGCTCC CTGCCACCT GTGGAAGCAA CTGCGTGAT TGATGCGCCA CAGACTTTT 180
75 TCCCTCGAC CTGCGCGCGG TACCCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
TAGGGTGGTT TCCCCCCAG CTTCGGGCTT TGTITGGGTT TGATTGTGTT TGGCTCTTCG 300
CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCTTTCTT 360
TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTGCCG GCGGGGCCCT 420
TGGCGGTGGA AGGAGGTGCT TCTGCGGAG ACCGCGGAC CGCGGTGCC GAGCGGGAG 480
GGCCGTAGGG GCCCTGAGAT GCGGAGCGGT GCCCGGGCCC GCTTACCTGC ACCGCTTGCT 540
80 CCGAGCGCGG GGGTCCGCT GCTAGGCTG CCGAAAAAGT CCTAGCGACA CTGCGCCGCG 600
GGCCCGGAG TCGCCCGGGA GCGCGAGCCC GCGTCCGAA GGCAGCCAGG CGGCGGGCGC 660
GGGGCGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTITACC GCTGCATTG 720
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 GCTCAGTTGA TTCAATAGAA TACCCATCTG TGCATGTTAT AATACCCACT GAAAAATGAAA 1020
 10 TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA 1080
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 25 TTACAATGAA AAAATGTGAT GTTACAGGAG GAAAAACTA TGCAATATC AAACCTATTG 2040
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 35 GCACCGATCC CAGGAGCATC GGCCGCTTCT GTGAACACTG CCCCACCTGT TATACAGCCT 2580
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 40 ATAAATTTAA GTCTCATCA GATTACAGAG TGTGAGGCTG AAAAAAGGAT AAGTTGATTC 2880
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 45 GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180
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 TACTGCCATA AAAAATAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAGCT 3780
 GAATGTTAA

55 A127 Protein sequence:
 Gene name: Integrin, beta 8
 Unigene number: Hs.52620
 ProbeSet Accession #: AA479726
 Protein Accession #: NP_002205.1
 60 Signal sequence: 1-39
 Transmembrane domains: 682-704
 EGF domain: 552-584
 INB domain: 54-469
 Cellular Localization: plasma membrane

65

1 11 21 31 41 51
 70 MCGSALAFFT AAFVCLQNDR RGPASFLNAA WVPSLVGLG QGEDNRCASS NAASCARCLA 60
 LGPECGWCQV EDFISGGSRs ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP 120
 GEVSIQLRPG AEANFMLKVH PLKKYFVDLY YLVDVSASMH NNIEKLNSVG NDLSRKMAPP 180
 SRDFRLGPGS YVDKTVSPYI SIHPERIHNQ CSDYNLDCMP PHGYIHVLSL TENITEPEKA 240
 VRHQKISGNI DTPEGGFDM LQAAVCESHI GWRKEAKRL LVMTDQTSHE ALDSKLAGIV 300
 VPNDGNCHLK NNIVYKSTIM EHPSLQQLSE KLIDNNINVI FAVQKQFHW YKDLLPLLP 360
 75 TIAGEIESKA ANLNLVVVEA YQKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGRK 420
 NVTSNDENVLF NVTVTMKKCD VTGGKNYAI KPIGFNETAK IHIHRNCSCQ CEDNRGPKGR 480
 CVDETFLDSK CFQCDENKCH FDEDFSSSES CKSHKDPVC SGRGVCVCGK CSCHKIKLGK 540
 VYGYKCEKDD FSCPYHHGNL CAGHGECEAG RCQCFSGWEG DRQCFPSAAA QHCVNSKGV 600
 80 CSRGTCVCG RCCECTDPSI GRPCEHCPTC YTACKENWNC MQCLHPHNLs QAILDQCKTS 660
 CALMEQHYV DQTSCECFSSP SYLRIFFIIF IVTFLIGLLK VLIIRQVILQ WNNENKIKSSS 720
 DYRVASAKKD KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETFRCNF

A128 DNA SEQUENCE

Gene name: G protein-coupled receptor 64

Unigene number: Hs.184942
 Probeset Accession #: AA435577
 Nucleic Acid Accession #: NM_005756
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

5

1 11 21 31 41 51
 1 AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTTCTGAA 60
 10 CTGCGGGTCA GGAATGGTTT CTCTGTGAG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA 120
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 TCCCTGGAG AGATACTGA TAATCCAGT TTGTACCAC CACCTGCTAA ATTATCTGTT 240
 GTCAGTTTGT CCCCCCTCTC CAATGAGGTT GAAACAACAA GCCTCAATGA TGTACTTTA 300
 15 AGCTTACTCC CTTCAAACGA AACAGAAAAA ACTAAATCA CTATAGTAAA AACCTTCAAT 360
 TCTTCAGGCG TCAAAACCCA GAGAAATATC TGCAATTGT CATCTATTG CAATGACTCA 420
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 CAACATATAA CGAATGGCAC CTAACTGGA GTCTGTCTC TAAGTGAATT AAAACGCTCA 540
 GAGCTCAACA AAACCTGCA AACCTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600
 GAGGCCCAA GCACATTAAA TTGTACATT ACAATAAAG TGAATAATAC AATGAATGCA 660
 20 TGTGCTGCAA TACCTGCCC TTCTCCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780
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 25 GCTGAGCCTC CAGATTATTC ACCTGTGACC CACAATGTTT CTTCTCCAAT AGGGGAGATT 960
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 30 CAAGTGTGTC AGATGGAGAA GGCTCTGTCC TTGGGAGGCC TGGAGCCTAA CCTCGCAGGA 1260
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 35 CAAGCTCCTG AGAACAGTAT TGGCACAATT ACTCTTCCCT CATGCTGATG GAATAATTTA 1560
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 45 CTCTGGACT CGTGGATTGC TCTGTATAAG ATGCAAGGCC TCTGATCTC AGTGGCTGTA 2160
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CTGACTTGTC TTGCAATAT TTCTTTCTG ATTATTTAA TTTCTGTGA TTTATATGTT 4620
 AAAATCAAAA ATGTTAAAT CAATGAAATA AATTGTCAGT TAAGA

- 5 A129 Protein sequence
 Gene name: G protein-coupled receptor 64
 Unigene number: Hs.184942
 Protein Accession #: NP_005747.1
 Signal sequence: 1-38
 GPS domain: 564-615
 10 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880
 Cellular Localization: plasma membrane

15 1 11 21 31 41 51
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 PSSNEVETTS LNDVTLSELLP SNTEKTKIT IVKTFNAGV KPQRNICLS SICNDSAPFR 120
 GEIMFOYDKE STVPQNHIT NGTLTGVLSL SELKRSELNK TLQTLSEYF IMCATAEQS 180
 20 VCLADHPRGP PFSSSQSIPV VPRATVLSQV PKATSFAPPP DYSPVTHNVP SPIGEIQPLS 240
 PQPSAPIASS PAIDMPPQSE TISSPMPQTH VSGTPPPVKA SPSSPTVSAP ANVNTTSAPP 300
 VQTDIVNTSS ISDLENQVLQ MEKALSIGSL EPNLAGEMIN QVSRLLHSPP DMLAPLAQRL 420
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 25 NSIGITITLPS SLNNLPAHD MELASRVQFN FFETPALFQD PSLENLSLIS YVISSSVANL 540
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 SHLTSPGVLL DLRSRTVLPA QMMALTFITY IGCGLSSIFL SVTLVTYIAP EKIRRDYPSK 660
 ILIQLCAALL LNLVFLDS WIALYKMQGL CISVAVFLHY FLVVSFTWMG LEAFHMYLAL 720
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 30 AVFYITVGVY FCVIFLLNVS MFIIVLVQLC RIKKKKQLGA QKRTSIQDLR SIAGLTFLLG 840
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 NSDWSKTATN GLKKQTVNQV VSSSSNSLQS SSNSTNSTTL LVNNDCSVHA SGNNGMASTER 960
 NGVSFVQNG DVCLHDFTGK QHMFNEKEDS CNKGKRMALR RTSKRGSLEH IEQM

- 35 A130 DNA SEQUENCE
 Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 Probeset Accession #: AA460530
 Nucleic Acid Accession #: NM_003667
 40 Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 45 TCAGGAACGC GCGCTCTGGC GCTGCAGACG CCGGCTGAGT TGCGAGAGCC CACGGAGCGG 120
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 50 GCGCCACACA CTGTCATTGC GAGCCCGACG GCAGGATGTT GCTCAGGGTG GACTGCTCCG 360
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5 GAGACCTGGA GAATATTGG GACTGCTCTA TGGTAAACA CATTGCCCTG TTGCTCTTCA 2520
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 10 TGAGAAAGCA AACCTACGTC TGGACAAGAT CAAAACACCC AAGCTTGATG TCAATTAAC 2760
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 15 ATAAGAAGAG CTGAGGTGAA ACTCGGTTTA AA

A131 Protein sequence

15 Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 Protein Accession #: NP_003658.1
 Signal sequence: 1-22
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825
 20 Cellular Localization: plasma membrane

25 1 11 21 31 41 51
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 30 LNYNLDLDFP TAIRTLNLK ELGFHNNIR SIPEKAPVGN PSLITIRFVD NPIQFVGRSA 300
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 YNLLDELPSF SVQCKLQKID LRHNEIYEIK VDTFQQLLSL RSLNLAWNKI AIHFNAPST 420
 LPSLIKLDS SNLLSFPIT GLHGLTHLKL TGNHALQSLI SSENFPPELV IEMPYAYQCC 480
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 35 AVNMLTGVSS AVLAGVDAPT PGSPARHGAW WENGVGCHVI GFSLIFASES SVFLLTLAAL 660
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 STMGYVALI LLNSLCFLAM TIAYTKLYCN LDKGDLENIW DCSMKHIAL LLFTNCILNC 780
 PVAFLSFSSL INLTFISPEV IKFILLVVP LPACLNPLLY ILFNFHFKEE LVSLRKQTYV 840
 40 WTRSKIPSLM SINDDVEKQ SCDSTQALVT FTSSSITYDL PPSSVPSPAY PVTESCHLSS 900
 VAFVPC

A132 DNA SEQUENCE

45 Gene name: parathyroid hormone receptor 2
 Unigene number: Hs.159499
 Probeset Accession #: U25128
 Nucleic Acid Accession #: NM_005048
 Coding sequence: 143-1795 (underlined sequences correspond to start and stop codons)

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 55 TCTTCTACA GCGCTTCGG GCATGSCCG GCTGGGGGCG TCGCTCCAG TCTGGGTTG 180
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5 GGAGTAGTTT ATTACCTTCT ATTGGCATCA AGTTTTCCTC TAAATTAATG TATGGTATTT 2040
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 10 TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTCCTTG 2580
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 T

15 A133 PROTEIN SEQUENCE
 Gene name: parathyroid hormone receptor 2
 Unigene number: Hs.159499
 Protein Accession #: NP_005039.1
 Signal sequence: 1-25
 Pfam domain: 7tm_2 [141-420]
 20 Transmembrane domains: 177-197, 228-250, 253-275, 280-302, 320-342, 363-385, 398-419
 Cellular Localization: plasma membrane

25 1 11 21 31 41 51
 MAGLGASLHV WGHMLGSLC LARAQLDSDG TITIEEQIVL VLKAKVQCEL NITAIQLQEGE 60
 GNCFFPBDGL ICWFRGTGVR ISAVFCPPYI YDFNHKGVAF RHCNPNGTWD FMHSLNKTWA 120
 NYSDCRLRPLQ PDISIGKQEF FERLYVMYTV GYSISFGSLA VAILIIGYFR RLHCTRNYYH 180
 MHLFVSFMLR ATSIKPVKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV 240
 30 VMFIYFLATN YWILVEGLY LHNLIFFVAF SDTKYLWGFY LIGWGFPAAF VAAMAVARAT 300
 LADARCWELS AGDIKIWIYA PILAAIGLNF ILPLNTVRVL ATKIWNENAV GHDTKQYRK 360
 LAKSTLVVLV VFGVHYIYFV CLPHSPTGLG WEIRMHCELF FNSPQGFVFS IYCYCNGEV 420
 QAEVKMWSR WNLSDVWKRT PPGSRRCGS VLTIVTHSTS SQSQVAASR MWLISGKAAK 480
 35 IASRQPDSDI TLPYVWSNS EQDCLPHSFH ETKKEDSGRQ GDDILMEKPS RPNMESNPDE 540
 GCQGETEDVL

A134 DNA sequence
 Gene name: ESTs
 Unigene number: Hs.128899
 40 Probeset Accession #: AA983251.
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

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 GACCGGGAGA GGGAGAGCCG GCCCGAGGCT GCCCGGCTCC TGTGGGACCG CGCTGCAGCC 180
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 50 CCGCGGCGCG CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCTT 300
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 TCCGAGCAGC AGCCCCGGGG GCCTTCTGAC TGCATCCCGA GATTTCATC AGCGAGTGCA 420
 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480
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 55 CCGCGCGGAA AGCGCGCGGG GACAGTCAAT GACGAGGCGC GGGGGTCCGC GGGGCCACGA 600
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 TGTCTGCTGC TGCCTGCTCG GCGCGCGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC 780
 TGGCTGGAGC CGCAGGGCGT CTGCGCATC GCGCTTCCAGT ACTGCTGCTC CAGCGCGGAG 840
 60 GCGACGCGCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCGGAG 900
 GCGCGCTCGG ACCAGGGCGG CTGCGCAAT GACCGCCAGC AGGGCGCTGG CGAGCTGGC 960
 CGGCGCGACA AAGACGGGCG CCGACGGCTC GGCAGGGCTT CATGCTTAG GGTACCCAA 1020
 GGAGACGCGG AGGGTGGCGC CCCACCGCTG AGGGCTGGC AGCGGTGCTC CCTGAAGGC 1080
 TCCCGGAAGG GAAGGCAGCT CCTCAGGCTT TTCCCGGGGC TGTGCCCCG TGCAGAGCGC 1140
 65 CGCGGATTCC CATCTTCTCC ACGCGCGGCG CCTCTCCCC TGCAGCGGCC CGCCTTCCCC 1200
 ATCTACGTGC CGTTCCTCAT TGTGGCTCC GTGTTGTGCG CCTTTATCAT CTTGGGGTCC 1260
 CTGTGTGCGC CCGTTTGTCT GAGATGTCTC CGGCTAAGC AGGATCCCCA GCAGAGCCGA 1320
 GCGCCAGGGG GTAACCGCTT GATGGAGACC ATCCCATGA TCCCGAGTGC CAGCACTCC 1380
 CGGGGCTCGT CCTCAGCCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG GCGCACTCC 1440
 70 GGGGCGCGGG CGCCCCAAC AAGGTACAG ACCAACTGTT GCTTGGCGGA AGGGACCATG 1500
 AACACAGTGT ATGTCAACAT GCCCAGCAAT TTCTCTGTGC TGAAGTGTCA GCAGGCCACC 1560
 CAGATTGTGC CACATCAAGG GAGTATCTG CATCCCCAT ACGTGGGGTA CACGGTGCAG 1620
 CACGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCTGCA GCCTGGCTAC 1680
 AGGCAGATTG AGTCCCCCTT CCCTCACACC AACAGTGAAC AGAAGATGTA CCGAGCGGTG 1740
 75 ACTGTATAAC CGAGAGTCAC TGGTGGGTTT CTTTACTGAA GGGAGAGGAA GGCAGGGGTG 1800
 GATTCTCGAG GTGGAGTCC GCACATGTG GTGGTATTTA TGGCAGGATT CCTTTGGATG 1860
 GCTTCATTGG CCCCCAGACT GTATGAAAAC ATCTCGAAT TAGCATTTC GATATGTTT 1920
 CATCCAGGGT ATCATTGATT TATGATGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980
 80 TTGCTGTGGG GTGTATAACA AATGCTTGAG TCGAAGTGC CCTTGAGATA TGGTTGACGA 2040
 AAGAATTTTA TAAACTGATA AATTAAAGAT TTTTATTATG TTGTATTAT TATTCTTTT 2100
 TTGTTGTTGA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGAG GACTTTT 2160
 TTTTTTTTTT TTTTITTTAA TCAGACAGGG TCTTGCTCTG TTGCCCCAGC TGGAGTGCAG 2220
 TGGTGGGATC TCGGCTCACT GCAACTCAG CCTCTGGAT TCAGGCAACA CTCCTGCTC 2280
 AGCCTCCACC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCATAATTT TTGATTTTT 2340

5 TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA CCTCAAGCAA 2400
 TCTGCCTGTC TCAGCCTGCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCAGGCC 2460
 TGAGCCTTTT TTTTTCCTTA ATGCATCCAA GGTTAAGGGG AAGACGCAAA TAACAGGACT 2520
 ATTCTAAAG GAAACCTGTT TGAACCTCTG GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580
 GGCACACCTT AATTTCATTG TAAAAAGATA TATATATTTT GTCTATTTTT GTGCTTTTGG 2640
 GGGCCTATTT TGTGCTTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG AITTTCTACA 2700
 TTAATAAGAG ACTGAAATAA AITGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCAATT CATCCCTTC 2820
 10 TTGATTGTAT CTAAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATCTTTTT 2880
 TATATTGAAA TCATAAATA TCACCGCTG CTCTCTGAG TTACTTTTAA TTTTGCTTG 2940
 TGGTATAGGT TTGGCGTTTC CTTCGTTTG GTTTTCAGAG CCCCATGTCT ATATAGTCCT 3000
 GAGTGCAAGT AACTTACTATA CTTGTAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA 3060
 AAAAAATTTT TGTCTTAGT TATAAAAT CAAGAAATG TGTACAAAG ATACTTAGTA 3120
 TAGCTCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTACTTT 3180
 15 GCAGATCAT AGCTTTTATA TACTTTGTT ATCAAAATGG CTTATTTTTC AGGCATAAG 3240
 GATTGTTAAG AGAAAGCTT TTCAACGAAG GATTGCCCTT CTCTCCAC ACTGTTCTTG 3300
 ATTTCTCTC TCTTTCAGG CTCAACAGGC ACTGATTCA TTGCCAATGT TCCAATTTAT 3360
 CAAATTCAG TGAATTTATT TGTGTGTTCT TACTTATAT AAAAAAGAT AACTTTAAG 3420
 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTA ACAAATCGCT 3480
 20 GTATGGTATG GTCTTCTACA CATTATGTC TATAGATATC TATCGATCAT CTTTCTATTC 3540
 TGTTCATGA CTGAATAATG TAAACCAAGT GTTGGCAAT GGTATCATCA ATGATACTCA 3600
 TTTTATAA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660
 TGAATAAATA AAAAAAATA AAAAAAATA

25 A135 Protein sequence
 Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 30 Transmembrane domains: 402-424
 Cellular Localization: not determined

35 1 11 21 31 41 51
 | | | | |
 MLSGFLMSPS TQHRAQYTPG GKLPWEASI GAHTSRGRGS DRERESRFEA AGLMDRAAA 60
 GEAEKGNRGE PPAWIRAOQQ PRPPPAQQAP GTAAGGAQDP RLPRGRSRGR VRLPVKPPFA 120
 SGRQPRGSPD CIPRPPSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAEBSG 180
 40 PRGRRRGTVS DEARGSPGPR LLGDRPALSG DALSAAPRVVP CGALAARPSF HPGTPLRSCS 240
 CCMRLCWRRG RGPSPGYCHG WLDAQGVVRI GPQCFERFDG GDATICCGSC ALRYCCSSAE 300
 SRLDQGCND DRQGGAGEPG RADKDGPRRL GRASCLRGTD GDGEGAPPPV RAWQRCSPG 360
 PFKGRQLLRA PFGLLPRARR RGFPSPPRG PSPLQRPALP IYVFLIVGS VFVAFILGS 420
 LVAACCCRCL RPKQDPQQR APGGNRLMET IPMIPSAETS RGSRRSQSST AASSSSSANS 480
 45 GARAPPTRSQ TNCCLPBGTM NNVYVNMPTN FSVLNCQCAT QIVPHQGGYL HPPYVGTVQ 540
 HDSVPMTAVE PFMDDLQPGY RQIQSPFPHT NSEQRMYPV TV

50 A136 DNA SEQUENCE
 Gene name: selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Nucleic Acid Accession #: NM_000450
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
 | | | | |
 ATGATTGCTT CACAGTTTCT CTGAGCTCTC ACTTTGGTGC TTCTCATTAA AGAGAGTGGG 60
 GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATGTT 120
 CAGCAAAAGT ACACACACCT GGTGCAATT CAAAACAAAG AAGAGATTGA GTACTTAAAC 180
 60 TCCATATTGA GCTATTACAC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACATGTG 240
 TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAAGCT GGCCTCCAGT 300
 GAACCCAAAC ATAGGCAAAA AGATGAGGAC TGGTGGAGA TCTACATCAA GAGAGAAAAA 360
 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
 GCTGCCTGTA CCAATACATC CTGAGTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480
 65 TACACTTGCA AGTGTGACCC TGGCTTCAGT GGAATCAAGT GTGAGCAAT TGTGAAGTGT 540
 ACAGCCCTGG AATCCCTGGA GCATGGAAGC CTGGTTTGCA GTCAACCCACT GGGAAACTTC 600
 AGCTACAATT CTCTCGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
 ACCATGCAAT GTATGTCTCT TGGAGAATGG AGTCTCTCTA TTCCAGCCTG CAATGTGTTT 720
 GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTTGGA 780
 70 AGCTTCCCAT GGAACACAACT CTGTACATT GACTGTGAAG AAGGATTGTA ACTAATGGGA 840
 GCCCAGAGAG TTCACTGTAC CTGATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900
 GCTGTGACAT GCAGGCGGCT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960
 CCTGCTGGAG AGTTCACTCT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020
 75 TTGAGGGGAC CAGCCAGAGT TGAATGCACC ACTCAAGGGC AGTGGACACA GCAATCCCA 1080
 GTTGTGTAAG CTTTCCAGTG CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT 1140
 CTTCCTAGTG CTTCTGGCAG TTTCCGTTAT GGGTCCAGCT GTGAGTTCTC CTGTGACGAG 1200
 GGTTTGTGTT TGAAGGGATC CAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260
 GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCG GAAGGGTTG 1320
 GTGAGGTGTG TCAATCCCC TATTGGAGAA TTCACCTACA AGTCTCTCTG TGCCCTCAGC 1380
 80 TGTGAGGAGG GATTGTAATT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440
 TGGACAGAG AGGTTCTCTC CTGCCAAGTG GTAAATGTT CAAGCCTGGC AGTTCCGGGA 1500
 AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGCCA CTGTGTGCAA GTTCCGCTGT 1560
 CCTGAAGGAT GGACGCTCAA TGGCTCTGCA GCTGGACAT GTGGAGCCAC AGGACACTGG 1620
 TCTGGGCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCTTT GGTAGCTGGA 1680
 CTTTCTGCTG CTGAGCTCTC CCTCTGACA TTAGACCAAT TTCTCTCTG GCTTCGGAAA 1740

TGCTTAGCGA AAGCAAAGAA ATTTGTTCTT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

5 A137 Protein sequence:
Gene name: Selectin E (endothelial adhesion molecule 1)
Unigene number: Hs.89546
Probeset Accession #: M24736
Protein Accession #: NP_000441
10 Signal sequence: 1-22
Transmembrane domains: 555-573
C-lectin domain: 23-139
Cellular Localization: plasma membrane

15
1 11 21 31 41 51
MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRVTHLVAI QNKKEIEYLN 60
SILSYSPSY WIGIRKVNIV WVVVGTQKPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK 120
20 DVGMMNDRRC SKKLLALCYT AACTNTSCSG HGECEVETINN YTCKCDPGFS GLKCEQIVNC 180
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240
ECDAVINPAN GFVECEQNPNG SFPWNITCTF DCEGFELMAG AQLQCTSSG NWDNEKPTCK 300
AVTCRAVRQP QNGSVRCSSS PAGEFTFKSS CNFTCEEGFM LQGFPAQVECT TQGWTOQIIP 360
VCEAFQCTAL SNPERGYMNC LPSASGSFRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEMDN 420
25 EKPTCEAVRC DAVHQPFGKL VRCASPIGE FTYKSSCAPS CEEGFELYGS TQLECTSQGQ 480
WTEEVPSQCV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540
SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLNLRLK CLRKAKKVPV ASSCQSLESD 600
GSYQKPSYIL

30 A138 DNA SEQUENCE:
Gene name: ESTs, Weakly similar to JB0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Nucleic Acid Accession #: AA487468
35 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60
CTACACTCAG CTTTGGGTCT CTGCTCTCTA CTGCTCAGAG TTTCTTCCAA CCTTGCCATT 120
GCAATAAAAA AGGAAAGAG GCTCTCTCAG ACCTCTCAA GAGGATGGGG AGATGACATC 180
ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
ATGGTTATTC ATCACTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGCC 300
45 CAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
GAAACCACTG ATAAGAAATT ATCACTGAT GGGCAATATG TGCTTAGAAT CATGTTTGTA 420
GACCTCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTTAACAG ATTGTACACA 480
TATGAGCCTC GGGATTATCC CCTATTGATA GAAACATGA AGAAGCATT AAGACTTAT 540
CAGTCAGAGC TATAAGAGAT GATAGAAAA AGCCTTCACT TCAAAGAAGT CAAATTTCAT 600
50 GAAGAAACCC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTATTA 660
TTACTATTTA GTTTTTTAA TGTGTTTGA ATAGTCTTAT TAAATAAAT GTTTTTTAA 720
TCTGAAAAA AAAAAA AAAAAA

55 A139 Protein sequence:
Gene name: ESTs, Weakly similar to JB0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Protein Accession #: none found
60 Signal sequence: 1-23
Transmembrane domains: none found
Cellular Localization: secreted

65 1 11 21 31 41 51
MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK 60
PLMVIHLED CQYSQALKKV FAQNNEIQEM AQNKFIMLNL MHETTDKNLS PDGQVVPRI 120
70 FVDPSITVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

A140 DNA SEQUENCE
Gene name: TMPRSS3a
Unigene number: Hs.298241
Probeset Accession #: AI538613
75 Nucleic Acid Accession #: AB038157
Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
ACCGGGCACC GGACGGCTCG GGTACTTTG TTTCTAATTA GGTATGCCC GTGTGAGCCA 60
GGAAGGGCT GTGTTTATGG GAAGCCAGTA ACCTGTGGC CTACTATCTC TTCGTGGTG 120
CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGC 180
AGAGGTCTCT AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGA AGCCCCCTTC 240

5 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCCTGTTC ACCAGATGCA 300
 GATGCTGTTC CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTC AATCATGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
 TCAGGGAACT ACAGATGTG CTCTCTCTT AAGTGTATG AGCTGATAGC TGGATGTGAC 480
 GGAGTCTCG ATTGCAAGA CGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600
 AAGGGTCACT ACGCAATGT TGCCTGTGCC CAACTGGGT TCCCAAGCTA TGTGAGTTCA 660
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT 720
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 10 TGTGCTCTG GCCACGTGGT TACCTTGCAG TGCACAGCCT GTGTTCATAG AAGGGGCTAC 840
 AGCTACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900
 CTTCACTTCC AGGCTACCA CCTGTGGGG GGCTCTGTCA TCACGCCCT GTGGATCATC 960
 ACTGTGACG ACTGTGTTA TGACTTGTAC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020
 CTAGTTTCC TGTGGACAA TCCAGCCCA TCCACTTGG TGGAGAAGAT TGTCTACCA 1080
 15 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCGGGCCA 1140
 CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCTTCCCA ACTCTGAAGA GAACTTCCCC 1200
 GATGGAAGA TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGAAGCC 1260
 TCCCTGTGC TGAACCAAGC GGCCTGCCCT TTGATTCCA ACAAGATCTG CAACCAAGG 1320
 GACGTGTAG CTCCCTCAT CTCCCTCTCC ATGCTCTGCG CGGGTACCT GACGGGTGGC 1380
 20 GTGGACAGCT GCCAGGGGGA CAGCGGGGG CCCCTGGGT GTCAAGAGAG GAGGCTGTGG 1440
 AAGTTAGTGG GAGCGACGAC CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
 TACACCGTGG TACCTCTCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTCT AGGTGATGAA GACAGCCCGA 1620
 25 TCCTCCCTG GACTCCCTG TAGGAACCTG CACACGAGCA GACACCTTGG GAGCTCTGAG 1680
 TTCGGGCACT AGTAGCAGGC CGGAAAGAG CACCTTCCA TCTGATTCCA GCACAACCTT 1740
 CAAGCTGCTT TTGTGTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTGG CCCAGGCTGG 1800
 AGTGCACTGG CGAAATCCTT GCTCACTGCA GCCTCGCTT CCTGGTTCA AGCGATTCTC 1860
 TTGCTCAGC TTCCCGAGTA GCTGGGACCA CAGGTGCCCG CCACCAACCC CAACTAATT 1920
 30 TTGTATTTTT AGTAGAGACA GGGTTTACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
 CCTCAAATGA TGTGCTGCT TCAGCTCCC ACAGTCTGG GATTACAGG ATGGGCCACC 2040
 ACGCTAGCC TCACTCTCTT TTCTGATCTT CACTAAGAAC AAAAAGAAC GCACACTTGA 2100
 AGGGCGGCTT TTCCCTCTGG TCCATCTGGT TTCTCTCCA GGGGTCTTGC AAAATTCTCT 2160
 ACGAGATAAG CAGTTATGTG ACCTCAGCTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
 35 GCACCAAGCC AGAAGTGCAG AACTGCAGT ACTGCACTT TTCATCTCTA GGGACCAAGAA 2280
 CCAAAACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
 ATGACTCGTT TAAGGCCTAT TTTCTGATT TCTTTGATG ATTTGGTGTG TGACGTATTA 2400
 TTGTCTTGT ATTCCAAATA ATATGTTTC TCCCTCAAA AAAAAAAAAA AAAAAAAAAA 2460
 AAAAAA

40 **A141 Protein sequence:**
 Gene name: TMPS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Protein Accession #: BAB20077
 45 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 Tryp_SPC domain: 216-444
 Cellular Localization: plasma membrane

50
 1 11 21 31 41 51
 | | | | |
 MGENDPFAVE APFSFRSLPG LDDLKISFVA PDADAVAAQI LSLLPLKFFP IIVIGIILI 60
 55 LALAIGLGIH FDCSGKYRRC SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GQNAVILQVP 120
 TAASWKTMCs DDMKHGAYNV ACAQLGFPSY VSSDNLRVSS LBGQFREBFV SIDHLLPDDK 180
 VTALHSHVYV REGCASGRHV TLQCTACGHR RGYSSRIVGG NMSLLSGWPW QASLQFQGYH 240
 LCGSVITPL WIITAABCVY DLVLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSHYKPKR 300
 LGNDIALMLK AGPLTFNEMQ QPVCLPNSSE NFPDGVKWT SGWGEDTGA GDASPLVNH 360
 60 AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVDSOQGD SGGPLVQQR RLWKLVGATS 420
 FGGCAEVNK PGVYTRVTSF LDWIEQMER DLKT

65 **A142 DNA SEQUENCE**
 Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Nucleic Acid Accession #: none found
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

70
 1 11 21 31 41 51
 | | | | |
 CCAACAGAT TTGCAGATCA AGGAGAACCC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60
 75 CTGAGATCTT TGCCTAGCT ACATCCTCAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120
 CGGCTGCTCC TATTGCTGAG CTGCCTGGCC AAAACAGGAG TCTGGGTGA TATCATCATG 180
 AGACCCAGCT GTGCTCTCG ATGGTTTAC CACAAGTCCA ATTGCTATGG TTACTTCAGG 240
 AAGCTGAGCA ACTGGTCTGA TGCAGAGCTC GAGTGTCACT CTTACGGAAA CGGAGCCAC 300
 CTGGCATCTA TCTGTAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360
 80 CAGAGAAGCC AGCCGATATG GATTGGCTG CACGACCCAC AGAAGAGGCA GCAATGGCAG 420
 TGGATTGATG GGGCCATGTA TCTGTACAGA TCTGTGCTG GCAAGTCCAT GGGTGGGAAC 480
 AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTAA CTGGAGCAG CAACGAATGC 540
 AACAGAGGCC AACACTTCT GTGCAAGTAC CGACCATAGA GCAAGAATCA AGATTCTGCT 600
 AACTCTGTCA CCAGCCCGCT CTCTTCTCT TCTGTAGCC TGGCTAAATC TGCTCATTTA 660
 TTCAGAGGGG AAACCTAGCA AACTAAGAGT GATAAGGGCC CTACTACACT GGCTTTTTTA 720

5 GGCTTAGAGA CAGAAACTTT AGCATTGGGC CCAGTAGTGG CTTCTAGCTC TAAATGTTTG 780
 CCCCGCCATC CCTTTCCACA GTATCCTTCT TCCTCTCTCC CCTGTCTCTG GCTGTCTCGA 840
 GCAGTCTAGA AGAGTGCAAT TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAAT 900
 AAAGATTGGA AGACAGAAGG AAGAACTCA GGAGTAAGCT TCTAGACCCC TTCAGCTTCT 960
 ACACCTTCTT GCCTCTCTC CATTCCTGTC ACCCACCCC AGCCACTCAA CTCTGCTTG 1020
 TTTTTCCTTT GGCCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGGTTG ATGTGGGCCA 1080
 TACATTCCTT TAATAAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA

10 A143 Protein sequence:
 Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Protein Accession #: none found
 15 Signal sequence: 1-22
 Transmembrane domains: none found
 C-type lectin domain: 47-156
 Cellular Localization: secreted

20 1 11 21 31 41 51
 MASRSMRLLL LLSCLAKTV LGDIIMRPS APGWFFYHKS CYGYFRKLRL WSDAELEQCS 60
 YGNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQOWQWIDG AMYLRSWSG 120
 25 KSMGGNKHCA EMSSNNNFLT WSSNECNKRQ HFLCKYRP

30 A144 DNA SEQUENCE
 Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

35 1 11 21 31 41 51
 GCGGAACACC GCGCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
 TCCTCTGTGG ACCTCTCGCG TCCTCTCTCC TTCTCCAGGT TTGCTGGCTG CAGTGCAGCG 120
 CCTCCGAGCC GTGCCGGGGC GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180
 CGGAGCAGGA GCGCGGCCAG CGCTCGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240
 40 CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAAGGGTC 420
 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
 ACAGCATCAC GGGGCGGGGG GCAGACAGCC CCCCTGAGGG TGCTCTCGCT GTAGAGAAGG 540
 45 AGACAGGCTG GTTGTGTTTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
 TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGA GACCCCATG AACATCTCCA 660
 TCATCGTGAC CGACAGAAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCGAGGGA 720
 GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840
 50 AGGACCCACA CGACCTCATG TTCACAATTC ACOGGAGCAC AGGCACCATC AGCCTCATCT 900
 CCAGTGGCCT GGACCGGGAA AAGTCCCTTG AGTACACACT GACCATCCAG GCCACAGACA 960
 TGGATGGGGA CGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCCT GATGCCAATG 1020
 ACAATGCTCC CATGTTTGAC CCCCAGAAGT ACGAGGCCCA TGTGCTGAG AATGCACTGG 1080
 GGCATGAGGT CGAGAGGCTG ACGGTCACTG ATCTGGACGC CCCCAACTCA CCAGCGTGGC 1140
 55 GTGCACCTTA CCTTATCATG GCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
 CTGAGAGCAA CAGGGGCATC CTGACAACCA GGAAGGGTTT GGATTTTGAG GCCAAAAACC 1260
 AGCACACCCT GTACGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCCCAACCT 1320
 CCACAGCCAC CATAGTGGTC CAGTGGAGG GAGACCTGTG TTTGTCCAC 1380
 CCTCCAAAGT CGTTGAGGTC CAGAGGGCA TCCCACTGG GAGACCTGTG TGTGCTTACA 1440
 60 CTGCAGAAGA CCTGTACAG GAGAATCAAA AGATCAGCTA CCGCATCCCT AGAGACCCAG 1500
 CAGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCA AGCTGTGGC ACCCTCGACC 1560
 GTGAGGATGA CGAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620
 ATGGAAGCCC TCCCACCACT GSCACGGGAA CCTTCTGCT AACACTGATT GATGTCAACG 1680
 ACCATGGCCC AGTCCCTGAG CCGCTCAGA TCACCATCTG CAACCAAGC CCGTGTGCGC 1740
 65 ACGTGCTGAA CATCAGGAC AAGGACCTGT CTCGCCACAC CTCCTCTTTC CAGGCCACG 1800
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTTT TCTCTGTCTG 1920
 ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGGAC TGCCATGGCC 1980
 ATGTGGAAC CTGCCCCTGA CCTTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
 70 TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100
 TCAAGGAGCC CCTCTACTC CCAAGAAGAT ACACCCGTA CAAGCTCTTC TACTATGGCG 2160
 AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220
 AGGCCAGGCC GGAGGTGGTT CTCCGCAATG ACGTGGCACC AACCATCATC CGACACCCA 2280
 75 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGCAA CTTTATAATT GAGAACCCTGA 2340
 AGGCGGCTAA CACAGACCCC ACAGCCCGC CCTACGACAC CCTCTTGGTG TTGCACTATG 2400
 AGGGCAGCGG CTCCGACGCC GCGTCCCTGA GCTCCCTCAC CTCCTCCGCG GCAGACATGT 2520
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAAGAAGCTG AACGTACGGC 2580
 80 CACAGAGCAT CTCGAAGGGG GCGGAGAGCA GGCTATGAGT CTGAGCTTAG AGTGGTGGCT 2700
 GGAAGTGGCC GTAGCAACTT GCGGAGAGCA GCGATTGAGT TTCAGCACTG AAAACCTCTC 2760
 TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCGATTGAGT TTCAGCACTG AAAACCTCTC 2820
 ACCTGGGCC AGGGTTGCTT CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCGTAAAA 2880
 TGCTCAACCC TGTGCTCTGG GCGTGGGCTT GCTGTGACTG ACCTACAGTG GACTTCTCT 2940
 CTGGAATGGA ACCTTCTTAG GCTTCTGCT GCAACTTAAT TTTTTTTTTT AATGCTATCT

TCAAAAAGTT AGAGAAAGTT CTTCAAAAGT GCAGCCAGAG GCTGCTGGGC CCACTGGCCG 3000
 TCTGCAATT CTGTTTCCA GACCCCAATG CCTCCATTG GGATGGATCT CTGCGTTTTT 3060
 ATACTGAGTG TGCCTAGGTT GCCCCTTATT TTTTATTTTC CCTGTGCGT TGCTATAGAT 3120
 GAAGGGTGAG GACAATCGTG TATATGTACT AGAACTTTTT TATTAAGAA A

A145 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675

Cellular localization: plasma membrane

1 11 21 31 41 51
 MGLPRGFLAS LLLQVCWLQ CAASEPCRAV PREAEVTLEA GGAEQEPGQA LGKVFMCPCG 60
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
 KGPPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKSTGWLLEN KPLDREBIK 180
 YELPGHNVSE NGASVEDPMN ISIIITDQND HKPKPTQDTF RGSVLGVLV GTSMVQVTAT 240
 DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TMDGDGSTT TAVAVVEILD ANDNAPMFDQ QKYEAHVPEV AVGBEVQRLT VTDLDPNSP 360
 AMRATYLMG GDDGDHPTIT THPESNQIL TTRKGLDPEA KNQHTLYVEV TNEAPVLKL 420
 PTSTATIVVH VEDVNEAPVF VPSKVNVEVQ EGIPTGEPVC VYTAEDPKKE NQKISYRILR 480
 DPAGWLANDP DSGQVTAAGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLTLID 540
 VNDHGPVEEP RQITICNQSP VRHVLNITDK DLSPHSTPFQ AQLTDDSDIY WTAENVNEED 600
 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILFVL 660
 GAVLALLFL LVLLLLVRKK RKIKEPLLLP EDDTRDNVYF YGEGGGGEED QDYDITQLHR 720
 GLEARPEVVL RNDVAPTIIIP TPMYRPRPAN PDBIGNFIE NLKAANTDPT APPYDTLLVF 780
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKLA DMYGGGEDD

A146 DNA SEQUENCE:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Nucleic Acid Accession #: NM_003318
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GGAAATCCTT TTTTCTTTT TTTGAGATGG AGTTTCACCTC TTGTTGCCA GGCTGGAGTG 60
 CAATGGCACA ATCTCAGCTT ACTGCAACCT CCGCTCCCGG GGTTCAGCGG ATTCCTCTGC 120
 CTGAGCCTCT CAAGTAGCTG GGATTACAGG CATGTGCCAC CACCCCTGGC TAACTAATTT 180
 CTTTCTATT TAGTAGAGAT GGGGTTTAC CATGTTGGTC AGGCTGGTCT TGAACCTCTG 240
 ACCTCAGGTG ATCCACTGCG CTGGGCTCC CAAAGTGCTA GGATTACAGC CGTGAAACTG 300
 TGCTGGCTG ATCTCTTTT TGTGTGTGA TTTTGAAC AGGGTCTCCG TTGTTCCGCC 360
 AGGCTGGAGT GCAGTGGTGC GATCTTGGCT CACTATAACC TCCACCTCCT GGTTCACAGT 420
 GATCCTCCCA CTTTAGCTCT CTGAGTAGCT GTGATTACAG GCGTGACCA CCACACCCGG 480
 CTAAATTTTG TATTTTATT AGAGACAGGG TTTCAACATG TTGGCCAGGC GTTCTCTCAA 540
 CTCTGGACT CAAGGATCC GCCTGCTCC ACTTCCCAA GTCCCGAGAT TACAGGTGTG 600
 AGTCACATG CTCACCTTA TAATCTTAA GTCATTTTT CTGCTCCATT TCTTCTTAG 660
 GGTCTCTACA ACAAATCTGC ATTAGGCGGT ACAATAATCC TTAACCTCAT GATTACAAA 720
 AGGAAGATGA AGTGATTCAT GATTAGAAA GGGGAAGTAG TAAGCCCACT GCACACTCCT 780
 GGATGATGAT CCTAAATCCA GATACAGTAA AAATGGGGTA TGGGAAGGTA GAATACAAAA 840
 TTTGGTTTAA ATTAATATCT TAAATATCTA AAAACATTT TGGATACATT GTTGATGTGA 900
 ATGTAAGACT GTACAGACTT CTTAGAAAAC AGTTTGGGTT CCATCTTTTC ATTTCCCGAG 960
 TGCAGTTTTG TGTAGAAATG GAATCCGAGG ATTTAAGTGG CAGAGAATTG ACAATTGATT 1020
 CCATAATGAA CAAAGTGAGA GACATTAAAA ATAAGTTTAA AAATGAAGAC CTACTGATG 1080
 AACTAAGCTT GGAATAAAAT TCTGCTGATA CTACAGATAA CTCGGGAAC GTTAACCAAA 1140
 TTATGATGAT GGCAAAACAC CCAGAGGACT GGTGAGTTT GTTGCTCAA CTAGAGAAAA 1200
 ACAGTGTTC GCTAAGTGAT GCTCTTTTAA ATAAATGAT TGGTGGTTAC AGTCAAGCAA 1260
 TTGAAGCGCT TCCCCAGAT AAATATGGCC AAAATGAGAG TTTTGCTAGA ATTCAGTGA 1320
 GATTGCTGTA ATTAAGAGCT ATTCAAGAGC CAGATGATGC ACGTGACTAC TTTCAATGG 1380
 CCAGAGCAAA CTGCAAGAAA TTTGCTTTTG TTCATATATC TTTTGCACAA TTTGAAGTGT 1440
 CACAAGGTAA TGTCAAAAAA AGTAAACAC TTCCTCAAAA AGCTGTAGAA CGTGAGCAG 1500
 TACCACTAGA AATGCTGGAA ATTGCCCTGC GGAATTTAAA CCTCCAAAAA AAGCAGCTGC 1560
 TTTCAAGAGA GGAAGAGAAAG AATTATACAG CATCTACGGT ATTAAGTACC CAAGATCAT 1620
 TTTCCGGTTC ACTTGGGCAT TTACAGAAATA GGAACACAG TTGTGATTCC AGAGGACAGA 1680
 CTACTAAAGC CAGGTTTTTA TATGGAGAGA ACATGCCACC ACAAGATGCA GAAATAGGTT 1740
 ACCGGAATTC ATTGAGACAA ACTAACAAAA CTAACAGTCT ATGCCCATTT GGAAGAGTCC 1800
 CAGTTAACCT TCTAAATAGC CCAGATTGTG ATGTGAAGAC AGATGATTCA GTTGACTCTT 1860
 GTTTATGAA AAGACAAACC TCTAGATCAG AATGCCGAGA TTTGTTGTG CCTGGATCTA 1920
 TAACCAAGTG AAATGATTCC TGTGAATTAA GAAATTTAAA GTCTGTTCAA AATAGTCATT 1980
 TCAAGGAACC TCTGGTCTCA GATGAAAAGA GTTCTGAAC TATTATTACT GATTCAATAA 2040
 CCCTGAAGAA TAAACCGGAA TCAAGTCTTC TAGCTAAATT AGAAGAACT AAAGAGTATC 2100
 AAGAACCAGA GGTTCAGAG AGTAACCCAGA AACAGTGGCA AGCTAAGAGA AAGTCAGAGT 2160
 GTATTAAACA GAATCTGCT GCATCTTCAA ATCACTGGCA GATTCCGGAG TTAGCCCGAA 2220
 AAGTTAATAC AGAGCAGAAA CATACCATT TTGAGCAACC TGTCTTTTCA GTTTCAAAAA 2280
 AGTCACCAAC AATATCAACA TCTAAATGGT TTGACCCAAA ATCTATTGTG AAGACACCAA 2340

WO 03/042661

GCAGCAATAC CTGGATGAT TACATGAGCT GTTTTAGAAC TCCAGTTGTA AAGAATGACT 2400
 TTCCACCTGC TTGTGAGTTG TCAACACCTT ATGGCCAACC TGCCGTGTTT CAGCAGCAAC 2460
 AGCATCAAT ACTTGCCACT CCACTTCAA ATTTACAGGT TTTAGCATCT TCTTCAGCAA 2520
 ATGAATGCAT TTGGTTTAAA GGAAGAATTT ATTCCATATT AAAGCAGATA GGAAGTGGAG 2580
 GTTCAAGCAA GGTATTTTCT GTGTTAAATG AAAAGAAACA GATATATGCT ATAAATATG 2640
 TGAACCTAGA AGAAGCAGAT AACCAAACCT TTGATAGTTA CCGGAACGAA ATAGCTTATT 2700
 ACCAGTACAT CTACATGGTA ATGGAGTGTG GAAATATTGA TCTTAATAGT TGGCTTAAAA 2760
 AGAAAAATC CATGTATCCA TGGGAACGCA AGAGTTACTG GAAAAATATG TTAGAGGCAG 2820
 TTCACCAAT CCATCAACAT GGCATTGTTT ACAGTGTCTT TAAACCAAGT AACTTTCTGA 2880
 TAGTTGATGG AATGCTAAAG CTAATTGATT TTGGGATGTC AAACCAATG CAACCAAGATA 2940
 CAACAAGTGT TGTAAAGAT TCTCAGTTG GCACAGTTAA TTATATGCCA CCAGAAGCAA 3000
 TCAAGATAT GTCTTCTCC AGAGAGAATG GGAATCTAA GTCAAAGATA AGCCCCAAAA 3060
 GTGATGTTG GTCCTTAGGA TGTATTTTGT ACTATATGAC TTACGGGAAA ACACCATTTT 3120
 AGCAGATAAT TAATCAGATT TCTAAATTAC ATGCCATAAT TGATCCTAAT CATGAAATTG 3180
 AATTTCCTGA AATTCAGAG AAAGATCTTC AAGATGTGTT AAAGTGTGTT TAAAAAGGG 3240
 ACCCAAAACA GAGGATATCC ATTCTGAGC TCCTGGCTCA TCCATATGTT CAAATTCAAA 3300
 CTCATCCAGT TAACCAAAATG GCCAAGGAAA CCACTGAAGA AATGAAATAT GTTCTGGGCC 3360
 AACTGTGTTG TCTGAATTCT CCTAACTCCA TTTTGAAAGC TGCTAAAACT TTATATGAAC 3420
 ACTATAGTGG TGGTGAAAGT CATAATTCTT CATCTCCAA GACTTTTGAA AAAAAAGGG 3480
 GAAAAAATG ATTTGCAGTT ATTCTGAATG TCAGATAGGA GGTATAAAT ATATTGGACT 3540
 GTTATATCTT TGAATCCCTG TGGAAATCTA CATTTGAAGA CAACATCACT CTGAAGTGT 3600
 ATCAGCAAAA AAAATTCAGT GAGATTATCT TTAAGAGAAA ACTGTAAAA TAGCAACCAC 3660
 TTATGGCACT GTATATATTG TAGACTTGT TTCTCTGTTT TATGCTCTG TGTAATCTAC 3720
 TTAACATCTT TTTACTCTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAAGTTT 3780
 TAAATAAAGT TTTGTGGCTA AATGA 3840

A147 Protein sequence:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Protein Accession #: NP_003309
 Signal sequence: none found
 Transmembrane domains: none found
 Protein Kinase Domain: 510-775
 Cellular Localization: cytoplasmic and nuclear

1 11 21 31 41 51
 MNKVRDIKKN FKNEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPEDWL SLLKLEKNS 60
 VPLSDALLAK LIGRYSAIE ALPPDKYQON ESFARIQVRF AELKAIQEPD DARDYFQMAR 120
 ANCKKFAFVH ISFAQFELSQ GNVKSKQLL QKAVERGAVP LEMLEIALRN LNLQKKLLS 180
 EEEKKNSLAS TVLTAQESFS GSLGHLQNRN NSCDSRGQRT KARFLYGENM PPQDAEIGYR 240
 NSLRQTNKTK QSCPFGRPV NLLNSPDCIV KTDDSVVPCF MKRQTSRSEC RDLVVPKSKP 300
 SGNDSCLELN LKSVQNSHF EPLVSDKSS ELIITDSITL KNTKESLLA KLEETKEYQE 360
 PEVPESNQKQ WQARKRSECI NQNPAASSNH WQIPELARKV NTEQKHTTPE QPVFSVSKQS 420
 PPISTSKWFD PKSICKTPSS NTLDDYMSCF RTPVVKNDFF PACQLSTPYG QPACFQQQOH 480
 QILATPLQNL QVLASSSANE CISVKGRIYS ILKQIGSGGS SKVFQVINEK KQIYAIKVVN 540
 LEEADNQTLN SYRNEIAYLN KLQGHSDKII RLYDYBITDQ YIYMVMCEGN IDLNSWLKKK 600
 KSIDPWERKS YWKNMLEAVH TIHQHGIHVS DLKPFANFLIV DGMKLKIDFG IANQMOPDIT 660
 SVVKDSQVGT VNYMPPEAIK DMSSRENGK SKSKI SPKSD VMSLGCILYI MTKGTPFQQ 720
 IINQISKLHA IIDPNHRIEF PDIPEKDLQD VLKCLKRDV KQRISIPELL AHPYVQIQTH 780
 PVNQMARGT BEMKYVLGQL VGLNSPNSIL KAAKTLYEHY SGSESHNSSS SKTFEKKRGK 840
 K

A148 DNA SEQUENCE

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
 Unigene number: Hs.258583
 Probeset Accession #: NM_012152
 Nucleic Acid Accession #: NM_012152
 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CTTCTTAAA TTTCTTTCTA GGAATGTCAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60
 GACAAGCACA TGGACTTTT TTATAATAGG AGCAACACTG ATACTGTGCA TGACTGGACA 120
 GGAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTTT TCTGCCTGTT TATTTTTTTT 180
 TCTAATTCTC TGGTCATGCG GGCAGTGATC AAAAACAGAA AATTTCATTT CCGCTTCTAC 240
 TACCTGTTGG CTAATTAGC TGCTGCGGAT TTCTTCTGCT GAATTGCCTA TGTATTCTCTG 300
 ATGTTTAAAC CAGGCCAGT TTCAAAAAC TTGACTGTCA ACCGCTGTTT TCTCCGTCAG 360
 GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCGTGGAG 420
 AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA 480
 CTGCTCATTT TGCTGTCTG GGCATGCGCC ATTTTATGTT GGGCGGTCCC CACACTGGGC 540
 TGAATTTGCC TCTGCAACAT CTCTGCTGTC TCTTCCCTGG CCCCATTTA CAGCAGGAGT 600
 TACCTTGTTT TCTGGACAGT GTCCAACTC ATGGCCTTCC TCATCATGTT TGTGGGTGAC 660
 CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAACGTCT TGTCTCGCA TACAAGTGGG 720
 TCCATCAGCC GCCGAGGAC ACCCATGAAG CTAATGAAGA CGGTATGAC TGTCTTAGGG 780
 GCGTTTGGG TATGCTGGAC CCGGGGCTG GTGGTCTGTC TCCTGACGG CCTGAAGTGC 840
 AGCAGTGTG GCGTGCAGCA TGTGAAAAGG TGGTCTCTGC TGCTGCGCT GCTCAACTCC 900
 GCGTGAACC CCATCATCTA CTCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG 960
 ATGATCTGCT GCTTCTCTCA GGAGAACCA GAGAGGCGTC CCTCTCGCAT CCGCTCCACA 1020
 GTCTCAGCA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080

GTCTGCAATA AAAGCACTTC CTAAACTCTG GATGCCTCTC GGGCCACCCA GGTGATGACT 1140
 GTCTTAGG

- 5 **A149 Protein sequence:**
 Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
 Unigene number: Hs.258583
 ProbeSet Accession #: NM_012152
 Protein Accession #: NP_036284
 10 Signal sequence: none found
 Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295
 Cellular Localization: plasma membrane

15 1 11 21 31 41 51
 | | | | | |
 MNECHYDKHM DFFYNRSNTD TVDDWTGTLK VIVLCVGTFF CLFIFFSNLS VIAAVIKNRK 60
 FHPPFYLLA NLAAADFPAG IAYVPLMFNT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL 120
 20 LVIAVERHMS IMRMVHSNL TKGRVTLIL LVNAIAIFMG AVPTLGWNL CNISACSSLA 180
 PIYSRSYLVF WTVSNLMAFL IMVVYLRIY VYVKRKTIVL SPHTSGSISR RRTPMKIMKT 240
 VMTVLGAFVW CWTPLGVLL LDGLNCRQCG VQHVKRWFLL LALLNSVVPN IISYKDEDM 300
 YGTMKGMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

25 Prostate

- A150 DNA SEQUENCE**
 Gene name: ESTs
 Unigene number: Hs.293616
 30 ProbeSet Accession #: AW043782
 Nucleic Acid Accession #: none found
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

35 1 11 21 31 41 51
 | | | | | |
 AGCAACGACG CGGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GGGCGCTGTG 60
 CCTGCTGCTG AGCAGCGCGG CGSAGAGCCA GCTGCTCCCC GGGAACTACT TCACCAATGA 120
 40 GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCAATCCCG GCGCCTGGCA 180
 GTGTGACGGG CTGCGTGAAT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
 GTCGAAATGT GGGCCAACTT TCTTCCCCTG TGCCAGCGGC ATCCATTGCA TCATTGGTGG 300
 CTTCCGGTGC AATGGGTGTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
 AAACCCCTCTG CTTTGTCTCA CGGCCCGCTA CCACTGCAAG AACGGCCTCT GTATTGACAA 420
 GAGCTTTCAT TCGATGAGAG AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
 45 AAGTTCTCAA GAACCGGCA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540
 TTACCCGAGC ATCAGCTATG CCATCATCGG CAGCTCGTTC ATTTTGTGTC TGGTGGTGGC 600
 CCTGCTGSCA CTGGCTTTCG ACCACCAAGC GAAGCGGAAC AAACCTCATGA CGCTGCCCCG 660
 GCACCGGCTG CAGCAGCGTG TGCTGCTGTC CCGCCTGGTG GTCCCTGGAC ACCCCACCA 720
 CTGCAACGTC ACCTACAAGC TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780
 50 GAATGCGTGG GAAGTAGGCT CCCCACCTCT CTACTCCGAG GCCTTGTCTG ACCAGAGGCC 840
 TGCGTGGTAT GACCTTCTTC CACCGCCCTA CTCTTCTGAC ACAGGAATCT TGAACCAAGC 900
 CGACCTTGCC CCCTACCGCT CCGGCTCCGG GAGTGCCCAAC AGTGCCAGCT CCCAGGAGC 960
 CAGCAGGCTG CTGAGCGTGG AAGACACCA CACAGCCCGG GGGCAGCCTG GCCCCAGGA 1020
 GGGCACTGCT GAGCCGAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAGG TATAAGTCCC 1080
 55 AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTC TAACAATTG 1140
 TGCTCATGGG AAGCTCTTTA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200
 AACTATCTCT GCATTCCCTT CCTCCCCAGC ACTTCAGAGA TGTTTTCTG GGTCTCTAGT 1260
 TGACATGATC TGTGTGTGCT CTTTCTGTC AGGTCACTCT TCCCTTGGGA CCGAGATCA 1320
 CACCCTCATT TTTCACATTA TTCTGTTTCT GTTGGAGAGA CAGCATATAA AACAGTATTG 1380
 60 AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGAGA 1440
 CGCTGGAGCC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTTAG 1500
 ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCAACCCCC CAAAAAATT CCATTGTAGC 1560
 ATCAAAACCT GCTTTCACCA ATCCTATTG ATGCCCCAG TTCAGCAGAG TCAGTGGCCA 1620
 AAGAAAACCT TGGACGTGAG TAACACCTT CAGCAGTCCG AACGTTATT TGGTTTGTG 1680
 65 AAGGACTCTG AAACCATCTA CCCTGTATAA ATTCTGGCTT TAGAAATTTG CCCAAGAAATG 1740
 CTCATTCTGA GAGCTTCTCT CAGCAGCATA TATCATCAGC CTCATCTTAA AATAGGCAGG 1800
 GAGCCCTTCC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC 1860
 TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCAAC CTCOCAGCTG 1920
 70 ACCTGCCCGT AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT 1980
 GTATGTCCCT GTGGCCCAAC CCCAGCCTGT CTGTCTCAIT CATGCAGCCT CAACACTGGC 2040
 TCCAAAGTT CCCTTAACAC TTGCAAGTCT CTTTATACCT GTGCATTGG ACTTAGGGAC 2100
 ACTGTCTTCT ATCACAAGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160
 CTGCACTGTG CAGCTCTCTT TTCCCAAGGT CCAATAACCA GCACCTCTAG TTAGAGTTAG 2220
 75 GGTCAAGGTC AGGCCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGCAAG 2280
 AGACAATTG GAGTCAAGAT TTTCCATTG GATCTATTTT AAATCTTTTA GAAATGCATT 2340
 TGAAACAGTT TGTTTGTTTT TTCCCTTCTA GTTAAGGGAC TATTATATG TGTATAGGAA 2400
 AGCTGTCTCT TTTTGTGTTT TTCTTTAAAC AAGGTCCAAA GAAAGATGCA AAGGAGATC 2460
 ACACCCCTGC CCGCTGAGC CCGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520
 80 ACATTGTGTC ATTGTGTCAC TTTGAGTTA TATTATATCA AGTTCITGAA GGAAGCAGAA 2580
 AGAGGGACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTTTT 2640
 TTCTCTGTGT CCACTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAACGTT 2700
 AGGTGTTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATAGGAA CCAGGTAGAG 2760
 CCACTCGGG CAGCTGTCA CATTTCAGAA CTTCCTTCCG CAGCTGAAGA AATGTTCACT 2820

AACCTGTTTG ACGCTAATTA AACAGAGGCC TGCAGGAAGT GGGGCTAAAG TGGCATTTCAG 2880
 TGATCCTGTT CTGTAGACTT TTCTTCTTT TTTAACCCTA ATCCAAAGGA TGTTCAGAA 2940
 AAGCTAGCCA CTGGTATTTT GTTTTGTGTT AAAAAAAGAA AAGAAAGAAA 3000
 AACGGAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
 5 CTGAGTAATC CAATAAGAA CTTTGTATGA CAGCCAGAA GTGTAGAAC TCTGGCTGAA 3120
 CATTTCATCT CCGTGTAGTC AGAAGGGCTT TATTTCTCCC TTGTATGGG CCCTTCTTC 3180
 TTTCTGGTGC TCTGGAAGTT GTTAGAGGA AAGAATTCTA ATTTAATTA ATTGCGCAGT 3240
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCACTCTAG GAAAAACAAA TGGTTTATG 3300
 10 AGATAAGGGA TGCCTACTAA TGCTTTTATA AAACAAACAG GCACATTTT ATTATAGATT 3360
 TGATTTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAGC GGCAGGTTT 3420
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480
 TTTTAACTC ATTCACACCA GGAAGCTTTT TTATACATTG CCTAAATCTA GSCCAACAG 3540
 AAAATAGTCT CATCTCTTTT TTTCTCAAT GAGATCCGTG TTTTATTTA GCATTAAAT 3600
 15 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660
 TTTTAAAAA ATGCACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAACTG 3720
 GAAAGGTTG GTGTCGTGTC TTTTGTGTT TTGGTTAGGC TTGGTTTGT TTTTAAATT 3780
 TTATACTTC TAATAAATTT GCAGTTTCAT TCTTCTGTT TGTGCAAAWG GMMCTAMARM 3840
 AAMMAAAAC AWYTTTGGGG GGGCTTGGGC CTCGAAAAA GTTTTAAACA CCACCTCGGG 3900
 TGGGCGGGG GGGCCACGT AGGTACGGCG ACCACGCGG CCCAAACGG ACCCCAGAAG 3960
 20 GAAACCTGG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACGGCGCGG 4020
 GGAAACCGCA GAGTGTTCG TAAACACAC CCGAAGAGAG AACTCAGAAG CACACAGCG 4080
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

25 A151 Protein sequence:
 Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Protein Accession #: none found
 30 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

35
 1 11 21 31 41 51
 | | | | |
 MWLLGPLCLL LSSAAESQLL PGNNFTNECN IPGNFMCNSG RCIPGAWQCD GLPDCFDKSD 60
 40 EKECPKAKSK CGPTFFPCAS GIHCCIIGRFR CNGFEDCPDG SDBENCTANP LLCSTARYHC 120
 KNLGCLDKSF ICDGQNNQCD NSDEESCESS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180
 VIFVLVALL ALVLHQRKR NMLTLFVER LQHPVLLSRL VVLDHPHCN VTYNVNNGIQ 240
 YVASQAEQNA SEVGSPPSYS EALLDQRPW YDLPPPPYS DTESLNQADL PPRSRSGSA 300
 NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTEEV

45 A152 DNA SEQUENCE
 Gene name: Transmembrane protease, serine 2 (TMPRSS2)
 Unigene number: Hs.105807
 Probeset Accession #: T48536
 50 Nucleic Acid Accession #: NM_005656.1
 Coding sequence: 57-1535 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
 | | | | |
 GTCATATGTA ACATTCCAGA TACCTATCAT TACTGATGTC TGTGATAAC AGCAAGATGG 60
 CTTTGAATC AGGGTACCA CCAGCTATTG GACCTTACTA TGAATAACAT GGTATACCAAC 120
 CGGAAACCC CTATCCCGCA CAGCCCACTG TGGTCCCGAC TGTCTACGAG GTGCATCCGG 180
 CTCAGTACTA CCGCTCCGCC GTGCCCACTG AGGCCCGAG GGTCTCTGAC CAGGCTTCCA 240
 60 ACOCCTGCTG CTGCACGCGC CCCAAATCCC CATCCGGGAC AGTGTGACCT TCAAGACTA 300
 AGAAAGCACT GTGCATCACC TTGACCTCGG GGACCTTCTT CGTGGGAGCT GCGCTGGCGG 360
 CTGGCCTACT CTGGAAGTTC ATGGGCAGCA AGTGCTCCAA CTCTGGGATA GAGTGCAGCT 420
 CCTCAGGTAC CTGCATCAAC CCTCTAACT GGTGTGATGG CGTGTACAC TGCCCGGGCG 480
 GGGAGGACGA GAATCGGTGT GTTCGCTCT ACAGACCAAA CTTCATCCTT CAGATGTACT 540
 CATCTCAGAG GAAGTCTGTG CACCCTGTGT GCCAAGACGA CTGGAACGAG AACTACGGGC 600
 65 GGGCGGCTG CAGGACATG GGCTATAAGA ATAAATTTTA CTCTAGCCAA GGAATAGTGG 660
 ATGACAGCGG ATCCACGAGC TTTATGAAC TGAACACAG TGCCGGCAAT GTCGATATCT 720
 ATAAAAAAT GTACCACTGT GATGCCTGTT CTTCAAAAGC AGTGGTTTCT TTACGCTGTT 780
 TAGCCTGGGG GTTCAACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGGC GGTGAGAGCG 840
 CGCTCCCGGG GGCCTGGCCC TGGCAGGTCA GCCTGCACGT CCAGAAGCTC CAGTGTGCG 900
 70 GAGGCTCCAT CATCACCCCC GAGTGGATCG TGACAGCCGC CCAGTGGTG GAAAAACCTC 960
 TTAACATCC ATGGCATTTG ACGGCATTTT CGGGGATTTT GAGACATCT TTCATGTTCT 1020
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 AGAACATGA CATTCGCTG ATGAAGCTGC AGAAGCTCT GACTTTCAAC GACCTAGTGA 1140
 AACCACTGTG TCTGCCAAC CCAGGCATGA TGCTGCAGCC AGAACAGCTC TGTGGAATTT 1200
 75 CCGGTGGGG GGCACCGAG GAGAAAGGA AGACCTCAGA AGTGTGAAC GCTGCCAAGG 1260
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 CAGCATGAT CTGTGCGGCG TTCTGTCAGG GGAACGTCGA TTCTTGCCAG GGTGACAGTG 1380
 GAGGCTCTCT GGTCACTTCG AACCAACAATA TCTGGTGGCT GATAGGGGAT ACAAGCTGGG 1440
 80 GTTCGCTG TGCCAAAGCT TACAGACAG GAGTGTACCG GAATGTGATG GTATTCAACG 1500
 ACTGGATTTA TCGACAATG AAGGCAACCG GCTAATCCAC ATGGTCTTCG TCCTTGAAGT 1560
 CGTTTACAA GAAACCAATG GGGCTGGTTT TGCTTCCCGG TGCTATGATT ACTCTAGAG 1620
 ATGATTGAGA GGTCACTTCA TTTTATTAA ACAGTGAAC TGTCTGGCTT TGGCACTCTC 1680
 TGCCATACTG TGCAGGCTGC AGTGGCTCCC CTGCCAGCC TGCTCTCCCT AACCCCTGT 1740

COGCAAGGGG TGATGGCCGG CTGGTTGTGG GCACTGGCCG TCAATTGTGG AAGGAAGAGG 1800
 GTTGAGAGCT GCCCCATTG AGATCTTCCT GCTGAGTCCT TTCCAGGGGC CAATTTTGA 1860
 TGAGCATGGA GCTGTCACTT CTCAGCTGCT GGATGACTTG AGATGAAAAA GGAGAGACAT 1920
 5 GGAAGGGGAG ACAGCCAGST GCCACCTGCA GCGGCTGCCC TCTGGGGCCA CTGGTAGTG 1980
 TCCCCAGCCT ACTTCACAG GGGATTTTGC TGATGGGTTT TTAGAGCCTT AGCAGCCCTG 2040
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 AAGGGGAACA GAAACATTTT TGTTCTTATG GGGTGAGAAAT ATAGACAGTG CCCTTGGTGC 2160
 GAGGGAAGCA ATTGAAAGG AACTTGCCTT GAGCACTCCT GGTGAGGTG TCCACCTGCA 2220
 10 CATTGGGTGG GGTCTCTGGG AGGGAGACTC AGCCTTCCTC CTCATCCTCC CTGACCTGTC 2280
 TCCTAGCACC CTGGAGAGTG AATGCCCTT GGTCCCTGGC AGGGCGCCAA GTTTGGCACC 2340
 ATGTGGCCCT CTTCAGGCTT GATAGTCATT GGAAATTGAG GTCCATGGGG GAAATCAAGG 2400
 ATGTCAGTT TAAGGTACAC TGTTTCCATG TTATGTTTCT ACACATTGAT GGTGGTGACC 2460
 CTGAGTTCAA AGCCATCTT

A153 Protein sequence:

Gene name: Transmembrane protease, serine 2 (TMPRSS2)
 Unigene number: Hs.105807
 20 Probeset Accession #: T48536
 Protein Accession #: NP_005647.1
 Signal sequence: none found
 Transmembrane domains: 85-107
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MALNSGSPFA IQPIYENHGY QPENFYPAQP TVVPIVYEVH PAQYYPSPVP QYAPRVLTQA 60
 30 SNPVVCTQPK SPSGTVCSTK TKKALCITLT LGTFLVGAAL AAGLWKPFG SKCSNSGIEC 120
 DSSGTCINPS NWCDDVSHCP GGEDENRCVR LYGNPFLQMQ YSSQRKSWHP VCQDDWNNY 180
 GRAACRDMY KNNFYSSQGI VDDSGSTSPM KLNTSAGNVD IYKLYHSDA CSHKAVVSLR 240
 CLACGVNLNS SROSRIVGGE SALPGAMPWQ VSLHVQNVHV CGGSIITPEW IVTAACHVEK 300
 PLANPWHMTA FAGILRQSPM FYGAGYQVQK VISHPNYDSK TKNDIALMK LQKPLTFNDL 360
 35 VKPVCPLNPG MMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLLIETQRC NSRYVYDNL 420
 TPAMICAGFL QGNVDSQGD SGGPLVTSNN NIWNLIGDTS WSGSCAKAYR PGVYGNVMPV 480
 TDWYRQMKK NG

A154 DNA SEQUENCE

Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039
 40 Unigene number: Hs.129179
 Probeset Accession #: AI694767
 Nucleic Acid Accession #: AI694767
 Coding sequence: 130-1086 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CAGAGAGGCT GTATTTCAGT GCAGCCTGCC AGACCTCTTC TGGAGGAAGA CTGGACAAAG 60
 GGGGTACACG ATTCTCTCCA TACGGTTGAG CCTCTACCTG CCTGGTGCTG GTCACAGTTC 120
 50 AGCTTCTTCA TGATGGTGGG TCCCAATGGC AATGAATCCA GTGCTACATA CTTCATCCTA 180
 ATAGGCCTCC CTGGTTTAGA AGAGGCTCAG TTCTGGTTGG CCTTCCCATT GTGCTCCCTC 240
 TACCTTATTG CTGTGCTAGG TAACCTGACA ATCATCTACA TTGTGCGGAG TGAGCAGCAG 300
 CTGCATGAGC CCATGTATAT ATTCTTTGTC ATGCTTTTCA GCATTGACAT CCTCATCTCC 360
 ACCTCATCCA TGCCCAAAAT GCTGGCCATC TTCTGGTTCA ATTCCACTAC CATCCAGTTC 420
 55 GATGCTGTGC TGCTACAGAT GTTTGCCATC CACTCCTTAT CTGGCATGGA ATCCACAGTG 480
 CTGCTGGCCA TGGCTTTTGA CCGCTATGTG GCCATCTGTC ACCCACTGGG CCATGCCACA 540
 GTACTTACGT TGCTCTGGTG CACCAAAATT GGTGTGGCTG CTGTGTGGTG GGGGGCTGCA 600
 CTGATGGCAC CCTCTCCTGT CTTCATCAAG CAGCTGCCCT TCTGCGCTCA CAATATCCTT 660
 TCCCATTCCT ACTGCTTACA CCAAGATGTC ATGAAGCTGG CCTGTGATGA TATCCGGGTC 720
 60 AATGTGCTCT ATGGCCCTAT CGTCATCATC TCCGCCATTG GCTGAGACTC ACTTCTCATC 780
 TCCTTCTCAT ATCTGCTTAT TCTTAAGACT GTGTGGGGCT TGACACGTGA AGCCAGGCC 840
 AAGGCATTGG GCACTTGGGT CTCTCATGTG TGTGCTGTGT TCATATTCTA TGTAACCTTC 900
 AITGGATTGT CCATGGTGCA TCGCTTAGC AAGGGGGGTG ACTCTCCACT GCCCGTCACT 960
 TTGGCCAATA TCTATCTGCT GGTTCCTCCT GTGCTCAACC CAATTGTCTA TGGAGTGAAG 1020
 65 ACAAGGAGGA TTGACAGCGG CATCTCTGGA CTCTTCCATG TGGCCACACA GCCTTCAGAG 1080
 CCTAGGTTGT CAGTGATCAA ACTTCTTTTC CATTGAGAGT CCTCTGATTC AGATTTTAAT 1140
 GTTAACATTT TGGGAAGCAG TATTCAGAAA AAAAAATTCCT TTAATAAAAA TACAACCTAG 1200
 ATCCCTCAAA TATGAACTG GTTGGGGAAT CTCCATTTT TCAATATTAT TTTCTCTTT 1260
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 70 TTTTCATTTT ACCATGCAGT CCAATCTAA ACTGCTTCTA CTGATGTTT ACAGCATTCT 1380
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 ACTCCCAACC ACATTGGATC TCAGAAAAAT ACTGTCTTCA AAATGACTTC TACAGAGAAG 1560
 AAATATTTT TCCTCTGGAC ACTAGCACTT AAGGGGAAGA TTGGAAGTAA AGCCTTGAAA 1620
 75 AGAGTACATT TACCTACGTT AATGAAAGTT GACACACTGT TCTGAGAGTT TTCACAGCAT 1680
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 TTAGTACCTC CATGTAGACC ATGGGAAAAAT TGATGTTTCA TGGGGATCAG TGAATTTAAAT 1800
 GGGGTCAAAA AAGTATAAAA ATTAATAAAA AAAGACTTCA TGCCCAATCT CATATGATGT 1860
 GGAAGAAGCT TTAAGAGAGC CAACAGGATA GTGGGTTAGA GATTTCAGAG GTCTTACATT 1920
 80 TTCTARAGGA GGTATTTAAT TTCTTCTCAC TCATCCAGTG TTGTATTTAG GAATTTCTGT 1980
 GCAACAGAAC TCAATGGCTT AATCCCACTA GCTATTGCTT ATTGTCTGCT TCCAATTGCC 2040
 AATTACCTGT GTCTTGGGAG AAGTGATTTC TAGGTTCACC ATTATGGAAG ATTCTTATTC 2100
 AGAAAGCTGT CATAGGCTT ATAGCAAGTT ATTTATTTT AAAAGTTCCA TAGGTGTTTC 2160
 TGATAGGCAG TGAGGTTAGG GAGCCACCAG TTATGATGGG AAGTATGGA TGGCAGGTGT 2220
 TGAAGATAAC ATTGGCCTTT TGAATGTGAC TGTAGCTGG AAAAGTGAGG AATCTTCAGG 2280

5
10
15

ACCATGCTTT ATTGGGGCT TTGTGCAGTA TGGAACAGGG ACTTTGAGAC CGGGAAGCA 2340
ATCTGACTTA GGCATGGGAA TCAGGCATTT TTGCTTCTGA GGGGCTATTA CCAAGGGTTA 2400
ATAGGTTTCA TCTTCAACAG GATATGACAA CAGTCTTAAC CAAGAACTC AAATTACATA 2460
TACTAAACA TGTGATCATA TATGTGTAA GTTTCATTTT CTTTTCAAT CCTCAGGTTT 2520
CCTGATATGG ATTCCTATNA CATGCTTTCA TCOCCTTTG TAATGGATAT CATATTGGGA 2580
AATGCCTATT TAATACITGT ATTGCTGCT GGACTGTAAG CCCATGAGGG CACTGTTTAT 2640
TATTGAATGT CATCTCTGT CATCATTGAC TGCTCTTGC TCATCATTTGA ATCCCCCAGC 2700
AAAGTGCCTA GAACATAATA GTGCTTATGC TTGACACGG TTATTTTICA TCAAACTGA 2760
TTCTTCTGT GCTGAACACA TAGCCAGGCA ATTTCCAGC CTCTTTTGA TTGGGTATTA 2820
TTAAATTTTA GCCATTACTT CCAATGTGAG TGGAGTGAC ATGTGCAATT TTTATACCTG 2880
GCTCATAAAA CCTCCCATG TGCAGCCTTT CATGTTGACA TTAATGTGA CTGGGAAGC 2940
TATGTGTAC ACAGAGTTAA TTAACNGAA AGGCTTGNA ATTTTGTGN AANNAACTG 3000
TGGCNGAG GCCNCAACC CTTTTNNNA ATTGGCAAN NTCCCACTT GTANTTGGT 3060
AAGGAGGCCA GTTGGATAAG TGAAAATAA AGTACTATG TGTG

A155 PROTEIN SEQUENCE

Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039
Unigene number: Hs.129179
Protein Accession #: not available
Signal sequence: none found
Pfam domain: 7tm_1 [43-293]
Transmembrane domains: 29-51, 57-79, 82-104, 203-225, 239-261, 273-295
Cellular Localization: not determined

30
35

1 11 21 31 41 51
MVDPNGNESS ATYFILIGLP GLEEAQFWLA FPLCSLYLIA VLGNLTIIYI VRTEHSLHEP 60
MYIFLCMLSG IDILISTSSM PKMLAIFWEN STTIQFDACL LQMPAIHSLS GMBSTVLLAM 120
AFDRVAICH PLRHATVLT PLVTKIGVAA VVRGAALMAP LPVFIKQLPF CRSNILSHSY 180
CLHQDVMLKA CDDIRNVVY GLIVIIISAIG LDSLLISFSY LLILKTVLGL TREAQAKAFG 240
TCVSHVCAVF IFYVPIGLS MVHRFSKRDR SPLPVILANI YLLVPPVLNP IYGVKTKKEI 300
RQRILRLPHV ATHASEP

A156 DNA SEQUENCE

Gene name: vasoactive intestinal peptide receptor 1
Unigene number: Hs.198726
Probeset Accession #: X77777
Nucleic Acid Accession #: NM_004624.1
Coding sequence: 57-1544 (underlined sequences correspond to start and stop codons)

45
50
55
60
65
70
75
80

TCGAGCCTG CGAGGGTGG TGGTGGTGGT GGTGGTGGCC CTCGCCGCC TCATCATGC 60
CTCTCTCTCC TCTGCTCTCG CTCAGGCGCC TCGGTGGCGG TTGGTGGCG GTTACGGCGC 120
TGGTGGTGGC GCGCGCGCGG GCTGCTCTC GGGAGGCGCG GGGCGGATCT CCGCGCGCAG 180
GCGCGCGCGG CCGAGGTGGG GTGCGCGCGC GGAGGCGGCT CGAGCTTGTG GCTGCGCGCT 240
CGCTCTTGGG CTCTCTGCTG CAGGAGGAGT GTGACTATGT GCAGATGATC GAGGTGCAGC 300
ACAGCAGTG CCTGGAGGAG GCCCAGCTGG AGAATGAGAC AATAGGCTGC AGCAAGATGT 360
GGGACAACT CACTGCTCG CCAGCCACCC CTCGGGGCCA GGTAGTTGTC TTGGCCTGTC 420
CCCTCATCTT CAGCTCTTC TCCTCCATTC AAGGCCGCAA TGTAAGCCGC AGCTGCACCG 480
ACGAAGGCTG GACGCACCTG GAGCCTGGCC GGTACCCCAT TGCTGTGAG ACCTGCTACA 540
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CCATTGGCTA CGGCTGTCC CTCGCCACC TTCTGGTGGC CACAGCTATC CTGAGCCTGT 660
TCAGGAAGCT CCACTGCAGC CGGAATACA TCCACATGCA CCTCTTCATA TCCTTCATCC 720
TGAGGGCTGC CGCTGTCTC ATCAAGACT TGGCCCTCTT CGACAGCGGG GAGTGGAGCC 780
AGTGTCCGA GGGCTCGGTG GGTGTGAGG GCCTCTACCT GTACACCTG CTGCGCTCT 840
TGGCTAATCT TTCTGCTG CTGGTGGAG GCCTCTACCT GTACACCTG CTGCGCTCT 900
CCTTCTCTCT TGAGCGGAG TACTTCTGGG GGTACATACT CATCGGCTGG GGGGTACCCA 960
GCACATTAC CATGGTGGG ACCATCGCCA GGATCCATTT TGAGGATTAT GGTCTGCTCA 1020
GGTGTGGGA CACCATCAAC TCCTCACTGT GGTGGATCAT AAAGGGCCCC ATCTCTACCT 1080
CCATCTTGGT AAACITCATC CTGTTTATT GCATCATCCG AATCCTGCTT CAGAAACTGC 1140
GGCCCCCAGA TATCAGGAAG AGTGACAGCA GTCCATATCT AAGGCTAGCC AGGTCCACAC 1200
TCCTGCTGAT CCCCCTGTTT GGAGTACACT ACATCATGTT CGCCTTCTTT CCGGACAATT 1260
TTAAGCCTGA AGTGAAGATG GTCTTTGAGC TCGTGTGGG GTCTTTCCAG GGTTTTGTGG 1320
TGGCTATCCT CTACTGCTTC CTCAATGGTG AGGTGCAGGC GGAGCTGAGG CGGAAGTGGC 1380
GGCGCTGGCA CTGCGAGGC GTCTGGGCT GGAACCCCAA ATACCGGCAC CGTGGGGAG 1440
GCAGCAACGG CGCCAGTGC AGCAGCAGG TTTCATGCT GACCGCGCT AGCCAGGTG 1500
CCGCGCGCTC CTCAGCTTC CAAGCGAAG TCTCCCTGGT CTGACCAACA GGATCCAGC 1560
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GGCACTCTCT AGAAGACGCA GCGCTAGAGC CTGCTGGAG CGTTTCTAGC AAGTGAGAGA 1740
GATGGGAGCT CCTCTCTGG AGGATGAGG TGGAACTCAG TCATTAGACT CCTCTCCAA 1800
AGGCCCCCTA CGCCATCAA GGGCAAAAG TCTACATACT TTCACTGTA CTCTGCCCC 1860
TGCTGGCTCT TCTGCCAAT TGGAGGAAG CAACCGTGG ATCTCTAAC AACACTGGT 1920
TGACCTGAGG CGAGGAAGT TCTGCCCGG AAGGTCAACA GCACCAACAC CACGGTAGT 1980
CCTGAAATCT CCACTTGTCT GTCAAGTTC TTTGGGTAA GCATTACCA CTAGGCATT 2040
GACTGAAGAT GCAGCTCACT ACCCTATTCT CTCTTACGC TTAGTTATCA GCTTTTAAA 2100
GTGGGTATT CTGAGTTT TGTTTGGAGA GCACACCTAT CTAGTGGTT CCCCACGAA 2160
GTGAGCTGC CCTGGGTCA GTCTGGTGG AGGAAGTGC AACCAAGGA CTGAGGAGC 2220
CTGAGCCTC TGGGAATGA GAAGGCGCC ACCAGCGAT GCTAGTCTC GGAATAAGC 2280
TACTGTCTCT CCAAGTCTCA GTGGCTCAT CTGTCAAGT GGACTCTGC ACACAGCCA 2340
TTCTTATCTC TCTGTGCTGT GGAAGCAACA GGAATCAAGA GACTGCCCTC CTGTCCACC 2400
CACCTATGTG CCAACTGTTG TAACTAGGCT CAGAGATGTG CACCATGGG CTCTGACAGA 2460

5
AAGCAGATCC TCACCTCTGCT ACACATACAG GATTTGAAGT CAGATCTGTC TGATAGGAAT 2520
GTGAAGACAC GGACTCTTAC TGCTAAGTTT TGTGTATGTT AACCAGCCAG ATCCTCTTGG 2580
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CTGGTCACAG CCTCCTCTGT CTGCCCTTCA CCCAGTGGC CACTCAGCTT CCTACCCACA 2760
CCTCTGCCAG AAGATCCCTT CAGGACTGCA ACAGGCTTGT GCAACAATAA ATGTTGGCTT 2820
GGAAAAAAA AAAA

10 A157 Protein sequence:
Gene name: vasoactive intestinal peptide receptor 1
Unigene number: Hs.198726
Probeset Accession #: X77777
Protein Accession #: JC2195
Signal sequence: none found
15 Transmembrane domains: 181-202, 214-236, 255-277, 290-311, 332-354, 377-399, 408-430
Cellular Localization: plasma membrane

20
1 11 21 31 41 51
MPPPPLLSLR RLGGGWSAVT RLVVAAAGAR SRQGRGSRG AGGGGRGGVA RRRRLRLRAA 60
RSLGSSSLQE ECDYVQMI EV QHKQCLEBAQ LENETIGCSK MMDNLTCPA TPRGQVVVLA 120
CLFLFKLFSS IQGRNVSRSC TDEGWTLEP GPYPIACGLD DKAASLDEQQ TPFYGSVKITG 180
YTIGVGLSLA TLLVATALLS LFRKLHCTRN YIHMLFISF ILRAAAVPIK DLALFDSGES 240
25 DQCEGSGVGC KAAMVFPQYC VMANFFWLLV EGLYLYTLLA VSPFSEKRYF WGYILIGWGV 300
PSTFTMVWTI ARIHFEDYGL LRCWDITNSS LWNIIKGPIL TSILVNFIIL ICIIRILLQK 360
LRPPDIRKSD SSPYRRLARS TLLLIPLFGV HYIMFAPFPD NFKPEVKMVF ELVVGSPQGF 420
VVAILYCFLN GEVQABLRRK WRRWHLQGV LWNPKYRHPG GGSNGACTST QVSMLTRVSP 480
30 GARRSSSPQA EVSLV

35 A158 DNA SEQUENCE
Gene name: ESTs
Unigene number: Hs.29383
Probeset Accession #: AW207206
Nucleic Acid Accession #: AL133619
Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCCCCCA GCTCGCGAC CCCGGGCTCT 60
CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCTT TGAGGCGCGA GAGCCCGCAG 120
CTCAGGACAG GCCACCGGCA GAAACGGAAC CTGGAGCTGG AGAAAAAGCT CAGATTCTCTG 180
CAGCAGCAGC ACTCGGAGAT GCTGGCCAA GCTCCATGAG AGATCGAGCA TCTGAAGCGG 240
45 GAAACACAGG GTGAGCGGCG GCGGGGCCCT AGGCGGCCCC TGCTCCCCA GGCACACTCA 300
ACACTGCCCG TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACAGC CCTGGGCTCA 360
GGGGGAACAC AGGACGGGGA GCCCTCCAG ACTGTCTTGG CCCACCTGGC TGCACTGGCC 420
CCTGTATGCC AACCCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC CGCTACCTCT 480
AGCCGTGGCT GGACGATGTT ATGCAGCCAA GCACAGCAGC TGCTGCTCTC GGGGAAGCCA 540
50 GGGCCTGAGG TCATTGCAGG GCGGCAGGTG GCCACAGGGT GCTCCCCAGA CCTCCCTCT 600
CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CCTGCCCTGC TAGATCTTTG 660
CCTCAGATTG CTGCTGTGGC CAGGCCAGG ATTTCCAGCC CTATGGCTCT GAGTCCTCAC 720
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55 GCATCTCCCC ATCTGACAG CCGCCCCCAC CCAGCCAGG ATCTCTGGCT GTGTCTCAA 900
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60 GACAGGACAC GGAAGAGGCC CATGCTTCC CTGGGACCT GCTGTTCAT GTGTCCCAAG 1200
CCCTCCTGCT TTCAGATGG CCCCTCAGGA AACCACTTT CCAGGGCCTC TGCTCCCTTG 1260
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65 TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500
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70 ACCCACTTA GGCAGTGGCA AGTGTCTATC CGGAGCTGT GGAATACCAA CCTCTGTCAG 1800
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75 AAACGGCGCC TGCATGCTC AGTGTCTGA

80 A159 Protein sequence:
Gene name: ESTs
Unigene number: Hs.29383
Probeset Accession #: AW207206
Protein Accession #: T43457
Signal sequence: none found
Transmembrane domains: 303-322
Cellular Localization: not determined


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1      11      21      31      41      51
5      |      |      |      |      |      |
MSGAGVAAGT RPPSSPTPGS RRRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60
QQQHSEMLAK LHEEIEHLKR ENKGEFARGP RPALPPQHS TLPLPQHRNT AINSSTRLGS 120
GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWIDAATS SRGWTMLCSQ AQHVLLSGSP 180
GPEVIAGRQV ATGCSPLPFP PSRAEMGRNP WDSPPCARSL PQIAAVARPR ISSPMALSPH 240
MLGAQGIWTH SIQGSPLPAIW AATMGTKGGS RVLPFCHLSK ALPHPDSPGH PAQDPGLWSQ 300
10      |      |      |      |      |      |
AHFPLSLGLG LITSGOHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVEGGP FPSRCGNSSE 360
LFWAKCGPSR QPQPCSGADA DRTREEMLS LGTCCSMCPK PSCFPDGPSP NHLSRASAPL 420
GARWVCINGV WVEPGGSPSA RLKEGSSRTH RPPGKRGRLA GGSADTVRSP ADSLSMSSFQ 480
SVKSISNSAN SQGKARPQPG SFNKQDSKAD VSQKADLEE PLLHNSKLDK VPGVQQQARK 540
EKAASNAGA ACMGNSQHQG RQMAGAGHPF MILPLPLRKP TTLRQCEVLI RELWNTNLLQ 600
15      |      |      |      |      |      |
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LKQTPKNFNA ERQKRLQAMQ KRRLERSVL

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A160 DNA SEQUENCEGene name: LIV-1 protein, estrogen regulated

Unigene number: Hs.79136

Probeset Accession #: U41060

Nucleic Acid Accession #: NM_012319.2

Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

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GCGGAGACGA AGCGCGAATG GCGAGGAAGT TATCTGTAAT CTGTATCCTG ACCTTTGCCC 180
TCTCTGTAC AAATCCCTTT CATGAACATA AAGCAGCTGC TTCCCCCCAG ACCACTGAGA 240
AAATTAGTCC GAATTGGGAA TCTGGCATTG ATGTTGACTT GGCATTTTCC ACACGGCAAT 300
ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAAATA TTCTTTGTCA GTTGAAGGGT 360
35      |      |      |      |      |      |
TCAGAAAAAT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG 420
ACCCAGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG 480
AGCATCACTC AGACCCAGAG CATCACTCTG ACCATGATCA TCACTCTCAC CATAATCATG 540
CTGCTTCTGG TAAAAATAAG CGAAAAAGCTC TTTGCCAGA CCAATGACTCA GATAGTTTCAG 600
GTAAGATATC TAGAAACAGC CAGGGGAAAG GAGCTCACCG ACCAGAACAT GCCAGTGGTA 660
40      |      |      |      |      |      |
GAGGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACTG 720
TCTCTGAAGG AACTCATTCT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAATCTCTCC 780
CCAAAGATGT AAGCAGCTCC ACTCCACCCA GTGTCAATC AAAGAGCCGG GTGAGCCGGC 840
TGGCTGTGTG GAAAAACAAAT GAATCTGTGA GTGAGCCCGG AAAAGGCTTT ATGTATTCCA 900
45      |      |      |      |      |      |
GCATGGGCAT CCAGGTTCCG CTGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCATCA 1020
TCAACCAAAAT TGATGCTAGA TCTGTCTGTA TTATACAAAG TGAAAAGAAG GCTGAAATCC 1080
CTCCAAAGAC CTATTCAATTA CAAATAGCCT GGGTTTATCT TAGTGCTCTC CATGAATCGG GTGTTTTTCA 1200
TCAGTTTCTT GTCTCTGCTG GGGGTTATCT TAGTGCTCTC CATGAATCGG GTGTTTTTCA 1260
50      |      |      |      |      |      |
AATTTCTCTT GAGTTTCTCT GTGGCAGTGG CCGTTGGGAC TTTGAGTGGT GATGCTTTTT 1260
TACACCTTCT TCCACATTCT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACCAG 1320
CAATGGAAAT GAAAGAGGGA CCACTTTTCA GTCACTGTCT TTCTCAAAAC ATAGAAGAAA 1380
GTGCTATTTT TGATTCACAG TGGAGGGGTC TAACAGCTCT AGGAGGCGTG TATTTCATGT 1440
55      |      |      |      |      |      |
TCTTGTGTGA ACATGCTCTC ACATGATGTA AACAATTTAA AGATAAGAAG AAAAAGAAATC 1500
AGAAGAAACC TGAATAATGAT GATGATGTGG AGATTAAGAA GCAAGTTGTC AAGTATGAAT 1560
CTCACTTTTC AACAAATGAG GAGAAAGTAG ATACAGATGA TCGAAGTGA GGTATTATAC 1620
GAGCAGACTC ACAAGAGCCC TCCCACTTTG ATTCTCAGCA GCCTGCAGTC TTGGAAGAAG 1680
AAGAGGTGAT GATAGCTCAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG 1740
60      |      |      |      |      |      |
GGTGCAAGAA TAAATGCCAT TCACATTTC ACGATACACT CGGCCAGTCA GACGATCTCA 1800
TTCAACACCA TCATGACTAC CATCATATTC TCCATCATCA CCACCACCAA AACCAACATC 1860
CTCAGATGCA CAGCCAGCGC TACTCTCGGG AGGAGCTGAA AGATGCGCGC GTGCGCAATT 1920
75      |      |      |      |      |      |
TGGCCTGGAT GGTGATAATG GGTGATGGCC TGCACAAATT CAGCGATGGC CTAGCAATTG 1980
GTGCTGCTTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTGTCT GTGTTCTGTC 2040
ATGAGTTGCC TCATGAATTA GGTGACTTTG CTGTTCTACT AAAGGCTGGC ATGACCGTTA 2100
AGCAGGCTGT CCTTTATAAT GCATTGTTCAG CCATGCTGGC GTATCTTGA ATGGCAACAG 2160
65      |      |      |      |      |      |
GAATTTTCAT TGGTCATTAT GCTGAAAATG TTTCTATGTG GATATTGTGA CTACTGCTG 2220
GCTTATTCAT GTATGTTGCT CTGGTTGATA TGGTACCTGA AATGCTGCAC AATGATGCTA 2280
GTGACCATGG ATGTAGCCGC TGGGGGTATT TCTTTTACA GAATGCTGGG ATGCTTTTGG 2340
GTTTGGGAAT TATGTTACTT ATTTCCATAT TTGAACATAA AATCGTGTTC CGTATAAAT 2400
70      |      |      |      |      |      |
TCTAGTTAAG GTTTAAATGC TAGACTAGCT TAAAAAGTTG TCATAGTTTC AGTAGGTCAT 2460
AGGGAGATGA GTTTGTATGC TGTACTATGC AGCGTTTAAA GTTAGTGGGT TTTGTGATT 2520
TTGTATTGAA TATTGCTGTC TGTACAAAG TCAGTTAAAG GTACGTTTAA ATATTTAAGT 2580
TATCTATCTT TGGAGATAAA ATCTGTATGT GCAATTCACC GGTATTACCA GTTATTATG 2640
75      |      |      |      |      |      |
TAAACAGAGG ATTTGGCATG ACATGTTCTG TATGTTTCAG GGAATAATGT CTTTAATGCT 2700
TTTTCAGAAA CTAACACAGT TATTCCTATA CTGGATTTTA GGTCTCTGAA GAACCTGCTG 2760
TGTTTAGGAA TAAGATGTG CATGAAGCCT AAAATACCAA GAAAGCTTAT ACTGAATTTA 2820
AGCAAGAGAA TAAAGAGGAA AAGAGAAGAA TCTGAGAATT GGGGAGGCAT AGATTCTTAT 2880
80      |      |      |      |      |      |
AAAAATCACA AAATTGTTG TAAATTAGAG GGGAGAAATT TAGAATTAAG TATAAAAGG 2940
CAGAATTAGT ATAGAGTACA TTCATTAAAC ATTTTGTGTA GGATTATTTC CGTAAAAAC 3000
GTAGTGAGCA CTCTCATATA CTAATTAGTG TACATTTAAC TTTGTATAAT ACAGAAATCT 3060
AAATATATTT AATGAATTCA AGCAATATAC ACTTGACCAA GAAATTGGAA TTTCAAAATG 3120
TTGTCGCGGG TTATATACCA GATGAGTACA GTGAGTAGTT TATGTATCAC CAGACTGGGT 3180
TATTGCGAAG TTATATACCA CCAAAAGCTG TATGACTGGA TGTCTGGTT ACCTGGTTTA 3240
CAAAATATTC AGAGTAGTAA AACTTTGATA TATATGAGGA TATTAAACT ACATAAGTA 3300
TCATTGTATT CGATTCAGAA AGTACTTTGA TATCTCTCAG TGCTTCAGTG CTATCAATTG 3360

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GAGCAATTGT CTTTATATAC GGTACTGTAG CCATACTAGG CCTGTCTGTG GCATTCTCTA 3420
GATGTTTCTT TTTTACACAA TAAATTCCTT ATATCAGCTT G

5 A161 PROTEIN SEQUENCE

Gene name: LIV-1 protein, estrogen regulated
Unigene number: Hs.79136
Protein Accession #: NP_036451
Signal sequence: 1-21
Pfam domain: Zip[591-743]
Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745
Cellular Localization: plasma membrane

15 1 11 21 31 41 51
MARKLSVILI LTFALSVTNP LHELKAAAPP QTTEKISPNW ESGINVDLAI STRQYHLQQL 60
FRRYGENNSL SVEGFRKLLQ NIGIDKIKRI HIHHDHHDHS DHEHHSDBER HSDHEHHSDB 120
EHSDDHHDHS HINHAASGKN KRKALCPDHD SDSGKDPN SQKGAHRPE HASGRRNVKD 180
SVSASEVIST VYNTVSEOTH FLETIETPRP GKLPKDVSS STPPSVTSKS RVSRLAQKRT 240
NESVSEPRKG FMYSRNTNEN PQECFNASKL LTHSGMGIVQ PLNATEPNYL CPAIINQIDA 300
RSLIHTSEK KAEIPPKTYS LQIAMVGGFI AISHIISPLSL LGVILVPLMN RVFFKFLSP 360
LVALLAVGTLG GDAPLHLLPH SHASHHSHS HEPPAMEMKR GPLFSLSSQ NIEESAYFDS 420
TWKGLTALGG LYFMFLVEHV LTLIKQFKDK KRKQKPPEN DDDVEIKQL SKYESQLSTN 480
25 ESKVDTDDRT EGYLRADQSE PSHPDSQQPA VLEEEVVMIA HAHPQEVYNE YVPRGCKNKC 540
HSHFDHTLGG SDDLHHDHHD YHHILHHDH QNHHPHSHSQ RYSREELKDA GVATLAWMVI 600
MGDGLHNFSD GLAIGAATFE GLSSGLSTSV AVPCHELPEE LGDFAVLLKA GMTVKQAVLY 660
NALSLMLAYL GMATGIFIGH YAENVSMWIF ALTAGLFMYV ALVDMVPEML HNDASDHGCS 720
RWGYFFLQNA GMLLGFGLML LISIFERKIV FRINF

30 A162 DNA sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
Unigene number: Hs.87223
Probeset Accession #: AA250737
Nucleic Acid Accession #: NM_001203
Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
CGCGGGGCGC GGAGTCGGCG GGGCCTCGCG GGACGCGGGC AGTGCAGAGA CCGCGGCGCT 60
GAGGACGCGG GAGCGCGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT 120
GTGAAGGAA AGGAAGATCA TTTCATGCCT TGTGTATAAA GGTTCAGACT TCTGCTGATT 180
CATAACCATT TGCTCTCTAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAGACC 240
TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA 300
45 AATGTGGGCA CCAAGAAAGA GATGGTGAG AGTACAGCCC CCACCCCGG TCCAAAGGTC 360
TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420
GAGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCGCTGT GGTCACTTCT 480
GGTTGCTAGT GACTAGAAGG CTCAGATTTT CAGTGTGGGG AACTCCCAT TCCTCATCAA 540
AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAGAAGCT ACACCTTACA 600
50 CTGCTTCATG TGAAAAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCTTTACTT 660
ATATCTGTGA CTGTCTGTAG TTTGCTCTTG GTCTTATCA TATTATTGTT TTAATCTCGG 720
TATAAAGAGC AAGAAACCCG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAACCTTAC 780
ATTCTCTCTG GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840
TCAGGCTCTC CTCTGCTGGT CCAAGGACT ATAGCTAAGC AGATTGAGT GGTGAACAG 900
55 ATTGGAAGAG GTGCTATGG GGAAGTTTGG ATGGGAAAGT GCGGTGGGGA AAGGTTAGCT 960
GTGAAGTGT TCTTACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020
ACAGTGTGTA TGAGGCATGA AAACATTTTG GTTTTCATTG CTGCAGATAT CAAAGGGACA 1080
GGGTCTCTGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140
60 TATCTGAAGT CCACCAACCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC 1200
AGTGGCTTAT GTCAATTACA CACAGAAATC TTTAGTACTC AAGGCARACC AGCAATTGCC 1260
CATCGAGATC TGAAGAGTAA AAACATTCTG GTGAAGAAAA ATGGAACTTG CTGTATTGCT 1320
GACCTGGGCC TGGCTGTGTA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380
ACTCGAGTTG GCACCAACCG CTATATGCCT CCAGAGGTGT TGGACGAGAG CTTGAACAGA 1440
AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCTCAT CCTTTGGGAG 1500
65 GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC 1560
CTAGTCCCA GTCACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGAT CAAAGAGTTA 1620
OGCCCCAT TCCCAACCG GTGGAGCAGT GATGAGTGT TAAGGCAGAT GGGAAAACTC 1680
ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTTAAGAAA 1740
ACACTTGCCA AAATGTGAGA GTCCACAGAC ATTAACCTCT GATAGGAGAG GAAAAGTAAG 1800
70 CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTGTGG GCAGAGCAAA AGACATCAAA 1860
TAAGCATCCA CAGTACAAGC CTTGAACATC GTCTGCTTC CCAGTGGGTT CAGACCTCAC 1920
CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980
TCTGTTGTA GCGGAGAAAA CGTTGGGTA ACTGTGTCAA GATATGATGC AT

75 A163 Protein sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
Unigene number: Hs.72472 / Hs.87223
Probeset Accession #: AA250737 / U89326
Protein Accession #: NP_001194
Signal sequence: 1-13
Transmembrane domains: 128-144
PFAM domains: activin_receptor [30-111], protein kinase [204-491]
Cellular Localization: plasma membrane


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1      11      21      31      41      51
|      |      |      |      |      |
5  MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHCPE DSVNNICSTD GYCFTMIEED 60
   DSGLPVVTSQ CIGLEGSDFO CRDTPIPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD 120
   GPIHHRALLI SVTVCSLLLV LILLFCYFRI KRQETRPFRYS IGLEQDETYI PPGESLRDLI 180
   BQSQSSSGSGS GLPLLQRTI AKQIQMVKQI KGGRYGEVMM GKWRGEKVAV KVFPTEBAS 240
   WFRETEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300
   MLKLAYSSVS GLCHLATEIF STQKPAIAH RDLKSKNILV KKNGTCCIAH LGLAVKFISD 360
10  TNEVDIPFNT RVGTKRYMPP EVLDESLNRN HFQSYIMADM YSFLILWEV ARRCVSGGIV 420
   EEYQLPYHDL VPSDPSEYEDM REIVCIKKLR PSFPNRWSSD ECLRQMKLM TECWAHNPAS 480
   RLTAALRVKKT LAKMSESQDI KL

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A164 DNA sequence

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15  Gene name:          ESTs
   Unigene number:     Hs.157601
   Probeset Accession #: W07459
   Nucleic Acid Accession #: AC005383
   Coding Sequence:     328-2751 (underlined sequences correspond to start and stop codons)
20

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1      11      21      31      41      51
|      |      |      |      |      |
25  GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGGTAGAAG TGAAGTACTT 60
   TTTTATTTCG AGACCTGGGC CGATGCCGCT TTAAAAACG CGAGGGGCTC TATGCACCTC 120
   CCTGGCGGTA GTTCTCCGGA CCTCAGCCGG GTGCGGTGCT GCGGCCCTCT CCCAGGAGAG 180
   ACAAAACAGT GTCCACGCTG GCAGCCGCGC CCGGGGCGCC CCTCCTGTGA TCCCGTAGCG 240
   CCCCCTGGCC CGAGCCGCGC CCGGGTCTGT GAGTAGAGCC GCCCGGGCAC CGAGCGCTGG 300
   TCCCGGCTCT CCTTCGGTTA TATCAACATG CCCCCTTTCC TGTGTCTGGA GGCGGCTCTG 360
   GTTTTCTCTG TTTCCAGAGT GCCCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAACAAA 420
   GAAACCATCG GGAAGATTTT AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480
   ATCATGTTTC TGTAGATGGG GTCTAACAGC GTCGGGAAG GAGGCTTTGA AAGGTCCAAG 540
   CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600
   GCATTCCAGT TCAATTCCAC TCCTCATCTG GAATTCCTCT TGGATTCAIT TTCAACCCAA 660
   CAGGAAGTGA AGGCAAGAAT CAAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720
   CTTCCTCTGA AATACCTTCT GCACAGAGGG TTGCTGGAG GCAGAAATGC TTCTGTGCCC 780
   CAGATCTCTA TCATCGTCA CACTGTGTTT GCTGTGGGG TCAGGTTTCC CAGTGGGAG 840
   CAGCTGAAGG AAAGGGGTGT CGAGCCTAGA GGGCAGCAGC TGCTGTGTGG TGAGCAGGTG 900
   GAGGTGCGCA CCAACGCGCT CTTCAGCACC CTCAGCAGCT CGGCCATCTG CTCACGCGCC 960
   ACGCCAGACT GCAGGTCGTA GGCTCACCCC TGTGAGCACA GGACCTTGCG GGTGCTGGCT 1020
   GAGTTCGCTG GCATATGCCCC ATGCTGGAGA GGATCGCGCG GGACCTTGCG GGTGCTGGCT 1080
   GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTTCTTAA CCCACCTTGC CACTGTCTAC 1140
   AGGACCACCT GCCAGGCCCC CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1200
   CCAGAAGGAC TGAAGCGCTA CAGTGCCTC TGCCCGCTGG CCTTTGAGG GGAGGCTAAC 1260
   TGTGCCCTGA AGCTGAGCCT GGAATGCAGG GTGCGCTTCC TCTTCTGCT GGCAGCTCT 1320
   GCGGGCACC A CTCTGACGG CTTCCTGCGG GCCAAAGTCT TCGTGAAGG GTTTGTGCGG 1380
   GCGGTGCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG 1440
   CTGGTGGCGG TGCTGTGGG GAGATACCA GATGTGCTCT ACCTGGTCTG GAGCCTCGAT 1500
   GGCATTTCCT TCGGTGTGG CCCACCTTG ACGGGCAGTG CCTTGGGCA GCGGCGCAGG 1560
   CGTGGCTTGG GGAGGCCAC CAGACAGGCG CAGGACCGCG CACGTAGAGT GGTGTTTGG 1620
   CTCACTGAGT CACTCTCCGA GATGAGGTT GCGGGCCGAG CGGTGACGC AAGGGCGCGA 1680
   GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG GCGGTGCGGG CAGAGCTGGA GGAGATCACA 1740
   GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAATCCCT 1800
   GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG CGGCCAGGCT GCGGACACA AGCCCTGGAC 1860
   CTCGTCTTCA TGTGGACAC CTCTGCCTCA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1920
   AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTGCGC 2040
   CTGGTGGTGT ATGGCAGCCA GGTGCAGACT GCCTTCGGGC TGGACACCAC ACCACCCCG 2100
   GCTGCGATGC TGCGGGCCAT TAGCCAGGCC CCTACCTAG GTGGGGTGGG CTCAGCAGGC 2160
   ACGGCCCTGC TGCACATCTA TGACAAAGTG ATGACCTGCC AGAGGGGTGC CCGGCTTGGT 2220
   GTCCCCAAGC CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCCGTTCCT 2280
   GCCCAGAAGC TGAGGAACAA TGGCATCTCT GTCTTGGTGG TGGGGTGGG GCTGTCTCTA 2340
   AGTGAGGGTC TCGGAGGCT TGCAGGTCCC CCGGATTCCC TGATCCAGT GGCAGCTTAC 2400
   GCGGACCTGC GGTACCAACA GAGCGTGTCT ATGTAGTGGC TGTGTGAGA AGCCAAGCAG 2460
   CCAGTCAACC TCTGCAAAAC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CCTGCAGAA 2520
   GGGAGCTACC GCTGCAAGTG TCGGGATGGC TGGGAGGGCC OCCACTGCGA GAACCGTGAG 2580
   TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGGATT TTAGAGCGCC CCTGAGGCAC 2640
   ATGGCTCCCG TGCAGGAGGG CAGCAGCGGT ACCCTCCCA GCAACTACAG AGAAGGCTG 2700
   GGCACGTAAA TGTGTCTTAC CTCTGTGAGG GTCTGTGCCC AGGATGTCCC AACTGCAGCC 2760
   TTCCCGCGT GGCACGAGCC ACTATTCTCA CTGAGGAGGG AGGATGTCCC AACTGCAGCC 2820
   ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTCAACCCACA AACGATGTG TGAAGAGTT 2880
   TTGATGTGTA AGTAATAACC CACTTCTGT ACCTGCTGTG CCTTGTGAG GCTATGTCAT 2940
   CTGCCACCTT TCCCTTGAGG ATAAACNAGG GGTCTGTAAG ACTTAAATTT AGCGGCTTGA 3000
   CGTTCCTTTG CACACAATCA ATGCTCGCCA GAATGTGTGT GACACAGTAA TGCCAGCAGC 3060
   AGGCCTTTAC TAGAGCATCC TTTGAGCGGC GAAGGCCACG GCCTTTTCAAG ATGGAAGACA 3120
   GCAGCTTTTC CACTTCCCCA GAGACATCTT GGATGCATTT GCATTGAGTC TGAAAGGGGG 3180
   CTTGAGGGAC GTTGTGACT TCTTGGGAC TGCCCTTTGT GTGTGGAAGA GACTTGAAGA 3240
   GGTCTCAGAC TGAATGTGAC CAATTAAACA GCTTGTGTA TGTGGGGGA GGGGCTGAGT 3300
80  TGTGATGGG CCCAGGTCTG GAGGGCCACG TAAATCGTCT CTGAGTGTG AGCAGTGTCC 3360
   ACCTTGAGG TCTTC

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A165 Protein sequence

Gene name: ESTs
 Unigene number: Hs.157601
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: none found
 VGM domains: 49-223; 341-518; 529-706
 BGF domains: 298-333; 715-748
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
15  MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SQMWCSAAV DIMFLDGSN 60
    SVGKGSFERS KHFAITVCDG LDISFPRVRV GAFQFSSTPH LEFPDLSFST QQEVKARIKR 120
    MVFRGGRTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180
    FAVGVRFPRW SELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
    PCEHRTLEMW REFAGNAPCW RGSRRTLAVL AAHCFYYSWK RVFLTHPATC YRTTCFPGPCD 300
    SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
    RAKVPVRRPV RAVLSSEDSRA RVGVATYSRE LLVAVPVGEY QDVPLDVNSL DGIPFRGGPT 420
    LTGSALRQAA ERGFGSATRT QQDRPRRVVV LLTSEHSEDE VAGPARHARA RELLLLGVS 480
    BAVRALEEEI TGSPKHVMVY SDPQDLFNQI PELQGLKCSR QRPQCRTQAL DLVFMLD TSA 540
    SVGPENPAQM QSPVRSALQ FEVNPDTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
    APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVL T GGRGAEDAAV PAQKLNNNGI 660
    SVLVVGVGPV LSEGLRLLAG PRDSLIHVAA YADLRHQDV LIEMLOGEAK QPVNLCCKPSP 720
    QNBSGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETFLR HMAPVQEGSS 780
    RTPPSNYREG LGTEMVPTFW NVCAPGP
  
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A166 DNA sequence

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR
 Unigene number: Hs.37744
 Probeset Accession #: AA011176
 Nucleic Acid Accession #: AF272890
 Coding Sequence: 87-1520 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
40  TGCTACCGCG GCGCGGGCTT CTGGGGTGTG CCCCACACAC GCGCCAGCCG TGCCACACCC 60
    CCGCGCCCGG GCGCTCGCAG CTGCGCATGG GCGCGGGGGT GCTGCTCCTG GCGCGCTCCG 120
    AGCCCGGTAA CCGTGTGCTG GCGGCACCGC TCCCGCAAGG CGCGGCCACC GCGCGCGCGC 180
    TGCTGGTGGC CGGCTGCGCG CCGGCTCGGT TGCTGCTTCC CGCCAGAGAA AGCCCGGAGC 240
    CGCTGTCTCA GCAGTGGACA GCGGGCATGG GTCTGCTGAT GCGGCTCATC GTGCTGCTCA 300
    TCGTGGCGGG CAATGTGCTG GTGATGCTGG CCATCGCCAA GACGCGCGGG CTGCAGACGC 360
    TCACCAAACT CTTCATCATG TCCTGTGCCA GCGCGCAACT GGTGATGGGG CTGCTGGTGG 420
    TGCGGTGCGG GCGCCACCAT GTGGTGTGGG GCGGCTGGGA GTACGGCTCC TTCTTCTGGG 480
    AGCTGTGGAC CTCACTGGAC GTGCTGTGCG TGACGGCCAG CATCGAGACC CTGTGTGTCA 540
    TTGCGCTGGA CCGCTACCTC GCCATCACCT CGCCCTTCCG CTACCAAGAG CTGCTGACGC 600
    GCGCGCGGGC GCGGGGCGCT GTGTGCAACG TGTGGGCCAT CTGGGCGCTG GTGTCTTCC 660
    TGCCCACTCT CATGCACTGG TGGGGGCGGG AGAGCGACGA GCGCGCGCGC TGCTACAAAG 720
    ACCCAAGTGT CTGCACTTTC GTCAACCAAC GGGCTCAAGC CATCGCCTCG TCCGTAGTCT 780
    CCTTCTACGT GCCCCTGTGC ATCATGGGCT TCGTGTACCT GCGGGTGTTC GCGAGGCC 840
    AGAAGCAGGT GAAGAAGATC GACAGCTGCG AGCGCGGTTT CCTCGGCGGC CAGCGCGCGC 900
    CGCCCTCGCC CTGCGCCTCG CCGCTCCCGG CGCCCGCGCC GCGCGCGCGA CCGCGCGGCC 960
    CGCGCGCGCG CGCGCGCACG GCCCGGCTGG CCAACGGGGG TGCGGGTAAG GCGCGGCCCT 1020
    CGCGCTGCTG GCGCCTAGCG GAGCAGAAGG CGCTCAAGAC GCTGGGCATC ATCATGGGGG 1080
    TCTTCAAGCT CTGCTGGCTG CCCTTCTTCC TGGCCAAAGT GGTGAAGGCC TTCCACCGCG 1140
    AGCTGTGTGC CGACCGCTCT TCGTCTTCT TCAACTGGCT GGGCTACGCC AACTCGGCCT 1200
    TCAACCCCAT CATCTACTGC GCGAGCCCGG ACTTCGCGAA GGCCTTCCAG GGAAGTCTCT 1260
    GCTGCGCGCG CAGGGCTGCC GCGCGGCGCC ACGCGACCCA CGGAGACCGG CCGCGCGCCT 1320
    CGGGCTGTCT GCGCGGGCCC GGAACCCCGC CATCGCCCGG GCGCGCCTCG GACGACGACG 1380
    ACGACGATGT CGTGGGGGCC ACGCGCGGCC CGCGCCTGCT GGAGCCCTGG GCGCGCTGCA 1440
    ACGCGGGGCG GCGGGGGGAC AGCGACTCGA GCGTGGACGA GCGGTGCGCG CCGCGCTTGG 1500
    CCTCGGAATC CAAGGTGTAG GCGCGGGCGC GGGGCGCGCA CTCGGGCGAC GCGTTCACAG 1560
    GGGAAAGAGG AGATCTGTGT TTACTTAAGA CCGATAGCAG GTGAACCTGA AGCCCACAAT 1620
    CCTGCTCTGA ATCATCCGAG GCAAGAGAGAA AAGCCACGGA CCGTTGCACA AAAAGGAAAG 1680
    TTTGGGAAGG GATGGGAGAG TGGCTTCTCT ATGTCTCTTG TTG
  
```

A167 Protein sequence

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR
 Unigene number: Hs.37744
 Protein Accession #: AA011176
 Signal sequence: none found
 Transmembrane domains: 62-84, 95-117, 135-157, 177-198, 226-248
 Pfam domain: 7tm_1 [75-377]
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
80  MGAGVLVLGA SEPGNLSSAA PLPDGAATAA RLLVPASPPA SLLPPASESP EPLSQWNTAG 60
    MGLMALIVL LIVAGNVLVI VAIKTPRLQ TLTNLFIMSL ASADLVNGLL VVPFGATIVV 120
  
```


WO 03/042661

WGRWEYGSFF CELMTSDVVL CVTASIELTC VIALDRYLAI TSPFRYQSLT TRARARGLVC 180
 TVWATISALVS FLPIIMHWRW AESDEARRCY NDPKCCDFVT NRAYAIASSV VSFYVPLCIM 240
 AFVYLRVPRE AQKQVKIDS CERRFLGGPA RPPSPSPSPV PAPAPPPPPP RPAATAATAP 300
 LANGRAGKRR PSRLVALREK KALKTLGIIM GVFTLCWLFP FLANVVKAPH RELVFDRLFV 360
 FFNMLGYANS AFNPIIYCRS PDRKAPQGL LCCARRAARR RHATHGDRPR ASGCLARPGP 420
 PPSPGAASDD DDDDDVVGATP PARLLEPWAG CNGGAADSD SSLDEPCRPG FASESKV

A168 DNA sequence

Gene name: CEGP1
 Unigene number: Hs.222399
 Probeset Accession #: AA256485
 Nucleic Acid Accession #: AJ400877
 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GGCGTCCGCG CACACCTCCC CGCGCCGCGG CCGCCACCGC CCGCACTCCG CCGCCTCTGC 60
 CCGCAACCGC TGAGCCATCC ATGGGGTTCG CGGGCCGCAA CGGTCCCGGG GCGGCCTGGG 120
 CGGTGCTGCT GCTGCTGCTG CTGCTGCGCG CACTGCTGCT GCTGGCGGGG GCCGTCCCGC 180
 CGSGTCCGGG CCGTGCAGCG GGGCCGCGAG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240
 ATGACTGCCA TGCCGACGCC CTGTGTGAGA ACACACCCAC CTCCTACAAG TGCTCCTGCA 300
 AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAAATGAGC 360
 TCAATGGAGG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATCGT TGCACTTGTT 420
 TTGATGGCTT CATGTGGCTT CATGACGGTC ATAATTGTCT TGATGTGGAC GAGTGCCTGG 480
 AGAACATATG CGGCTGCCAG CATACCTGTG TCAACGTCAT GGGGAGCTAT GAGTGTCTGT 540
 GCAAGGAGGG GTTTTTCCTG AGTGACAAAT AGCACACCTG CATTCAACCGC TCGGAAGAGG 600
 GCCTGAGCTG CATGAATAAG GATCACGGCT GTAGTCACAT CTGCAAGGAG GCCCCAGAGG 660
 CGAGCGTCGC CTGTGAGTGC AGGCCTGGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720
 TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG 780
 GCCCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG 840
 AGCGACAGGA CACTGTCCTG GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG 900
 ATAAACGGGT GAAACGGCGG CTGCTCATGG AAACGTGTGC TGTCAACAAT GGAGGCTGTG 960
 ACCGCACCTG TAAGGATACT TCGACAGGTG TCCACTGCAG TTGTCTCTGT GGATTCACCT 1020
 TCCAGTTGGA TGGGAAGACA TGTAAAGATA TTGATGAGTG CCAAGCCCGC AATGGAGGTT 1080
 GTGATCAATT CTGCAAAAC ATCGTGGGCA GTTTTGACTG CGGCTGCAAG AAGGAGTTTA 1140
 AATTATTAAC AGATGAGAAG TCTTGCCAAG ATGTGGATGA GTGCTCTTGT GATAGGACCT 1200
 GTGACCACAG CTGCATCAAC CACCTGGGCA CATTGTCTTG TGCTTGCAAC CGAGGGTACA 1260
 CCCTGTATGG CTTCACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGGAGGCT 1320
 GTCAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CCAAGTCCAC CCGGTGTACA 1380
 AGCTCCACTG GAATAAAAAA GACTGTGTGG AAGTGAAGGG GCTCCTGCCC ACAAGTGTGT 1440
 GACCCCGTGT GTCCCTGCAC TCGGTAAGA GTGGTGGAGG AGACGGGTGC TTCTCAGAT 1500
 GTCACCTCGG CATTCACTCT TCTTCAGATG TCACCAACAT CAGGACAAGT GTAACTTTTA 1560
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 AGGCGCTCCA CAGGAGCAG TTTCACTTCC AGCTCTCAGG CATGAACCTC GACGTGGCTA 1920
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 CAGAAAACCA ATGTGTCACT TGCAGGGCTG GGACCTATTA TGATGGAGCA CGAGAAGCT 2040
 GCATTTATG TCCAAATGGA ACCCTCCAAA ATGAGGAAGG ACAAATGACT TGTGAACCAT 2100
 GCCCAAGACC AGGAATATCT GGGGCCCTGA AGACCCAGCA AGCTTGGAAAT ATGTCTGAAT 2160
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 ACTTTGATGG CTCCACAAC ATAACCCAGT GTAAAAACAG AAGATGTGGA GGGGAGCTGG 2520
 GAGATTTCAC TGGGTACATT GAATCCCAAA ACTACCCAGG CAATTACCCA GCCAACACCG 2580
 AGTGTACGTG GACATCAAC CCACCCCCCA AGCGCCGCTC CCGATCGTGT GTCCCTGAGA 2640
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 GAGATGGCAG GCTCTATGCA TCTGAGAAC ATCAGGAAT ACTTAAGGAT AAGAACTTA 2940
 TCAAGGCTCT GTTTGATGTC CTGGCCCATC CCCAGAACTA TTTCAGTAC ACAGCCAGG 3000
 AGTCCCGAGA GATGTTTCCA AGATCGTTCA TCCGATTGCT ACGTTCCTAA GTGTCCAGT 3060
 TTTTGAGACC TTACAAATGA CTCAGCCAC GTGCCACTCA ATACAAATGT TCTGCTATAG 3120
 GGTGCTGGG ACAGAGCTGT CTTCTCTG CTGTGACGA CAGTCCGGTA TTGCTGCCTC 3180
 CGTATCAGT GACTCAATT AGTTCAATT TTATAGATA TACAGATATT TTGTTAAAT 3240
 GAACCTGGTT TTTCTTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT 3300
 CAGCTTCTCA CTGCTGTGGG CGGATGTCTT GATAGATCA CGGCTGGCT GAGCTGGACT 3360
 TTGCTCAGCC TAGGTGAGAC TCACCTGTCC TTCTGGGGTC TTACTCTCC TCAAGGAGTC 3420
 TGTAGTGAA AGGAGGCCAC AGAATAAGCT GCTTATTCTG AAACCTCAGC TTCTCTAGC 3480
 CCGGCCCTCT CTAAGGGAGC CCTCTGACT CGTGTGAGG CTCTGACCAG GCAGAACAGG 3540
 CAAGAGGGGA GGAAGGAGA CCCCTGCGAG CTCCTCCAC CCACCTTGAG ACCTGGGAGG 3600
 ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGTAGC CAGGAACCTG 3660
 AGTTCTAAGC AGTGCTCGTG AAAAAAAGAA GCAGAAAGAA TTAGAATAAA ATAAAAACTA 3720
 AGCACTTCTG GAGACAT

A169 Protein sequence

Gene name: CEGP1
 Unigene number: Hs.222399

Probeset Accession #: AA256485
 Protein Accession #: CAB92285
 Signal sequence: 1-31
 Transmembrane domains: none
 PFAM domains: EGF-like_domains [49-84,132-167,177-213,286-321,407-442] CUB_domain [809-918]
 Cellular Localization: may be secreted

1 11 21 31 41 51
 10 | | | | |
 MGAVAGNRNRP AANAVLLLLL LPPPLLLLAG AVPPGRGAA GPQEDVDECA QGLDDCHADA 60
 LQNTPTSYK CSCKPGYQGE GRQCEDIDEC GNELANGGVH DCLNIPGNYR CTCFDGFMIA 120
 HDHGNCLDLD ELENNGGCG HTCVNVWGSY ECKCKGFFL SDNQHCTIHR SEBGLSCMKN 180
 DHGCSHICKE APRGSVACBC RPFELAKNQ RDCILTCNHG NGGQHSDD TADGPECSCH 240
 15 PQYKMGHTDGR SCLEREDTVL EVTESNTTSV VDGDKRVKRR LLMETCAVNN GGCRTCKDT 300
 STGVHSCPCV GFTLQLDGKT CKDIDECQTR NGGCDHPCGN IVGSPDCGCK KGFLLTDEK 360
 SCQDVDECSL DRTCDHPCIN HPGTACACN RGYTLYGPTH CGDTNECSIN NGGCGQVCVN 420
 TVGSYEQCH PQYKLHWNKK DCVEVKGLLP TSVSPRVSLH CGKSGGGDGC FLRCHSGIHL 480
 SSDVTITRTS VTFKLNEGKC SLKNAELFPE GLRPALPEKH SSVKESFRYV NLTCSSGRQV 540
 20 PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCOLSCIVKR TEKRLRAIR TLRKAVHREQ 600
 PHLQLSGMNL DVAKCPPTS ERQASGCGV QGHAEHQCVS CRAGTYDGA RERCILCPNG 660
 TQNEBECMSL DRPCRPQNS GALKTPAWN MSECGLQCP GEYSADGFAP CQLCALGTFO 720
 PEAGRTSCFP CGGLATKHQ GATSFQDCET RVQCSGHEFY NTTTHRCIRC PVGTQYQEPG 780
 RNCVSCFAGN TTDFDGSIN ITQCKNRCG GELGDFTVYI ESPNYRGNYP ANTECTWTIN 840
 25 PPPKRRILIV VPEIFLPIED DCGDYLVMRK TSSNSVTTY ETCQTYERPI APTSRSKKLW 900
 IQFKNSEBNS ARGFQVPTV YDEYQELIE DIVRDGRLYA SENHQEILKO KKLKALFDV 960
 LAHPNQYFKY TAQESREMPF RSPIRLLRSK VSRFLRPYK

A170 DNA sequence
 Gene name: DEME-6 protein (KIAA0452)
 Unigene number: Hs.125783
 Probeset Accession #: AL039402
 Nucleic Acid Accession #: AF007170
 Coding sequence: 1-1725 (underlined sequences correspond to stop codon)

1 11 21 31 41 51
 35 | | | | |
 AAGGAGGCGG CTTCGGGAA AAGCGACCCG AGGACTCCTG AGAGCAGCCT CCATGAGGCC 60
 CTGACCACTG CATGACCGC CCTGACCTC TTCTCACCA ACCAGTTCTC AGAAGCACTC 120
 40 AGCTACCTCA AGCCAGAAC CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC 180
 CTGAGATGTC AGCCCATGAT GACCTTTGAC CCTCAGGACA TCCTGCTTGC CGGCACATG 240
 ATGAAGGAGG CACAGATGCT GTGTGAGAGG CACCGGAGGA AGTCTTCTGT AACAGATTCC 300
 TTCAGCAGCC TGGTGAACCG CCCCACTCTG GGCCTATTCA CTGAAGAAGA AATCCACGCT 360
 45 GAGGTCTGCT ATGACAGATG CCTGCTGCG AGAGCAGCCC TGACCTTCTC GCAGGACGAG 420
 AACATGCTGA GCTTCTATCA AGGCGGCATC AAGTTTGAAC ACAGCTACCA GACCTACAAG 480
 GAGCTGGACA GCCTTGTTCA GTCTCACAA TACTGCAAGG GTGAGAACCA CCGCAGCTTT 540
 GAAGGAGGAG TGAAGCTTGG GTTAGGGGCC TTCAACCTGA CACTGTCCAT GCTTCTCTACT 600
 AGGATCTTGA GGTCTGTGGA GTTTGTGGGG TTTTCAGGAA ACAAGGACTA TGGGCTGCTG 660
 50 CAGCTGGAGG AGGAGCGCTC AGGGCACAGC TTCGCTCTG TGCTCTGTGT CATGCTCCTG 720
 CTGTGCTACC ACACCTTCTC CACCTTCGTG CTGGGTACTG GGAACGTCAG CATGAGGAG 780
 CGCGAGAGC TCTTGAAGCC CTACCTGAAC CGGTACCTTA AGGGTGCCAT CTCTCTGTT 840
 TTTGAGGAGG GAATCTGAAT CATTAAAGGC AACATTGATG CAGCCATCCG GCGTTTCGAG 900
 GAGTGTCTGT AGGCCAGCA GCACCTGGAAG CAGTTTCACC ACATGTGCTA CTGGAGACTG 960
 55 ATGTGTGCTC TCACCTACAA GGGCCAGTGG AAGATGTCTC ACTTCTACGC CGACCTGCTC 1020
 AGCAAGAGAG ACTGCTGGTC CAAGGCCACC TACATTTACA TGAAGGCCGC CTACCTCAGC 1080
 ATGTTTGGGA AGGAGGACCA CAAGCCGTTT GGGGACGAGC AAGTGGAAAT ATTTGAGACT 1140
 GTGCCAGGCC TGAAGCTCAA GATTGCTGGG AAATCTCTAC CCACAGAGAA GTTTGCCATC 1200
 CGGAAGTCCC GSGCTACTT CTCTCCAC CCTATCTGCG TGCCAGTGCC TGCTCTGGAA 1260
 60 ATGATGTACA TCTGGAACCG CTAGCCGCTG ATTGGGAAGC AGCCGAAACT CACGGATCGG 1320
 ATACTTGAGA TTACTACTAA GGCTGAAGAG ATGCTGGAGA AAGGCCGAGA GAACGAGTAC 1380
 TCAGTGGATG ACAGAGTCTT GGTGAAATG TTGAAAGGCC TGTGTCTGAA ATACCTGAGC 1440
 CGTGTCCAGG AGGCCGAGGA GAATTTTAGG AGCATCTCTG CCAATGAATA GAAGATTAAA 1500
 TATGACCACT ACTTGATCCC AAACGCCCTG CTGGAGCTGG CCCTGCTGCT TATGGAGCAA 1560
 65 GACAGAAAG AGAGGCCAT CAACTTTTGG GAATCTGCCA AGCAAACTA CAAGAATTAC 1620
 TCCATGGAGT CAAGGACACA CTTTCAATC CAGGCAGCCA CACTCCAAGC CAAGTCTTCC 1680
 CTAGAGAAAC GCAGCAGATC CATGGTCTCA TCAGTGTCTT TGTAGCTTTG TGCAGCAGTT 1740
 CCGGCTGGA AGACAGAGAG AGCTCTGAA AACATTTCAA AATACCCCT 1800
 CCGCTGCCC TGCCCTGCTT TTGGGTCCA CCGCACTCC AGTTGGATGG CACAACATAG 1860
 70 TGTATCCGTG CAGAAGCGA GCTGGCATTT TCACAGTGT AGCCAGGGG CTTTGCCAG 1920
 GGCAGAGCAG GTGAGCCCT CTGCTGCCC TATCACACAT ACGGTACTT GCTTTTCACT 1980
 GTGATGTTTA AGAGAATGTA TGAACAGTTT ACATTTTCTC TAGAAATACA TTGATGGGAT 2040
 CACAGTTGCG TTTAAAAACC AACACAAATC AACCACTGT AAGTCTTTGT CTTCACCTAT 2100
 TATCATCTGG AGGTAAATCT CTTTATATGA TGATGCCAAA GGGCAAAATG CTTTCAAAT 2160
 75 TCAGCAAGTT CTGACGTTGT GTGACGGAAG GTCTTCAGA GGAAGCTGAG AATGCTGGG 2220
 AGAGGCTTAG CCTCAGGCTT CAATGCTTCT GGGGTGGGCG ATGAGGATGT ACACAGACAC 2280
 CCACTACCTT ACTACTCACA CTTCAATTCA CTCTTTTGT AAAATTTCAA TTTAAAAATC 2340
 AAGCAGTCT TTTTGTGAG ATAAAATCTG AGCTCTTCTG TAGAAAAATC AATCTCTACC 2400
 AGTAGAAAT GCCAGGCTT GATGGAAGAG CTGTGTAGCC CTTTCTATGC CAAAGCCAGG 2460
 80 AAATTTGGGG GGCAGGAGGA GGTCTCAGA ATCCAGTCTG TATCTTTGCT GTATGCCAAA 2520
 CTGAACCCAC TGGGAAATAA TTATGAACA TAAAAATCTT CTGTACTTCA TCCAAGGTA 2580
 CATTGCTTA CTGACAGCAT TTTTGTAAA ACTGTTATTC TTGAAAAAAA AAAAAAAA 2640
 AA

A171 Protein sequence

Gene name: DEME-6 protein (KIAA0452)
 Unigene number: Hs.125783
 ProbeSet Accession #: AL039402
 Protein Accession #: AAC39582
 Signal sequence: none
 Transmembrane domains: 210-226
 Cellular Localization: plasma membrane

10 1 11 21 31 41 51
 1 MTALDLFLTN QFSEALSYLK PRTKESMYHS LTYATILEMQ AMMTFDFQDI LLAGNMKEA 60
 2 OMLQQRHRRK SSVTDSFSSL VNRPTLGQFT EEEIHAECY AECILQRAAL TFLQDENMVS 120
 3 FIKGGIKVRN SVQTYKELDS LVQSSQYCKG ENHPHFEGGV KLGVGAFNLT LSMPLTRILR 180
 15 4 LLEFVGFSGN KDYGLLQLEE GASGHSFRSV LCVMLLLCYH TFLTFLVLTG NVNIREARKL 240
 5 LKPYLNRYPK GAIFLFFAGR IEVIKGNIDA AIRRFEBCE AQOHWKQFHH MCYWEIWMCF 300
 6 TYKGGWKMSY PYADLLSKEN CWSKATYIYM KAAYLSMFGK EDHKPFQDDE VELFRAVPL 360
 7 KLKIAKSLP TEKFAIRKSR RYFSSNPISL FVPALMMYI WNGYAVIGKQ PKLTDGILEI 420
 8 ITKAEMLEK GPENEYSVDD ECLVKLLKGL CLKYLGRVQE AEENFRSISA NEKKIKYDHY 480
 20 9 LIPNALLELA LLLMBQDRNE EAIKLLESBK QNYKNYSMBE RTHFRIOAAT LQAKSSLENS 540
 10 SRSMVSSVSL

A172 DNA sequence

Gene name: EST
 Unigene number: Hs.200102
 ProbeSet Accession #: AL117406
 Nucleic Acid Accession #: none found
 Coding sequence: 1-4044 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51
 1 ATGACTAGGA AGAGGACATA CTGGGTGCCC AACTCTTCTG GTGGCCTGGT GAATCGTGGC 60
 2 ATCGACATAG GCGATGACAT GGTTCAGGA CTTATTATATA AAACCTATAC TCTCCAAGAT 120
 35 3 GGGCCCTGGA GTCAGCAAGA GAGAAATCCT GAGGCTCCAG GGAGGGCAGC TGICCCACCG 180
 4 TGGGGGAAGT ATGATGCTGC CTTGAGAAC ATGATTCCCT TCCGTCCCAA GCGGAGGTTT 240
 5 CCTGCCCTCC AGCCCTCTGA CAATGCTGGC CTGTTCTCCT ACCTCACGCT GTCATGGCTC 300
 6 ACCCGCTCA TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACACCAT CCCTCCACTG 360
 7 TCAGTCCATG ATGCTCAGA CAAAATGTC CAAAGGCTTC ACCGCTTTG GGAAGAAGAA 420
 40 8 GTCTCAAGGC GAGGGATTGA AAAAGCTTCA GTGCTTCTGG TGATGCTGAG GTTCCAGAGA 480
 9 ACAAGGTTGA TTTTCGATGC ACTTCTGGGC ATCTGCTTCT GCATGCTGAG TGTACTGGGG 540
 10 CCAATATTGA TTATACCAA GATCCTGGAA TATTCAGAAG AGCAGTTGGG GAATGTTGTC 600
 11 CATGGAGTGG GACTCTGCTT TGCCCTTTTT CTCTCCGAAT GTGTGAAGTC TCTGAGTTTC 660
 45 12 TCTCCAGTTT GGATCATCAA CCAAGCACA GCCATCAGGT TCCGAGCAGC TGTTCTCTCC 720
 13 ATCAGCTTCT TCACCGGTGA TGTAACCTAC CTGTTTGAAG GGGTGTGCTA TGGACCCCTA 840
 14 GTACTGATCA CCTGCGCATC GCTGGTCATC TGCAGCATT CTTCCTACTT CATTATTGGA 900
 15 TACACTGCAT TTATTGCCAT CTTATGCTAT CTCTGGTTT TCCCACTGGC GGTATTTCATG 960
 50 16 ACAAGAATGG CTGTGAAGGC TCAGCATCAC ACATCTGAGG TCAGGACCA GCGCATCCGT 1020
 17 GTGACCAAGT AAGTTCTCAC TTGCATTAA CTGATTAAAT TGTACACATG GGAGAAACCA 1080
 18 TTTGCAAAAT TCATTGAAGG TATGGAAGT CTGACTTTCT GCTCCAAACC TGGTGATGGC 1140
 19 ATGGCCCTCA GCATGCTGGC CTCTTGAAT CTCTTCTGGC TGTCTAGTTT CTTTGTGCTT 1200
 20 ATTGCAGTCA AAGGTCTCAC GAATTCACAG TCTGCAAGT TGAGGTTCAA GAAGTTTTC 1260
 55 21 CTCACAGAGA GCGCTGTTT CTATGTCCAG ACATTACAAG ACCCCAGCAA AGCTCTGGTC 1320
 22 TTTGAGGAGG CCACTTGTTC ATGGCAACAG ACCTGTCCCG GGATCGTCAA TGGGGCACTG 1380
 23 GAGCTGGAGA GGAAGGAGGC TGCTTCTGAG GGGATGACCA GGCCTAGAGA TGCCCTCGGG 1440
 24 CCAAGAGGAG AAGGGACACG CTTGGGCCCA GAGTTGCACA AGATCAACT GGTGGTGTCC 1500
 25 AAGGGGATGA TGTTAGGGGT CTGCGGCAAC ACGGGGAGTG GTAAAGACAG CCGTGTGTCA 1560
 60 26 GCCATCTCGG AGGAGATGCA CTTGCTCGAG GCGTGGTGG GGGTGACAGG AAGCCTGGCC 1620
 27 TATGTCCTCC AGCAGGCTTG GATGCTCAGC GGGAAACATCA GGGAGAACAT CCTCATGGGA 1680
 28 GGCGCATATG ACAAGGCCCC ATACCTCCAG GTGCTCCACT GCTGCTCCCT GAATCGGGAC 1740
 29 CTGGAACCTT TGCCCTTTGG AGACATGACA GAGATTGGAG AGCGGGGCTT CAACCTCTCT 1800
 30 GGGGGGCGAGA AACAGAGGAT CAGCTGGGCC CGCGCGTCT ATTCCGACCG TCAGATCTAC 1860
 65 31 CTGCTGGAGC ACCCCCTGTC TGCTGTGGAC GCCACGTTGG GGAAGCACAT TTTTGAGGAG 1920
 32 TGCATTAAGA AGACATCTAG GGGGAAGACG GTGCTCTCGG TGACCCACCA GCTGCAGTAC 1980
 33 TTAGAATTTT GTGGCCAGAT CATTTTGTTG GAAATGGGA AAATCTGTGA AAATGGAAC 2040
 34 CACAGTGAGT TAATGCAGAA AAAGGGGAAA TATGCCCAAC TTATCCAGAA GATGCACAG 2100
 35 GAAGCCACTT CGGACATGTT GCAGGACACA GCAAGATAG CAGAGAAGCC AAAGGTAGAA 2160
 70 36 AGTCAGGCTC TGGCCACCTC CTTGGAAGAG GGTCTCTTGA GTTGGAGGGT CTACCAACAC 2220
 37 CAGCTCACAC AGGAGGAGGA GATGGAAGAA GGCTCCTTGA GTTGGAGGGT CTACCAACAC 2280
 38 TACATCCAGG CAGCTGGAGG TTACATGCTC TCTTGCAATA TTTTCTCTCT CGTGTGCTG 2340
 39 ATCGCTTCTT TAACGATCTT CAGCTTCTGG TGGCTGAGCT ACTGGTTGGA CGAGGGCTCG 2400
 40 GGGACCAATA GCAGCGGAGA GAGCAATGGA ACCATGGCAG ACCTGGGCAA CATTGCAGAC 2460
 75 41 GTGGGGGTCT GCTCCTCAGG GATTTTCACC AAAGTACGGA GGAAGGCATC CACGGCCCTG 2520
 42 CACAACAAGC TCTTCAACAA GGTTTTCGCG TGCCCATGTA GTTCTTTTGA GCTCTTGGCC 2580
 43 ATAGGCCGGC TTTTGAACCTG CTTGCGAGGG GACTTGGAAC AGCTGGACCA GCTCTTGGCC 2640
 44 ATCTTTTCAG AGCAGTCTCT GGTCTGTGCC TTAATGGTGA TCGCGCTCTT GTTGATTGTC 2700
 80 45 AGTGTGCTGT CTCCATATAT CTTGTTAATG GGAGCCATAA TCATGGTTAT TTGCTTCATT 2760
 46 TATTATATGA TGTTCAGAAA GGCATCTGGT GTGTTCAGAA GACTGGAGAA CTATAGCCGG 2820
 47 TCTCCTTTAT TCTCCACATC CCTCAATCTT CTGCAAGGCC CTGATGCCGA GAATAACTAC 2880
 48 GGAAAGACTG AAGACTTCAT CAGCCAGTTT AAGAGGCTGA CTGATGCCGA GAATAACTAC 2940
 49 CTGCTGTGTT TTCTATCTTC CACACGATGG ATGGCAATGA GGTGGAGAT CATGACCAAC 3000
 50 CTTGTGACCT TGGCTGTTGC CCGTTCGTG GCTTTTGGCA TTCTCTCCAC CCGCTACTCC 3060
 51

5 TTTAAAGTCA TGGCTGTCAA CATCGTGTCTG CAGCTGGCGT CCAGCTTCCA GGCCACTGCC 3180
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 CCACAGCATG GGGAAATCAT ATTTACAGAT TATCACATGA AATACAGAGA CAACACACCC 3360
 ACGTGCTTC ACGCATCAA CCTGACCATC CGGGCCACG AAGTGGTGGG CATCGTGGGA 3420
 AGGACCGGCT CTGGGAAGTC CTCCTTGGGC ATGGCTCTCT TCGGCTTGGT GGAGCCCATG 3480
 GCAGGCGGGA TTCTCAITGA CGGCTGGAC ATTTGCAGCA TCGGCTTGGG GGACTTGGCG 3540
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 CTAGATCCCT TTGACCGTCA CACTGACCAG CAGATCTGGG ATGCCTTGGG GAGGACATTC 3660
 10 CTGACCAAGG CCATCTCAAA GTTCCCCAAA AAGCTGCATA CAGATGTGGT GGAAAAAGGT 3720
 GGAACCTTCT CTGTGGGGGA GAGGCAGCTG CTCTGCATTG CCAGGGCTGT GCTTTCGCAAC 3780
 TCCAAGATG TCCTTATCGA TGAAGCCACA GCCTCCATTG ACATGGAGAC AGACACCCCTG 3840
 ATCCAGCGCA CAATCCGTGA AGCCTTCCAG GGCTGCACCG TGCTCGTCAT TGCCCAACCGT 3900
 GTCACCACTG TGCTGAACCTG TGACCACATC CTGGTTATGG GCAATGGGAA GGTGGTAGAA 3960
 15 TTTGATCGGC CGGAGGTACT GCGGAAGAAG CCTGGGTCTT TGTTCGAGC CCTCATGGCC 4020
 ACAGCCACTT CTCTACTGAG ATAAGGAGAT GTGGAGACTT CATGGAGGCT GGCAGCTGAG 4080
 CTCAGAGGTT CACACAGTGT CAGCTTCGAG GCCACAGTC TCGACCTTC TTGTTTGGAG 4140
 ATGAGAACTT CTCTGTGAAG CAGGGGTAAA TGTAGGGGGG GTGGGGATTG CTGGATGGAA 4200
 ACCCTGGAAT TGCGTACTTG ATGGCTCTCA AGACCTTAGA ACCCCAGAAC CATCTAAGAC 4260
 20 ATGGGATTCA GTGATCATGT GGTTCCTCCTT TTAACCTACA TGCTGAATA TTTTATAATA 4320
 AGGTAAAGC TTATAGTTTT CTGATCTGTG TTAGAAGTGY TGCAAATGCT GTACTGACTT 4380
 TGTAAATAT AAAACTAAGG AAAACTCAAA AAAAAA AAAA

25 Al73 Protein sequence
 Gene name: EST
 Unigene number: Hs.200102
 Probeset Accession #: AL117406
 Protein Accession #: none found
 Signal sequence: none found
 30 Transmembrane domains: 169-185, 199-215, 275-291, 304-320, 387-403, 770-786, 829-845, 907-923, 927-943, 1018-1034
 PFAM domains: ABC_transporter [502-673], ABC_membrane_region [163-432, 771-1060]
 ATP-binding_domains [508-516, 1139-1147]
 Cellular Localization: plasma membrane

35 1 11 21 31 41 51
 MTRKRTYVWP NSSGGGLVNRG IDIGDDMVSG LIYKTYTLQD GPWSQQRNP EAPGRAAVFP 60
 WQKYDAALRT MIPFPRKPRF PAPQPLDNAG LPSYLTVSWL TPLMIQSLRS RLDENTIPPL 120
 40 SVHDASDNV QRLHRLWEEF VSRRGIEKAS VLLVMLRFQR TRLIFDALLG ICPCIASVLG 180
 PILIIPKILE YSEEQLGNNV HGVGLCFALP LSECVKSLSP SSSWIINQRT AIRFRAAVSS 240
 FAFELIQLFK SVIHITSGEA ISFFTGDVNY LPEGVICYGLP VLITCASLVI CSISSYFIIG 300
 YTAFLAILCY LLVFPPLAVFM TRMAVKAQHH TSEVSDQRIR VTSEVLTCIK LIKMYTWEKF 360
 45 FAKIIEGMES LTPCSKPGDG MAPSMLASLN LLRLSVFFVP IAVKGLTNSK SAVMRFKKFF 420
 LQESPVPYVQ TLQDPSKALV FEEATLSWQQ TPCGIVNGAL ELERNHASE GMTRPRDALG 480
 PEEEGNSLGP ELHKINLVVS KGMMLGVCNG TGSGKSSLLS AILEEMHLE GSVGVQGSIA 540
 YVPQGANIVS GNIRENLMG GAYDKARYLQ VLNCCSLNRD LELLFPDGMT EIGERGLNLS 600
 GGQKQRIELA RAVYSDRQIY LLDPLSAVD AHVGRHIFEE CIKKTLRGKT VVLVTHQLQY 660
 50 LEFCQGIILL ENKICENGT HSELMQKKGK YAQLIQMHK EATSDMLQDT AKIAEKPKVE 720
 SQALATSLSE SLNGNAVPEH QLTQEEEMEE GSLSWRVYHH YIQAAGGYMV SCIIFFVVL 780
 IVFLTIPEFW WLSYWLQEQS GTNSSRESNG TMADLGNLAD NPQLSPYQLV YGLNALLLIC 840
 VGVCSGIFT VKTRKASTAL HNKLFNKVFR CPMSFFDTIP IGRLLNCPAG DLEQLDQLLP 900
 IFSEQLVLS LMVIAVLLIV SVLSPYILLM GAIMVICFI YMMFKKAIG VFKRLNYSR 960
 55 SPLFSHILNS LQGLSSIHVY GKTEDPISQF KRLTDAQMNY LLLFLSSTRW MALRLHMTN 1020
 LVTLAVALFV AFGISSTPYS PKVMVAVNVL QLABSFQATA RIGLETEAQF TAVERILQYM 1080
 KMCVSEAPLE MEGTSCPCQW PQHGEIIPQD YHMYRDNTP TVLHGINLTI RGHEVVGIVG 1140
 RTGSGKSLG MALFRIVPEFM AGRILIDGVD ICSIGLEDLR SKLSVIPQDP VLSGTLIRPN 1200
 LDPPDRHTDQ QINDALERTF LTKAISKFPK KLETDVVENG GNFSVGERQL LCIARAVLRN 1260
 60 SKILIDEAT ASIDMETDTL IQRTIREAFQ GCTVLVIAHR VTTVLNCDHI LVMGNKRVVE 1320
 FDRPEVLRKK PGSLFAALMA TATSSLR

65 Al74 DNA sequence
 Gene name: ESTs
 Unigene number: Hs.128899
 Probeset Accession #: AA983251
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51
 ATGCTGTCTG GCTTCTTGAT GAGTCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60
 GGAAGAAAC TTCCGTGGGA GCCTTCCATC GGTGGGCACA CTTCCCGAGG GCGAGGCAGC 120
 75 GACCGGGAGA GGGAGAGCCG GCCCGAGGCT GCCCGGCTCC TGTGGGACCG CGCTGCAGCC 180
 GGGGAGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GATCCCGCGC CCAGCAGCAG 240
 CCGCGGCCGC CGCCAGCTGG GCAAGCTCCC GGGACTCGCG CTGGGGGCGC GCAGGACCTT 300
 CGCTGCGTC CTGGACGTTT CCGGGGAGG GTCCGGTTGC CAGTGAAACC TCCAGAGGCT 360
 TCCGAGCAGC AGCCCCGGGG GCCTTCTGAC TGATCCCGA GATTTCATC AGCAGATGCA 420
 80 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGCTG AGGACGCGGA TGGCTTAGGA 480
 GCTCCTGGAC CTAGGGCCCG CGCTCGTCGC CTCTGGGGG TCGCGGCAGA GGGGAGTGGC 540
 CCGCGCGGAA AGCGCGCGGG GACAGTCAGT GACGAGGCCG GGGGTTCGCC GGGGCCACGA 600
 CTTCTCGAG AGCGTCTGCG GCTCTCTGGA GACGCGCTGT CCGCGCCGAG GGTGGTGCCA 660
 TGTGGGCGC TCGCGCTCG TCCGTCTCCT CATCTCGAA CGCGCTTCG CTCTGCGAGC 720
 TGTCTGCTGC TCGCTGTCTG GCGGCGGGGG CGAGGGCCCA GCGCGAGTA CTGCCACGCG 780

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TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 840
GGCGAGCCCA CCATCTGCTG CGGCAGCTGC GCCTTGCCTC ACTGCTGCTC CAGCGCCGAG 900
CGCGCGCTGG ACCAGGGGCG CTGGGACAAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGCG 960
CGCGCGGACA AAGACGGGCG CCGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020
GGAGACGGCG AGGGTGCCTC CCTCAGGGCT TTCCCGGGCG TGCTGCCCGG TGCCAGACGC 1080
TCCCGGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGCG TGCTGCCCGG TGCCAGACGC 1140
CGCGGATTCC CATCTTCTCC ACGCGGCGCG CCCTCTCCCG TGCCAGCGGC CGCCTTGCCC 1200
ATCTACGTGC CGTTCCTCAT TGTGGCTCC GTGTTTGTG CCTTTATCAT CTGGGGTCC 1260
CTGGTGGCAG CCTGTGCTG CAGATGTCTC CGGCCTAAGC AGGATCCCA GCAGAGCCGA 1320
GCCCCAGGGG GTAACCGCTT GATGGAGACC ATCCCATGA TCCCGAGTGC CAGCACCTCC 1380
CGGGGGTCTG CCTCAGCCCA GTCCAGCACA GCTGCCAGT CCAGCTCCAG CGCCAACTCC 1440
GGGCGCCGCG CGCCCCAAC AAGGTACAG ACCAAGTGT TCTCTGTGC TGAAGTGTCA GCAGGCCACC 1500
AACAACTGTG ATGTCAACAT GCCACGAAT TTCTGTGTC TGAAGTGTCA GCAGGCCACC 1560
CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCAT ACGTGGGGTA CACGGTGCAG 1620
CAGCACTCTG TCGCCATGAC AGCTGTGCCA CCTTCTAGG ACGGCGTGA GCCTGGCTAC 1680
AGGCAGATTG AGTCCCCCTT CCCTCACACC AACAGTGAAC AGAAGATGA CCCAGCGGTG 1740
ACTGTATAAC CAGAGTACAC TGGTGGGTTC CTTTACTGAA GGGAGAGGAA GGCAGGGGTG 1800
GATTCTCGAG GTGGAAGTCC GCACATGTCC GTGGTATTTA TGGCAGGAT CCTTTGGATG 1860
GCTTCATTTC CCCCCAGACT GTATGAAAC ATCTCCGAAT TAGCATTCTT GGATATGTTT 1920
CATCCAGGGT ATCATTGATT TATGATGGA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980
TTGCTGATGG GTGTATAACA AATGCTTGG TCCGAAGTGC CCTTGAGATA TGGTGTGACA 2040
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TTGTTGTTGA CTGCACAGG TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTTT 2160
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TATATTGAAA TCATAAATA TCACCGCTG CTCTCTGAG TTACTTTTAA TTTTGCTTG 2940
TGGTTATGGT TTGGCGTTT CTTCTGTTG GTTTTCAGAG CCCCATGCT ATATAGTCTC 3000
GAGTGCAAGT AATTACTATA CTTGTAATG AAGATCAGTA TTTCTGCTA GATCTGATA 3060
AAAAATTTT TGTCTTAGT TATAAAAT CAAGAAATG TGTACAAAG ATACTTAGTA 3120
TAGCTCTCA GCCATAACCT GAGACTGGG ATGAATTTA AACAGATAC GATTACTTT 3180
GCAGATCATA AGGCTTTTA TACTCTGTT ATCAAAATG CTTATTTT AGGCATAG 3240
GATTGTAAG AGAAAGCTT TTCACGAAG GATTGCCTT CTCTCCAC ACTGTTCTG 3300
ATTTCTCTC TCTTTAGGC CTCAACAGC ACTGATTCA TTGCCAATG TCCAATTT 3360
CAAATTCAG TGAATTTAT TGTGTGTT TACTTATAT AAAAAAGAT AACTTAAAG 3420
ATGTGCAAGT ACATTTCAC CTGCTAGCAC AACAGTAT TTGTAATTA ACAATCGCT 3480
GTATGGATG GTCTTCTACA CATTTATGTC TATAGATATC TATCGATCAT CTTTCTATT 3540
TGTTTCATGA CTGAATAATG TAAACCAAG GTTGGCAAT GGTATCATCA ATGATACTCA 3600
TTTTTTAATA ACCAAGGCA GGGGAAATC ATTTTACTTA TTAATAATA TTTTATGAT 3660
TGAAAAAAA AAAAAAAA AAAAAAAA

A175 Protein sequence

Gene name: ESTs
Unigene number: Hs.128899
Protein Accession #: none found
Signal sequence: 1-11
Transmembrane domains: 402-424
Cellular Localization: not determined

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65
70

1 11 21 31 41 51
MLSGFLMSPS TQHRAYTPG GKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60
GEAEKGNRGE PFAWIRAQQ PRPPPAQAP GTAAGGAQDP RLPRGRSRGR VRLPVKPPPA 120
SGRQPRGPSD CIPRPPSASA THKAVPKGTG PPAEDGDGLG APGRARRRR LLGVAAEGSG 180
PRGKRRTVTS DEARGSPGPR LLGDRPALSG DALSAAPRVV CGALAARPSP HFGTPLRSCS 240
CCWLRCWRRG RGPSGEYCHG WLDAGVWRI GFQCPERFDG GDATICGSC ALRYCCSSAE 300
ARLDQGGCDN DRQOGAGEPG RADKDGPRRL GRASCLRGTD GDGEGAPPV RAWQRCSPBG 360
SPKGRQLLRA PFGLLPRARR RGFPSSPRGG PSPLQRPALP IYVPFLVGS VFVAFIILGS 420
LVAACCCRL RPKQDPQQR APGGRNRLMET IPMIPASST RGSSSRQSST AASSSSSANS 480
GARAPPTRSQ TNCCLPEGTM NNYYNMPIN FSVLNCQAT QIVPEQGQYL HPFVGVTVQ 540
HDSVPMTAVP PFMDGLQPGY RQIQSPFPH T NSEQMYPV TV

A176 DNA SEQUENCE

Gene name: ESTs, Weakly similar to QGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
Unigene number: Hs.19322
Probeset Accession #: AA088458
Nucleic Acid Accession #: AA088458
Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
GCCCTTGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60

5 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAAGGTTT GGAGATGATG 120
 GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAAGGAGG CCAGCGCGCG 180
 CTGGGCGCAGA GCAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCTGG GGGAGCTGCT GCGTGCAGCC 300
 TGTGCCAGCC GGGGCTGCCC CCGTCTCTCC TCGGGGCCCC CCGTCCCTGC CTGACGTCC 360
 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCTCTCATG TGAAGGAGCA GAACCGACTC 420
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCAGC AGCTGGAGCA GGAGAAGTCG 480
 GCGCTCATT AAGCAGCTGT TGAAGGCCGC GCGCTGAGCC AGCAGGACGG GGGACCTCTG 540
 10 GATTCCACCT TCATCTAGTC CTGTGGGCC CGGTGGGCC CCAGGGCCAG CCTGGCACTC 600
 AGCCCTTGA GGTGGGGCGC CCATCGCAC CCACCTCTC TGGCTGGAGA CCGCGGCGAG 660
 GCGGCGGAC AGTCCCGGAG TGGGGGCTT CTGCGCGCC TTGCCAGATG GGCTCCCCAG 720
 GCGTGCCTCC GGTGCTGCCC CGCACCGAGC GCTTGACTCC GTTTGGGCTC CTGGTTGYTG 780
 ACATGGGCTG GGGGCTCTCT TGAATCGCA TAACTCGAG CTACTACTGG CCGCTGTCTG 840
 15 TGGACAGTGG GTTACCCCTC CATGAGTTAG CGTCCCGCG TTTCCAGCG TGCGGCGCTG 900
 GGTCCCTCT TCAGGGAAG GCACTGCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC 960
 AGAGGGCGCG GGGCGGCTCC GACGCGGCTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020
 CAGGACCGAG TGCTGTGAGC TGGAGCGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCTC 1080
 GTAAGCGGGG GGTGCTGCCC TGGCTGGGGA GCGCCAGGGA TAGCGGTGCG ACTTCAGGTT 1140
 CTGGCCAGCG CTGCTCAGC CTGGCTGCG CCGATCGGA CGCGGGTGG GCGAGAGCTT 1200
 20 GCGCTGCTG TGCCTCCAC AGACCTCGG GTGATGGCTT TCCCTCTCTT GCGCGGAGCG 1260
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 GACAGCTCCC AGGCAAGTCA TAGGCAAGC CTGTTTCCCC CGACTCAGGA TTTCCAAGGC 1380
 CTGGGGTCTT GCTCACCCCC CTGTGCTCTC ACGCCAGGCC TGTCCCCAGG TTTCACTGCG 1440
 25 GAGAGGGCAC GTCCCTCAGC CAAGGAAAC GAGAACCCCC AGGGTACAGG AGGAGGCTGG 1500
 GCGAGGTCCC CTGGGTGTC ACTCCCTCAG CCGCTGCCCA GCGCCACTCC CGCTGGTGCT 1560
 GGAGTAGCGA CTGGTGGGGG GCGCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTCAACA 1620
 GAAACCGAGG CACGGCAACA GCATCGATGG GTTCTGACG CAGGGGCCCC CGATGCGGGG 1680
 TCAGTGTGTT TGGGGCGCAG GCGCTCGATG GCGGGGTGAG TGGTGGGGG GCGCAGGGCC 1740
 30 CCGACAGCG GTGCTAGTGG TGGGGGCGC AGGGCCCCCT CGTGTCCAG GCATTTGGT 1800
 ACACTGTCCC ACAGGCAACC TGCTCAGAG GAGGGGCGCT GGCAGGCGAG GTGGCACTC 1860
 CTTTCCGAG CCCAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTTCC 1920
 TGCTGCACCT GGTCTGCAGG GGTGTCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT 1980
 GCGCTCTTAC CCGTGAAGTG GGAGTGGGCT TTTCCAGGGA CATAAGGATG TCAGGCGCTG 2040
 35 ACCTCTGCGG CAGGAAAGGG TGCAAGTCTT GAGGGCTGT GCGCCACAGC CCGACACCCC 2100
 AGGTGAGCTG CAGGCGAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCGCTCAGCA 2160
 GCGTGGGCTC TGCCCAACAG GCGCTCCCCA CGTCTGCTT TGAGGGTGCC TGCCATGCCC 2220
 TGGGGGATCC TGGCATTTT ACTGAGTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG 2280
 GGTGACTTCA TCAGGAGACC GCGCACATAG AGCTGGAACC CGCAGCTGAA GCGGAAATGT 2340
 40 GAGACAGGCT GGCACCTCCG GAAAACTGC CTTTCAGCCT TGGTGTCCG TGCAAGGTGA 2400
 AAAGAAATAG GTCTCCAG TTTACAGCTT GAAATCAGGC TAGTGAGTGG CCCTGGAGAC 2460
 CACGAGGGGA GAATTTAAG GCGCCGCGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT 2520
 GCAGAGCTCG CTGAGGCTT GCGCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAAGATGT 2580
 GAGCAGGCTC CTTGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGAGGT ACATACAGCT 2640
 45 GCGTGTGACA GTGATGACA CCGGAAATG TCTCAGGATG TTGAATGTG TCCTTGGGGG 2700
 CAGAAGTGTG CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACACCA GGCCTCAGGA 2760
 TTTTGTGTTT ATCAAGTTCC AAGGAAAGG AACATCTCAG CCGGGCGTGG TGGTTCAAGC 2820
 CTGGAATCCC AGCATTTGAG CCGAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880
 CCCCATCTCT ACARAAAAA AAAAGAAAG AAAGAAATG AGAGATCCAG GTTTAAAAAT 2940
 50 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000
 TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAGTA ACAGTGTGTT ATATATCTAA 3060
 AGAATAAAA GAGATTCTG GAAACATGAA AAAAA

A177 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

60 1 11 21 31 41 51
 | | | | |
 GCGGAACACC GCGCGCGCGT CGCGGAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
 TCCTCTGTGG ACCTCTGCGG TCTCTCTCTC TTCTCCAGGT TTGCTGGCTG CAGTGGCGGG 120
 65 CTTCCGAGCC GTGCGCGGGG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180
 CCGAGCAGGA GCGCGGCCAG GCGCTGGGGA AAGTATTCTT GGGCTGCCCT GGGCAAGAGC 240
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCATCTGTGG GAATGGCGAG ACAGTCCAGG 300
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA GGTATCTTAC 360
 GAAGACACAA GAGAGATGAG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAGGGGTC 420
 70 CTTTCCCCAA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACAC AAGATTTTCT 480
 ACAGCATCAC GGGGCGGGGG GCAGACAGCC CCCCTGAGGG TGTCTTGGCT GTAGAGAAGG 540
 AGACAGGCTG GTTGTGTGTT AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
 TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGG GGACCCCATG AACATCTCCA 660
 TCATCTGTAC CGACAGGAAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCGAGGGA 720
 GTGTCTTAGA GGGAGTCTTA CCAAGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
 75 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAA 840
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 CCAATGGGCT GAGCGGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
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5 CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCCACTGG GGAGCCTGTG TGTTCTACA 1440
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 ATGGAAGCCC TCCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680
 ACCATGGCCC AGTCCCTGAG CCCCCTCAGA TCACCATCTG CAACCAAGC CCTGTGCGCC 1740
 ACGTGTGAA CATCAGCGAC AAGGACCTGT CTCCCCACAC CTCCCCTTTC CAGGCCGAGC 1800
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTT TCTCTGTCTG 1920
 10 ACCATGGCAA CAAGAGCAGC CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
 ATGTGGAAC CTGCCCCTGA CCTGGAAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
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 TCAAGGAGCC CCTCTACTC CCAGAAGATG ACACCGTGA CAACGTCTTC TACTATGGCG 2160
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 15 AGGCCAGGCC GGAGGTGGTT CTCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340
 AGGCGGCTAA CACAGACCCC ACAGCCCCGC CCTACGACAC CCTCTTGGTG TCGACTATG 2400
 AGGCGAGCGG CTCGACGCTC GCGTCCCTGA GCTCCCTCAC CTCTCCGCC TCCGACCAAG 2460
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCGCTT CAAGAAGCTG GCAGACATGT 2520
 20 ACGTGTGGCG GGAGGACGAC TAGGCGGCT GCCTGACAGG CTGGGGACCA AACGTCAGGC 2580
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 25 TGCTCAACCC TGTGTCTCTG GCCTGGGCTC GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
 CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTTTTTTT AATGCTATCT 2940
 TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGGCCAGA GCTGCTGGGC CCACTGGCCG 3000
 TCCTGCATTT CTGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTTT 3060
 30 ATACTGAGTG TGCTAGGTT GCCCTTATT TTTTATTTTC CCTGTTGCGT TGCTATAGAT 3120
 GAAGGGTGAG GACAACTGTG TATATGTACT AGAACTTTT TATTAAAGAA A

A178 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675

Cellular localization: plasma membrane

1 11 21 31 41 51
 45 MGLPRGFLAS LLLLQVCNLQ CAASEPCRAV FREAEVTLBA GGAEQEPGQA LGKVFMGCPG 60
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
 KGPPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGMLLLN KPLDREBIK 180
 YELFGHAYSE NGASVEDPMN ISLIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
 50 DEODRIYTYN GVAVYSHSQ EPKDPHDLME TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TDMDGDSSTT TAVAVVEILD ANDNAPMFDK QKYEAVHPEN AVGHEVQRLT VTDLDAFNSP 360
 AWRATYLLIM GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEFVC VYTAEDPDKE NQKISYRILR 480
 DPAGWLAMPD DSQGVTAAGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLTLID 540
 55 VNDHGPVPEP RQITICNQSP VRHVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
 TVVLSLKKEFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGGFILFVL 660
 GAVLALLFL LVLVLLVRKK RKIKEPLLLP EDDTRDNVFI YGEBGGGEED QDYDITQLHR 720
 GLEARPEVVL RNDVAPTIIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

A179 DNA SEQUENCE

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
 Unigene number: Hs.258583
 Probeset Accession #: NM_012152
 Nucleic Acid Accession #: NM_012152
 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 70 CTCTTTTAAA TTCTTTCTA GGATGTTTCA TTCTTTCCA CAATGAATGA GTGTCACTAT 60
 GACAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTGCA TGACTGGACA 120
 GGAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTTT TCTGCCTGTT TATTTTTTTT 180
 TCTAATCTCT TGGTCATGCG GGCAGTGATC AAAAACAGAA AATTTCATTT CCCCTCTCAC 240
 75 TACCTGTTGG CTAATTAGC TGCTGCCGAT TTCTTCGCTG GAATTGCCCTA TGTATTCCTG 300
 ATGTTTAACA CAGGCCCACT TTCAAAACTT TTGACTGTCA ACCGCTGGTT TCTCCGTGAG 360
 GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT GSCCGTGGAG 420
 AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGCTGACA 480
 CTGCTCATTT TGCTGTCTG GGCATCGGCC ATTTTATAGG GGGCGGTCCC CACACTGGGC 540
 80 TGGAAATTGCC TCTGCAACAT CTCTGCCCTG TCTTCCCTGG CCCCATTTC CAGCAGGAGT 600
 TACCTTGTIT TCTGACAGT GTCCAACTTC ATGGCCTTCC TCAATCATGT TGTGGTGTAC 660
 CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAAGCTCT TGTCTCCGCA TACAAGTGGG 720
 TCCATCAGCC GCCCGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780

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GCCTTTGTGG TATGCTGGAC CCCGGGCGTG GTGGTTCTGC TCCTCGACGG CCTGAACTGC 840
AGGCAGTGTG GCGTGCAGCA TGTGAAAAGG TGGTTCTGTC TGCTGGCGCT GCTCAACTGC 900
GTCGTGAACC CCATCATCTA CTCTACCAAG GACGAGGACA TGTATGGCAC CATGAAGAAG 960
ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGGGGTC CCTCTGGCAT CCGCTCCACA 1020
GTCCTCAGCA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080
GTCTGCAATA AAAGCACTTC CTAAACTCTG GATGCCTCTC GGCCCAACCA GGTGATGACT 1140
GTCITAGG

A180 Protein sequence:
Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
Unigene number: Hs.258583
Probeset Accession #: NM_012152
Protein Accession #: NP_036284
Signal sequence: none found
Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295
Cellular Localization: plasma membrane

1 11 21 31 41 51
MNECHYDIKHM DFFYNRSNTD TVDDWTGTRL VIVLCVGTFP CLPIFFPSNSL VIAAVIKNRK 60
FHFFPYLLA NLAAADFFAG IAYVFLMPT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL 120
LVIAVERHMS IMRMVHSNL TKKRVTLILL LVWAIAPMG AVPTLGMNCL CNISACSSLA 180
PIYSRSYLVF WTVSNLMAPL IMVVVYLRIV VYVIRKTNVL SPHTSGSISR RRTPMKLMKT 240
VMTVLGAPVF CWTPLGLVLL LDGLNCRQCG VQHVWRKFWLL LALLNSVVPV IYISYKDEDM 300
YGTMKMKICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAFCNK STS

A181 DNA SEQUENCE
Gene name: ESTs
Unigene number: Hs.162859
Probeset Accession #: AA569531
Nucleic Acid Accession #: AA569531
Coding sequence: 1-504 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
ATGACCTACA GTTACTCATT TTTCAGGCCT GAGTIGATCG TTAATCATCT TAATTATGTT 60
CATTCTGAAG CCAACAGGAG AACCAAGACC AAAACITTTAT TGCTCTGCTG TCATTTCCTT 120
GATGAAACCT CTGGACTAAG CACACATCTT CCTTGTTTAT CTCTCTCAA GGAGTGTGGA 180
GTGCTTCATC TGACATCCA CGGGAAGAAG GAAGACATGA GAATCACCCA ACAGTCTTCC 240
CAGCTATACC TGTGGGACAT GGGTGGTTT ACAATATTTA AGAACCTGTG GATGAGCCTC 300
ATACCCAGAG GGAACAAACG CTCGCCAAA AGAGTTACAG AAACCATCCT GAGAGATTTT 360
AAGCAGAAGC AAGGTTCAA GATCCAAGAG GAGAGACGAA GAGAGTCTGC AGGACCAAAC 420
CTCTCTTCAT TCTGGTTTGT GGGGAATGCT GGAAGAGGAG ACAGGCCCCA GATTTGGGCA 480
GGAAGTAAAC AGTTTTCAGG CTGAGGCCAA TCTGAGCAGG AACATTCCAA TATTTCTTCA 540
GCTACGTTGT CCCAGCACT CACTGGTTAA CCTTTTATGT CCACCATTTG TGGATTTTCA 600
AGCTACTTGT CAATGGTGAA TATTGATCAT CATCATTATC TACTGAGCTG CTACCATATC 660
CCAGCTACTC CTTCGATGTT GTTCATTATT TTCTCAACAC TCAGCATATT TGCAATATGT 720
TATGTAATAT CACAGACAAG GAAACTGAAC GCAGAAATGT TTTATTTCTT GCCAATATC 780
ACATGAGGAT GAACAATGAA ACCGATTGTA AACCAAGGAT GTCTGATTCC AACATCTCTG 840
GGTCCCTTTT CACTCTGATA TGCTGCAATT AAAAAGCCAT TTCTAAGACT GT

55
60
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A182 Protein sequence:
Gene name: ESTs
Unigene number: Hs.162859
Probeset Accession #: AA569531
Protein Accession #: none found
Signal sequence: 1-46
Transmembrane domains: none found
Cellular Localization: not determined

1 11 21 31 41 51
MTYSYSFFRP ELIVNHLNYV HSEANRRRTK KTLISLLSPL DETSGLSTHL PCLSLSKSCG 60
VLHLDIHGKK EDMRITQSS QLYLWDMGGF TIFENLWMSL IPRGNKRSFK RVTETILRDF 120
KQKQSSKIQE ERRRESAGPN LSSFWFVGNA GRGDRPQIWA GSKQPSG

A183 DNA SEQUENCE
Gene name: ESTs
Unigene number: Hs.179809
Probeset Accession #: N95796
Nucleic Acid Accession #: XM_050197
Coding sequence: 310-1971 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
TCACACGTGC CAAGGGGCTG GCTCAGCGGA ACCAGCCTGC ACGCGCTGGC TCGGGGTGAC 60
AGCCGCGCGC CTGGGCCAGG ATCTGAGTGA TGAGACGTGT CCCCCTGAG GTGCCCCACA 120
GCAGCAGGTG TTGAGCATGG GCTGAGAAGC TGGACCGGCA CCAAAGGGCT GGCAGAAATG 180
GGCGCTGGC TGATTCTTAG GCAGTTGGCG GCAGCAAGGA GGAGAGGCGC CAGCTTCTGG 240
AGCAGAGCGG AGACGAAGCA GTTCTGGAGT GCCTGAACGG CCCCCTGAGC CTAACCGGCC 300

5 TGGCCCACTA TGGTCCAGAG GCTGTGGGTG AGCCGCTGC TCGGCACCG GAAAGCCAG 360
 CTCTTGTG TCAACCTGCT AACCTTTGGC CTGAGGGTGT GTTGGCCGC AGGCATACCC 420
 TATGTGCCGC CTCTGCTGCT GGAAGTGGGG GTAGAGGAGA AGTTCATGAC CATGGTGTG 480
 GGCAATTGGT CAGTGTGGG CCTGGTCTGT GTCCCGCTCC TAGGCTCAGC CAGTGAACAC 540
 TGGCGTGGAC GCTATGGCCG CCGCGGCCCT TTCATCTGGG CACTGTCTCT GGGCATCTCT 600
 CTGAGCCTCT TTCTCATCCC AAGGGCCGCG TGGCTAGCAG GGCTGCTGTG CCGGATGCC 660
 AGGCCCTGAG AGCTGGCACT GCTCATCTGT GGCCTGGGGC TGCTGGACTT CTGTGGCCAG 720
 GTGTGCTTCA CTCCACTGGA GGCCTGCTC TCTGACCTCT TCCGGGACCC GGACCACTGT 780
 CGCCAGGCTT ACTCTGTCTA TGCTTCATG ATCAGTCTTG GGGGCTGCCT GGGCTACCTC 840
 10 CTGCTTGGCA TTGACTGGGA CACCAGTGCC CTGGCCCTCT ACCTGGGCAC CCAGGAGGAG 900
 TGCTCTTTG GCCTGTCTAC CCTCATCTTC CTCACCTGCG TAGCAGCCAC ACTGTCTGGT 960
 GCTGAGGAGG CAGCGCTGGG CCCACCGAG CCAGCAGAAG GGCTGTGGGC CCCCTCTTG 1020
 TGGCCCACT GCTGTCCATG CCGGGCCCGC TTGGCTTTCC GGAACCTGGG GCGCTGTCT 1080
 CCGCGCTGC ACCAGCTGTG CTGCGCATG CCCCGACCC TGCGCCGCT CTCTGTGGCT 1140
 15 GAGCTGTGCA TGTGATGGC GCTGATGGC GAGCGGGCA CCGAGGCCG GAGACACTAT 1200
 GAGGGGCTGT ACCAGGGCGT GCCCAGAGCT GAGCGGGCA CCGAGGCCG GAGACACTAT 1260
 GATGAAGCG TTCCGATGGG CAGCCTGGG CTGTTCTGCT AGTGCGCCAT CTCTGTGGT 1320
 TTCTCTCTG TCATGGACCG GCTGTGGCAG CGATTGGCA CTGAGCAGT CTATTGGCC 1380
 AGTGTGGCAG CTTTCCCTGT GGTGCGCGT GCCACATGCC TGTCACACAG TGTGGCCGT 1440
 20 GTGACAGCT CAGCGCCCT CACCGGGTTC ACCTTCTCAG CCCTGCAGAT CCTGCCCTAC 1500
 ACACTGSCCT CCTCTACCA CCGGAGAAAG CAGGTGTTC TGCCCAAATA CCGAGGGGAC 1560
 ACTGAGAGTG CTAGCAGTGA ACACGTGGT GCTGGAGCA GTGGCCTGCT CCCACTCCA 1620
 GGAGCTCCCT TCCCTAATGG ACACGTGGT GCTGGAGCA GTGGCCTGCT CCCACTCCA 1680
 CCGCGCTCT GCGGGGCTC TGCTGTGAT GTCTCCGTAC GTGTGGTGT GGTGAGGCC 1740
 25 ACGGAGGCCA GGTGTGTTC GGGCGGGGC ATCTGCTGG ACCTGCCAT CTGTGATGT 1800
 GCCTTCTGCT GTGCCAGGT GCGCCATCC CTGTTATGG GCTCCATGT CCAGCTCAGC 1860
 CAGTCTGTCA CTGCTATAT GGTGTCTGCC GCAGGCTGG GTCTGGTGC CATTACTTT 1920
 GCTACACAGG TAGTATTTGA CAGAGCGAC TTGGCCAAAT ACTCAGCGTA GAAACTTCC 1980
 AGCACATTGG GGTGAGGGC CTGCTCACT GGTGCCAGC AAGTAATGT GCTCTCTCT 2040
 30 ATGGGGCTG CCGGCTGGCC GCCAGTTCT GTTGTGCCA AAGTAATGT GCTCTCTCT 2100
 GCCACCTGT GCTGCTGAGG TGCTGAGTG CACAGCTGGG GGCTGGGGG TCCCTCTCT 2160
 CTCTCCCGC TCTTAGGGC TGCTGAGTG GAGGCTTCC AAGGGGTTC CAGTCTGGAC 2220
 TTATACAGGG AGGCCAAG GGTCCATGC ACTGGAATG GGGGACTCT CAGGTGGAT 2280
 ACCCAGGCTC AGGGTAAAC GCTAGCTCC TAGTGTAGG ACACCTAGAG AAGGGTTTT 2340
 35 GGGAGCTGAA TAAACTCAGT CACCTGGTT CCATCTCTA AGCCCTTAA CCTGCAGCT 2400
 CGTCTAATGT AGCTCTTGA TGGAGTTTC TAGGATGAA CACTCTCCA TGGGATTGA 2460
 ACATATGAA GTTATTGTA GGGGAAGAGT CCTGAGGGC AACACACAG AACAGGCTG 2520
 CCTCAGCCCC ACAGGCACTG GTCTTTTTG CTGANTCCA CCCCCCTCT CTTACCTCT 2580
 TT

A184 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.179809
 Probeset Accession #: N95796
 Protein Accession #: XP_050197
 Signal sequence: none
 Transmembrane domains: 21-43, 53-75, 90-112, 125-147, 160-182, 199-221, 323-345, 350-372, 379-401
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MVQLRVVSR LRRHKAQLLL VNLITFGLEV CLAAGITYVP PLLLEVGVVE KPMIMVLGIG 60
 55 PVLGLVCPVL LGSASDHWRG RYGRRRPFIM ALSLGLLSL FLIPRAGWLA GLLCDFRPL 120
 ELALLILGVG LIDFCQVCF TPLEALLSDL FRDPDHCRA YSVYAFMISL GGLGLYLLPA 180
 IDWDTALAP YLTQEECLF GLLTLIFLTC VAATLLVAEE AALGPTPEAE GLSAPSLSPH 240
 CCPCRARLAF RNLGALLPRL HOLCCRMPT LRLFLVAELC SWMALMTFTL FYTDFVGEGL 300
 60 YQGVPRAEFG TEARRHYDEG VRMGLGLFL QCAISLVFSL VMDRLVQRF TRAVYLASVA 360
 AFPVAAGATC LSHSVAVVA SAALTGTFTS ALQILEYTLA SLYHREKQVF LPKYRGDTGG 420
 ASSEDSLMS FLPGPKPGAP PFNGHVAGG SGLLPPFPAL CGASACDVSV RVVVGEPTEA 480
 RVVPGRGICL DLAILDSAPL LSQVAPSLFM GSTVQLSQSV TATMVSAAGL GLVAYFATQ 540
 VVFDKSDLAK YSA

A185 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.11260
 Probeset Accession #: R73640
 Nucleic Acid Accession #: AK002126
 Coding sequence: 1-1593 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 75 ATGGTTCGCC GGGGGCTGCT TGCGTGGATT TCCCGGGTGG TGGTITTGCT GGTGCTCCTC 60
 TGCTGTGCTA TCTCTGTCT GTACATGTTG GCTGACACCC CAAAGGTGA CGAGGAGCAG 120
 CTGGCACTGC CCAGGCCCAA CAGCCCAAG GGAAGGAGG GGTACCAAGC GCTCCTTCAG 180
 GAGTGGGAGG AGCAGCACCG CAACCTACGT AGCAGCCTGA AGCGGCAGAT CGCACAGCTC 240
 80 AAGGAGGAGC TGCAGGAGAG GAGTGAGCAG CTCAGGAATG GGCAGTACCA AGCCAGGAT 300
 GCTGCTGGCC TGGGTCTGGA CAGGAGCCCC CCAGAGAAA CCCAGGCCA CCTCCTGGCC 360
 TTCTGCACT CGCAGGTGGA CAGGAGCAG GTGAATGCTG GGTCAAGCT GGCACAGAG 420
 TATGACAGAG TGCTTTTGA TAGCTTTACT CTACAGAGG TGTACCAAGT GGAGACTGGC 480
 CTTACCCGCC ACCCGAGGA GAAGCTGTG AGGAAGGACA AGCGGATGA GTTGGTGGAA 540
 GCCATTGAAT CAGCCTTGA GACCTGAAC AATCCTGCAG AGAACAGGCC CAATCACCTG 600

5 CCTTACACGG CCTCTGATT CATAGAAGGG ATCTACCGAA CAGAAAGGGA CAAAGGGACA 660
 TTGTATGAGC TCACCTTCAA AGGGGACCAC AAACAAGGAT TCAACCGCT CATCTTATTT 720
 CGACCATTCG GCGCCATCAT GAAAGTGAAA AATGAAAAGC TCAACATGCC CAACACGCTT 780
 ATCAATGTTA TGTGCTCTT AGCAAAAAGG GTGGACAAGT TCGGGCAGTT CATGCAGAA 840
 TTCAAGGAGA TGTGATTGA GCAGGATGGG AGAGTCCATC TCACTGTTGT TACTTTGGG 900
 AAAGAAGAAA TAAATGAAGT CAAAGGAATA CTGAAAACA CTTCCAAAGC TGCCAACTTC 960
 AGGAACITTA CCTTCATCCA GCTGAATGGA GAATTTTCTC GGGGAAAGGG ACTTGATGTT 1020
 GGAGCCCGCT TCTGGAAGGG AAGCAACGTC CTCTCTTTT TCTGTGATGT GGACATCTAC 1080
 10 TTCAATCTG AATTCTCTAA TACGTGTAGG CTGAATACAC AGCCAGGGAA GAAGGTATTT 1140
 TATCCAGTTC TTTTCAGTCA GTACAATCCT GGCATAATAT ACGGCCACCA TGATGCACTC 1200
 CCTCCCTTGG AACAGCAGCT GGTTCATAAG AAGGAAACTG GATTTTGGAG AGACTTTGGA 1260
 TTTGGGATGA CGTGTGAGTA TCGGTGAGAC TTTCATCAATA TAGTGGGTT TGATCTGGAC 1320
 ATCAAGAGCT GGGGCGGAGA GGATGTGCAC CTTTATCGCA AGTATCTCCA CAGCAACCTC 1380
 ATAGTGTAC GAGCGCTGT GCGAGGACTC TTCCACCTCT GGCATGAGAA GCGCTGCATG 1440
 15 GACGAGCTGA CCCCCGAGCA GTACAAGATG TGCATGCACT CCAAGGCCAT GAACGAGGCA 1500
 TCCACGGCC AGCTGGGCAT GCTGTGTTC AGGCACGAGA TAGAGGCTCA CCTTCGCAAA 1560
 CAGAAACAGA AGACAAGTAG CAAAAAACA TGA

20 **A186 Protein sequence:**
 Gene name: ESTs
 Unigene number: Hs.11260
 Probeset Accession #: R73640
 Protein Accession #: NP_060841
 25 Signal sequence: 1-26
 Transmembrane domains: none found
 Cellular Localization: not determined

30 1 11 21 31 41 51
 | | | | | |
 MVRRLGLAWI SRVVVLLVLL CCAISVLYML ACTPKGDEEQ LALFRANSPT GKEGYQAVLQ 60
 EWESQHRNYV SSLKRQIAQL KEELQERSEQ LRNGQYQASD AAGLGLDRSP PEKTQADLLA 120
 FLHSQVDAE VNAGVKLATE YAAVFDST LQKVYQLETG LTRHPPEKPV RKDKRDELVE 180
 AIESALBTLN NPAENSPNER PYTASDFIEG IYRTERDKGT LYELTFKGDH KHEFKRLILF 240
 35 RFPGPIMKVI NEKLAMANTL INVIVPLAKR VDKFRQFMQN FREMCIEQDG RVHLTVVYFG 300
 KEELINEVKGI LENTSKAANF RNFTPIQLNG EFSRGRGLDV GARFWKGSNV LLFPDQVDIY 360
 FTSEFLATCR LNTQPGKKVF YPVLFSQYNP GLIYGHDAV PPLEQQLVIK KETGFWRDFG 420
 FQMTQYRSD FNIIGGFOLD IKGWGGEVDH LYRKYLHSLN IIVRTFVRGL FHLWHEKRCM 480
 40 DELTPEQYKM CMQSKAMNEA SHGQLGLMVF RHEIEAHLRK QKQKTSKKKT

A187 DNA SEQUENCE
 Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 Probeset Accession #: N51919
 45 Nucleic Acid Accession #: AF189723
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
 | | | | | |
 ATGATTCTCT TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60
 ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120
 TTTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180
 TCTCAGTTTA AAAATCCCTT TATTATGCTG CTCTGGCTT CTGCAGTCAT CAGTGTTTTA 240
 55 ATGCATCAGT TGATGATGCG CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTTCAGTT 300
 GCCTTTGTTT AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360
 CCAGAAAGCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGCCCG AGACTTGTGT 420
 CCAGGTGATA CAGTTTGCTT TTCTGTTGGG GATAGAGTTC CTGCTGACTT ACCTTGTGTT 480
 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTGTT 540
 60 AAGGTGACAG CTCCTCAGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600
 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTGAT TGGAAACAGG 660
 GAAAATCTG AATTTGGGGA GGTTTTAAAT ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720
 CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGTGATA 780
 ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAA ATATCCTGGA AATGTTTACT 840
 65 ATTAGTGTAA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCATTTGT GGTTCAGTGT 900
 ACGCTAGCTC TTGGTGTATT GAGAATGGTG AAGAAAAGGG CCATTGTGAA AAGCTGCCT 960
 ATTTGTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAACTGGG AACACTGAGC 1020
 AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGATGCG TGAGGTTACT 1080
 GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTTGTGATG GTGATGTTGT TCATGGATT 1140
 70 TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200
 AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAATTGCTCT TGCAATGAAG 1260
 ATGGGTCTTG ATGGAATCTA ACAAGACTAC ATCAGAAAAA CTGAATACCC TTTTAGCTCT 1320
 GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACGAAACAC AGCAGGACAG ACCAGAGATT 1380
 TGTTTTATGA AAGGTGCTTA CGAACAAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440
 75 GGGCAGACTT TGACTTCTG TCAGCAGCAG AGAGATGTGT ACCAACAGAA GAAGGCACGC 1500
 ATGGGCTCAG CGGGACTCAG AGTTCTTGCT TTGGCTTCTG GTCTGAACT GGGCAGCTG 1560
 ACATTTCTTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620
 ACAACACTCA TTGCTCTCAG AGTATCAATA AAAATGATTA CTGGAGATT 1680
 GCAGTTGCAA TGCCAGTGT TCTGGGATTG TATTCACAAA CTTCAGATC AGTCTCAGGA 1740
 80 GAAGAAATAG ATGCAATGGA TGTTCAGCAG CTTTCACAAA TAGTACCAA GGTTCAGTA 1800
 TTTTACAGAG CTAGCCCAAG GCACAAGATG AAAATTATTA AGTCGCTACA GAAGAACGGT 1860
 TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920
 ATTGGAGTTG CGATGGGCCA GACTGTGACA GATGTTTCA AAGAGGCAGC AGACATGATC 1980
 CTAGTGGATG ATGATTITCA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGATTTAT 2040

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10
AATAACATTA AAAATTTTGT TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACITTA 2100
ATCTCATTTG CTACATTAAT GAACTTTTCT AATCTCTCA ATGCCATGCA GATTTTGTGG 2160
ATCAATATTA TTATGGATGG ACCCCAGCT CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220
GATGTCAATC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACCTGATA 2280
CTTAAATAC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTGTGT CTTCTGGCGT 2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400
TTTTTTGACA TGTTCAATGC ACTAAGTTCC AGATCCCAGA CCAAGTCTGT GTTTGAGATT 2460
GGACTCTGCA GTTATAGAAT GTTTTGCTAT GCAGTTCTTG GATCCATCAT GGGACAATTA 2520
CTAGTTATTT ACTTTCCTCC GCTTCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
GATCTGTGT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTGA GTTCGACATC ATCATCTTTT 2700
CTTGAAGTAT GA

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25
A188 Protein sequence:
Gene name: ATPase, Ca++ transporting, type 2C, member 1
Unigene number: Hs.106778
Probeset Accession #: N51919
Protein Accession #: AAF27813
Signal sequence: none found
Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
Cellular Localization: not determined

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1 11 21 31 41 51
MIPVLTSKIA SELPVSEVAS ILQADLQNGL NKCEVSHERRA PHGWNEFDIS EDEPLWKKYI 60
SQFKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVTV AFVQYRSEK SLEELSKLVP 120
PECHCVRBKG LEHTLARDLV PGDTVCLSVG DRVPADLRLF EAVDLSDIES SLTGETTPCS 180
KVTAPQPAAT NGDLASRSNI AFMGTILVRG KAGGVVIGTG ENSEPFGEVFK MMQAEAPKT 240
PLQKSMDLIG KQLSPYSPFI IGIIMLVGWL LKGDILEMPT ISVSLAVAAI PEGLEPIVTV 300
TLALGVMRMV KKRAIVKLP IVELGCGNV ICSDKTGTLT KNEMTVTHIF TSDGLHAEVT 360
GVGYNQFGEV IVDGDVVHGF YNPVSRIVE AGCVNDNAVI RNNTLMGKPT EGALIALAMK 420
MGLDGLQDDY IRKAEYPPFS EQKMAVKCV HRTQQRPEI CFMKGAYBOV IKYCTTYQSK 480
GQTLTLTQQQ RDVYQBEKAR MGSAGLRVLA LASGPGLQL TFLGLVGIID PPRTGVKEAV 540
TTLIASGVSI KMITGDSQBT AVAIASRLGL YSKTSQSVSG EEDIAMDVQQ LSQIVPKVAV 600
FYRASPRHMK KIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVMAGTGT DVCKEADMI 660
LVDDDFQTIM SAIEEGKIY NNINPFVRFO LSTSIALLTL ISLATLMNPF NPINAMQILW 720
INIMDGPPA QSLGVEPVOK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780
ELRDNVITPR DTTMTPTCFV FFDMPNALSS RSQTKSVFBI GLCSNRMFCY AVLGSIMGQL 840
LVIYFPPLQX VFQTESLSIL DLLFLGLTGS SVCIVABIHK KVERSREKIQ KHVSSTSSSF 900
LEV

45
50
A189 DNA SEQUENCE
Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Nucleic Acid Accession #: N62096
Coding sequence: 1-1284 (underlined sequences correspond to start and stop codons)

55
60
65
70
75
1 11 21 31 41 51
ATGGGCTACC AGAGGCAGGA GCCTGTCTATC CGSCGCAGA GAGGATTGCC TTATTCAATG 60
AAGCAGACTG GGTTCCTTT GGAATATATG CTTTATTTCT GGGTTTCATA TGTACAGAC 120
TTTTCCTCTG TTTTATTTAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACAGTCT 180
TTGGTCAATA AAACITTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTCTC TCAGTTTITG 240
TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATACTTT GAGCAAGATT 300
TTTCAAGAA TCCAGGAGT TGATCTCTGA AACGTGTTTA TTGGTCGCCA CTTCAATTAT 360
GGACTTTCCA CAGTTACCTT TACTCTGCTT TTATCTGTGT ACGAAATAT AGCAAGACTT 420
GGAAAGGTCT CCCTCATCTC TACAGGTTTA ACAACTCTGA TTCTTGGAAT TGTAAATGGCA 480
AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAAG ACGCTTGGGT ATTGCAAAAG 540
CCCAATGCCA TTCAAGCGGT CGGGGTATG TCTTTTGCAT TTATTTGCCA CCRAACTCC 600
TTCTTAGTTT ACAGTTCTCT AGAAGAAACC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT 660
ATGTCCATCG TGATTCTGT ATTATCTGT ATATTCTTG CTACATGTGG ATACTTGACA 720
TTTACTGGCT TCACCAAGG GGAATTATTT GAAAATTACT GCAGAAATGA TGACCTGGTA 780
ACATTTGGAA GATTTTGTTA TGGTGTCACT GTCAATTGTA CATACCTAT GGAATGCTTT 840
GTGACAAGAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTCATC GGTTTTCCAC 900
ATTGTTGTAA CAGTGATGGT CATCACTGTA GCCACGCTTG TGTCAATTGT GATTGATGTC 960
CTCGGGATAG TTCTAGAACT CAATGGTGTG CTCTGTGCAA CTCCCTCAT TTTTATCAAT 1020
CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCGA TAAGATTATG 1080
TCTTGTGCA TGCTTCCCAT TGGTGTGTG GTGATGTTT TTGATTTGT CATGGCTATT 1140
ACAAATACTC AAGATGCGAC CCATGGGCAG GAAATGTTCT ACTGCTTCC TGACAATTTC 1200
TCTCTACAA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260
ATTAGTATCT TTAACCTCGA GTAA

80
A190 Protein sequence:
Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Protein Accession #: none found
Signal sequence: none found
Transmembrane domains: 28-50, 66-88-112-134, 142-164, 217-239, 260-282, 298-320, 327-348, 359-381

Cellular Localization: plasma membrane

5
1 11 21 31 41 51
| | | | |
MGYQRQEPVI PPQRGLPYSM KQAGFPPLGIL LLFWVSIVTD FSLVLLIKGG ALSGTDITYQS 60
LVNKTGFPFG YLLSLVLQPL YPFIAMISYN IAGDTLSKV FQRIQGVDP NVFIGRHPII 120
GLSTVTFITLP LSLYRNIAKL GKVSLISTGL TTLILGIVMA RAISLGHPIH KTEDAWVFAK 180
PNAIQAVGVM SFAFICHNS FLVYSSLEBP TVAKMSRLIH MSIVISVFIC IFPATCGYLT 240
10 FTGFTQGDLP ENYCRNDDL TFGFRFCYGT VILTYPMBCF VTRIVIANVP FGGNLSVVFH 300
IVVTVMVITV ATLVSLIDC LGIVLELNGV LCATPLIFII PSACYLKSE EPRTHSDKIM 360
SCVMLPIGAV VMVFGFVMAI TNTQDCTHGQ BMFYCFPDNF SLTNTSESHV QQTTLQLSTLN 420
ISIFQLE

15 A191 DNA SEQUENCE
Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Nucleic Acid Accession #: N62096
20 Coding sequence: 1-1203 (underlined sequences correspond to start and stop codons)

25
1 11 21 31 41 51
| | | | |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCGAGT TTTCCCTTGT TTTATTGATA 60
AAAGGAGGGG CCTCTCTGG AACAGATACC TACCAGTCTT TGGTCAATAA AACTTTGGGC 120
TTTCCAGGGT ATCTGTTCTT CTCTGTTCTT CAGTTTTTGT ATCCTTTTAT AGCAATGATA 180
AGTTACATA TAATAGCTGG AGATACTTTG AGCAAAGTTT TTCAAAGAAT CCCAGGAGTT 240
GATCCTGAAA ACGTGTATT TGGTCCGCC TTCAATTATG GACTTTCCAC AGTTACCTTT 300
30 ACTCTGCCCT TATCCTTGTA CGAAATATA GCAAAGCTTG GAAAGTCTC CCTCATCTCT 360
ACAGGTTTAA CAACTCTGAT TCTTGGAAAT GTAAATGGCAA GGGCAATTTC ACTGGGTCCA 420
CACATACCAA AACAGAGAAGA CGCTTGGGTA TTTGCAAAGC CCAATGCCAT TCAAGGGGTC 480
GGGGTTATGT CTTTTCGATT TATTGGCCAC CATAACTCCT TCTTAGTTTA CAGTTCCTCTA 540
GAAGAACCCA CAGTAGCTAA GTGGTCCCGC CTTATCCATA TGTCCATCGT GATTTCGTGA 600
35 TTTATCTGTG TATCTTTGAC TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAGGGG 660
GACTTATTGG AAAATTAATG CAGAAATGAT GACCTGGTAA CATTTGGAAG ATTTTGTTAT 720
GGTGTCACTG TCATTTTGAC ATACCCATAG GAATGCTTTG TGACAAGAGA GGTAAATTGCC 780
AATGTGTTTT TTGGTGGGAA TCITTCATCG GTTTCCACA TTGTTGTAAC AGTGATGGTC 840
ATCACTGTAG CCACGCTTGT GTCATTGCTG ATTGATTGCC TCGGATAGT TCTAGAACTC 900
40 AATGGTGTGC TCTGTGCAAC TCCCCTCAIT TTTATCAITC CATCAGCCTG TTATCTGAAA 960
CTGTCTGAAG AACCAAGGAC AACTCCGAT AAGATTATGT CTTGTGTCAT GCTTCCCAT 1020
GGTGTGTGG TGATGGTTT TGGATTGCTC ATGGCTATTA CAAATACTCA AGACTGCACC 1080
CATGGGCAGG AAATGTTCTA CTGCTTCTCT GACAATTTCT CTCTACAAA TACCTCAGAG 1140
TCTCATGTTC AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200
45 TAA

A192 Protein sequence:
50 Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Protein Accession #: none found
Signal sequence: 1-26
Transmembrane domains: 45-61, 92-108, 117-132, 191-207, 274-290, 297-313, 335-351
55 Cellular Localization: plasma membrane

60
1 11 21 31 41 51
| | | | |
MGYQRQEPVI PPQPSLVLLI KGGALSGDT YQSLVNKTFG FPGYLLSLV QFLYFFIAMI 60
SYNIIAGDTL SKVFQRIQGV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSLS 120
TGLTTLILGI VMARAIISLG HIPKTEDAWV FAKPNAIQAV GVMSFAPICH HNSFLVYSSL 180
EPTVAKWSR LIHMSIVISV PICIFPATCG YLTPTGFTQG DLFENYCRND DLVTFGRFCY 240
65 GVTIVITPM ECFVTRIVIA NVFPGNLS VPHIVVTMV ITVATLVSL IDCLGIVLEL 300
NGVLCATPLI FIIPACYLK LSEPRTHSD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT 360
HGQEMFYCFP DNFSLTNTSE SHVQQTQLS TLNISIFQLE

A193 DNA SEQUENCE
70 Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Nucleic Acid Accession #: N62096
Coding sequence: 1-1140 (underlined sequences correspond to start and stop codons)

75
1 11 21 31 41 51
| | | | |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCGAG TCAATAAAAC TTTCCGCTTT 60
CCAGGCTATC TGCTCTCTC TGTCTCTCAG TTTTGTATC CTTTATAGC AATGATAAGT 120
80 TACAATATA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 180
CCTGAAAACG TGTATTATGG TCGCCACTTC ATTATTGGAC TTCCACAGT TACCTTTACT 240
CTGCCTTTAT CCTGTACCG AAATATAGCA AAGCTTGGAA AGGTCTCCCT CATCTCTACA 300
GGTTTAACAA CTCTGATTCT TGAATTGTA ATGGCAAGGG CAATTTCACT GGGTCCACAC 360
ATACCAAAAA CAGAAGACGC TTGGGTATTT GCAAAGCCCA ATGCCATTCA AGCGTGTCGG 420

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GTTATGCTT TTGCATTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480
 GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCGTATTT 540
 ATCTGTATAT TCTTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600
 TTATTGAAA ATTACTGCAG AAATGATGAC CTGTAACAT TTGGAAGATT TTGTTATGGT 660
 GTCACGTCA TTTTACATA CCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720
 GTGTTTTTGT GTGGGAATCT TTCATCGGTT TTCCACATG TTGTAACAGT GATGGTCAAT 780
 ACTGTAGCCA CGCTTGTGTC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840
 GGTGTGCTCT GTGCAACTCC CCTCATTTT ATCATTCCAT CAGCCTGTTA TCTGAAACTG 900
 TCTGAAGAAC CAAGGACACA CTCGATAAG ATTATGCTT GTGTCATGCT TCCCATTTGGT 960
 GCTGTGGTGA TGGTTTGTGG ATTCGTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT 1020
 GGGCAGGAAA TGTCTACTG CTTTCTGAC AATTCTCTC TCACAAATAC CTCAGAGTCT 1080
 CATGTTTCAGC AGACACACA ACTTCTACT TAAATATTA GTATCTTCA ACTCGAGTAA

A194 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 24-40, 70-86, 95-111, 171-186, 253-269, 276-292, 314-330
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MG YQRQEPVI PPQVKNKTFG PGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVPQRIQVD 60
 PENVPIGRHF IIGLSTVFT LPLSLYRNIA KLGRVSLIST GLTTLILGIV MARAISLGPH 120
 IPKTEDAWVF AKPNAIQAVG VMSFAPICHH NSFLVYSSLE EPTVAKWSRL IHMSIVISVF 180
 ICIFFPATCGY LFTFTGFTQGD LPENYCRNDD LVTFGRFCYG VIVILTYPME CFVTREVIAN 240
 VFFGGLSSV FHIVVTVMVI TVATLVSLLI DCLGIVLELN GVLCAATPLIF IIPSACYLKL 300
 SEEPRTSHSDK IMSCVMLEIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NPSLTNTSES 360
 HVQQTTLQST LNISIFQLE

A195 DNA SEQUENCE:

Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Nucleic Acid Accession #: N62096
 Coding sequence: 1-1389 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCGAGA GAGATTTAGA TGACAGAGAA 60
 ACCCTTGTTT CTGAACATGA GTATAAGAG AAAACCTGTC AGTCTGCTGC TCTTTTAAAT 120
 GTGTCAACT OGATTATAGG ATCTGGTATA ATAGGATTGC CTTATTCAAT GAAGCAAGCT 180
 GGGTTTCCTT TGGGAATATT GCTTTTATTC TGGGTTTCAAT ATGTTACAGA CTTTCCCTT 240
 GTTTTATGTA TAAAGGAGG GGCCTCTCT GGAACAGATA CCTACCAGTC TTTGGTCAAT 300
 AAAACTTTGG GCTTCCAGG GTATCTGCTC CTCTCTGPTC TTCAGTTTGT GTATCCTTTT 360
 ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAAAGT TTTTCAAAGA 420
 ATCCAGGAG TTGATCCTGA AAACGTGTTT ATTGGTGGCC ACTTCATTAT TGGACTTTCC 480
 ACAGTTACCT TTACTCTGCC TTTATCCTTG TACCGAAATA TAGCAAGCT TGGAAAGGTC 540
 TCCCTCATCT CTACAGTTT AACAACTCTG ATTCTTGGAA TTGTAATGTC AAGGGCAATT 600
 TCACCTGGTC CACACATACC AAAACAGAA GAGCCTTGGG TATTTGCAA GCCCAATGCC 660
 ATTCAAGCGG TCGGGGTAT GTCTTTTGCA TTTATTGGCC ACCATACTC CTCTTAGTT 720
 TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC 780
 GTGATTTCTG TATTATCTG TATATCTTT GCTACATGT GATACTTGAC ATTACTGGC 840
 TTCACCCAG GGGACTTATT TGAATAATAC TGCAAAATG ATGACCTGGT AACATTGGA 900
 AGATTTTGT ATGGTGTGAC TGTCAATTTG ACATACCTTA TGGAAATGCT TGTGACAAGA 960
 GAGGTAATTG CCAATGTGT TTTGGTGGG AATCTTTCAT CGGTTTCCA CATTTGTGTA 1020
 ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCAATGC TGATTGATG CCTGGGATA 1080
 GTTCTAGAGA TCAATGGTGT GCTCTGTGCA ACTCCCTCA TTTTATCAT TCCATCAGCC 1140
 TGTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTGTC 1200
 ATGCTTCCCA TTGGTGTGT GGTGATGGTT TTTGGATTG TCATGGCTAT TACAAATACT 1260
 CAAGACTGCA CCCATGGGCA GGAAATGTTT TACTGCTTC CTGACAATTT CTCTCTCACA 1320
 AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACCTT CTACTTTAAA TATTAGTATC 1380
 TTTCAATGA

A196 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 37-53, 66-82, 109-125, 155-172, 180-196, 255-271, 338-354, 361-377, 399-415
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MG YQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLPYSMKQA 60

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GFPIGILLLP WVSIVTDFSL VLLIKGALS GTDTYQSLVN KTFGPPGYLL LSVLQFLYPF 120
IAMISYNIIA GDTLSKVFQR IPGVDPENVF IGRHPIIGLS TVTPTLPLSL YRNIAKLGKV 180
SLISTGLTTL ILGIUMARA I SLGPHIPKTE DAMVFAKPA IQAVGVMSFA PICHENSFLV 240
YSSLEPPTVA KWSRLIHMSI VISVPICIFP ATCGYLTFTG FTQGDLEFNY CRNDLIVTFG 300
RFCYGVTVIL TYPMECFVTR EVIANVFFPG NLSSVFHIVV TVMVITVATL VSLILDCLGI 360
VLEINGVLCA TPLIFIIPSA CYLKLSEEP R THSKIMSCV MLPIGAVVMV FGFVMAITNT 420
QDCTHQEMP YCFPDNFSLT NTSSEHVQQT TQLSTLNI SI PQ
  
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A197 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.31608
 Probeset Accession #: H18836
 Nucleic Acid Accession #: NM_017636
 Coding sequence: 1-3501 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

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20 1 ATGGAGGATG CCTTCGGGGC AGCCGTGGTG ACCGTGTGGG ACAGCGATGC ACACACCAAG 60
    GAGAAGCCCA CGATGCTTA CGAGAGAGCTG GACTTCACGG GGGCCGGCCG CAAGCACAGC 120
    AATTCTCTCC GGCTCTCTGA CCGAACGGAT CCAGCTGCAG TTATATAGTCT GGTTCACACGC 180
    ACATGGGGCT TCCGTGCCCC GAACCTGGTG GTGTCACTGC TGGGGGGATC GGGGGGCCCC 240
    GTCTCCAGA CCTGGCTGCA GGACCTGCTG GTCGTGGGC TGGTGGGGC TGCCAGAGC 300
    ACAGGAGCCT GGATTGTCTG TGGGGTCTG CACACGGGCA TCGGCCGCA TGTGGTGTG 360
    GCTGTACGGG ACCATCAGAT GGCCAGCACT GGGGGACCA AGGTGGTGGC CATGGGTGTG 420
    GCCCCTTGGG GTGTGGTCCG GAATAGAGAC ACCCTCATCA ACCCCAAGGG CTCGTTCCTC 480
    GCGAGGTACC GGTGGCGCGG TGACCCGGAG GACGGGGTCC AGTTTCCCTT GGACTACAAC 540
    TACTGGGCTT TCTTCTTGGT GGACGACGGC ACACACGGCT GCCTGGGGGG CGAAGAACCGC 600
    TTCCGCTTTC GCCTGGAGTC CTACATCTCA CAGCAGAAGA CGGCGTGGG AGGGACTGGA 660
    ATTGACATCG CTTCTCTGCT CCTCCTGATT GATGGTGATG AGAAGATGTT GACGCGAATA 720
    GAGAAGCCCA CCCAGGCTCA GCTCCCATGT CTCCTCGTGG CTGGCTCAGG GGGAGCTGCG 780
    GACTGCTGCG CGAGACCTCT GGAAGACACT CTGGCCCAAG GGAGTGGGGG AGCCAGGCAA 840
    GGCGAAGCCC GAGATCGAAT CAGCGCTTTC TTCCCAAAG GGGACCTTGA GGTCTGCGAG 900
    GCCCAGGTGG AGAGGATTAT GACCCGGAAG GAGCTCTTGA CAGTCTATTG TTCTGAGGAT 960
    GGGTCTGAGG AATTGAGAGC CATAGTTTTC AAGGCCCTTG TGAAGGCCCTG TGGGAGCTCG 1020
    GAGGCTCAGC CCTACCTGGA TGAGCTGCGT TTGGCTGTGG CTTGGAACCG CGTGGACATT 1080
    GCCCAGAGTG AACTCTTTCG GGGGGACATC CAATGGCGGT CCTTCCATCT CGAAGCTTCC 1140
    CTCATGAGCG CCTGCTGAA TGACCGGCTT GAGTTCGTGC GCTTGTCTAT TCCCAAGGCG 1200
    CTCAGCCTGG GCCACTTCTT GACCCCGATG CGCCTGGCCC AACTCTACAG CGCGCGGCC 1260
    TCCAACTGCG TCATCGCAAC CCTTTTGGAC CAGGCGTCCC ACAGCGCAGG CACCAAAGCC 1320
    CCAGCCCTAA AAGGGGGAGC TGCGGAGCTC CGGCCCTCG ACCTGGGGCA TGTGCTGAGG 1380
    ATGCTGCTGG GGAAGATGTG CGCGCCGAGG TACCCCTCCG GGGGCGCCTG GGACCTCAC 1440
    CCAGGCCAGG GCTTCGGGGA GAGCATGTAT CTGCTCTCGG ACAAGGCCAC CTGCGGCTC 1500
    TGCTGGATG CTGGCTCGG GCAGGCCCCC TGGAGCGACC TGCTTCTTTG GGCACCTGTT 1560
    CTGAACAGCG CACAGATGGC CATGTACTTC TGGGAGATGG GTTCCAATGC AGTTTCTCTA 1620
    GCTCTTGGGG CCTGTCTGCT GCTCCGGGTG ATGGCACGCC TGGAGCCTGA CGCTGAGGAG 1680
    GCAGCACGGG AACTCTTTCG GCGTTCAAG TTTGAGGGGA TGGCGTTGA CCTCTTTGGC 1740
    GAGTGCTATC GCAGCAGTGA GGTAGGGGCT GCGCGCTCC TCTTCCGTG CTGCGGCTC 1800
    TGGGGGATG CCACTTGCTT CCAGCTGGCC ATGCAAGCTG ACGCCCGTGC CTCTTTTGGC 1860
    CAGGATGGGG CATCTGCTCT GCTGACACAG AAGTGGTGGG GAGATATGGC CAGCACTACA 1920
    CCCATCTGGG CCTGCTTCTT CGCCTTCTTT TGCCCTCCAC TCATCTACAC CGCCTCATC 1980
    ACCCTCAGGA AATCAGAAGA GGAGCCACA CGGAGGAGC TAGAGTTTGA CATGATAGT 2040
    GTCAATTAAT GGAAGGGGCC TGTCCGGAGC GGGGACCCAG CCGAGAAGAC GCGCTGGGG 2100
    GTCCCGGCC AGTCCGGCGG TCCGGTGTG TGGCGGGGCC GCTGCGGGG GCGCCGGTGC 2160
    CTACCGCGCT GGTTCACATT CTGGGGCGCG CGGTGACCA TCTTCATGGG CAACGTGGTGC 2220
    AGCTACCTGC TGTCTCTGCT GCTTTCTCG CGGTGCTGC TCGTGGATT CTACCGCGG 2280
    CGCCCGGCT CCTCGAGCT GCTGCTCTAT TCTGGGCTT TCAAGCTGCT GTGCGAGGAA 2340
    CTGCGCCAGG GCCTGAGCGG AGCGGGGGC AGCTCGCCA GCGGGGGCCC GGGGCTGGC 2400
    CATGCTCAC TGAGCCAGCG CCTGCGCTC TACTCGCG ACAGCTGGA CCACTGCGAC 2460
    CTAGTGGCTC TCACCTGCTT CTTCTGGGC GTGGCTGCC GGTGACCCC GGTCTTGTAC 2520
    CACCTGGGCC GCACGTCTCT CTGCATGAC TTCACTGTTT TCAAGGTGCG GCTGCTTAC 2580
    ATCTTCAGG TCAACAACA GCTGGGGCCC AAGATGCTCA TCGTGAGCAA GATGATGAAG 2640
    GACGTGTTCT TCTTCTCTTT CTCTCTCGC GTGTGGCTGG TAGCTATGG GGTGCCACG 2700
    GAGGGGCTCC TGAGGCCAGG GGACAGTGAC TTCCCAAGTA TCTTGGCGCG GGTCTTCTAC 2760
    CGTCCCTACC TGAGATCTT CGGCGAGATT CCGCAGGAG ACATGGAGCT GGCCCTCATG 2820
    GAGCACAGCA ACTGCTGTC GGAGCCCGGC TTCTGGGCAC ACCCTCTCTG GGGCCAGGCG 2880
    GGCACTCGG TCTCCAGTA TGCCAACTGG CTGGTGGTGC TGCTCTGT CATCTTCTG 2940
    CTGCTGCCA ACATCTGCT GGTCAACTTG CTCATTGCCA TGTTCAGTTA CACATTGCG 3000
    AAGTACAGG GCAACAGCGA TCTCTACTGG AAGGCGCAG GTTACCGCT CATCCGGAA 3060
    TTCCACTCTC GGGCCGCGCT GGGCCCGCCC TTATCGTCA TCTCCACTT GGGCTCTCTG 3120
    CTCAGGCAAT TGTGCGAGG ACCCCGGAGC CCCCAGCGCT CCTCCCGGC CCGTGGCAT 3180
    TTCCGGGTTT ACCTTCTTAA GGAAGCGAG CGGAAGCTGC TAACGTGGGA ATCGGTGCAT 3240
    AAGGAGAACT TTCTGCTGGC ACGCGCTAGG GACAAGCGGG AGAGCGACTC CGAGCTCTG 3300
    AAGCGCAGT CCCAGAGGT GGACTTGGCA CTGAAACAGC TGGGACACAT CCGGAGTAC 3360
    GAACAGCGC TGAAATGCT GGAGCGGGAG GTCCAGCAG GTAGCCCGT CCGGGGTGG 3420
    GTGCGCGAGG CCTGAGCGG CTCTGCTTG CTGCCCCAG GTGGGCGGCC ACCCCTGAC 3480
    CTGCTGGGT CCAAGAGCTG A
  
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A198 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.31608
 Probeset Accession #: H18836
 Protein Accession #: none found

Signal sequence: none found
 Transmembrane domains: 214-230, 537-556, 642-662, 730-752, 760-782, 815-837, 842-864, 877-899, 973-995
 Cellular Localization: plasma membrane

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1	11	21	31	41	51							
MEDAFGA	AVV	TVWDS	DAHTT	EKPTD	AYGEL	DFTGAGR	KHS	NFLRL	SDRTD	PAAVY	SLVTR	60
TWGFRA	PNLV	VSVLG	SGGP	VLQTL	QDLL	RRGLV	RRAQS	TGAWI	VTGGL	HTGIG	RHVGV	120
AVRDHQ	MAST	GGTKV	VAMGV	APHG	VVRND	TLINP	KGSFP	ARYRN	RGDPE	DGVQ	PPLDYN	180
YSAPFL	VDDG	THGCL	GGENR	FRLRL	ESYIS	QKRTG	VGGTG	IDIPV	LLLLI	DGDEK	MLTRI	240
ENATQA	LQPC	LLVAG	SGGAA	DCLAE	TLEDT	LAPGS	GGARQ	GEARD	RIRRF	FPKGD	LEVLQ	300
AQVERI	MRK	ELITV	YSSD	GSEEF	FETIV	LKALV	KACGS	EASAY	LDEL	LAVAM	NRVDI	360
AQSELP	RGDI	QWRSP	HLBAS	LMALL	NDNR	EFVRL	LISHG	LSLGH	FLTPM	RLAQL	YSAAP	420
SNSLIR	NLD	QASHS	AGTKA	PALKG	GAEL	RPPDV	GHVLR	MLLGM	KCAPR	YPSGG	AWDFH	480
PGQFG	ESMY	LLSDK	ATSP	SLDAG	LQAP	WSDLL	LWALL	LNRAQ	MAMVF	WEMGS	NAVSS	540
ALGAC	LLRV	MARLE	PDABE	AARRK	DALF	PEGMG	VDLFG	ECYRS	SEVRA	ARLLL	RRCFL	600
WGDA	TCQLA	MQADA	RAFFA	QDGV	QLLTQ	KWGD	MASTT	PIWAL	VLAFF	CPPLI	YTRLI	660
TFRK	SEBPT	REELE	PDMS	VINGE	GPVGT	ADPAE	KTPIG	VPRQS	GRPGC	CGRC	CGRR	720
LRRWF	FWGA	PVTIF	MGNV	SYLLF	LLLF	RVLV	DFOFA	PPGLE	LLLY	FWAFT	LLCEE	780
LRQGL	SGGG	SLASG	GGPG	HASLS	QRLRL	YLAD	SNQCD	LVALT	CFLIG	VGCR	LTPGLY	840
HLGR	TVLCID	FMVFT	VRLLH	IFTVN	KQGP	KIVIV	KMMK	DVFFL	FPFPG	VNLV	AYGVAT	900
EGLR	PRDSD	FPSIL	RRVFF	RFYQL	IFGQI	PQEDM	VDALM	EHSNC	SESPG	FWAHP	PQAQA	960
GTCV	SQYANW	LVLVL	LIWIFL	LWANIL	LVNL	LIAMP	SYTFG	KVQGN	SDLYW	KAQRY	RLIRE	1020
PHSR	PALAPP	FIVIS	HLRL	LRQL	CRPRS	POPS	PALEH	FRVLS	KEAE	RKLLT	WESVH	1080
KENP	LARAR	DKRES	DSERL	KRTSQ	KVDLA	LKQL	GHI	REY	EQRL	KVL	ERE	1140
VAEAL	SRSAL	LPPGG	PPPPD	LP	PSKD							

A199 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.40808
 Probeset Accession #: AA054237
 Nucleic Acid Accession #: AA054237
 Coding sequence: 1-894 (underlined sequences correspond to start and stop codons)

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1	11	21	31	41	51							
ATGAG	AGCCG	CGCTCGT	CACGG	CGCTC	AGCCT	CGGCC	TCAGC	CTGTG	CTCC	CTGGG	60	
CTGCT	CGTCA	CGCCAT	CTT	CACCG	ACCA	TGGT	ACGAG	ACCG	ACCCG	CGCC	ACAAG	120
GAGAG	CTGCG	AGCCG	AGCCG	CGCG	GGCGC	GACCC	CCCGG	ACCA	GAGAA	CCGCT	GATG	180
CCGCT	GTGCG	ACCTG	CCGCT	CGCGG	ACTCG	CCCCG	CTGG	CGCG	CGGCT	GCTC	CCGGG	240
GGCCG	GGGCG	CGCGG	ACCCG	CGAGT	CCTCG	CGCTG	CTGCC	TGGG	CGCTG	CGG	CTGGAC	300
GGCGA	GTGCG	GCCGG	CCCCCT	CTTGC	CCACC	TACTG	GGGCC	TCTGG	AGGAA	GTGTA	CTTCTC	360
CTGGG	CATCG	ACCGG	GCAT	CGAC	CCCCCT	ATCCT	GAAAG	GTATT	CGCGA	GCGAT	GCACG	420
GCCAT	CAAGT	ACCACT	TTTC	TCAG	CCCCATC	CGCTT	GCGAA	ACATT	CTCTT	TAATT	TAACC	480
AAGAC	CATAC	AGCAAG	ATGA	GTGG	CACCTG	CTTCA	TTAA	GAAGA	ATCAC	TGCTG	GCCTC	540
CTCGG	CATG	CCGTAG	CCGT	CCTTC	CTCTG	GGCTG	CATTG	TGGC	CACAGT	CAGTT	CTTCTC	600
TGGG	GAGAGA	GCTTG	ACCCA	GCACG	TGGCT	GGACT	CTCGT	TCCTC	CATGAC	AGGG	ATATT	660
TGCAC	CAATT	CCCTC	GTAC	TTATG	CCGCC	AGTAT	CTCGT	ATGAT	TTGAA	CCGG	CTCCCA	720
AAGCT	AATT	ATAGC	CTGCC	TGCTG	ATGTG	GAAC	ATGGT	ACAG	CTGGT	CATCT	TTTGC	780
GCCTG	GTGCA	GTTTAG	GCTT	TATGT	GGCA	GCTG	GAGTC	TCTG	CATGC	TTATC	CGGTT	840
ATTAG	CCGGA	CCAAG	ATTG	ACAG	CTAAG	TCTG	CAGAG	ACTC	CACGT	ATGA		

A200 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.40808
 Probeset Accession #: AA054237
 Protein Accession #: none found
 Signal sequence: 1-18
 Transmembrane domains: 179-201, 209-231, 257-279
 Cellular Localization: plasma membrane

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1	11	21	31	41	51							
MEPRAL	VTAL	SLGLS	LCSLG	LLVTA	IFTDH	WYETD	PRRHK	ESCERS	RAGA	DPPD	QKNRLM	60
PLSHL	PLRDS	PPLGR	LLPG	GPGR	ADPESW	RSLLG	LGLLD	ABOGR	PLFAT	YSGL	MRKCYF	120
LGIDR	DIDL	ILKGI	AQRCT	AIKYH	FSQPI	RLRNP	PFNLT	KTIQ	QDEWL	LHLR	RITAGF	180
LGMAV	AVLLC	GCIVAT	VSFP	WEBSL	TQVA	GLLFL	MTGIP	CTISL	CTYAA	SISYD	LNRLP	240
KLII	SLPADV	EHGGS	WSIFC	AWCSL	GFI	AGGL	CIAYF	ISRTK	IAQLK	SGRD	STV	

A201 DNA SEQUENCE

Gene name: CDA14
 Unigene number: Hs.26813
 Probeset Accession #: N32912
 Nucleic Acid Accession #: NM_016570
 Coding sequence: 1-1134 (underlined sequences correspond to start and stop codons)

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1	11	21	31	41	51							
ATGAG	GCAG	TGAAT	CGGAA	AAAAA	CTTTA	AGTTT	GGTAA	AAGAG	TGGA	TGCTT	TTCCG	60
AAGG	TTCTG	AGAG	CTATG	AGAG	ACTCA	GCCAG	TGGAG	GTAC	AGTTT	CTA	ATAGCA	120

5 TTTACAATA TGCGTTTATT AACATAATG GAATTCCTCAG TATATCAAGA TACATGGATG 180
 AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAT TAAGAATTAA TATAGATATT 240
 ACTGTTGCCA TGAAGTGTC AATATGTTGA GCGGATGTAT TGGATTAGC AGAAACAAATG 300
 GTTGATCTG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360
 10 AAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAGA GCATTCACTT 420
 CAAGATGTGA TATTTAAAA TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480
 GATGATTCAT CACAGTCTCC AATGTCATGC AGAATTCATG GCCATCTATA TGTCAATAAA 540
 GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCCTCG TGGTCATGCA 600
 CATTTGGCAG CACTTGTCAA CCATGAATCT TACAATTTT CTATAGAAT AGATCATTG 660
 15 TCTTTTGGAG AGCTTGTCC AGCAATTATT AATCCTTTAG ATGAACTGA AAAAATTGCT 720
 ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAACAA ACTACATACA 780
 TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAA 840
 CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTTATGA AATATGATCT CAGTCTCTT 900
 ATGGTGACAG TTACTGAGGA GCACATGCCA TTCTGGCAGT TTTTGTAAAG ACTCTGTGGT 960
 20 ATTGTTGGAG GAATCTTTTC AACACAGGC ATGTACATG GAATTGAAA ATTTATAGTT 1020
 GAAATAATT GCTGTCGTT CAGACTTGA TCCTATAAAC CTGTCAATTC TGTTCCTTTT 1080
 GAGGATGGC ACACAGACAA CCACCTACCT CTTTATAGAA ATAATACACA TTGA

20 **A202 Protein sequence:**
 Gene name: CDA14
 Unigene number: Hs.26813
 Probeset Accession #: N32912
 Protein Accession #: NP_057654
 25 Signal sequence: none found
 Transmembrane domains: none found
 Cellular Localization: nuclear

30 1 11 21 31 41 51
 | | | | |
 MRRLNRKKTIL SLVKELDAPP KVPESYVETS ASGGTVSLIA FTTMALLTIM EPSVYQDTWM 60
 KYEYVDKDF SSILRINIDI TVAMKQYVG ADVLDLAETM VASADGLVYE PTVFDLSPQQ 120
 KEWQRLQLI QSLRQEEHSL QDVIFKSAFK STSTALPPRE DDSSQSFNAC RIHGHLYVNK 180
 35 VAGNPHITVG KATPHRGRHA HLAALVNHES YNPSHRIDHL SFGELVPAII NPLDOTEKIA 240
 IDHNQMFQYF ITVVPTKLEH YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL 300
 MVTVTSEHMP FVQFFVRLCG IVGGIFSTTG MLHGIGKPIV EIICCRFLRG SYKPVNSVFP 360
 EDGTDNHLPL LLENNTN

40 **A203 DNA SEQUENCE**
 Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)
 Unigene number: Hs.44926
 Probeset Accession #: S79876
 45 Nucleic Acid Accession #: NM_001935.1
 Coding sequence: 76-2301 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
 | | | | |
 CGCGCGTCTC CGCGGCCCGC GTGACTTCTG CCTGCGCTCC TTCTCTGAAC GCTCACTTCC 60
 GAGGAGACGC CGACGATGAA GACACCGTGG AAGATTCTTC TGGGACTGCT GGGTGTGCT 120
 CGCCTTGTC CCACTATCAC CGTGCCCGTG GTTCTGCTGA ACAAGGCAC AGATGATGCT 180
 55 ACAGCTGACA GTGCGCAAACT TTAACCTCTA ACTGATTACT TAAAAATATC TTATAGACTG 240
 AAGTTATACT CCTTAAGATG GATTTAGAT CATGAATATC TCTACAAACA AGAAAAATAAT 300
 ATCTTGATAT TCAATGCTGA ATATGGAAAC AGCTCAGTTT TCTTGGAGAA CAGTACATT 360
 GATGAGTTTG GACATCTCAT CAATGATTAT TCAATATCTC CTGATGGGCA GTTTATTCTC 420
 TTAGAATACA ACTAAGTGAA GCAATGGAGG CATTCTTACA CAGCTTCATA TGACATTAT 480
 GATTTAAATA AAAGGCAGCT GATTACAGAA GAGAGGATTC CAACCAACAC ACAGTGGGTC 540
 60 ACATGCTCAC CAGTGGGTCA TAAATTGGCA TATGTTTGGG ACAATGACAT TTATGTTAAA 600
 ATTGAACCAA ATTTACCAAG TTACAGAAATC ACATGGACGG GGAAGAGAATA TATAATATAT 660
 AATGGAATAA CTGACTGGGT TTATGAAGAG GAAGTCTTCA GTGCCTACTC TGCTCTGTGG 720
 TGGTCTCCAA ACGGCACCTT TTAGCATAT GCCCAATTTA ACGACACAGA AGTCCCACTT 780
 65 ATTGAATACT CCTTCTACTC TGATGAGTCA CTGCACTACC CAAAGACTGT ACGGGTTCCA 840
 TATCCAAAGG CAGGAGCTGT GAATCCAACT GTAAAGTTCT TTGTTGTAAT TACAGACTCT 900
 CTCAGCTCAG TCACCAATGC AACTTCCATA CAAATCACTG CTCTGCTTC TATGTTGATA 960
 GGGGATCACT ACTTGTGTGA TGTGACATGG GCAACACAAG AAAGAATTTC TTTGCACTGG 1020
 CTAGGAGGGA TTCAAGAACTA TTCGGTCATG GATATTTGTG ACTATGATGA ATCCAGTGGA 1080
 70 AGATGGAAGT GCTTAGTGGC ACGGCAACAC ATTGAAATGA GTACTACTGG CTGGGTTGGA 1140
 AGATTTAGGC CTTCAGAAAC TCATTTTACC CTTGATGGTA ATAGCTTCTA CAAGATCATC 1200
 AGCAATGAAG AAGGTTACAG ACACATTGTC TATTTCCAAA TAGATAAAAA AGACTGCACA 1260
 TTTATTACAA AAGGCACCTG GGAAGTCATC GGGATAGAAAG CTCTAACCAAG TGAATTATCTA 1320
 TACTACATTA GTAATGAATA TAAAGGAATG CCAGGAGGAA GGAATCTTTA TAAATCCAA 1380
 75 CTATGACT ATACAAAAGT GACATGCTC AGTTGTGAGC TGAATCCGGA AAGGTGTGAG 1440
 TACTATTCTG TGTCAATTCAG TAAAGAGGCG AAGTATTATC AGCTGAGATG TTCCGGTCTC 1500
 GGTCTGCCCC TCTATACTCT ACACAGCAGC GTGAATGATA AAGGGCTGAG AGTCTGTGAA 1560
 GACAACTCAG CTTTGGATAA AATGCTGAGC AATGTCCAGA TGCCCTCCAA AAAAATGGAC 1620
 TTCAATATTT TGAATGAAC AAAATTTTGG TATCAGATGA TCTTGCTTCC TCATTTTGAT 1680
 80 AAATCCAGGA AATCTCTCT ACTATTAGAT GTGATGACAG GCCATGTAG TCAAAAAGCA 1740
 GACACTGTCT TCAGACTGAA CTGGGCCACT TACCTTGCAA GCACAGAAAA CATTATAGTA 1800
 GCTAGCTTTG ATGGCAGAGG AAGTGGTTAC CAAGGAGATA AGATCATGCA TGCAATCAAC 1860
 AGAAGACTCG GAACATTGGA AGTTGAAGAT CAAATTGAAG CAGCCAGACA ATTTTCAAAA 1920
 ATGGGATTTG TGGACAACAA ACGAATTGCA ATTTGGGGCT GGTCAATGAG AGGGTACGTA 1980
 ACCTCAATGG TCCTGGGATC GGGAAAGTGG GTGTTCAGT GTGGAATAGC CGTGGCGCCT 2040

5 GTATCCCGGT GGGAGTACTA TGACTCAGTG TACACAGAAC GTTACATGGG TCTCCCAACT 2100
 CCAGAAGACA ACCTTGACCA TTACAGAAAT TCAACAGTCA TGAGCAGAGC TGAAAAATTTT 2160
 AAACAAGTTG AGTACCTCCT TATTCATGGA ACAGCAGATG ATAACGTTCA CTTTCAGCAG 2220
 TCAGCTCAGA TCTCCAAAGC CCTGGTCGAT GTTGGAGTGG ATTTCCAGGC AATGTGGTAT 2280
 10 ACTGATGAAG ACCATGCAAT AGCTAGCAGC ACAGCACACC AACATATATA TACCCACATG 2340
 AGCCACTTCA TAAAACAATG TTTCTCTTTA CCTTAGCACC TCAAAATACC ATGCCATTTA 2400
 AAGCTTATTA AAACCTATTT TTGTTTTCAT TATCTCAAAA CTGCACTGTC AAGATGATGA 2460
 TGATCTTTAA AATACACACT CAAATCAAGA AACTTAAGGT TACCTTTGTT CCCAAATTTT 2520
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 15 TTGAATTATC CGGTGGGTTT TTATTGTTA AAATCATTTT TGCATCAGCT GCTGAAACAA 2640
 CAAATAGGAA TTGTTTTTAT GGAGGCTTTG CATAGATTCC CTGAGCAGGA TTTTAACTTT 2700
 TTTCTAATCG GACTGGTTC AATGTTGTTT TCTTCTTTAA AGGGATGGCA AGATGTGGGC 2760
 AGTGATGTCA CTAGGGCAGG GACAGGATAA GAGGGATTAG GGAGAGAAGA TAGCAGGGCA 2820
 TGCTGGGAA CCCAAGTCCA AGCATACCAA CACGAGCAGG CTACTGTCTG CTCCCTCGG 2880
 20 AGAAGAGCTG TTCACCAAGA GACTGGCACA GTTTCTGAG AAAGACTATT CAAACAGTCT 2940
 CAGGAAATCA AATATCGAAA GCACTGACTT CTAAGTAAAC CACAGCAGTT GAAAGACTCC 3000
 AAAGAAATGT AAGGGAAACT GCCAGCAACG CAGCCCCAG GTGCCAGTTA TGGCTATAGG 3060
 TGCTACAAAA ACACAGCAAG GGTGATGGGA AAGCATTGTA AATGTGCTTT TAAAAAATAA 3120
 TACTGATGTT CCTAGTGAAG GAGGCGCTTT GAAACTGAGA TGTGAACACA TCAGCTTGCC 3180
 25 CTGTAAAGAT ATGAAATAT TTGTATCACA AATCTTAAT TGAAGGAGTC CTGTCATCAA 3240
 TTTTCTTAT TTCATTCTTT TGAGTGCTTT AATTAAGAAT ATATTTTAACT TTCCTTGGAC 3300
 TCATTTTAAA AAATGAACA TAAATACAA TGTATGATAT TATTATTCCT ATTCTACATA 3360
 CTATGGAATT TCTCCAGTC ATTTAATAAA TGTGCCTTCA TTTTTC

25 A204 Protein sequence:
 Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)
 Unigene number: Hs.44926
 30 Probeset Accession #: S79876
 Protein Accession #: NP_001926.1
 Signal sequence: none found
 Transmembrane domains: 6-28
 DPPIV_N_term domain: 43-557
 35 Peptidase_S9 domain: 558-635
 Cellular Localization: plasma membrane

40 1 11 21 31 41 51
 MKTPWKILG ILGAAALVTI ITVPVVLINK GTDDATDSR KTYTLTDYLK NTYRLKLYSL 60
 RWISDHEYLY KQENNLVFN AEYGNSSVPL ENSTFDEFGH SINDYSISPD GQFILLEYN 120
 VKQWRHSYTA SYDIYDLNKR QLITEERIFN NTQWVWSPV GHKLAYVWNN DIYVKLEPNL 180
 PSYRITWTGK EDIYINGITD WVYEEVPSA YSALWNSPNG TFLAYAQFND TEVPLIEYSF 240
 45 YSDESQYYPK TVRVYPRKAG AVNPTVKFFV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300
 CDTWTATQER ISLQWLRIQ NYSVMDICDY DESSGRWNCL VARQHIEMST TGVNVRFRPS 360
 EPHTLDGNS FYKIISNEEG YRHICYFQID KKDCTPITKG TWEVIGIEAL TSDYLYIYN 420
 EYKGMPPGGRN LYKIQLDIYT KVTCLSCBLN PERCQYYSVS FSKEAKYQYL RCGSGPLPLY 480
 TLHSSVNDKG LRVLEDNSAL DKMLQNVQMP SKKLDPIILN ETKEFYQMIL PPHEFRSKKY 540
 50 PLLLDVYAGP CSQKADTVFR LHWATYLAST ENIIIVASF DG RGSQYQDKI MHAINRRLGT 600
 FEVEDQIEAA RQFSKMGFVD NKRIAINGWS YGGYVTSMLV GSGSGVFCKG IAVAPVSRNE 660
 YDSVYTERY MGLPTPEDNL DEYRNSTVMS RAENFRQVEY LLIHGTADDN VHFQQAQIS 720
 KALVDVGVD FQAMWYTEDH GIASSTAHQH IYTHMSHFIX QCFSLP

55 A205 DNA SEQUENCE
 Gene name: predicted exon
 Unigene number: none found
 Probeset Accession #: none found
 Nucleic Acid Accession #: none found
 60 Coding sequence: 1-261 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
 ATGGCTCTGG CGAAGGTGAG GGAGCCAAAC GCAAATGACA ATGCCATCAG AGTTGACAAC 60
 AGAAGTGTGA TTAAAGTGGG TGCTAACCAG TGTTCCCTGC ATGAGGCAGA AAGTGAATCC 120
 AGAAACCCCTC AGGAGCTCTG GATGGGCGCT CTCTCTTGA TGGGGGTCTC AGAAGCATGT 180
 GTGGAATGA GGCCTCTGTC AGTCTGGTCC CTGAGAGATG ACAAGGAGCA GAGCCCCCAC 240
 CAGCCACAC TGGATGTCTA A

70 A206 Protein sequence:
 Gene name: predicted exon
 Unigene number: none found
 75 Probeset Accession #: none found
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 46-68
 Cellular Localization: not determined

80 1 11 21 31 41 51
 MALAKVREFN ANDNAIRVDN RSVIKVRANQ CSLHFAESSE RNPQELMWGL LLLMGVLEAC 60
 VEMRPLSVWS LRDDKEQSPH QPTLDV

A207 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.222886
 Probeset Accession #: AI672225
 Nucleic Acid Accession #: none found
 Coding sequence: 1-462 (underlined sequences correspond to start and stop codons)

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10      1      11      21      31      41      51
      |      |      |      |      |      |
      ATGCCAAATG CTGAGTTAGA AGCAAAGAGC CTGGAAGCA GTAAATGTTT AAAAAGTCT 60
      CTCATACTTG CTGTATGTTG TGGATCAGCA AATATAGTCA GGCCTCTACT TGAGCAAAAT 120
      ATTGATGTAT CTTCTCAAGA TCTGGACAGA CGGCCAGAGA GTATGCTGTT TCTAGTCATC 180
15      ATCATGTGGA CCAGTTTGTG GGAAGACAAT CTTTCCATGG GCTGGGGGAA GCTAGAAGAT 240
      TTTATGGCTA TTGAAGAAGA AATGAAGAAG CACGGAAGTA CTCATGTGGG ATTCCAGAA 300
      AACCTGACTA ATGGTGCCGC TGCTGGCAAT GGTGATGATG GATTAAITCC TCCAAGGAAG 360
      AGCAGAACAC CTGAAAGCCA GCAATTTCTT GACACTGAGA ATGAAGAGTA TCACAGGTTT 420
      GTCAAAGATC AGATAGTTGT AGATATGCGG CGTTATTCTT GA
  
```

A208 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.222886
 Probeset Accession #: AI672225
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 16-38
 Cellular Localization: not determined.

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30      1      11      21      31      41      51
      |      |      |      |      |      |
      MPNAELEAKS LGSSKCLKTA LILAVCCGSA NIVSPILLEQN IDVSSQDLDR RPESMLFLVI 60
      IMWTSFVEDN LSMGWGKLED FMAIEEEMKK HGSTHVGFPE NLTNGAAGN GDDGLIPPRK 120
35      SRTPEQQPP DTENEYHRP VKDQIVVDMR RYF
  
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A209 DNA SEQUENCE

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1
 Unigene number: Hs.23796
 Probeset Accession #: NM_014253
 Nucleic Acid Accession #: NM_014253
 Coding sequence: 65-8242 (underlined sequences correspond to start and stop codons)

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45      1      11      21      31      41      51
      |      |      |      |      |      |
      GACTGCTTGC ATTAAAGGAC TTCCTCATCC TTTTITTCAT GAAACTGAGC TTGCTTAATC 60
      AGAGATGGAG CAAACTGACT GCAAACCCCTA CCAGCCTCTA CCAAAAGTCA AGCATGAAAT 120
      GGATCTAGCT TACACAGTTT CTTCTGATGA GAGTGAAGAT GGAAGAAAC CAAGACAGTC 180
50      ATACAACCTC AGGGAGACCC TGCACGAGTA TAACCGAGAG CTGAGGATGA ATTACAATAG 240
      CCAGAGTAGA AAGAGGAAAG AAGTAGAAAA ATCTACTCAA GAGATGGAAT TCTGTGAAAC 300
      CTCTCAGACT CTGTGCTCTG GCTACCAAAC AGACATGCAC AGCGTTTCTC GGCATGGCTA 360
      CCAGCTAGAG ATGGGATCTG ATGTGGACAC AGAGACAGAA GGTGCTGCCT CACCTGACCA 420
      TGCACTAAGA ATGTGGATAA GGGGAATGAA ATCAGAGCAT AGTTCTCTGT TGTCCAGCCG 480
      GGCCAACTCT GCATTATCCT TGACTGACAC TGACCATGAA AGGAAGTCTG ATGGGGAATA 540
      TGGTTTCAAA TTCTCTCTCT TTTGTTGTGA CATGGAGGCT CAAGCTGGGT CTAATCAAGA 600
      TGTGACAGAC AGCCACACAC ACCAGTTTAC CTTCAGACCC CTCCCACGCG CAOCTCGGCC 660
      TOCTCATGCC TGCACCTGTG CCAGGAAGCC ACCCCTGCA GCGGACTCTC TTCAGAGGAG 720
      ATCAATGACT ACCCGCAGCC AGCCAGCCCC AGCTGCTCCA GCTCCCCCAA CCAGCAGGCA 780
      GGATTGAGTC CATCTGCATA ACAGCTGGGT CCTGAACAGC AACATACCAT TGGAGACCA 840
      GCATTCCCTG TTCAACATG GATCTGGTTC CTCTGGATC TTCAGTGCAG CCAGTCAGAA 900
      CTACCCCTCG ACATCCAATA CCGTGTACTC GCCCCTCCCG AGGCTCTTTC CTGGAAGCAC 960
      CTTTTCOOGA CCGCTCTTTC CTTTAAACAA ACCTTACAGG TGCTGCAACT GGAAGTGCAC 1020
      AGCATTGAGC GCCACTGCAA TCACAGTGAC TTTGGCCTTG TTAATAGCCT ATGTGATTGC 1080
65      AGTGCAATTG TTGGCCTGGA CTTGGCAGTT GCAACCAAGT GAAGGAGAGC TGTATGCAAA 1140
      TGGAGTTAGC AAAGGGAACA GGGGGACCGA GTCCATGGAC ACTACTTACT CTCCAATTGG 1200
      AGGAAAAGTT TCTGATAAAT CAGAGAAAAA AGTGTTCAG AAGGGACGGG CGATAGACAC 1260
      TGGAGAAGTT GACATTGGTG CACAGGTCA TGCAGACATT CCACCTGGTT TATTCTGGCG 1320
      TTTCCAGATT ACTATCCACC ATCCAATATA TCTGAAGTTC AATATTCTCT TAGCCAAGGA 1380
70      CTCTCTGCTG GGAATTTATG GCAGAAGAAA CATTCACCT ACACATACTC AGTTTGATT 1440
      TGTAAAACCT ATGGATGGCA AACAGCTGGT CAAGCAGGAC TCCAAGGGCT CTGATGATAC 1500
      ACAGCACTCC CCTCGAAGCC TGATCTTAAC TTGCTTTCAG GAGACAGGTT TCATAGAGTA 1560
      TATGATCAAA GGACCTTGGT ATCTGGCGTT TTACAATGAT GGAAGAAAGA TGGAGCAAGT 1620
      ATTCGTGTTA ACTACAGCAA TTGAAATAAT GGATGACTGT TCAACCAATT GCAATGGAAA 1680
75      TGGAGAGTGT ATCTCTGGCC ATTGTCAATT TTTCCAGGA TTCCTTGGAC CTGACTGTGC 1740
      TAGAGATTCC TGCCCTGTGC TGTGTGTGTG GAATGGAGAA TACGAGAAAG GACACTGTGT 1800
      TCGCCGGGAT GGTCTGAAAG GGCCAGAGTG TGACGTTCCG GAAGAACAAT GCATTGATCC 1860
      AACATGCTTT GGCCAGGCA CCTGCATCAT GGGAGTCTGC ATCTGTGTGC CAGGATACAA 1920
      AGGAGAAATA TGGAGGAAG AGGACTGCCT AGACCCAATG TGTTCCAACC ATGGCATCTG 1980
80      TGTAAAAGGA GAATGTCACT GTTCTACTGG CTGGGGAGGA GTTAACTGTG AAACACCACT 2040
      TCCTGTATGT CAAGAGCAGT GCTCAGGACA CGGAACCTTT CTCTGGAGCG CTGGAGTATG 2100
      CAGCTGTGAT CCAAGTGAAG CAGGATCTGA CTGCTCAACA GAGCTGTGTA CCATGGAGTG 2160
      TGGTAGCCAT GGAGTCTGCT CAAGAGGAAT TTGCCAGTGT GAAGAAGGCT GGGTAGGACC 2220
      AACATGTGAG GAACGCTCCT GTCATTCTCA TTGTACTGAG CATGGCCAAT GCAAAGATGG 2280
  
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	AAAATGTGAG	TGTAGCCCTG	GATGGGAGGG	CGACCACTGC	ACAATTGCTC	ACTACTTAGA	2340
	TGCTGTCCGA	GATGGCTGCC	CAGGGCTCTG	CTTTGGAAAT	GGAGATGTA	CCCTGGATCA	2400
	AAATGGTTGG	CAGTGTGTGT	GTCAGGTGGG	TTGGAGTGGG	ACAGGCTGCA	ATGTTGTCAT	2460
5	GGAAATGCCT	TGTGGAGATA	ACTTGGACAA	TGATGGAGAT	GGTTAAACCG	ACTGTGTGGA	2520
	TCCTGACTGT	TGTCAACAAA	GCAACTGTTA	TATAAGTCTT	CTCTGCCAGG	GCTCACCAGA	2580
	TCCTCTTGAC	CTCATTTCAGC	AAAGCCAAAC	TCTCTTCTCT	CAGCACACTT	CAAGACTTTT	2640
	TTATGATCGA	ATCAAAATCC	TCATTGGCAA	GGACAGTACT	CATGTCATTC	CTCCTGAGGT	2700
	GTCATTTCAG	AGCAGGCGTG	CCTGTGTGAT	TCGAGGCCAA	GTGGTGGCCA	TAGATGGAAC	2760
10	TCCTCTAGTG	GGAGTGAATG	TCAGTTTCTT	GCACCACAGT	GATTATGGGT	TTACCATCAG	2820
	CCGGCAAGAT	GGAGGCTTTG	ACCTCGTGGC	CATCGGTGGC	ATCTCTGTCA	TCTTAATCTT	2880
	CGACCGATCC	CCTTTCTCTG	CTGAGAAGAG	AACACTCTGG	TTGCCCTGGA	ATCAGTTTAT	2940
	TGTGGTAGAG	AAAGTCACCA	TGCAGAGAGT	TGTATCAGAC	CGCCCATCCT	GCGATATCTC	3000
	CAACTTTATC	AGCCCAAACC	CTATTGTGCT	TCCTTCACCG	CTCACATCAT	TTGGAGGGTC	3060
15	CTGTCCAGAG	AGGGGAACCT	TTGTTCTCTG	GCTGCAGGTT	GTACAGGAGG	AAATTCCTAT	3120
	TCCTCCACAG	TTTGTGAGGC	TGAGTTACCT	GAGCAGCCGC	ACCCCTGGGT	ATAAAACCTT	3180
	GGTACGGATC	CTTCTGACAC	ATTCAACGAT	TCCCGTAGGC	ATGATAAAG	TACACCTCAC	3240
	AGTAGCTGTG	GAAGGGCGAC	TCACACAGAA	GTGGTTTCCC	GCCGCAATTA	ATCTTGCTTA	3300
	CACATTTGCT	TGGAACAAGA	COGATATCTA	TGGACAGAAG	GTTTGGGGCC	TGGCAGAGGC	3360
20	TTTGGTATCT	GTGGGATATG	AATATGAAAC	GTGCCCTGAC	TTTATTCTCT	GGGAGCAAAG	3420
	GACAGTCGTT	TTACAGAGTT	TTGAGATGGA	TGCTTCTAAC	CTAGGAGACT	GGTCTTTGAA	3480
	TAAGCATCAC	ATTTTGAATC	CTCAAAGTGG	AATCATACAT	AAAGGGAATG	GAGAAAATAT	3540
	GTTCATTTC	CAGCAGCCCC	CAGTCATATC	AACATAATG	GGTAATGGAC	ACCAAAGGAG	3600
	TGTAGCTGTC	ACCAACTGCA	ATGGCCGAGC	CCACAACAC	AAACTCTTTG	CTCCTGTGCG	3660
25	CTTAGCTTCT	GGCCCTGATG	GCAGTGTGTA	TGTTGGCGAC	TTCAATTTTG	TAAGGAGAAT	3720
	ATTTCCTCTG	GGAACTCTCG	TTAGTATTTT	GGAAATTAAG	ACAAGTCTTG	CTCACAAATA	3780
	CTATCTGGCT	ATGGACCTTG	TGCTGGAATC	ACTCTATCTA	TCAGACACCA	ATACTCGCAA	3840
	AGTCTCAAG	TTGAAATCTC	TTGTGGAGAC	GAAAGATCTG	TCCAAGAAAT	TTGAAGTGGT	3900
	GGCAGGAATC	GGTGATCAGT	GCCTTCCCTT	TGACCCAGAGT	CATTGTGGAG	ATGGTGGGAG	3960
	AGCATCGGAA	GCTTCACTGA	ATAGCCCTCG	AGGCATCACA	GTGTATAGGC	ATGGATTTAT	4020
30	TTACTTTGTG	GATGGGACTA	TGATTGCGAA	AATTGATGAG	AATGCTGTGA	TCACAACCTG	4080
	AATCGGCTCA	AATGGTCTGA	CTTCCACACA	ACCACTGAGC	TGTGACTCAG	GAATGGACAT	4140
	CACCTCAGGT	CGATTAGAGT	GGCCAAACAGA	CCTTGACAGT	AATCCTATGG	ACAATTCATT	4200
	GTATGTCTTG	GATAACAACA	TTGTGCTGCA	AATTTCTGAG	AACAGGCGTG	TTCCGATCAT	4260
	CGCAGGACGC	CCCATTCACT	GCCAGGTGCC	AGGCATCGAT	CATTTCCTGG	TCAGCAAGGT	4320
35	AGCAATTAC	TCCACTCTAG	AGTCAGCGAG	GGCCATCAGT	GTCTCCACCA	GCGGCTGCT	4380
	CTTCATAGCT	GAAACAGACG	AGAGGAAAGT	AAACCGCATT	CAGCAAGTAA	CCACCAATGG	4440
	GGAGATCTAC	ATCATGCGTG	GTGCCCCAC	TGACTGTGAC	TGCAAAATGG	ATCCAAATGG	4500
	TGACTGTTTT	TCAGGTGATG	GTGGCTATGC	CAAAGATGCA	AAGATGAAAG	CCCCTTCTCT	4560
40	CTTAGCAGTG	TGCGCTGATG	GAACCTCTA	TGTGGCAGAC	CTCGGAAATG	TTCGAATTGG	4620
	TACCATCAGC	AGGAACCAAG	CCCACCTGAA	TGACATGAAC	ATTTATGAGA	TTGCTTCACC	4680
	CGCTGATCAG	GAACGTGACC	AGTTCACTGT	AAATGGAACC	CACCTACACA	CCCTGAACCT	4740
	GATAACAAGG	GACTATGTTT	ATAACTTCAC	CTACAATTCT	GARGGTGACT	TGGGCGGAT	4800
	TACCAGCAGC	AATGGCAATT	CAGTGCACAT	TGCGCGTGAT	GCAGGCGGAA	TGCCGCTATG	4860
45	GCTTGTGGTG	CCTGGCGGAC	AGTATACCTG	GCTGACTATA	AGCAGCAATG	GAGTCTTGAA	4920
	AAGAGTGTCA	GCCCAAGGCT	ATAATCCGGC	CTTAATGACC	TATCCAGGAA	ACACAGGGCT	4980
	TCTGGCTACC	AAAAGTAAAG	AAAATGGATG	GACAACCGTT	TATGATGATG	ACCCCGAGGG	5040
	ACACCTGACC	AATGCAACGT	TTCCCACTGG	AGAGGTGAGC	AGCTTCCACA	GTGACCTGGA	5100
	GAAGCTGACA	AAAGTGAGGC	TAGATACTTC	CAACCGTGAA	AATGTCTCTA	TGTCAACCAA	5160
50	CTTGACGSCA	ACTAGTACCA	TATATATTTT	AAAACAAGAA	AATACTCAAA	GTACCTATCG	5220
	GGTGAATCCA	GATGGTTCCC	TGCGTGTGAC	TTTTGCCAGC	GGGATGGAGA	TGGGCTCTAG	5280
	CTCAGAGCCC	CACATCTCTG	CAGGGGCGAGT	CAACCTTACC	CTGGGCAAT	GCAACATCTC	5340
	ATTGCCCGGA	GAGCACAATG	CAAACTCTAT	CGAGTGGCGG	CAGAGGAAGG	AGCAAAACAA	5400
	AGGCAATGTT	TGCGCTTTTG	AAAGGAGGCT	GAGGGCCGAC	AACAGAAACC	TACTCTCCAT	5460
55	AGATTTTGAT	CATATAACCC	GCACAGGAAA	GATCTATGAT	GACCATCGAA	AATTCACCTT	5520
	TGGAATTCCT	TATGACCAGA	CTGGGCGACC	CATTCTGTGG	TCTCTGTGTA	GCAGATATAA	5580
	TGAAGTGAAC	ATCACATATT	CACCTTCGGG	ATTGGTGAGC	TTTATTCAAA	GAGGAACGTT	5640
	GAATGAAAAA	ATGGAATATG	ACCAGAGTGG	GAATAATTAT	TCAAGAACTT	GGGCTGATGG	5700
	GAATAATTGG	AGCTATACCT	ACTTAGAAAA	ATCTGTGATG	CTTCTCTTAC	ACAGCCAGCG	5760
60	GCGTACATC	TTTGAGTATG	ACCAATCAGA	TTGCTGCTG	TCAGTTACCA	TGCTAGCAT	5820
	GGTGGCCGAC	AGCTTACAAA	CCATGCTTTC	AGTGGGCTAC	TACCTTAATA	TCTACACCCC	5880
	ACCGGACAGT	AGCACTTCTT	TTATCCAAGA	CTATAGTCGA	GATGGCCGAT	TGCTACAGAC	5940
	CCGTGATCTG	GGGACAGGGC	GCAGAGTCTT	ATACAAGTAC	ACCAAGCAAG	CAAGGCTTTC	6000
65	TGAGGTTCTC	TATGATACCA	CTCAGGTGAC	ATTAAACATAT	GAAGAGTCTT	CTGGAGTGAT	6060
	TAAGACAATA	CACCTGATGC	ATGACGAGAT	CATCTGCACA	ATCAGATACA	GGCAACAGG	6120
	ACCTCTTATT	GGACGCCAGA	TTTTAGATT	CAGTGAAGAA	GGCCTTGTGA	ATGCAAGGTT	6180
	CGACTACAGC	TACAACAATT	TCCGAGTCAC	AAGCATGCAA	GCTGTAATCA	ATGAAACCCC	6240
	TTTGCTCTATA	GATCTTTACC	GATATGTTGA	TGCTCTGCG	AGAACAGAGC	AGTTTGGAAA	6300
	ATTCACTGTA	ATTAAATTAC	ATTAAATCA	GGTCATAACT	ACTACAGTGA	TGAACACAC	6360
70	CAAAATCTTC	AGTGCCAAATG	GACAAGTCAT	TGAAGTCCAA	TATGAATCC	TAAAGGCAAT	6420
	TGCTCTACTG	ATGACCAATC	AATATGATAA	TGTGGGCCGA	CATGGTAATA	TGTGCATAAG	6480
	GGTAGGAGTA	GATGCCAATA	TAACAAGGTA	CTTCTATGAA	TACGATGCTG	ATGGGCAACT	6540
	TCAGACTGTT	TCTGTAAATG	ACAAAACCCA	GTGGCGTTAT	AGTTACGATC	TGAATGGAGA	6600
	CATCAACCTC	TTAAGCCATG	GGAAGAGTGC	TGCTCTTACT	CCCTCCGAT	ATGACCTCCG	6660
	AGACCGCATC	ACCAGATTAG	GAGAAATCA	GTATAAAATG	GATGAAGATG	GCTTTCTGAG	6720
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	TAAGTCCAGC	CTAGGGCAGC	ACCTTCAGTT	CTTTGTGAC	GCGACCGCGA	ACCCCAATAG	6900
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	TGTTGTTGCT	GGCAGATGGA	CAACGGCCTA	TCATCACATA	TGGAACAGT	TGAACCTCCT	7260
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A210 Protein sequence:

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1
 Unigene number: Hs.23796
 Probeset Accession #: NM_014253
 Protein Accession #: NP_055068
 Signal sequence: none found
 Transmembrane domains: 318-340
 Cellular Localization: plasma membrane

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A211 DNA SEQUENCE:

Gene name: Solute carrier family 26, member 4
 Unigene number: Hs.159275
 Probeset Accession #: AF030880
 Nucleic Acid Accession #: NM_000441
 Coding sequence: 225-2567 (underlined sequences correspond to start and stop codons)

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 TTTTCTCTAA GTGCCAACAA TTTTCTAGAT ATTATATACA ACACAGGCTT TGATCTTGGG 3780
 GACTTTTCCC ATATATTTCA CACTGGAGTG AATGAAAGTT TACTTCATT CTAGAGAAAA 3840
 60 GTTATACCCA GGTCCCAAT TGAGAAATGC TTGCTTGATT GAAAGCGACA TCATCCCTTG 3900
 GTATATCCA GGGATTGGTT TCAGGACCCC TGCAATTACC AAAATTGTG CACACTCAAG 3960
 TCTCGACGT ACCCTGCGCT AAAGATAGAA TGCTTCTCT GTTTTCTCT TGAATACAA 4020
 CCAGAACAA TGTGTCTATT TCTGAAAGAA TAGGATTAAT GATCATACAA ATGGGTTAAT 4080
 CCGAATTCT GGTGTAAAT CTGGTTACAG CATAACTAGG ATTATAATGC TGCCTCATTT 4140
 65 TCACAGCACT ACTGTCTTAT ATTGACAACA AATCATCTCG CTAAGAGTGT AATGTAGGCC 4200
 AGGCGCGGTG GCTCATGCC GTAAATCCCAG CACTTTGGGA GCGCGAGGCG GGTGGATCAC 4260
 GAGGTCAAGA GATCGAGACC ATCCTGGCTA ACATGGTAAA ACCCGCTCT TACTAAAAAT 4320
 AGAAAAAAG AAATTAGCCT AGCGTGGTGG CTGGCGGGCG CCGTAGTCC CAGCTATTTG 4380
 GAGGCTAAG CAGGAGAAAT GCGTGAACC CGGGAGGCGG AGCTTGCACT GAGCGAGGT 4440
 70 CGTGCCACTG CACTCCAGCC TGGGCGACAG AGCAAGACTC CGTCTCAAAA AAAAAAATA 4500
 AAAAAAATA AGAGTGAATG TAATAGTCTT GCAGAAATG AATGAATACC TTTGTTCAAT 4560
 AAAGGAAAAA TGCACTGCTC ACTTTTGA AGGAAATGCC AAGTTAGCT TTTACACAA 4620
 GGCTAGAGTT TGTAAATTT GGGTTCAATT GTGATGACAT AAGTCAGCAA ACTGCGGGA 4680
 75 TACTGTCTCT TCTATGTATT TTGTGAATAG TAAGCATAAT TTTAGTTTGT TATTATCAAT 4740
 GAAAAATTTA CTTGAAATTA AAGCTGCCTT TTGTTATATT TTTAACCTAT AGGATAAGAT 4800
 TCCAGTATG TATATGAGTT TTAACAAAT AATCATGTACA TTTGAAATA 4860
 TTTGCACACA TTTAAAAATA AATGTAAAGT TGTCTTTTAA ACTACTCGGA TGTGCTCTT 4920
 CTGAACAAAA

A212 Protein sequence:

80 Gene name: Solute carrier family 26, member 4
 Unigene number: Hs.159275
 Probeset Accession #: AF030880
 Protein Accession #: O43511
 Signal sequence: none found

Transmembrane domains: 81-103, 109-131, 136-158, 185-207, 221-243, 245-267, 270-291, 295-317,
347-369, 386-408, 420-442, 448-470, 486-508
Cellular Localization: plasma membrane

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1 11 21 31 41 51
MAAPGGRSEP PQLPEYSCSY MVSRRPVYSEL AFQQQHERRL QERKTLRESL AKCCSCSRKR 60
AFGVLTLPV ILEWLPKYRV KEWLLSDVIS GVSTGLVATL QGMAYALLAA VPVGYGLYSA 120
10 FFPIITYFIF GTSRHISVGP FVVSLMVGS VVLSMAPDEH FLVSSSNGTV LNTTMDTAA 180
RDTARVLIA ALTLVLGIIQ LIFGGLQIGF IVRYLADPLV GGFTTAAAFQ VLVSQLKIVL 240
NVSTKNYNGV LSIIYTLVEI FQNIQDNLN DFTAGLLTIV VCMVAVKELND RFRHKIPVPI 300
PIEVIVTIIA TAISYGANLE KNYNAGIVKS IPRGFLPPEL PVSLSFSEML AASFSIAVVA 360
YIAIVSVGVK YATKYDYTID GNQEFIAFGI SNIFSGFPFC FVATTALSRT AVQESTGGKT 420
15 QVAGIISAAI VMIAIALGK LLEPLQKSVL AAVVIANLKG MFMQLCDIPR LWRQNKIDAV 480
IWFVTCIVSI ILGLDLGLLA GLIFGLTLTV LRVQFPSPWNG LGSIPSTDIY KSTKNYKNIE 540
EPQGVKILRF SSPIFYGNVD GFKKCIKSTV GFDAIRVYNK RLKALRKIQK LIKSGQLRAT 600
KNGIISDAVS TNNAFEPDED IEDLEELDIP TKEIEIQVDW NSELPVKVNV PKVPIHSLVL 660
20 DCGAISFLDV VGVRSRLRVIV KEFQRIDNVV YFASLQDYVI EKLEQCGFFD DNIRKDTFFL 720
TVHDAILYLQ NQVKSQEGQG SILETITLIQ DCKDTLELIE TELTEBELDV QDEAMRTLAS 780
QDEAMRTLAS

25 A213 DNA SEQUENCE:
Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]
Unigene number: Hs.98280
Probeset Accession #: AA418000
Nucleic Acid Accession #: NM_021614
30 Coding sequence: 458-2197 (underlined sequences correspond to start and stop codons)

35 1 11 21 31 41 51
CGGCGGCAGC AGCCCATGCC TCCGGTGCAA CAGCTGCGCC TCCTCCGGTG CCCCGGCGGC 60
GGGGGCGGGA GATAACCTGT CCTGCTGCT CCGCACCTCC TCGCCGCGCG GCGCCTTCG 120
GACCCGCACC TCCTCCCGCG TGTCGGGCTC GTCTGCTGCT TGCTGCTGCT GCTCGTCGCG 180
CGGCGGCAGC CAGCTCAATG TGAGCGAGCT GACGCGTCC AGCCATGCCA GTGCGCTCCG 240
GCAGCAGTAC GCGCAGCAGT CCGCGCAGCA GTGCGCGTCC GCCTCCCACT ACCACCACTG 300
CCACAGCCTG CAGCCCGCGC CCGAGCCGAC GGGCAGCCTC GGCAGTCTGG GCTCCGCGCC 360
40 CCGCTCTGCG CACCACCACC ACCACCOCGA CCGGCGCGAC CACCAGCACC ACCAGCCCCA 420
GGCGCGCCGC GAGAGCAACC CCTTCACCGA AATAGCCATG AGCAGCTGCA GGTACAACGG 480
GGGCGTCATG CGGCGGCTCA GCAACTTGA GCGCTCCGCG CGGAGCTGGC GCGCGTCTCT 540
CTCAGAGGCG CAGCCCTGCT AGCCCCCGCG GTCTGTGGGA GGAGGTGGCG GCGCGTCTCT 600
CCGCTCTGCA GAGCCTGCGC CCGCGCGCGC TGTTTGTGTC TCAGCCCCCG AGATCGTGGT 660
45 GTCTAAGCCC GAGCACAACA ACTCCAACA CCTGGGCTCT TATGGAACCG CGGCGGAGG 720
CAGCACTGGA GAGAGCGGCG GCGGTGGAGG GAGCGGGCAC GGCAGCAGCA GTGGCACCAC 780
GTCCAGCAAA AAGAAAAACC AGAACATCGG CTACAAGCTG GGCACCGCGC GCGCGCTGTT 840
CGAAAAAGCG AAGCGGCTCA GCGACTACGC GCTCATCTTC GGCATGTTCC GCATCGTGGT 900
CATGGTCATC GAGACCGAGC TGTCGTGGGG CGCTCATGAC AAGGCGTGGC TGTATTCTCT 960
50 AGCTCTGAAA TGCCTTATCA GTCTCTCCAC GATCATCTCG CTCGGTCTGA TCATGTTGTA 1020
CCACGCCAGG GAAATACAGT TGTTTATGGT GGAACAATGA GCAGATGACT GGAGAAATAGC 1080
CATGACTTAT GAGCGTATTT TCTTCACTG CTGGAATAA CTGGTGTGIG CTATTCTATC 1140
CATACCTGGG AATTATACAT TCACATGGAC GGCCCCGCTT GCCTTCTCTCT ATGCCCATC 1200
CACAACCAAC GCTGATGTGG ATATTATTTT ATCTATACCA ATGTTCTTAA GACTCTATCT 1260
55 GATTGCCAGA GTTCATGCTT TACATAGCAA ACTTTTCACT GATGCTCTCT CTAGAAGCAT 1320
TGGAGCACTT AATAAGATAA ACTTCAATAC ACGTTTGTGT ATGAAGACTT TAATGACTAT 1380
ATGCCCAAGG ACTGTACTCT TGGTTTTTAG TATCTCATT TGGATAATTG CCGCATGGAC 1440
TGTCGAGGCT TGTGAAAGGT ACCATGATCA ACAGGATGTT ACTAGCAACT TCCTTGGAGC 1500
GATGTGGTGG ATATCAATAA CTTTCTCTCT CATTGGTTAT GGTGACATGG TACCTAACAC 1560
60 ATACTGTGGA AAAGGAGTCT GCTTACTTAC TGGAAATTAT GGTGCTGGTT GCACAGCCCT 1620
GGTGTAGCT GTATGGGCAA GGAAGCTAGA ACTTACCAAA GCAGAAAAAC ACGTGCACAA 1680
TTTCTATGAT GATACTCAGC TGAATAAAG AGTAAAAAAT GCAGCTGCCA ATGTACTCAG 1740
GGAAACATGG CTAATTTACA AAAATACAAA GCTAGTGAAA AAGATAGATC ATGCAAAAGT 1800
AAGAAAAAT CATACGAAAT TCTTGCAAGC TATTTCATCA TTAAGAAAGT TAAAAATGGA 1860
65 GCAGAGGAAA CTGAATGACC AAGCAAAACAC TTTGGTGGAC TTGGCAAGA CCCAGAACAT 1920
CATGTATGAT ATGATTTCTG ACTTAAACGA AAGGAGTGAA GACTTCGAGA AGAGGATGTT 1980
TACCTCGGAA ACRAAACTAG AGACTTTGAT TGGTAGCATC CACGCCCTCC CTGGGCTCAT 2040
AAGCCAGACC ATCAGGCGAG AGCAGAGAGA TTTCAATGAG GCTCAGATGG AGAGCTACGA 2100
70 TAAGCAAGTC ACTTACAATG CTGAGCGGTC CCGTCTCTCG TCCAGGAGGC GCGCGTCTCT 2160
TTCCACAGCA CCACCAACTT CATCAGAGAG TAGCTAGAAG AGAATAAGTT AACCAAAAA 2220
TAAGACTTTT TGCCATCATA TGGTCAATAT TTTAGCTTTT ATGTATAAGC CCCTATGGTT 2280
CTAATCAGCG TTATCCGGGT TCTGATGTCA GAATCCTGGG AACCTGAACA CTAAGTTTAA 2340
GGCCAAAAAT AGTGAAAACT CTTTCTTTT CTTTCAGATG CACAGGGAAT GCACCTATTA 2400
75 TTGCTATATA GATTGTTCTT CTTGTAATTT CACTAATCTT TTATTCATCG ACTTCAACA 2460
AACCITACTA CTACATTATA TGATATATAA TAAAAAAGT TAATTTCCGA

80 A214 Protein sequence:
Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]
Unigene number: Hs.98280
Probeset Accession #: AA418000
Protein Accession #: NP_067627
Signal sequence: none found
Transmembrane domains: 135-157, 168-190, 208-230, 254-276, 306-328, 342-364, 373-394

	1	11	21	31	41	51	
5							
	MSSCRYNGGV	MRPLSNLSAS	RRLNHEMDSE	AQPLQPPASV	GGGGGASSPS	ADAAAAAASV	60
	SSAPEIVVSK	PERDNNNLIA	LYTGGGGST	GGGGGGGGSG	HGSSSGTKSS	KKKNQNIYK	120
	LGHRRALPEK	RKRLSOYALI	PGMPGIVVMV	IETELSWGAV	DKASLYSLAL	KCLISLSTII	180
10							
	LLGLIIVYHA	RETLQFMVDN	GADDWRIAMT	YERIFFICLE	ILDCAIHPIF	GNYFTFTWAT	240
	LAFSYPASTT	TADVDDIILSI	PMFLRLVILA	RVMLLHSHKFL	TDASSRSIGA	LNKNINPTFR	300
	VKMTLMTICP	GTVLLVFSIS	LWIIAAWTVR	ACERYHDDQD	VTSNPLGAMW	LISITPLSTG	360
	YQDMVPNTYC	QKGVCLLTPI	AGAGCTALVV	AVVARKLELT	KAEXHVSFNM	MDLQTLKRVK	420
15							
	NAAANVLRET	WLIYKNTKLV	KKIDHAKVRK	HQRKFLQAIH	QLRSVKMEQR	KLNDQANTLV	480
	DLAKTQNIYM	DMISDLNERS	EDPEKRVITL	ETKTLTIGSS	THALPGLISQ	TIRQQQRDPI	540
	EAQMSYDKH	VTYNAERSRS	SSRRRSRSTT	APPTSSSS			

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Gene name:	CGI-86 protein
Unigene number:	Hs.109201
Probeset Accession #:	AW161450
Nucleic Acid Accession #:	NM_016029
Coding sequence:	228-1097 (underlined sequences correspond to start and stop codons)

50 AGATTGCCAT GAATCTTGCA AA

Gene name:	CGI-86 protein
Unigene number:	Hs.109201
Probeset Accession #:	AW161450
Protein Accession #:	NP_057113
Signal sequence:	1-26
Transmembrane domains:	183-206, 221-243
Cellular Localization:	plasma membrane

70 MPTWAWIITN KMGKKRIENF KSGVDADSSY FRIFKTRHD

75

Gene name:	Homo sapiens mRNA; cDNA DKFpZp56401763 (from clone DKFpZp56401763)
Unigene number:	Hs.27373
Probeset Accession #:	FL3036
Nucleic Acid Accession #:	AC012478
Coding sequence:	1-1896 (underlined sequences correspond to start and stop codons)

80

1	11	21	31	41	51	
<u>ATGCGCGCG</u>	<u>TGCGCGTGC</u>	<u>CGCGCGCTC</u>	<u>CTGCGCTGC</u>	<u>TGCTGCTGC</u>	<u>GCTCTGGCC</u>	60
GCTCCGCGCG	CCGCGGCCAG	CAGAGCGAG	TCGCTCTCG	CGCGGTGGCC	CGAACCCGAG	120
CGCGAGTTCG	GGCCACCGCG	CGCGCGCGGG	CGCGGGAACA	CCACCGCGTT	TGGGTCTGGG	180
GCGGCGGGCG	GCACGCGGAC	CTCAGCTCC	AACACGAGTG	GCGACGCGCTT	GGTGACCGAG	240

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ATTTCATCC TCCTCCGCGA CCTACCCACC CTCAAGGCGAG CCGTGATCGT GCGGTTCCGC 300
TTTACCACCC TCCTCATCGC CTGCTGCTG CTGCGGCTCT TCAGGTCCGG AAAGAGGTTA 360
AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGG AATGGGCGCA 420
CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
TCCTTGCCGG CTGCACTGAG ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCTT 540
GTGCCCCCACC CCTTCATCCT CGACATTGAC CTTCCAGCAA GATGCAGTGG AAGGCTGAT 600
GGTGGAAATCA GACCTGGTAA AACCTGTTTC CCAGCCTGGT GGCATCCTGT GGAAGTTGG 660
TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGGAAG CCTCTGCGT CAGAGGTGTT 720
GAAACAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGCCTGTC AGGCATCTGC 780
TCAGACTGTG ACTGGCAAGC TCGTTTCCAC GTCAACCAA TGGAGTTGCT TCTGCCACCC 840
TTTGGGCATC CCTTTAAAGT GCCCCTACT TCTACTCCC ATGGTTTTCG ACAAATGTCAG 900
CTGAATCTCA TGGAAAAGCT GGATTCCTCT GCCTTACGCA GAAACACCCG GGCTCCATCT 960
GCCAGGTGCT TGCCACTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
CCTTGGTGGC ACTTCAGGCG CACAGGCTCT CCAATAAAAA CCCTTTACAC ACAAACCATG 1080
AGTACTTGGC LTTTGAAGCT TTTCTGTTGT GCGCGCCAGC GGGGCACCTT TTGTGAAGAC 1140
AGAGCAGTGA CTAAGGTTCT CCAGGCTAGC TCTTTCTCCA AACAGCTCGC CTGGAAGCCA 1200
GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260
ACCCATCCTC TCAGGTTGGC TCGTTTCAGT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG 1320
AGGGTGTTC GCGCTCCGCG CGACTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCAACT 1380
TGCTTTTGG CTTTGAAGAT TCTGTTGAGG CGCCATCCTC ACCTTGACCT CTTCTACAAA 1440
ATCTGTCTCC CTTGCTGTGC CGTGGAAAC CTAAGGGAAG CCAAGAGAAG CTCAGTGACT 1500
GTCTTGTGCT CATTTAGGCA GAGCCCAACA AAGGCAGCTG CTGCCACGG GGAGCTGTCT 1560
AAACGAGGGC CCAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620
GCGAACCTGC AGACAATTCC AGATAACCAA GGCCAGGAAG GCCCAGTGA GGATGTCACT 1680
CACCTGGGAG GAGACTTGGG TGGGGTGGCA AATTTCTATT TGGAGGAAGA GGGTTTCCAG 1740
GATGGCAGAT GCCAGAAGAT GGTCTGATG TCTGAGGAAG GGCCACCTAG TTGACAGGA 1800
TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCCTTCCTT 1860
TCCCCCGAC AGCCCCCTGT TCTGTCCAGG CCTTGA
  
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A218 Protein sequence:

Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
 Unigene number: Hs.27373
 Probeset Accession #: F13036
 Protein Accession #: FGENESH predicted
 Signal sequence: 1-27
 Transmembrane domains: 94-115, 448-469
 Cellular Localization: not determined

1 11 21 31 41 51
 MRVPLPAPL LPLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTTRFGSG 60
 AAGSGSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAF FTLIIACLL LRVRPSKRL 120
 KKTRKYDIIT TPAERVEMAP LNEEDDEDED STVFDIKYRV SLPAALRRQL PGQTLTLTVP 180
 VPPPFILID LPARCSGRPD GGIRPGKTCF PAWHPFVSW SAATWGVKW TWKPSVCGGV 240
 ETKINVMYKT PAPSCVSGIC SDCHWQARFH VITMELLPP FGHFPKVPPT STPHGFRQLQ 300
 LNLMEKLDSS ALRRNTRAPS ARCLPLVLA EAAAESDLN PWWHPSATGS PIKTLTYQTM 360
 STLGLDVFCG AGQRTGFCED RAVTKVLQGS SFSKQLRWKP ALESGFPHHL RLLRECPFLS 420
 THPVLARS D AQQASLTGR RVFRKPRQSL HGGGSAGTAT CLLVLKILL RHPHLDLFYK 480
 ICLPCCAVEH LREARSSVT VLASFQSPQ KAAAHGEFV KRGPSGLTR HTCPCWGITH 540
 ANLQTIPTDQ GQEGPRESDVT HPGGDLDGVA NFYLEEBGFQ DGRQKMWLM SEEGPPLTG 600
 CERLTGSHHF SSHSKWSFPL SPRQLFLSR P

A219 DNA SEQUENCE

Gene name: selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Nucleic Acid Accession #: NM_000450
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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ATGATGCTT CACAGTTCT CTCAGCTCTC ACTTGGTGC TTCTCATTAA AGAGAGTGA 60
GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
CAGCAAAGGT ACACACACCT GGTTCGAATT CAAACAAAG AAGAGATTGA GTACCTAAAC 180
TCCATATTGA GCTATTCAAC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG 240
TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAGAACTG GGTCCAGGT 300
GAACCCAACA ATAGGCAAAA AGATGAGGAC TGCCTGGAGA TCTACATCAA GAGAGAAAAA 360
GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
GCTGCCGTGA CCAATACATC CTGCACTGGC CACGCTGAAT GTGTAGAGAC CATCAATAAT 480
TACACTTGCA AATGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAT TGTGAATCTG 540
ACAGCCCTGG AGTCCCTGGA GCATGGAAGC CTGGTTTCCA GTCACCACT GGGAACTTC 600
AGCTACAATT CTCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
ACCATGCAGT GTATGTCTCT TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGTT 720
GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTTGA 780
AGCTTCCCAT GGAACACAC CTTGACATT GACTGTGAAG AAGGATTGA ACTAATGGGA 840
GCCAGAGGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAG 900
GCTGTGACAT GCAGGCGCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCAATTCC 960
CTGTCTGGAG AGTTCACCTT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020
TTGCAAGGAC CAGCCCAAGT TGAATGACCC ACTCAAGGCG AGTGGACACA GCAATATCCA 1080
GTTGTGAAG CTTTCCAGTG CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT 1140
CTTCTAGTG CTTCTGGCAG TTTCCGTTAT GGGTCCAGCT GTGAGTTCTC CTGTGAGCAG 1200
GGTTTTGTGT TGAAGGGATC CAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAC 1260
  
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GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320
GTGAGGTGTG CTCAATCCCC TATTGGAGAA TTCACCTACA AGTCCTCTTG TGCCCTCAGC 1380
TGTGAGGAGG GATTTGAATT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440
TGGACAGAAG AGGTTCTCTC CTGCCAAGTG GTAAAATGTT CAAGCCTGGC AGTTCCGGGA 1500
AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGGCA CTGTGTGCAA GTTCGCTGT 1560
CCTGAAGGAT GGAOGCTCAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG 1620
TCTGGCCTCG TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680
CTTTCTGCTG CTGGACTCTC CCTCCTGACA TTAGCACCAT TTCTCCTCTG GCTTCGGAAA 1740
TGCTTACGGA AAGCAAAGAA ATTGTCTCTT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

A220 Protein sequence:

Gene name: Selectin E (endothelial adhesion molecule 1)
Unigene number: Hs.89546
Probeset Accession #: M24736
Protein Accession #: NP_000441
Signal sequence: 1-22
Transmembrane domains: 555-573
C-lectin domain: 23-139
Cellular Localization: plasma membrane

1 11 21 31 41 51
MIASQFLSAL TLVLIIKESG AWSYNTSTEA MTYDEASAYC QQRYYTHLVAI QNKKEIEYLN 60
SILSYSPSYW WIGIRKVNNV WVVVGTKQPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK 120
DVGMWNDERC SKKCLALCYT AACTNTSCSG HGBCVETINN YTCCKDPGFS GLKCEQIVNC 180
TALESPEHGS LVCSEPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIACNVV 240
ECDAVTNPAN GFVECFQNPQ SPFWNTTCTF DCEBGFELMG AQSLOCTSSG NWDNEKPTCK 300
AVTCRAVRQP QNGSVRCSSS PAGEFTFKSS CNFTCEBGFM LQGPAGVECT TGGQWTQIP 360
VCEAFQCTAL SNFERGYMNC LPSASGSFRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWEN 420
EKPTCEAVRC DAVHQPPIKGL VRCAHSPIGE FTYKSSCAPS CEBGFELYGS TQLECTSQGQ 480
WTEEVFSCQV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHM 540
SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLWLRLK CLRKAKKFPV ASSCQSLSD 600
GSYQKPSYIL

Taxol ProstateA221 DNA SEQUENCE

Gene name: ESTs; Liprin A2
Unigene number: Hs.306480
Probeset Accession #: N51002
Nucleic Acid Accession #: N51002
Coding sequence: 1-3793 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
ATGATGTGTG AAGTGATGCC CACGATTAAT GAGGACACCC CAATGAGCCA AAGGGGGTCC 60
CAAAGCAGTG GCTCGGACTC AGACTCCCAT TTTGAGCAGC TGATGGTGAA TATGCTAGAT 120
GAAAGGGATC GTCTTCTAGA CACCTTTCGG GAGACCCAGG AAAGCCTCTC ACTTGCCAG 180
CAAAGACTTC AGGATGTCAT CTATGACCGA GACTCACTCC AGAGACAGCT CAATTGAGCC 240
CTGCCACAGG ATATCGAATC CCTAACAGGA GGGCTGGCTG GTTCTAAGGG GGCTGATCCA 300
CGGGAATTTG CTGCACTGAC AAAAGAATTA AATGCCTGCA GGGAAACAACT TCTAGAAAAG 360
GAAGAAGAAA TCTCTGAATC TAAAGCTGAA AGAAACAACA CAAGACTATT ACTGGAGCAT 420
TTGGAGTGCC TTGTGTCAAG ACATGAAAGA TCACTAAGAA TGACGGTGGT AAAACGGCAA 480
GCCAGTCTC CTCTCAGGAG ATCCAGTGAA GTTGAAATTC TCAAGGCAC TGAATCTTTG 540
TTTGAGCAC ACAGGCCCTT GGATGAAAAG GTTAGGGAGC GACTGAGGGT TTCTTTAGAA 600
AGAGTCTCTG CACTGGGAAG AGAACTAGCT GCTGCTAATC AGGAGATTGT TGCCCTTGGT 660
GAACAAATG TTCATATACA AAGAAAAATG GCATCAAGCG AGGGATCCAC AGAGTCAGAA 720
CATCTTGAA GGAATGGAACC TGGACAGAAA GTCCATGAGA AGCGTTTGT CAAATGTTCT 780
ATAGACTCAA CGATGAAAC TAGTCAAATA GTTGAACTAC AAGAAATGCT TGAAGAGCAA 840
AACTATGAAA TGGCCAGAT GAAAGAACGT TTAGCAGCCC TTTCTTCCC AGTGGGAGAG 900
GTGGAACAGG AAGCAGAGAC AGCAAGAAAG GATCTCATT AAACAGAGA AATGAACACC 960
AAGTATCAA GGGACATTAG GGAGGCCATG GCACAAAAGG AAGATATGGA AGAAGAAT 1020
ACAACCCCTT AAAAGCGTTA CCTCAGTGCT CAGAGAGAAT CTACCTCCAT ACATGACATG 1080
AATGATAAAC TAGAAAAATG GTTAGCAAT AAAGAAGCTA TCCTACGGCA GATGGAAGAG 1140
AAAAACAGAC AGTTACAAGA ACGTCTTGAG CTAGCTGAAC AAAAGTTGCA GCAGACCATG 1200
AGAAAGGCTG AAACCTTGCC TGAAGTAGAG GCTGAAGTGG CTCAGAGAAT TGCAGCCCTA 1260
ACCAAGGCTG AAGAGAGACA TGGAAATATT GAAGAAGCTA TGAGACATTT AGAGGGTCRA 1320
CTTGAAGAGA AGAATCAAGA ACTTCAAAGA GCTAGGCAAA GAGAGAAAAAT GAATGAGGAG 1380
CATAACAGA GATTATOGGA TACGGTTGAT AGACTTCTGA CTGAATCCAA TGAAGCCCTA 1440
CAACTACACT TAAAGGAAAG AATGGCTGCT CTAGAAGAAA AGAATGTTTT AATTCAAGAA 1500
TCAGAACTT TCAGAAAGAA TCTTGAAGAA TCTTTACATG ATAAGGAAAG ATTAGCAGAA 1560
GAAATTGAAA AGCTGAGATC TGAACCTGAC CAATTGAAA TGAGAACTGG CTCTTTAATT 1620
GAACCCACAA TACCAAGAAC TCATCTAGAC ACCTCAGCTG AGTTGCGGTA CTCAGTGGGA 1680
TCCTTAGTGG ACAGCCAGTC TGATTACAGA ACAACTAAG TAATAAGAAG ACCAAGGAGA 1740
GGCCGATGG GTGTGGAAG AGATGAGCCA AAGGTGAAAT CTCTTGGGGA TCACGAGTGG 1800
AATAGAACTC AACAGATTGG AGTACTAAG AGCCACCCCT TTGAAAGTGA CACTGAAATG 1860
TCTGATATTG ATGATGATGA CAGAGAAACA ATTTTGTAGT CAATGGATCT TCTCTCTCCA 1920
AGTGGTCATT CGAGTGCCCA GACGCTAGCC ATGATGCTTC AGGAACAATT GGATGCCATC 1980
AACAAAGAAA TCAGGCTAAT TCAGGAAGAA AAAGAACTCA CAGAGTTGGT TGCTGAAGAA 2040
ATTGAAAAAT GAGTGCTTAG TGTGAGCCTC GAAGGCCTGA ATTTGGCAAG GGTCCACCCA 2100

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GGTACCTCCA TTACTGCCTC TGTTACAGCT TCATGCTGG CCAGTTCATC TCCCCCAGT 2160
GGACACTCAA CTCCAAGACT CACCCCTCGA AGCCCTGCCA GGGAAATGGA TCGGATGGGA 2220
GTCATGACAC TGCCAAGTGA TCTGAGGAAA CATCGGAGAA AGATTGCAGT TGTGGAGAAA 2280
GATGGTCGAG AGGACAAAGC AACAAATTAAT TGTGAAACTT CTCTCTCTCC TACCCCTAGA 2340
GCCCTCAGAA TGACTCACAC TCTCCCTTCT TCCTACCACA ATGATGCTCG AAGTAGTTTA 2400
TCTGTCTCTC TTGAGCCAGA AAGCCTCGGG CTGGTAGTGT CCAACAGCAG CCAAGACTCT 2460
CTTCACAAG CCCCAAGAA GAAAGGAATC AAGTCTTCAA TAGGACGTTT GTTTGGTAAA 2520
AAAGAAAAAG CTGCACTTGG GCAGCTCCGA GGCCTTATGG AGACTGAAGC TGCAGCTCAG 2580
GAGTCCCTGG GGTAGGCAA ACTCGGAAGT CAAGCTGAGA AGGATCGAAG ACTAAGAGAA 2640
AAGCATGAAC TTCTTGAAGA AGCTCGGAGA AAGGGATTAC CTTTGGCCCA GTGGGATGGG 2700
CCAACTGTGG TCGCATGGCT AGAGCTTTGG TTGGGAATGC CTGCGTGGTA CGTGGCAGCC 2760
TGCGAGCCA ACGTGAAGAG TGGTGCCATC ATGTCGTCTT TATCTGCAC TGAGATCCAG 2820
AGAGAAATTG GAATCAGCAA TCCACTGCAT CGCTTAAAC TTGATTAGC AATCCAGGAG 2880
ATGGTTCCCT TAACAAGTCC TTCACTCTCT CCAACATCTC GAATCCTTC AGGCAACGTT 2940
TGGGTGACTC ATGAAGAAT GGAATACTT GCAGCTCCAG CAAAAACGAA AGAATCTGAG 3000
GAAGGAAGCT GGGCCCAAGT TCCCGTTTTT CTACAGACC CTGGCTTATG AGATATGAAT 3060
CATGAGTGA TTGGAATGA ATGGCTTCCC AGCTTGGGGT TACCTCAGTA CAGAAGTTAC 3120
TTTATGGAAT GCTTGTGAGA TGCAAGAATG TTAGATCACC TAACAAAAA AGATCTCCGT 3180
GTCCATTAA AAATGTGGA TAGTTCATC CGAACAGTT TACAATATG AATTATGTGC 3240
TTAAAGAGT TGAATATGA CAGAAAGAA CTAGAAAGAA GACGGAAGC AAGCCAACAT 3300
GAAATAAAG ACTGTTGGT GTGGAGCAAT GACCGAATTA TTCGCTGGAT ACAAGCAAT 3360
GGACTTCGAG AATATGCAAA TAATATACT GAGAGCGGTG TGCATGGCTC ACTTATAGCC 3420
CTGATGAAA ACTTTGACTA CAGCAGCTTA ACTTTATTAT TACAGATTCC AACACAGAAC 3480
ACCCAGGCAA GGCAGATTCT TGAAGAGAA TACAATAACC TCTTGGCCCT GGGAACTGAA 3540
AGGCGACTGG ATGAAGTGA TGACAAGAAC TTCAGACGTG GATCAACCTG GAGAAGCAG 3600
TTCTCTCTC GTGAAGTACA TGAATCAGC ATGATGCTG GGTCTCAGA AACATTACCA 3660
GCTGGATTGA GGTAAACAC AACCTCTGG CAATCAAGAA AAATGACAAC AGATGTTGCT 3720
TCATCAAGAC TGCAGAGGTT AGACAACCTC ACTGTTGCA CATACTCATG TCTCGAGTAA 3780
GGGCGCGCTT TAA

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A222 Protein sequence:

Gene name: ESTs; Liprin A2
 Unigene number: Hs.306480
 Probeset Accession #: N51002
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: none found
 AAA domain: 286-539
 SAM domain: 895-964, 1017-1084, 1105-1177
 Cellular Localization: not determined

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1 11 21 31 41 51
MMCEVMPTIN EDTPMSQRGS QSSGSDSDSH FEQLMVNMLD ERDLILDTLR ETQESLSLAQ 60
QRLQDVIYDR DSLQRLQNSA LPQDIESLTG GLAGSKGADP PEFAALTKEL NACREQLLEK 120
EEBISLKAEE RNNTLRLLLEH LECIVSRHER SLRMTVVKRQ AQSPSGVSSE VEVLKALKSL 180
FEHHKALDEK VREKLRVSLR KVSALREBELA AANQEIVALLR BQNVHIQRM ASSEGSTSESE 240
HLEGMFPGQK VHEKRLSNGS IDSTDETSQI VELQELLEKQ NYEMAQMKER LAALSSRVGE 300
VEQEAETARK DLIKTEEMNT KYQRDIREAM AQKEDMEERI TTLEKRYLSA QRESTSIHDM 360
NDKLENELAN KEAILRQMEB KNRQLQERLE LAEQKLQQTMM RKAETLEPEVE AELAQRIALA 420
TKABERHGN EERMRHLEGQ LEEKNQELQR ARQREKMEEB ENKRLSDTVL RLLTESNERL 480
QLHLKERMMA LEEKNVLIQE SETFRKNLEE SLHDKERLAE EYKLRSELD QLKMRGTGSLI 540
EPTTPRTHLD TSAELRYSVG SLVDSQSDYR TTKVIRPRPR GRMGVRRDEP KVKSIGDHEW 600
NRTQIGVLVS SHPFESDTEM SDIDDDDDRET IFSSMDLLSP SGHSDAQTLA MMLQEQLDAI 660
NKEIRLIQEB KESTELRAEB IENRVASVSL EGNLNLARVHP GTSITASVTA SSSLASSPPS 720
GHSTPKLTPR SPAREMDRMG VMTLPSDLRK HRRKIADVBE DGREDKATIK CETSPPPTPR 780
ALRMTHLTPS SYHNDARSSL SVSLEPESLG LGSANSSQDS LHKAPKKGKI KSSIGRLFGK 840
KEKARLQQLR GFMTETAAQA ESLGLGKLGAT QAEKDRRLKK KHELLEEARR KGLPFAQWDG 900
PTVVAVLELN LGMPAWYVAA CRANVKSgai MSALSDTEIQ REIGISNPLH RLKRLRLAIQE 960
MVSITSPPAP PTSRTPSGNV WVTHEEMENL AAPAKTKESE EGSWAQCFVP LQTLAYGDMN 1020
HEWIGNEWLP SLGLPQYRSY FMECLVDARM LDHLTKKDLR VHLKMVDSFH RTSLYGYIMC 1080
LKRLNYDRKE LERRREASQH EIKDVLVWSN DRIIRWIAI GLREYANNIL ESGVHGSLIA 1140
LDENFDYSSL TILLQIPTON TQARQILERE YNNLLALGTE RRLDESDDKN FRRGSTWRQ 1200
FPPREVHGIS MMPGSETLP AGFRLTTSG QSRKMTDVA SSRQLRLDNS TVRTYSCLIE

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A223 DNA SEQUENCE

Gene name: CDA14
 Unigene number: Hs.26813
 Probeset Accession #: N32912
 Nucleic Acid Accession #: NM_016570
 Coding sequence: 1- 1134 (underlined sequences correspond to start and stop codons)

75
80

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1 11 21 31 41 51
ATGAGGCGAC TGAATCGGAA AAAAAGCTTAA AGTTTGGTAA AAGAGTTGGA TGCCCTTCOG 60
AAGGTTCTCT AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120
TTTACAATAA TGCTTTTATT AACCATAAAT GAATCTCTAG TATATCAAGA TACATGGATG 180
AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAAT TAAGAATTAA TATAGATATT 240
ACTGTGTCGA TGAAGTGTCA ATATGTTGGA GCGGATGTAT TGGATTAGC AGAAACAATG 300
GTTGCTATGA CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360
AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAGAA GCATTCACTT 420
CAAGATGTGA TATTTAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480

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5 GATGATTCAT CACAGTCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCATAAAA 540
 GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCCTCG TGGTCATGCA 600
 CATTGGCAG CACTTGTCAG CCATGAATCT TACAATTTT CTCATAGAAT AGATCATTTG 660
 TCITTTGGAG AGCTTGTTC AGCAATTATT AATCCTTTAG ATGGAACTGA AAAAATGTCT 720
 ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAACAAA ACTACATACA 780
 TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAAAC 840
 CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTATGA AATATGATCT CAGTTCTCTT 900
 ATGGTGACAG TTAGTGAGGA GCACATGCCA TTCTGGCAGT TTTTGTAAAG ACTCTGTGGT 960
 10 ATTGTTGGAG GAATCTTTTC AACCAACAGSC ATGTTACATG GAATTGGAAA ATTATAGTT 1020
 GAAATAATTT GCTGTCGTTT CAGACTTGGG TCCTATAAAC CTGTCAATTC TGTTCCTTTT 1080
 GAGGATGGCC ACACAGACAA CCACCTTACCT CTTTTAGAAA ATAATACACA TTGA

15 A224 Protein sequence:
 Gene name: CDA14
 Unigene number: Hs.26813
 Probeset Accession #: N32912
 Protein Accession #: NP_057654
 20 Signal sequence: none found
 Transmembrane domains: none found
 Cellular Localization: nuclear

25 1 11 21 31 41 51
 | | | | | |
 MRRINRKRKL SLVKELDAPP KVPESYVETS ASGGTVSLIA PTTMALLTIM EPSVYQDTWM 60
 KYEYEVKDF SSKLRINIDI TVAMKQYVG ADVLDLAETM VASADGLVE PTVFDLSPQQ 120
 KEMQRLQLI QSRLEKEHSL QDVIPKSAPK STSTALPPRE DDSQSPNAC RIHGHLYVNK 180
 VAGNPHITVG KAIPHPRGHA HLAALVNHES YNPSHRIDHL SFGEIVPAII NPLDGTEDIA 240
 30 IDHNQMFQYF ITVVPKLIHT YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL 300
 MVTVTEEHMP FNQFPVRLCG IVGGIFSTTG MLHGIGKPIV EIICCRFRLG SYKPVNSVFP 360
 EDGHTDNHLP LLENNTN

35 Uterine
A225 DNA SEQUENCE:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 40 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
 | | | | | |
 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
 CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTCGTACAG TTTCTTCCAA CCTTGCCATT 120
 GCAATAAAAA AGGAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
 ACTTGGGTAC AAACCTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
 50 ATGGTTATTC ATCACTTGA GGAATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGGCC 300
 CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
 GAAACCACTG ATAAGAAATT ATCACTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
 GACCCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
 TATGAGCCTC GGGATTTACC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540
 CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAGAGAGT CAAATTTTCA 600
 55 GAAGAAAAAC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660
 TTAATAATTA GTTTTAAATA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTAAATA 720
 TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA

60 A226 Protein sequence:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Protein Accession #: none found
 65 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted

70 1 11 21 31 41 51
 | | | | | |
 MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK 60
 PLMWIHLED QQYSQALKKV PAQNEBIQEM AQNKPIMLNL MHETTDKNLS PDGQYVPRIM 120
 75 FVDFSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

80 A227 DNA SEQUENCE
 Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 Probeset Accession #: AA460530
 Nucleic Acid Accession #: NM_003667
 Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	GTGGGCGCAA	CGGGCACCTC	AGTCCCGGCC	GGGCTTCTCC	TGCGCGCCCA	CGCCGTGGGG	60
5	TCAGGAACGC	GGGCTCTGGC	GCTGCAGACG	CCCGCTGAGT	TGCAGAAGCC	CACGGAGCGG	120
	CGCCCGGCGC	GCCACGGGCC	GTAGCAGTCC	GGTGTGCTC	TCCGCCCCGG	TCCGGCTGGT	180
	GGCCCCCTAC	TTGGGGCACC	ATGGACACCT	CCCGGCTCGG	TGTGCTCCTG	TCCTTGCCTG	240
	TGCTGCTGCA	GCTGGCGACC	GGGGGCGAGT	CTCCAGGTG	TGGTGTGTTG	CTGAGGGGCT	300
	GCCCCACACA	CTGTCAATTG	GAGCCCGACG	GCAGGATGTT	GCTCAGGGTG	GACTGCTCCG	360
10	ACCTGGGGCT	CTCGGAGCTG	CCITCCCAAC	TCAGCGTCTT	CACCTCCTAC	CTAGACCTCA	420
	GTATGAACAA	CATCAGTCAG	CTGCTCCCGA	ATCCCCTGCC	CAGTCTCCGC	TTCTGGAGG	480
	AGTTACGCTC	TGCGGGAAC	GCTCTGACAT	ACATTCCCAA	GGGAGCATTG	ACTGSCCTTT	540
	ACAGTCTTAA	AGTTCTTATG	CTGCAGAATA	ATCAGCTAAG	ACAAGTACCC	ACAGAAGCTC	600
	TGCAGAAATT	GCGAAGCCTT	CAATCCCTGC	GTCCTGATGC	TAACCAATC	AGCTATGTGC	660
15	CCCCAAGCTG	TTTCAGTGGC	CTGCATTCCC	TGAGGCACTT	GTGGCTGGAT	GACAAATGCGT	720
	TAACAGAAAT	CCCCGTCCAG	GCTTTTAGAA	GTTTATCGGC	ATTGCAAGCC	ATGACCTTGG	780
	CCCTGAACAA	AATACACCAC	ATACCAGACT	ATGCCCTTGG	AAACCTCTCC	AGCTTGGTAG	840
	TTCTACATCT	CCATAACAAT	AGAATCCACT	CCCTGGGAAA	GAAATGCTTT	GATGGGCTCC	900
	ACAGCAATGA	GACTTTAGAT	TTAAATTACA	ATAACCTTGA	TGAATTCCTC	ACTGCAATTA	960
20	GGACACTCTC	CAACCTTAAA	GAACCTAGGAT	TTCAATAGCA	CAATATCAGG	TCGATACCTG	1020
	AGAAAGCATT	TGTAGGCAAC	CCITCTCTTA	TTACAATACA	TTTCTATGAC	AATCCCATCC	1080
	AATTTGTGAG	GAGATCTGCT	TTTCAACATT	TACCTGAAC	AAGAACACTG	ACTCTGAATG	1140
	GTGCTCTACA	AATAACTGAA	TTTCTCTGAT	TAACTGGAAC	TGCAACCTG	GAGAGTCTGA	1200
	CTTTAATCTG	AGCAGAGCTT	TCATCTCTTC	CTCAACCGT	CTGCAATCAG	TTACCTAATC	1260
25	TCCAAGTGCT	AGATCTGTCT	TACAACCTAT	TAGAAGATT	ACCCAGTTTT	TCAGTCTGCC	1320
	AAAAGCTTCA	GAAATTTGAC	CTAAGACATA	ATGAAATCTA	CGAAATTAAG	GTTGACACTT	1380
	TCCAGCAGTT	GCTTAGCCTC	CGATCGCTGA	ATTTGGGCTG	GAACAAAATT	GCTATTATTC	1440
	ACCCCAATGC	ATTTTCCACT	TTGCCATCCC	TAATAAAGCT	GGACCTATCG	TCCAACCTCC	1500
	TGTGCTCTTT	TCCATAAAT	GGGTTACATG	GTTTAACTCA	CTTAAATTA	ACAGGAAATC	1560
30	ATGCCCTTACA	GAGCTTGATA	TCATCTGAAA	ACTTTCAGAA	ACTCAAGGTT	ATAGAAATGC	1620
	CTTATGCTTA	CCAGTGTGCT	GCATTGAGAG	TGTGTGAGAA	TGCCATAAG	ATTCTAATC	1680
	AATGGAATAA	AGGTGACAAC	AGCAGTATGG	ACGACCTTCA	TAAGAAAGAT	GCTGGAATGT	1740
	TTCAAGCTCA	AGATGAACGT	GACCTTGAAG	ATTTCTGCT	TGACTTTGAG	GAAGACCTGA	1800
	AAGCCCTTCA	TTCAAGTGCAG	TGTTCACTT	CCCCAGGCC	CTTCAACCC	TGTGAACACC	1860
35	TGCTTGATGG	CTGGCTGATC	AGAATTGGAG	TGTGGAACAT	AGCAGTTCTG	GCACTTACTT	1920
	GTAATGCTTT	GGTGACTTCA	ACAGTTTTC	GATCCCTCT	GTACATTTC	CCCATTAAC	1980
	TGTTAATTGG	GGTCATCGCA	GCAGTGAACA	TGCTCACGGG	AGTCTCCAGT	GCCGTGCTGG	2040
	CTGGTGGGGA	TGCGTTCACT	TTTGCGCAGT	TTGCACGACA	TGGTGCCCTG	TGGGAGAAAT	2100
	GGGTGTGTTG	CCATGTCACT	GGTTTITTT	CCATTITTTG	TTCAAGATCA	CTGTITTTCC	2160
40	TGCTTACTCT	GGCAGCCCTG	GAGCGTGGGT	TCTCTGTGAA	ATATTCTGCA	AAATTGAAA	2220
	CGAAAGCTCC	ATTTTCTAGC	CTGAAAGTAA	TCATTTTGCT	CTGTGCCCTG	CTGGCCTTGA	2280
	CCATGGCGCG	AGTTCCCTCG	CTGGGTGGCA	GCAAGTATGG	CGCCTCCCTC	CTCTGCCCTG	2340
	CTTTGCCCTT	TGGGAGGCC	AGCACCATTG	GCTACATGTT	CGCTCTCATC	TTGCTCAATT	2400
	CCCTTTGCTT	CTCATGATG	ACCAATGCTT	ACACCAAGCT	CTACTGCAAT	TTGACCAAGG	2460
45	GAGACCTGGA	GAATATTGAG	GACTGTCTTA	TGGTAAACCA	CATTGCCCTG	TTGCTCTTCA	2520
	CCAACCTGAT	CCTAAACTGC	CCTGTGGCTT	TCTGTCTCTT	CTCCTCTTTA	ATAAACCTTA	2580
	CATTATCAG	TCTGGAAGTA	ATTAAAGTTA	TCCTTCTGTT	GGTAGTCCCA	CTTCTGTCAT	2640
	GTCTCAATCC	CCTTCTCTAC	ATCTTGTTCA	ATCTCACTT	TAAGGAGGAT	CTGGTGAGCC	2700
	TGAGAAAGCA	AACTACGCTG	TGGACAAGAT	CAAAACACCC	AAGCTTGATG	TCAATTAACT	2760
50	CTGATGATGT	CGAAACACAG	TCCGTGAGCT	CAACTCAAGC	CTTGGTAACC	TTTACCAGCT	2820
	CCAGCATCAC	TTATGACCTG	CCTCCAGATT	CGGTGCCATC	ACCAGCTTAT	CCAGTGACTG	2880
	AGAGCTGCCA	TCTTTCTCTC	TGGCATTTTG	TCCCATGTCT	CTAATTAAAT	TGTGAAGGAA	2940
	AATGTTTTC	AAGGTGAGAA	ACCTGAAAT	GTGAGATTGA	GTATATCAGA	GCAGTAATTA	3000
	ATAAGAGAG	CTGAGGTGAA	ACTCGGTTTA	AA			

A228 Protein sequence

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 Protein Accession #: NP_003658.1
 Signal sequence: 1-22
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825
 Cellular Localization: plasma membrane

	1	11	21	31	41	51	
65	MDTSRLGVLL	SLPVLLQLAT	GGSSPRSGVL	LRGCPHCHC	EPDGRMLLRV	DCSDLGLSEL	60
	PSNLSVFTSY	LDLSMNNISQ	LLPNPLPSLR	FLEELRLAGN	ALTYIPKGAF	TGLYSLKVLN	120
	LQNNQLRHVP	TEALQNLRS	QSLRLDANHI	SYVPPSCPSG	LHSLRLWLD	DNALTSIPVQ	180
	AFRSLSALQA	MTLALNKH	IPDYAFGNLS	SLVVLHLHNN	RIHSLGKKCF	DGLHSLTLD	240
70	LNYNMLDEFP	TAIRTLNLK	ELGFHNNIR	SIPEKAFVGN	PSLITIHFD	NPIQFVGRSA	300
	FQHLPELRTL	TLNGASQITE	FPDLTGATNL	ESLTLTGAQI	SSLPQTVCNQ	LENLQVLDLS	360
	YNLLLEDLPSP	SVCQKLQKID	LRHNEIYEIK	VDTPQQLSL	RSNLNLANKI	AIHFNAPST	420
	LPSLKLLDLS	SNLLSSFPIT	GLHGLTHLKL	TGNEHALQSLI	SSENFPELKV	IEMFYAYQCC	480
	APGVCEWAYK	ISNQWNGKDN	SSMDLHKKD	AGMFQAQDER	DLEDLFLDPE	EDLKALHSVQ	540
75	CSPSPGPFKP	CEHLLDGWL	RIGVWTIAVL	ALTCNALVTS	TVFRSPLYIS	PIKLLIGVIA	600
	AVNMLTGVS	AVLAGVDAPT	FGSFARHGAW	WENGVCCHVI	GFLSIPASES	SVFLLTLAAL	660
	ERGFVSVKSA	KPETKAPFSS	LKVIILLCAL	LALTMAAVPL	LGSKYGAAP	LCLPLFPFGE	720
	STMGYMVALI	LLNSLCFLMM	TIATYKLYCN	LDKQDLNIN	DCSMVKHIAL	LLFTNCLNLC	780
80	PVAFLSFSSL	INLTFISPEV	IKFILLVVVP	LPACLNPLLY	ILPNPHPKED	LVSLRKQTYV	840
	WTRSKHPSLM	SINSDDEKQ	SCDSQALVT	FTSSSTIYDL	PPSSVPSPAY	PVTESCHLSS	900
	VAFVPC						

Table 75: See Table 1

Table 76A depicts Seq ID No; UnigenelD; UnigeneTitle; PKey; Predicted Cellular Localization; and Exemplar Accession for each of the sequences in Table 78. The information in

Table 76A is linked by SeqID No to Table 78.

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Seq ID No:	Sequence ID No for sequences in table				
Pkey:	Unique Eos probeset identifier number				
ExAcon:	Exemplar Accession number, Genbank accession number				
UnigenelD:	Unigene number				
Unigene Title:	Unigene gene title				
Pred Subcell Loc:	Predicted sub-cellular localization				
Seq ID No	Pkey	ExAcon	UnigenelD	Unigene Title	Pred Subcell Loc
Seq ID 1 & 2	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipid	plasma membrane
Seq ID 3 & 4	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	plasma membrane
Seq ID 5 & 6	429423	AI016712	Hs.287797	integrin, beta 1 (fibronectin receptor,	plasma membrane
Seq ID 7 & 8	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	secreted
Seq ID 9 & 10	419172	AW338625	Hs.22120	ESTs; similar to TRANSMEMBRANE 4 SUPERF	plasma membrane
Seq ID 11 & 12	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
Seq ID 13 & 14	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
Seq ID 15 & 16	407836	T79340	Hs.200272	B-cell CLL/lymphoma 6, member B, zinc fi	intracell
Seq ID 17 & 18	414577	AK056548	Hs.72116	hypothetical protein FLJ20992 similar to	secreted
Seq ID 19 & 20	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	plasma membrane
Seq ID 21 & 22	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	secreted
Seq ID 23 & 24	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	secreted
Seq ID 25 & 26	429276	AF056085	Hs.198612	G protein-coupled receptor 51	plasma membrane
Seq ID 27 & 28	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	plasma membrane
Seq ID 29 & 30	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	secreted
Seq ID 31 & 32	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	intracell
Seq ID 33 & 34	418506	AA084248	Hs.85339	G protein-coupled receptor 39	plasma membrane
Seq ID 35 & 36	423961	D13666	Hs.136348	perostin (OSF-2os)	secreted
Seq ID 37 & 38	414812	X72755	Hs.77367	monokine induced by gamma interferon	secreted
Seq ID 39 & 40	417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	plasma membrane
Seq ID 41 & 42	417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	plasma membrane
Seq ID 43 & 44	424399	AI905687		AI905687:IL-BT095-190199-019 BT095 Homo	secreted
Seq ID 45 & 46	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	secreted
Seq ID 47 & 48	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	secreted
Seq ID 49 & 50	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	secreted
Seq ID 51 & 52	439569	AW602166	Hs.222399	CEGP1 protein	secreted
Seq ID 53 & 54	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
Seq ID 55 & 56	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	plasma membrane
Seq ID 57 & 58	411789	AF245505	Hs.72157	Adiccan	secreted
Seq ID 59 & 60	428698	AA852773	Hs.334838	KIAA1866 protein	plasma membrane
Seq ID 61 & 62	450098	W27249	Hs.8109	hypothetical protein FLJ21080	intracell
Seq ID 63 & 64	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	secreted
Seq ID 65 & 66	452747	BE153855	Hs.61460	lg superfamily receptor LNIR	plasma membrane
Seq ID 67 & 68	415539	AI733881	Hs.72472	BMP-R1B	plasma membrane
Seq ID 69 & 70	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
Seq ID 71 & 72	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
Seq ID 73 & 74	409079	W87707	Hs.82085	interleukin 6 signal transducer (gp130,	plasma membrane
Seq ID 75 & 76	442082	R41823	Hs.7413	ESTs	plasma membrane
Seq ID 77 & 78	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	plasma membrane
Seq ID 79 & 80	451398	AI793124	Hs.144479	ESTs	intracell
Seq ID 81 & 82	429220	AW207206		ESTs	plasma membrane
Seq ID 83 & 84	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	plasma membrane
Seq ID 85 & 86	423242	AL039402	Hs.125783	DEME-6 protein	plasma membrane
Seq ID 87 & 88	423242	AL039402	Hs.125783	DEME-6 protein	intracell
Seq ID 89 & 90	423242	AL039402	Hs.125783	DEME-6 protein	intracell
Seq ID 91 & 92	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
Seq ID 93 & 94	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
Seq ID 95 & 96	325372			Phase 2 & 3 Exons	cytoplasmic
Seq ID 97 & 98	450375	AA009647		a disintegrin and metalloproteinase doma	plasma membrane
Seq ID 99 & 100	426215	AW963419	Hs.155223	stanniocalcin 2	secreted
Seq ID 101 & 102	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	secreted
Seq ID 103 & 104	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
Seq ID 105 & 106	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
Seq ID 107 & 108	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	plasma membrane
Seq ID 109 & 110	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	secreted
Seq ID 111 & 112	446163	AA026880	Hs.25252	prolactin receptor	plasma membrane
Seq ID 113 & 114	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	plasma membrane
Seq ID 115 & 116	428179	AI127772	Hs.278696	serum/glucocorticoid regulated kinase-II	intracell
Seq ID 117 & 118	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	plasma membrane
Seq ID 119 & 120	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 121 & 122	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 123 & 124	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 125 & 126	115522	BE614387	Hs.333893	c-Myc target JPO1	intracell
Seq ID 127 & 128	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	plasma membrane
Seq ID 129 & 130	446051	BE048061	Hs.37054	ephrin-A3	plasma membrane
Seq ID 131 & 132	422048	NM_012445	Hs.288126	spodnon 2, extracellular matrix protein	secreted
Seq ID 133 & 134	410418	D31382	Hs.63325	transmembrane protease, serine 4	plasma membrane
Seq ID 135 & 136	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (tr	plasma membrane
Seq ID 137 & 138	422260	AA315993	Hs.105484	regenerating gene type IV	secreted

5	Seq ID 139 & 140	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KJAA119)	secreted
	Seq ID 141 & 142	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KJAA119)	secreted
	Seq ID 143 & 144	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 145 & 146	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 147 & 148	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 149 & 150	104888	AW939591	Hs.5940	mucin 13, epithelial transmembrane	plasma membrane
	Seq ID 151 & 152	420159	AJ572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	plasma membrane
	Seq ID 153 & 154	422330	D30783	Hs.115263	epiregulin	plasma membrane
10	Seq ID 155 & 156	452461	N78223	Hs.108106	transcription factor	intracell
	Seq ID 157 & 158	413324	V00571	Hs.75294	corticotropin releasing hormone	secreted
	Seq ID 159 & 160	412420	AL035668	Hs.73853	bone morphogenetic protein 2	secreted
	Seq ID 161 & 162	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	secreted
	Seq ID 163 & 164	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagonist	secreted
15	Seq ID 165	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (intracell
	Seq ID 166 & 167	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (intracell
	Seq ID 168 & 169	432829	W60377	Hs.57772	ESTs	intracell
	Seq ID 170 & 171	425721	AC002115	Hs.159309	uropod 1A	plasma membrane
	Seq ID 172 & 173	420370	Y13645	Hs.97234	uropod 2	plasma membrane
20	Seq ID 174 & 175	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.s.a	plasma membrane
	Seq ID 176 & 177	402075			ENSP00000251056:Plasma membrane calcium	secreted
	Seq ID 178 & 179	421110	AJ250717	Hs.1355	calthepin E	secreted
	Seq ID 180 & 181	451668	Z43948	Hs.326444	cartilage acidic protein 1	plasma membrane
	Seq ID 182 & 183	451668	Z43948	Hs.326444	cartilage acidic protein 1	secreted
25	Seq ID 184 & 185	451668	Z43948	Hs.326444	cartilage acidic protein 1	intracell
	Seq ID 186 & 187	408243	Y00787	Hs.624	interleukin 8	secreted
	Seq ID 188 & 189	422282	AF019225	Hs.114309	apolipoprotein L	secreted
	Seq ID 190 & 191	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	plasma membrane
	Seq ID 192 & 193	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	plasma membrane
30	Seq ID 194 & 195	404875			NM_022819: Homo sapiens phospholipase A2	intracell
	Seq ID 196 & 197	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (I	plasma membrane
	Seq ID 198 & 199	404977			Insulin-like growth factor 2 (somatomedi	secreted
	Seq ID 200 & 201	420876	AA918425	Hs.177744	ESTs	plasma membrane
	Seq ID 202 & 203	427747	AW411425	Hs.180655	serine/threonine kinase 12	intracell
35	Seq ID 204 & 205	420281	AI623693	Hs.323494	Predicted cation efflux pump	plasma membrane
	Seq ID 206 & 207	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	intracell
	Seq ID 208	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 209 & 210	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 211 & 212	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
40	Seq ID 213 & 214	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 215 & 216	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 217 & 218	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 219 & 220	405932			ESTs	intracell
	Seq ID 221 & 222	405932			C15000305:gi3806122[gb]AAC69198.1 (AF0	intracell
45	Seq ID 223 & 224	424008	R02740	Hs.137555	C15000305:gi3806122[gb]AAC69198.1 (AF0	plasma membrane
	Seq ID 225 & 226	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 227 & 228	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 229 & 230	444342	NM_014398	Hs.10887	putative chemokine receptor; GTP-binding	secreted
	Seq ID 231 & 232	421379	Y15221	Hs.103982	similar to lysosome-associated membrane	secreted
50	Seq ID 233 & 234	417079	U65690	Hs.81134	small inducible cytokine subfamily B (Cy	secreted
	Seq ID 235 & 236	412986	X81120	Hs.75110	interleukin 1 receptor antagonist	secreted
	Seq ID 237 & 238	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 239 & 240	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 241 & 242	447072	D61594	Hs.17279	cannabinoid receptor 1 (brain)	intracell
55	Seq ID 243 & 244	419723	AL120193	Hs.339810	tyrosylprotein sulfotransferase 1	secreted
	Seq ID 245 & 246	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	plasma membrane
	Seq ID 247 & 248	430890	X54232	Hs.2699	longevity assurance (LAG1, S. cerevisiae	plasma membrane
	Seq ID 249 & 250	456759	BE259150	Hs.127792	glypican 1	plasma membrane
	Seq ID 251	429466	M85835	Hs.12827	della (Drosophila)-like 3	secreted
60	Seq ID 252	429466	M85835	Hs.12827	ESTs	secreted
	Seq ID 253 & 254	419721	NM_001650	Hs.288650	ESTs	plasma membrane
	Seq ID 255 & 256	407034	U84540		aquaporin 4	secreted
	Seq ID 257 & 258	413472	BE242870	Hs.75379	gblHuman dystrobrevin isoform DTN-3 (DTN	secreted
	Seq ID 259 & 260	438380	T06430	Hs.6194	solute carrier family 1 (glial high affi	plasma membrane
65	Seq ID 261 & 262	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan BEHAB/b	secreted & plasma membrane
	Seq ID 263 & 264	419704	AA429104	Hs.45057	chondroitin sulfate proteoglycan 3 (neur	secreted
	Seq ID 265 & 266	444471	AB020684	Hs.11217	ESTs	intracell
	Seq ID 267 & 268	409395	U45745	Hs.336678	KJAA0877 protein	plasma membrane
	Seq ID 269 & 270	413063	AL035737	Hs.75184	dystrobrevin, alpha	secreted
70	Seq ID 271 & 272	433800	AI034361	Hs.135150	chitinase 3-like 1 (cartilage glycoprote	secreted
	Seq ID 273	458435	AI418718	Hs.144121	lung type-I cell membrane-associated gly	plasma membrane
	Seq ID 274	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	secreted
	Seq ID 275 & 276	424343	AW956360	Hs.4748	ESTs, Weakly similar to T46916 hypotheti	secreted
	Seq ID 277 & 278	424998	U58515	Hs.154138	adenylate cyclase activating polypeptide	plasma membrane
75	Seq ID 279 & 280	412709	AL022327	Hs.74518	chitinase 3-like 2	secreted
	Seq ID 281 & 282	435615	Y15065	Hs.4975	KJAA0027 protein	plasma membrane
	Seq ID 283 & 284	404049			potassium voltage-gated channel, KQT-like	plasma membrane
	Seq ID 285 & 286	418932	L34059	Hs.89484	NM_018937: Homo sapiens protocadherin be	plasma membrane
	Seq ID 287 & 288	404029			cadherin 4, type 1, R-cadherin (retinal)	plasma membrane
80	Seq ID 289 & 290	436480	AJ271643	Hs.87469	NM_018936: Homo sapiens protocadherin be	plasma membrane
	Seq ID 291 & 292	452401	NM_007115	Hs.29352	putative acid-sensing ion channel	intracell
	Seq ID 293 & 294	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 295 & 296	436895	AF037335	Hs.5338	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 297 & 298	421471	U90545	Hs.327179	carbonic anhydrase XII	plasma membrane
					solute carrier family 17 (sodium phospho	plasma membrane

5	Seq ID 299 & 300	428296	NM_003058	Hs.183572	solute carrier family 22 (organic cation	plasma membrane
	Seq ID 301 & 302	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	plasma membrane
	Seq ID 303 & 304	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter	plasma membrane
	Seq ID 305 & 306	410407	X66839	Hs.63287	carbonic anhydrase IX	plasma membrane
	Seq ID 307 & 308	453495	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	plasma membrane
	Seq ID 309 & 310	420737	L08096	Hs.99899	CD70 ; tumor necrosis factor (ligand) s	plasma membrane
	Seq ID 311 & 312	309931	AW341683		gbchd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	plasma membrane
	Seq ID 313 & 314	412719	AWD16610	Hs.816	ESTs	intracell
10	Seq ID 315 & 316	417034	NM_006183	Hs.80962	neurotensin	secreted
	Seq ID 317 & 318	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	plasma membrane
	Seq ID 319 & 320	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin	secreted
	Seq ID 321 & 322	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	plasma membrane
	Seq ID 323 & 324	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	secreted
15	Seq ID 325 & 326	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 327 & 328	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 329 & 330	429510	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	secreted
	Seq ID 331 & 332	406590	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	plasma membrane
	Seq ID 333 & 334	431846	BE019924	Hs.271580	uroplakin 1B	plasma membrane
20	Seq ID 335 & 336	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	secreted
	Seq ID 337 & 338	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	plasma membrane
	Seq ID 339 & 340	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	plasma membrane
	Seq ID 341 & 342	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	plasma membrane
	Seq ID 343 & 344	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	plasma membrane
25	Seq ID 345 & 346	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	secreted
	Seq ID 347 & 348	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	plasma membrane
	Seq ID 349 & 350	417542	J04129	Hs.82269	progesterone-associated endometrial prote	secreted
	Seq ID 351 & 352	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	plasma membrane
	Seq ID 353 & 354	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
30	Seq ID 355 & 356	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 357 & 358	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	secreted
	Seq ID 359 & 360	418462	BE001598	Hs.85266	integrin, beta 4	plasma membrane
	Seq ID 361 & 362	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	secreted
	Seq ID 363 & 364	439606	W79123	Hs.58561	G protein-coupled receptor 87	plasma membrane
35	Seq ID 365 & 366	404877			NM_005365:Homo sapiens melanoma antigen,	intracell
	Seq ID 367 & 368	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	plasma membrane
	Seq ID 369 & 370	109424	NM_005329	Hs.85982	hyaluronan synthase 3	plasma membrane
	Seq ID 371 & 372	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
40	Seq ID 373 & 374	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 375 & 376	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 377 & 378	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 379 & 380	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 381 & 382	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
45	Seq ID 383 & 384	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 385 & 386	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 387 & 388	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 389 & 390	409420	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kalinin	secreted
	Seq ID 391 & 392	332180	AF134160	Hs.7327	claudin 1	plasma membrane
50	Seq ID 393 & 394	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
	Seq ID 395 & 396	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
	Seq ID 397 & 398	439223	AW238299	Hs.250618	UL16 binding protein 2	plasma membrane
	Seq ID 399 & 400	409757	NM_001898	Hs.123114	cystatin SN	secreted
	Seq ID 401 & 402	428969	AF120274	Hs.194689	artemin	secreted
55	Seq ID 403 & 404	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 405 & 406	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 407 & 408	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 409 & 410	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
	Seq ID 411 & 412	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
60	Seq ID 413 & 414	414774	X02419	Hs.77274	plasminogen activator, urokinase	secreted
	Seq ID 415 & 416	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 417 & 418	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 419 & 420	428486	AW583497	Hs.184604	pancreatic polypeptide	secreted
	Seq ID 421 & 422	457489	AI693815	Hs.127179	cryptic gene	secreted
	Seq ID 423 & 424	432874	W94322	Hs.279651	melanoma inhibitory activity	secreted
65	Seq ID 425 & 426	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 427 & 428	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 429 & 430	404682			C9001188:gil12738842[ref]NP_073725.1 p	secreted
	Seq ID 431 & 432	428547	AW009166	Hs.99376	ESTs	secreted
70	Seq ID 433 & 434	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter	plasma membrane
	Seq ID 435 & 436	407242	M18728		gb:Human nonspecific crossreacting anti	plasma membrane
	Seq ID 437 & 438	407242	M18728		gb:Human nonspecific crossreacting anti	plasma membrane
	Seq ID 439 & 440	407242	M18728		gb:Human nonspecific crossreacting anti	plasma membrane
	Seq ID 441 & 442	432596	AJ224741	Hs.278461	mablin 3	secreted
	Seq ID 443 & 444	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	plasma membrane
75	Seq ID 445 & 446	423585	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	intracell
	Seq ID 447 & 448	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	secreted
	Seq ID 449 & 450	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 451 & 452	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 453 & 454	422109	S73265	Hs.1473	gastrin-releasing peptide	secreted
80	Seq ID 455 & 456	419235	AW470411	Hs.288433	neurotrophin	plasma membrane
	Seq ID 457 & 458	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	plasma membrane
	Seq ID 459 & 460	427333	AF067797	Hs.176658	aquaporin 8	plasma membrane
	Seq ID 461 & 462	417931	W95642	Hs.82961	trefol factor 3 (intestinal)	secreted
	Seq ID 463 & 464	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	secreted

5	Seq ID 465 & 466	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	secreted
	Seq ID 467 & 468	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	secreted
	Seq ID 469 & 470	452194	AI694413	Hs.332649	Ubiquitin-like protein FAT10777	plasma membrane
	Seq ID 471 & 472	452194	AI694413	Hs.332649	Ubiquitin-like protein FAT10777	plasma membrane
	Seq ID 473 & 474	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	secreted
	Seq ID 475 & 476	429010	Y18198	Hs.194725	one cut domain, family member 2	intracell
	Seq ID 477 & 478	431462	AW583572	Hs.256311	granin-like neuroendocrine peptide precu	secreted
	Seq ID 479 & 480	448243	AW369771	Hs.52620	integrin, beta 8	plasma membrane
10	Seq ID 481 & 482	426427	M86699	Hs.169840	TTK protein kinase	intracell
	Seq ID 483 & 484	428187	AI687303	Hs.285529	G protein-coupled receptor 49	plasma membrane
	Seq ID 485 & 486	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 487 & 488	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 489 & 490	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
15	Seq ID 491 & 492	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 493 & 494	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	secreted
	Seq ID 495 & 496	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	plasma membrane
	Seq ID 497 & 498	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum corn	secreted
	Seq ID 499 & 500	406400			kallikrein 8 (neuropsin/ovasin) (KLK8)	secreted
20	Seq ID 501 & 502	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	secreted
	Seq ID 503 & 504	420440	NM_002407	Hs.97644	mammaglobin 2	secreted
	Seq ID 505 & 506	428450	NM_014791	Hs.184339	KIAA0175 gene product	intracell
	Seq ID 507 & 508	446619	AU076543	Hs.313	secreted phosphoprotein 1 (osteopontin,	secreted
	Seq ID 509 & 510	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	secreted
25	Seq ID 511 & 512	453392	U23752	Hs.32964	SRX (sex determining region Y)-box 11	intracell
	Seq ID 513	431989	AW972870	Hs.291069	ESTs	
	Seq ID 514	439820	AL360204	Hs.283853	Homo sapiens mRNA full length Insert cDN	
	Seq ID 515 & 516	409178	BE393948	Hs.50915	kallikrein 5	secreted
30	Seq ID 517 & 518	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	secreted
	Seq ID 519 & 520	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
	Seq ID 521 & 522	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
	Seq ID 523 & 524	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 525 & 526	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 527 & 528	452097	AB002364	Hs.27916	a disintegrin-like and metalloprotease (secreted
35	Seq ID 529 & 530	416530	U62801	Hs.79361	kallikrein 6 (neurokin, zyme)	secreted
	Seq ID 531 & 532	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	plasma membrane
	Seq ID 533 & 534	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	plasma membrane
	Seq ID 535 & 536	412078	X69699	Hs.73149	paired box gene 8	intracell
	Seq ID 537 & 538	412078	X69699	Hs.73149	paired box gene 8	intracell
40	Seq ID 539 & 540	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	secreted
	Seq ID 541 & 542	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	secreted
	Seq ID 543 & 544	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	plasma membrane
	Seq ID 545 & 546	452792	AB037765	Hs.30652	KIAA1344 protein	plasma membrane
	Seq ID 547 & 548	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	plasma membrane
45	Seq ID 549 & 550	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 551 & 552	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 553 & 554	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 555 & 556	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 557 & 558	400290	H18836	Hs.31608	hypothetical protein FLJ20041	plasma membrane
50	Seq ID 559 & 560	410001	AB041036	Hs.57771	kallikrein 11	secreted
	Seq ID 561 & 562	418396	AI765805	Hs.26691	ESTs	plasma membrane
	Seq ID 563 & 564	451027	AW519204	Hs.40808	ESTs	plasma membrane
	Seq ID 565 & 566	446057	AA202227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	plasma membrane
	Seq ID 567 & 568	433466	AA508353	Hs.105314	relaxin 1 (H1)	secreted
55	Seq ID 569 & 570	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 571 & 572	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 573 & 574	414569	AF109298	Hs.118258	prostate cancer associated protein 1	plasma membrane
	Seq ID 575 & 576	413435	X51405	Hs.76360	carboxypeptidase E	secreted
	Seq ID 577 & 578	426501	AW043782	Hs.293616	ESTs	plasma membrane
60	Seq ID 579 & 580	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	plasma membrane
	Seq ID 581 & 582	408369	R38438	Hs.182575	solute carrier family 15 (H777) transport	plasma membrane
	Seq ID 583 & 584	412628	AI972402	Hs.306051	hypothetical protein MGC2648	secreted
	Seq ID 585 & 586	403047			NM_005656~Homo sapiens transmembrane pr	plasma membrane
	Seq ID 587 & 588	403047			NM_005656~Homo sapiens transmembrane pr	plasma membrane
65	Seq ID 589 & 590	408430	S79876	Hs.44926	dipeptidyl/peptidase IV (CD26, adenosine	secreted
	Seq ID 591 & 592	445413	AA151342	Hs.12677	CGI-147 protein	intracell
	Seq ID 593 & 594	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp56401763 (f	
	Seq ID 595 & 596	427958	AA418000	Hs.98280	potassium intermediate/small conductance	plasma membrane
	Seq ID 597 & 598	421887	AW161450	Hs.109201	CGI-86 protein	plasma membrane
70	Seq ID 599 & 600	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	secreted
	Seq ID 601 & 602	432101	AI918950	Hs.123642	EphA3	plasma membrane
	Seq ID 603 & 604	407786	AA687538	Hs.38972	tetraspan 1	plasma membrane
	Seq ID 605 & 606	416836	D54745	Hs.80247	cholecystokinin	secreted
	Seq ID 607 & 608	416539	Y07909	Hs.79368	epithelial membrane protein 1	plasma membrane
75	Seq ID 609 & 610	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 611 & 612	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 613 & 614	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 615 & 616	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 617 & 618	422424	AI186431	Hs.296638	prostate differentiation factor	secreted
	Seq ID 619 & 620	428970	BE276891	Hs.194691	retinoic acid induced 3	plasma membrane
80	Seq ID 621 & 622	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	secreted
	Seq ID 623 & 624	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 625 & 626	420610	AI683183	Hs.99348	distal-less homeo box 5	intracell
	Seq ID 627 & 628	425723	NM_014420	Hs.159311	dickkopf (Xenopus laevis) homolog 4	secreted

Seq ID 629 & 630	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (to	intracell
Seq ID 631 & 632	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	secreted
Seq ID 633 & 634	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	intracell

5 Table 76B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

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Pkey	CAT Number	Accession
424399	238951_1	AI905687 AI905624 AI905837 AI905623 AA340069 R75793 W72837 BE074512 AI905633 W72838 BE092421 AI127172 BE186013 AW070916 AI139456 AW176044 AW291960
429220	301384_1	AW207206 AW341473 AA448195 AI951341
450375	83327_1	AA009647 AA131254 AA374293 AW964405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

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Table 76C:

20

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

25

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402230	9966312	Minus	29782-29932
403047	3540153	Minus	59793-59968
404029	7671252	Plus	108716-111112
404049	3688074	Minus	75765-78155
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404877	1519284	Plus	1095-2107
404977	3738341	Minus	43081-43229
405932	7767812	Minus	123525-123713
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

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Table 77 provides Pkey; Seq ID No; Disease Indications; and Preferred Utility for sequences in Table 78. Seq ID No links the information in Table 77 to Table 78.

	Seq ID No:	Sequence ID No for sequences in table		
	Pkey:	Unique Eos probeset identifier number		
5	Disease Indications:	Diseases designated for coverage as described in Table 1		
	Preferred Utility:	Preference of utility, based partly upon predicted localization (Ab is antibody; sm is small molecule target; CTL is vaccine target)		
	Seq ID No	Pkey	Disease Indications	Preferred Utility
10	Seq ID 1 & 2	425023	angiogenesis	Ab, sm, CTL, imaging
	Seq ID 3 & 4	424503	pancreas, prostate, angiogenesis, bladder, lung	Ab, sm, imaging
	Seq ID 5 & 6	429423	angiogenesis	Ab, sm
	Seq ID 7 & 8	400289	angiogenesis, bladder, lung, cervical, ovarian, head & neck	Ab, sm, CTL, diagnostic
15	Seq ID 9 & 10	419172	angiogenesis, renal	Ab, sm, CTL, imaging
	Seq ID 11 & 12	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 13 & 14	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 15 & 16	407836	angiogenesis	CTL
20	Seq ID 17 & 18	414577	angiogenesis	Ab, CTL, diagnostic
	Seq ID 19 & 20	418738	angiogenesis, lung, ovarian, bladder & stomach, pancreas, uterine	Ab, sm, CTL, imaging
	Seq ID 21 & 22	428368	angiogenesis, head & neck, stomach	Ab, sm, diagnostic
	Seq ID 23 & 24	415138	angiogenesis, pancreas, stomach, lung, uterine	Ab, CTL, diagnostic
25	Seq ID 25 & 26	429276	angiogenesis, bladder, glioblastoma	Ab, sm, imaging
	Seq ID 27 & 28	418994	prostate, angiogenesis	Ab, CTL, imaging
	Seq ID 29 & 30	407975	angiogenesis, renal	Ab, CTL, diagnostic
	Seq ID 31 & 32	429113	angiogenesis, bladder and stomach	sm, CTL
30	Seq ID 33 & 34	418506	angiogenesis, ovarian, glioblastoma, uterine, lung, bladder, pancreas	Ab, sm, imaging
	Seq ID 35 & 36	423961	breast, colon, bladder, lung, fibrosis, pancreas, head and neck, ovarian	Ab, sm, diagnostic
	Seq ID 37 & 38	414812	breast, bladder, lung, Fibrosis, pancreas, colon, head and neck, cervical, stomach, renal, ovarian	Ab, CTL, diagnostic
	Seq ID 39 & 40	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab,CTL, imaging
35	Seq ID 41 & 42	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab, CTL, imaging
	Seq ID 43 & 44	424399	breast, uterine, head & neck	Ab, CTL, diagnostic
	Seq ID 45 & 46	422867	breast, ovarian, prostate, pancreas, lung, colon, uterine	Ab, CTL, diagnostic
	Seq ID 47 & 48	428227	breast, lung, bladder, ovarian, head & neck, fibrosis, colon, stomach, cervical	Ab, CTL, diagnostic
40	Seq ID 49 & 50	444381	breast, colon, bladder, lung, pancreas, head & neck, ovarian, stomach, uterine, renal, angiogenesis	Ab, CTL, diagnostic
	Seq ID 51 & 52	439569	breast, androgen withdrawal prostate, prostate, bladder	Ab, CTL, diagnostic
	Seq ID 53 & 54	411558	pancreas, prostate, stomach, breast, uterine, cervical, ovarian	Ab, sm, imaging
	Seq ID 55 & 56	400303	breast, ovarian, pros, stomach, uterine, bladder lung head & neck	Ab, sm, CTL, imaging
45	Seq ID 57 & 58	411789	pancreas, lung, breast, stomach, head & neck, ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 59 & 60	428698	breast, colon, lung, pancreas, stomach, head & neck, ovarian	Ab, sm, imaging
	Seq ID 61 & 62	450098	breast, lung, stomach, uterine	CTL
	Seq ID 63 & 64	421552	breast, ovarian, pancreas, cervical, uterine, prostate, lung, stomach, head & neck	Ab, sm, CTL, diagnostic
50	Seq ID 65 & 66	452747	breast, bladder, lung, head & neck, ovarian, stomach, uterine, pancreas	Ab, imaging
	Seq ID 67 & 68	415539	breast, prostate, ovarian, cervical, uterine	Ab,sm, CTL, imaging
	Seq ID 69 & 70	416636	breast, pancreas, uterine	Ab,sm, CTL, imaging
	Seq ID 71 & 72	416636	breast, pancreas, uterine	Ab,sm, CTL, imaging
55	Seq ID 73 & 74	409079	breast, prostate	Ab,sm, CTL, imaging
	Seq ID 75 & 76	442082	breast, prostate, ovarian	Ab, imaging
	Seq ID 77 & 78	400297	breast, bladder, colon, prostate	Ab,sm, CTL, imaging
	Seq ID 79 & 80	451398	breast, ovarian	CTL
60	Seq ID 81 & 82	429220	breast, prostate, benign prostatic hyperplasia	Ab, CTL, imaging
	Seq ID 83 & 84	421524	breast	Ab,sm, CTL, imaging
	Seq ID 85 & 86	423242	breast, renal, ovarian, prostate, colon	Ab, CTL, imaging
	Seq ID 87 & 88	423242	breast, renal, ovarian, prostate, colon	CTL
65	Seq ID 89 & 90	423242	breast, renal, ovarian, prostate, colon	CTL
	Seq ID 91 & 92	452190	breast, stomach, pancreas	CTL
	Seq ID 93 & 94	452190	breast, stomach, pancreas	CTL
	Seq ID 95 & 96	325372	breast	CTL
70	Seq ID 97 & 98	450375	breast, ovarian, head & neck, pancreas, lung, colon	Ab,sm, CTL, imaging
	Seq ID 99 & 100	426215	breast, lung, renal, colon, ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 101 & 102	425247	breast, ovarian, lung, colon, pancreas, head & neck, stomach, uterine, cervical, bladder	Ab, sm, CTL, diagnostic
	Seq ID 103 & 104	429353	breast, prostate	Ab, sm, CTL, imaging
75	Seq ID 105 & 106	429353	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 107 & 108	432201	breast, colon, lung chemo, ovarian, stomach, pancreas, uterine, cervical	Ab, sm, CTL, imaging
	Seq ID 109 & 110	427585	breast, lung, head & neck, pancreas, stomach, colon, ovarian, cervical	CTL
	Seq ID 111 & 112	446163	breast, cervical, uterine	Ab, sm, imaging
80	Seq ID 113 & 114	442117	breast, lung, bladder, pancreas, head & neck, stomach, ovarian, prostate	Ab, CTL, imaging
	Seq ID 115 & 116	428179	breast	sm, CTL
	Seq ID 117 & 118	431211	colon, bladder, lung, pancreas, head & neck	Ab, sm, imaging
	Seq ID 119 & 120	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
75	Seq ID 121 & 122	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 123 & 124	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 125 & 126	115522	colon, lung, bladder, pancreas	CTL
	Seq ID 127 & 128	452679	prostate, colon, pancreas, Taxol prostate	Ab,CTL, imaging
80	Seq ID 129 & 130	446051	colon, breast	Ab, sm, CTL, imaging
	Seq ID 131 & 132	422048	colon, pancreas, prostate	diagnostic
	Seq ID 133 & 134	410418	colon, bladder, lung, ovarian, pancreas, head & neck	Ab, sm, CTL, imaging
	Seq ID 135 & 136	446342	uterine, colon, prostate	Ab, sm, CTL, imaging
80	Seq ID 137 & 138	422260	colon, ovarian mucinous	Ab, sm, CTL, diagnostic
	Seq ID 139 & 140	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
	Seq ID 141 & 142	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
	Seq ID 143 & 144	111929	colon, breast, fibrosis	Ab, sm, imaging
80	Seq ID 145 & 146	111929	colon, breast, fibrosis	Ab, sm, imaging
	Seq ID 147 & 148	111929	colon, breast, fibrosis	Ab, sm, imaging

	Seq ID 149 & 150 104888	colon, stomach, uterine	Ab, imaging
	Seq ID 151 & 152 420159	bladder, stomach	Ab, sm, CTL, imaging
	Seq ID 153 & 154 422330	pancreas, colon, bladder	Ab, sm, CTL, imaging, diagnostic
5	Seq ID 155 & 156 452461	bladder, lung, head & neck, ovarian, glioblastoma, stomach, colon, cervical	CTL
	Seq ID 157 & 158 413324	bladder	Ab, sm, CTL, diagnostic
	Seq ID 159 & 160 412420	bladder, glioblastoma, lung, stomach	Ab, diagnostic
	Seq ID 161 & 162 416658	lung, ovarian, uterine, bladder	Ab, CTL, diagnostic
	Seq ID 163 & 164 407811	bladder, pancreas, stomach, uterine, lung	Ab, sm, diagnostic
10	Seq ID 165 402230	bladder	sm, CTL
	Seq ID 166 & 167 402230	bladder	sm, CTL
	Seq ID 168 & 169 432829	bladder	CTL
	Seq ID 170 & 171 425721	bladder	Ab, imaging
	Seq ID 172 & 173 420370	bladder	Ab, CTL, imaging
15	Seq ID 174 & 175 437852	bladder, lung	Ab, sm, CTL, imaging
	Seq ID 176 & 177 402075	bladder, lung, head & neck, cervical	diagnostic
	Seq ID 178 & 179 421110	bladder, pancreas, stomach, ovarian, lung	Ab, sm, diagnostic
	Seq ID 180 & 181 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
	Seq ID 182 & 183 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
20	Seq ID 184 & 185 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
	Seq ID 186 & 187 408243	bladder, stomach, head & neck, cervical	Ab, diagnostic
	Seq ID 188 & 189 422282	bladder, lung, head & neck	CTL, diagnostic
	Seq ID 190 & 191 425852	bladder, lung, head & neck	Ab, sm, CTL, imaging
	Seq ID 192 & 193 439738	bladder, lung, cervical	Ab, sm, CTL, imaging
25	Seq ID 194 & 195 404875	bladder	sm, CTL
	Seq ID 196 & 197 425883	bladder, pancreas	Ab, CTL, imaging
	Seq ID 198 & 199 404977	bladder, ovarian	Ab, sm, CTL, diagnostic
	Seq ID 200 & 201 420876	pancreas, bladder	Ab, sm, CTL, imaging
	Seq ID 202 & 203 427747	bladder, lung, ovarian, stomach	sm, CTL
30	Seq ID 204 & 205 420281	lung, bladder, ovarian, pancreas	Ab, sm, imaging
	Seq ID 206 & 207 446673	bladder	sm, CTL
	Seq ID 208 437553	bladder	Ab, CTL, imaging
	Seq ID 209 & 210 437553	bladder	Ab, CTL, imaging
	Seq ID 211 & 212 437553	bladder	Ab, CTL, imaging
35	Seq ID 213 & 214 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 215 & 216 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 217 & 218 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 219 & 220 405932	bladder, lung, head & neck, cervical	sm
	Seq ID 221 & 222 405932	bladder, lung, head & neck, cervical	Ab, sm, CTL, imaging
40	Seq ID 223 & 224 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 225 & 226 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 227 & 228 424008	bladder, head & neck, stomach, cervical	Ab, CTL, diagnostic
	Seq ID 229 & 230 444342	hepatitis C, lung, fibrosis, bladder	Ab, CTL, diagnostic
	Seq ID 231 & 232 421379	breast, pancreas, head & neck, lung, stomach, bladder, cervical, colon	Ab, diagnostic
45	Seq ID 233 & 234 417079	bladder, lung, head & neck, cervical	Ab, sm, CTL, imaging
	Seq ID 235 & 236 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 237 & 238 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 239 & 240 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 241 & 242 447072	glioblastoma, pancreas	sm, CTL
50	Seq ID 243 & 244 419723	glioblastoma	Ab, CTL, diagnostic
	Seq ID 245 & 246 419723	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 247 & 248 430890	glioblastoma, lung, cervical, bladder	Ab, CTL, imaging, diagnostic
	Seq ID 249 & 250 456759	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 251 429466	glioblastoma, uterine	
55	Seq ID 252 429466	glioblastoma, uterine	
	Seq ID 253 & 254 419721	glioblastoma, lung	Ab, sm, CTL, imaging
	Seq ID 255 & 256 407034	glioblastoma	Ab, CTL, diagnostic
	Seq ID 257 & 258 413472	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 259 & 260 436380	glioblastoma	Ab, CTL, diagnostic, imaging
60	Seq ID 261 & 262 426271	glioblastoma	Ab, CTL, diagnostic
	Seq ID 263 & 264 419704	glioblastoma	sm, CTL
	Seq ID 265 & 266 444471	glioblastoma, lung, colon	Ab, sm, CTL, imaging
	Seq ID 267 & 268 409395	glioblastoma	Ab, CTL, diagnostic
	Seq ID 269 & 270 413063	glioblastoma, ovarian, bladder, lung	Ab, CTL, diagnostic
65	Seq ID 271 & 272 433800	glioblastoma, lung	Ab, CTL, imaging
	Seq ID 273 458435	glioblastoma	
	Seq ID 274 458435	glioblastoma	
	Seq ID 275 & 276 424343	glioblastoma, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 277 & 278 424998	glioblastoma	Ab, CTL, diagnostic
70	Seq ID 279 & 280 412709	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 281 & 282 435615	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 283 & 284 404049	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 285 & 286 418932	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 287 & 288 404029	glioblastoma	Ab, sm, CTL, imaging
75	Seq ID 289 & 290 436480	glioblastoma	sm, CTL
	Seq ID 291 & 292 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 293 & 294 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 295 & 296 436895	breast, renal, ovarian, glioblastoma	Ab, sm, imaging
	Seq ID 297 & 298 421471	renal	Ab, sm, CTL, imaging
80	Seq ID 299 & 300 428296	renal	Ab, sm, CTL, imaging
	Seq ID 301 & 302 423508	renal, colon	Ab, CTL, imaging
	Seq ID 303 & 304 450001	renal, lung	Ab, sm, CTL, imaging
	Seq ID 305 & 306 410407	renal, lung, colon, stomach, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 307 & 308 453496	renal, prostate	Ab, sm, CTL, imaging

	Seq ID 309 & 310 420737	renal	Ab,sm, CTL, imaging
	Seq ID 311 & 312 309931	lung	Ab,sm, CTL, imaging
	Seq ID 313 & 314 412719	lung, head & neck, bladder, glioblastoma, cervical	CTL
5	Seq ID 315 & 316 417034	lung, head & neck, a couple cervical	Ab, CTL, diagnostic
	Seq ID 317 & 318 430486	lung, bladder, head & neck, cervical	Ab,sm, imaging
	Seq ID 319 & 320 413753	lung, bladder, head & neck, pancreas, cervical, colon	CTL, diagnostic
	Seq ID 321 & 322 425650	lung, head & neck, cervical, bladder	Ab, imaging
	Seq ID 323 & 324 423573	bladder, lung, head & neck, ovarian, pancreas, colon, stomach, uterine, cervical	Ab, CTL, diagnostic
10	Seq ID 325 & 326 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 327 & 328 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 329 & 330 429610	lung	CTL, diagnostic
	Seq ID 331 & 332 406690	lung, head & neck, pancreas, stomach, bladder, colon, cervical	Ab, imaging
	Seq ID 333 & 334 431846	lung, bladder, head & neck, uterine, cervical, stomach, ovarian	Ab, imaging
	Seq ID 335 & 336 422158	head & neck, bladder, lung, cervical, stomach	diagnostic
15	Seq ID 337 & 338 431958	lung, bladder, cervical, head & neck, ovarian, colon, prostate, pancreas, breast	Ab, CTL, imaging
	Seq ID 339 & 340 437044	head & neck, cervical, lung, bladder, breast, prostate, ovarian, stomach	Ab, imaging
	Seq ID 341 & 342 428484	lung, glioblastoma, bladder, head & neck, colon, cervical	Ab, sm, imaging
	Seq ID 343 & 344 429211	lung, bladder, head & neck, cervical, stomach	Ab, imaging
20	Seq ID 345 & 346 417389	ovarian, lung, bladder, uterine, cervical, pancreas, stomach	Ab, diagnostic
	Seq ID 347 & 348 431009	lung, bladder, head & neck	Ab, sm, imaging
	Seq ID 349 & 350 417542	lung	CTL, diagnostic
	Seq ID 351 & 352 449230	lung, cervical, head & neck, bladder, ovarian, colon	Ab, imaging
	Seq ID 353 & 354 410555	lung	Ab, sm, imaging
25	Seq ID 355 & 356 410555	lung	Ab, sm, imaging
	Seq ID 357 & 358 424687	head & neck, pancreas, lung, uterine, cervical, colon, stomach	Ab, sm, diagnostic
	Seq ID 359 & 360 418462	lung, bladder	Ab, imaging
	Seq ID 361 & 362 410274	lung, renal	diagnostic
	Seq ID 363 & 364 439606	lung, bladder, head & neck, cervical	Ab,sm, imaging
30	Seq ID 365 & 366 404877	lung, bladder	CTL
	Seq ID 367 & 368 444781	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 369 & 370 109424	bladder, lung	Ab, sm, CTL, imaging
	Seq ID 371 & 372 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 373 & 374 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
35	Seq ID 375 & 376 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 377 & 378 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 379 & 380 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 381 & 382 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 383 & 384 421817	lung, cervical, head & neck & bladder	Ab,sm, CTL, imaging
40	Seq ID 385 & 386 418678	lung, bladder, stomach, ovarian, pancreas & cervical	CTL
	Seq ID 387 & 388 418678	lung, bladder, stomach, ovarian, pancreas & cervical	CTL
	Seq ID 389 & 390 409420	lung, head & neck, pancreas, stomach, cervical, bladder	CTL, diagnostic
	Seq ID 391 & 392 332180	lung	Ab, sm, imaging
	Seq ID 393 & 394 408790	lung	Ab,sm, CTL, imaging
45	Seq ID 395 & 396 408790	lung	Ab,sm, CTL, imaging
	Seq ID 397 & 398 439223	lung, head & neck, cervical, bladder & colon	Ab, CTL, imaging
	Seq ID 399 & 400 409757	pancreas, stomach, lung, bladder, stomach	Ab, CTL, diagnostic
	Seq ID 401 & 402 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 403 & 404 428969	lung, cervical	Ab, CTL, diagnostic
50	Seq ID 405 & 406 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 407 & 408 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 409 & 410 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
	Seq ID 411 & 412 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
	Seq ID 413 & 414 414774	lung, bladder, head & neck, pancreas, stomach, ovarian	Ab, sm, diagnostic
55	Seq ID 415 & 416 407944	lung, head & neck	Ab, sm, imaging
	Seq ID 417 & 418 407944	lung, head & neck	Ab, sm, imaging
	Seq ID 419 & 420 428486	pancreas	Ab, CTL, diagnostic
	Seq ID 421 & 422 457489	pancreas, prostate, lung	Ab, CTL, diagnostic
	Seq ID 423 & 424 432874	pancreas, stomach	Ab, CTL, diagnostic
60	Seq ID 425 & 426 445891	stomach, pancreas, ovarian	Ab, CTL, imaging
	Seq ID 427 & 428 445891	stomach, pancreas, ovarian	Ab, CTL, imaging
	Seq ID 429 & 430 404682	pancreas	Ab, CTL, diagnostic
	Seq ID 431 & 432 429547	pancreas, head & neck, lung, ovarian	Ab, CTL, diagnostic
	Seq ID 433 & 434 425921	stomach, pancreas	Ab,sm, CTL, imaging
65	Seq ID 435 & 436 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 437 & 438 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 439 & 440 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 441 & 442 432596	pancreas, breast	CTL
	Seq ID 443 & 444 444006	pancreas, colon, lung, ovarian & cervical	Ab, CTL, imaging
70	Seq ID 445 & 446 423685	pancreas, uterine, colon	CTL
	Seq ID 447 & 448 428392	pancreas	Ab, CTL, diagnostic
	Seq ID 449 & 450 429597	pancreas, colon, stomach, lung	Ab,sm, CTL, imaging
	Seq ID 451 & 452 448030	pancreas, renal and stomach,	Ab,sm, imaging
	Seq ID 453 & 454 422109	pancreas, lung, colon	Ab, CTL, diagnostic
75	Seq ID 455 & 456 419235	pancreas, fibrosis, head & neck & lung	Ab, CTL, imaging
	Seq ID 457 & 458 449048	pancreas, ovarian, uterine, glioblastoma, head & neck & lung	Ab, CTL, imaging
	Seq ID 459 & 460 427333	pancreas, colon	Ab, sm, imaging
	Seq ID 461 & 462 417931	ovarian, pancreas, stomach, colon, uterine, prostate	Ab, diagnostic
	Seq ID 463 & 464 419216	pancreas, lung, stomach, cervical, prostate, head & neck	Ab, CTL, diagnostic
80	Seq ID 465 & 466 431629	pancreas, uterine, cervical, stomach	Ab, CTL, diagnostic
	Seq ID 467 & 468 413554	pancreas, glioblastoma	Ab, CTL, diagnostic
	Seq ID 469 & 470 452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
	Seq ID 471 & 472 452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
	Seq ID 473 & 474 426322	pancreas, bladder, stomach	Ab, diagnostic

	Seq ID 475 & 476 429010	pancreas	sm, CTL
	Seq ID 477 & 478 431462	pancreas, lung, glioblastoma	Ab, diagnostic
	Seq ID 479 & 480 448243	ovarian, uterine, lung, stomach, head & neck, glioblastoma, pancreas	Ab, sm, imaging
5	Seq ID 481 & 482 426427	ovarian, lung, head & neck, cervical, colon, uterine, stomach	sm, CTL
	Seq ID 483 & 484 428187	ovarian, uterine, colon, stomach	Ab, sm, CTL, imaging
	Seq ID 485 & 486 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 487 & 488 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 489 & 490 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
10	Seq ID 491 & 492 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 493 & 494 445537	ovarian, bladder, uterine, breast, lung, head & neck, renal, fibrosis, pancreas, cervical	Ab, CTL, diagnostic
	Seq ID 495 & 496 422278	ovarian, head & neck, bladder, cervical, lung	Ab, sm, imaging
	Seq ID 497 & 498 424620	ovarian	Ab, CTL, diagnostic
	Seq ID 499 & 500 406400	ovarian, uterine	Ab, CTL, diagnostic
15	Seq ID 501 & 502 431130	ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 503 & 504 420440	ovarian, uterine, cervical	Ab, CTL, diagnostic
	Seq ID 505 & 506 428450	ovarian, cervical, pancreas, lung	sm
	Seq ID 507 & 508 446619	ovarian, fibrosis, pancreas, head & neck, lung, colon	Ab, diagnostic
	Seq ID 509 & 510 436982	ovarian, fibrosis	Ab, CTL, diagnostic
20	Seq ID 511 & 512 453392	ovarian, lung, glioblastoma	CTL
	Seq ID 513 431989	ovarian	
	Seq ID 514 439820	ovarian, uterine, cervical, breast, prostate	
	Seq ID 515 & 516 409178	ovarian, breast	
	Seq ID 517 & 518 426514	ovarian, colon, bladder, lung, cervical	Ab, CTL, diagnostic
25	Seq ID 519 & 520 421478	ovarian, bladder	Ab, CTL, imaging
	Seq ID 521 & 522 421478	ovarian, bladder	Ab, CTL, imaging
	Seq ID 523 & 524 425776	ovarian, uterine, lung	Ab, sm, CTL, imaging
	Seq ID 525 & 526 425776	ovarian, uterine, lung	Ab, sm, CTL, imaging
	Seq ID 527 & 528 452097	ovarian	Ab, sm, diagnostic
30	Seq ID 529 & 530 416530	ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 531 & 532 431515	ovarian, prostate, lung	Ab, sm, CTL, imaging
	Seq ID 533 & 534 419452	ovarian, prostate, lung, breast, uterine	Ab, sm, CTL, imaging
	Seq ID 535 & 536 412078	ovarian	CTL
	Seq ID 537 & 538 412078	ovarian	CTL
35	Seq ID 539 & 540 411773	ovarian	Ab, sm, CTL, diagnostic
	Seq ID 541 & 542 407792	ovarian, uterine, cervical, pancreas	Ab, CTL, diagnostic
	Seq ID 543 & 544 431616	prostate, pancreas, colon	Ab, sm, CTL, imaging
	Seq ID 545 & 546 452792	prostate, uterine, breast	Ab, CTL, imaging
	Seq ID 547 & 548 400294	prostate, taxol prostate	Ab, sm, CTL, imaging
40	Seq ID 549 & 550 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 551 & 552 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 553 & 554 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 555 & 556 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 557 & 558 400290	prostate, colon	Ab, sm, CTL, imaging
45	Seq ID 559 & 560 410001	ovarian, prostate, uterine, cervical, lung	Ab, CTL, diagnostic
	Seq ID 561 & 562 418396	prostate	Ab, sm, CTL, imaging
	Seq ID 563 & 564 451027	prostate, uterine, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 565 & 566 446057	prostate	Ab, sm, CTL, imaging
	Seq ID 567 & 568 433466	prostate	Ab, CTL, diagnostic
50	Seq ID 569 & 570 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 571 & 572 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 573 & 574 414569	prostate	Ab, sm, CTL, imaging
	Seq ID 575 & 576 413435	prostate, glioblastoma, pancreas	Ab, sm, diagnostic
	Seq ID 577 & 578 426501	prostate, breast, glioblastoma, lung	Ab, CTL, imaging
55	Seq ID 579 & 580 448999	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 581 & 582 408369	prostate, lung, fibrosis, uterine, glioblastoma, cervical, ovarian	Ab, sm, CTL, imaging
	Seq ID 583 & 584 412628	prostate	Ab, CTL, diagnostic
	Seq ID 585 & 586 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
	Seq ID 587 & 588 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
60	Seq ID 589 & 590 408430	prostate	Ab, sm, CTL, imaging
	Seq ID 591 & 592 445413	prostate, colon, uterine, ovarian, lung, pancreas	diagnostic
	Seq ID 593 & 594 451982	prostate, bladder	CTL
	Seq ID 595 & 596 427958	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 597 & 598 421887	prostate	Ab, CTL, imaging
65	Seq ID 599 & 600 425071	prostate, colon, stomach, uterine, cervical, head & neck, pancreas	Ab, diagnostic
	Seq ID 601 & 602 432101	prostate, pancreas	Ab, sm, imaging
	Seq ID 603 & 604 407786	prostate, colon, uterine, stomach, inflammatory bowel disease, ovarian	Ab, sm, imaging
	Seq ID 605 & 606 416838	Prostate, Ewing, glioblastoma	Ab, CTL, diagnostic
	Seq ID 607 & 608 416539	ZD1839 resistant cancers, head & neck	Ab, sm, CTL, imaging
70	Seq ID 609 & 610 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 611 & 612 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 613 & 614 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 615 & 616 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 617 & 618 422424	bladder, pancreas, prostate, angiogenesis, colon, stomach, lung	Ab, CTL, diagnostic
75	Seq ID 619 & 620 428970	stomach, pancreas, colon	Ab, sm, imaging
	Seq ID 621 & 622 428330	uterine, ovarian, fibrosis, prostate, pancreas, lung, bladder, head & neck	Ab, sm, CTL, diagnostic
	Seq ID 623 & 624 439018	uterine, stomach, prostate	Ab, sm, CTL, imaging
	Seq ID 625 & 626 420610	uterine, ovarian endometrioid, lung	CTL
	Seq ID 627 & 628 425723	ovarian endometrioid, uterine, colon	Ab, CTL, diagnostic
80	Seq ID 629 & 630 456662	uterine, ovarian	CTL
	Seq ID 631 & 632 418281	uterine, ovarian	Ab, CTL, diagnostic
	Seq ID 633 & 634 429903	lung	sm

Table 78

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: NM_001400
Coding sequence: 251..1399

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	AAAGCTACAC	AAAAAGCCTG	GATCACTCAT	CGAACCACCC	CTGAAGCCAG	TGAAGGCTCT	180
	CTCGCCTCGC	CCTCTAGCGT	TCGCTCGGAG	TAGCGCCACC	CCGGCTTCTC	GGGGACACAG	240
	GGTTGGCACC	ATGGGGCCCA	CCAGCGTCCC	GCTGGTCAAG	GCCACCGCA	GCTCGGTCTC	300
	TGACTAGCTC	AACATGATA	TCATCGTCCG	GCATTACAAC	TACACGGGAA	AGCTGAATAT	360
15	CAGCGCGGAC	AAGGAGAACA	GCATTAAACT	GACCTCGGTG	GTGTTCAATC	TCATCTGCTG	420
	CTTTATCATC	CTGGAGAACA	TCCTTGCTCT	GCTGACCATT	TGGAATAACA	AGAAATTTCA	480
	CCGACCCATG	TACTATTTTA	TTGGCAATCT	GGCCCTCTCA	GACCTGTTGG	CAGGAGTAGC	540
	CTACACAGCT	AACCTGCTCT	TGCTGGGGGC	CACCACCTAC	AAGCTCACTC	CCGCCAGTGG	600
	GTTTCTGGCG	GAAAGGAGTA	TGTTTGTGGC	CCTGTGAGCC	TCCGTGTTCA	GTCTCCTCGC	660
20	CATCGCCATT	GAGCGCTATA	TCACAATGCT	GAAATGAAA	CTCCACAACG	GGAGCAATAA	720
	CTTCGCGCTC	TTCTTGCTAA	TCAGCGCCTG	CTGGGTGATC	TCCCTCATCC	TGGGTGGCCT	780
	GCCTATCATG	GGCTGGAATC	GCATCAGTGC	GCTGTCCAGC	TGCTCCACCG	TGCTGCCGCT	840
	CTACCAAGAG	CACATATATC	TCTTCTGCAC	CACGGTCTTC	ACTCTGCTTC	TGCTCTCCAT	900
25	CGTCATTCTG	TACTGAGAA	TCTACTCCTT	GGTCAGGACT	CCGAGCCGCC	GCCTGACGTT	960
	CCGCAAGAAC	ATTTCGAAGG	CCAGCGCAG	CTCTGAGAAG	TGCTGGGCGC	TGCTCAAGAC	1020
	CGTAATTATC	GTCTTGAGCG	TCTTCATGCG	CTGCTGGGCA	CCGCTCTTCA	TCTGCTCCTT	1080
	GCTGGATGTG	GGCTGCAAGG	TGAAGACCTG	TGACATCCTC	TTCAAGACCG	AGTACTTCTT	1140
	GGTGTGAGCT	GTGCTCAACT	CCGGCACCAA	CCCCATCATT	TACACTCTGA	CCAACAAGGA	1200
	GATGCGTCGG	GCCTTCATCC	GGATCATGTC	CTGCTGCAAG	TGCCCGAGCG	GAGACTCTGC	1260
30	TGGCAAAATC	AAGCGACCCA	TCATCGCGCG	CATGGAATTC	AGCCGACGCA	AATCGGACAA	1320
	TTCCCTCCAC	CCCCAGAAAG	ACGAAGGGGA	CAACCCAGAG	ACCATTATGT	CTTCTGGAAG	1380
	CGTCAACTCT	TCTTCTAGAA	ACTGGAAAGT	GTCCACCCAC	CCGAAGCCGT	CTTACTCTGG	1440
	TCGCTGGCCA	CCCCAGTGTG	TGGAAAAAAA	TCTCTGGGCT	TCGACTGCTG	CCAGGGAGGA	1500
	GCTGCTGCAA	CCGAGAGGGA	GGAAGGGGGA	GAATAOGAAC	AGCCTGGTGT	TGTCGGGTGT	1560
35	TGGTGGGTAG	AGTTAGTTCC	TGTGAACAA	GCCTGGGAA	GGGTGGAGAT	CAGGTCCCGG	1620
	CCTGGAATAT	ATATTCTACC	CCCCCTGAGC	TTTGATTTTG	CATGAGCCA	AAGGTCTAGC	1680
	ATTGTCAAGC	TCCTAAGAGG	TTCAATTGGC	CCCTCCTCAA	AGACTAATGT	CCCCATCTAG	1740
	AAGGCTCTCT	TTGTCTGGAG	CTTTGAGGAG	ATGTTTTCCT	TCACTTTAGT	TTCAAACCCA	1800
40	AGTGAGTGTG	TGCACITCTG	CTTCTTTAGG	GATGCCCTGT	ACATCCCAAC	CCCCACCTCT	1860
	CCTTCCCTCT	ATACCCCTCC	TCAACGTTCT	TTTACTTTAT	ACTTTAACTA	CCTGAGAGTT	1920
	ATCAGAGCTG	GGGTGTGGGA	ATGATCGATC	ATCTATAGCA	AATAGGCTAT	GTGAGTAGCG	1980
	TAGGCTGTGG	GAGATGAAG	ATGTTTGGGA	GGTGTAAGAC	AATGTCTCTC	GCTGAGGCCA	2040
	AAGTTTCCAT	GTAAGCGGGA	TCCGTTTTTT	GGAATTTGGT	TGAAGTCACT	TTGATTTCTT	2100
45	TAAAAACAT	CTTTTCAATG	AAATGTGTTA	CCATTTTATA	TCCATTGAAG	CCGAAATCTG	2160
	CATAAGGAAG	CCCCTTTTAT	CTAATGATA	TTAGCCAGGA	TCCTTGGTGT	CCTAGGAGAA	2220
	ACAGACAAAG	AAAACAAAGT	GAAAAACGAA	TGGATTAAC	TTTGCAAAAC	AAGGGAGATT	2280
	TCTTAGCAAA	TGAGTCTAAC	AAATATGACA	TCCGCTTTTC	CCACTTTTGT	TGATGTTTAT	2340
	TTCAAGATCT	TGTGTGATTC	ATTTCAAGCA	ACAACATGTT	GTATTTTGTG	GTGTTAAAG	2400
50	TACTTTTCTT	GATTTTGTAA	TGTATTGTTT	TCAGGAAGAA	GTCAATTTAT	GGATTTTCTT	2460
	AACCCGTTGT	AACTTTCTTA	GAATCCACCC	TCTTGTGCC	TTAAGCATT	CTTTAACTGG	2520
	TAGGGAACGC	CAGAACITTT	AAGTCCAGCT	ATTCATTAGA	TAGTAATTGA	AGATATGTAT	2580
	AAATATTACA	AAGAATAAAA	ATATATTACT	GTCTCTTTAG	TATGGTTTTT	AGTGCAATTA	2640
55	AACCGAGAGA	TGCTTTGTTT	TTTTAAAAAG	AATAGTATTT	AATAGGTTTC	TGACTTTTGT	2700
	GGATCATTTT	GCACATAGCT	TTATCAACTT	TTAAACATTA	ATAAACTGAT	TTTTTTAAAG	

Seq ID NO: 2 Protein sequence
Protein Accession #: NP_001391

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60	MGPTSVPLVK	AHRSSVSDYV	NYDIIVRHVN	YTGKLNISAD	KENSIKLTSV	VFILICCFII	60
	LENIFVLLTI	WTKKFPFRFM	YYFIGNLALS	DLLAGVAYTA	NLLSGNTTY	KLTPAQWFLR	120
	EGSMFVALSA	SVFSLLAIAI	ERYITMLKMK	LHNGSNFRL	PLLISACWVI	SLILGLPLIM	180
65	GMNCISALSS	CSVLPLVYHK	HYILPCTVVF	TLILLSIVIL	YCRIYSLVRT	RSRLTFRFN	240
	ISKASRSSEK	SLALLKTVII	VLSVFIACNA	PLFILLLLDV	GCKVKTCIL	FRAEYFLVLA	300
	VLNSGTNPPI	YTLTNKEMRR	AFIRIMSCKK	CPSGDSAGKF	KRPIIAGMEF	SRSKSDNSSH	360
	PQKDEGDNPE	TIMSSGNVNS	SS				

Seq ID NO: 3 DNA sequence
Nucleic Acid Accession #: NM_002205.1
Coding sequence: 1..3149

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	CGCCGACCCC	CGCTSSGTCC	GCTGCTGTTC	CTGCTSSGTC	CGCCGCCACC	CAGGGTGGGG	120
	GGCTTCAACT	TAGACGCGGA	GGCCCCAGCA	GTACTCTCGG	GGCCCCGGGG	CTCCTTCTTC	180
	GGATTCTCAG	TGGAGTTTTA	CGGCGCGGGA	ACAGACGGGG	TCAGTGTGCT	GGTGGGAGCA	240
80	CCCAAGGCTA	ATACCAGCCA	GCCAGGAGTG	CTGCAGGGTG	GTGCTGTCTA	CCTCTGTCTT	300
	TGGGGTGCCA	GCCCCACACA	GTGCACCCCC	ATTGAATTTG	ACAGCAAAAG	CTCTGGGCTC	360
	CTGAGTCTCT	CACGTGCCAG	CTCAGAGGGA	GAGGAGCCTG	TGGAGTACAA	GTCCCTGCAG	420
	TGGTTGGGGG	CAACAGTTGG	AGCCCATGGC	TCCTCCATCT	TGGCATGGGC	TCCACTGTAC	480
	AGCTGGCGCA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACCTGCTA	CCTCTCCACA	540
	GATACTTCA	CCGAATTCTT	GGAGTATGCA	CCCTGCCGCT	CAGATTTCAG	CTGGGCAGCA	600

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GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTOGATCCC TCTACAACCT CTCAGGGGAA 960
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CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAAAT TCAGAGACAA 1800
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Seq ID NO: 4 Protein sequence
Protein Accession #: NP_002196.1

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LESSLSSEEG KEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTCTYLS 180
DNFTRILEYA PCRSDFSWAA GQGYCQGGFS AEPTKTGRVV LGPGSYFWQ GQILSATQEQ 240
IAESYYPEYL INLVQQLQT RQASSIYDDG YLGYSVAVGE FSGDDTDEDV AGVPKGNLTY 300
GYVTILNGSD IRLSYNFSGE QMASYFGYAV AATDVNGDGL DDLLVGAPLL MDRTPDGRPQ 360
EVGRVYVYLQ HPAGIEPTPT LTLTGHDPEF RFGSSLTPLG DLDQDGYNDV AIGAPFPGET 420
QQGVVVFVFP GPGLGSKPS QVLQPLMAAS HTPDFFGSAL RGRDLGNGG YPDLIVGSFG 480
VDRKAVYRGR PIVSASASLT IFFAMPNPBE RSCSLEGNPV ACINLSFCLN ASGKHVADSI 540
GPTVELQLDW QKQKGGVRRR LFLASRQATL TQTLLIQNGA REDCREMKTY LRNESEPRDK 600
LSPHIALNLF SLDPQAFVDS HGLRPLALHYQ SKSRIEDKQ ILLDCGEDNI CVPDLQLEVF 660
GEQNEVYLDG KNALNLTPHA QNVGEGGAYE AELRVTPAPE AEYSGLVHRP GNFSSLSQDY 720
FAVNQSRLLV CDLGNPMKAG ASLNGGLRPT VPHLRDTKXT IQDFQILSK NLNNSQSDV 780
SFRLSEVAQA QVTINGVSKP EAVLFFVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840
SQGVLELSCP QALBQQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGLLHH QQRKRAPSR 900
SASSGPQILK CPEAECTRLR CELGPLHQBE SQSLQLHFRV WAKTFLOREH QPFSLQCEAV 960
YKALMPEYRI LPRQLPKER QVATAVQWTK AEGSYGVPLN IILAILFGL LLLGLLIYIL 1020
YKLGPFPRSL PYGTAMEKAQ LKPPATSDA
  
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Seq ID NO: 5 DNA sequence
Nucleic Acid Accession #: NM_002211.1
Coding sequence: 1..2397

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TATCCCATTG ACCTCTACTA CCTTATGGAC CTGTCTTACT CAATGAAAGA CGATTGGAG 480
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ATCTGTGAAT GTGAATGCCA AAGCGAAGGC ATCCCTGAAA GTCCCAAGT TCATGAAGGA 1440
AATGGGACAT TTGAGTGTGG CGCGTGCAGG TGCAATGAAG GGGCTGTGG TAGACATTGT 1500
GAATGCAGCA CAGATGAAGT TAACAGTGAA GACATGGATG CTTACTGCAG GAAAGAAAAC 1560
AGTTCAGAAA TCTGCAGTAA CAATGGAGAG TGGCTCTGCG GACAGTGTGT TTGTAGGAAG 1620
AGGATAAATA CAAATGAAT TTATTTCTGG AATTCTGCG AGTGTGATAA TTTCAACTGT 1680
GATAGATCCA ATGAGTGTGG TTGTGGAGGA AATGGTGTTC GCAAGTGTG TGTGTGTGAG 1740
TGCAACCCCA ACTACACTGG CAGTGCATGT GACTGTTCCT TGGATACTAG TACTTGTGAA 1800
GCCAGCAACG GACAGATCTG CAATGGCCGG GGCATCTGCG AGTGTGGTGT CTGTAAAGTGT 1860
ACAGATCCGA AGTTTCAAGG GCACACGTGT GAGATGTGTC AGACCTGCCT TGGTGTCTGT 1920
GCTGAGCATA AAGATGTGT TCAATGCAGA GCCTTCAATA AAGGAGAAAA GAAAGACACA 1980
TGACACAGG AATGTTCTTA TTTTAACATT ACCAAGGTAG AAGTCGGGA CAAATTACCC 2040
CAGCCGGTCC AACCTGATCC TGTGTCCAT TGAAGGAGA AGGATGTGA CGACTGTGG 2100
TTCTATTTTA GTATTTCAGT GAATGGGAAC AACGAGGTCA TGGTTCATGT TGTGGAGAAT 2160
CCAGAGTGTG CCACTGTGTC AGACATCAIT CCAATTGTAG CTGGTGTGGT TGCTGGAATT 2220
GTTCTTATTG GCCTTGCATT ACTGCTGATA TGAAGCTTT TAATGATAAT TCATGACAGA 2280
AGGAGATTGT CTAAATTGGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAATAAT 2340
CCTATTTTATA AGAGTGCCGT AACAACGTGT GTCAATCCGA AGTATGAGGG AAAATGA

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Seq ID NO: 6 Protein sequence
Protein Accession #: NP_002202.1

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1 11 21 31 41 51
MNLQPIFWIG LISSVCCVFA QTDENRCLKA NAKSGCECIQ AGFNGCWCTN STFLQEGMPT 60
SARCDLLEAL KKKGCPDDI ENPRGSKDIK KKNVITNRSK GTAEKLKPED ITQIQPQLV 120
LRLRSGEPQT FTLKFKRAED YPIDLYYLM LSYMKDDLE NVKSLGTDLM NEMRRITSDP 180
RIGFGSFVEK TVMPYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLTNKG VFNELVGRQR 240
ISGNLDSPEG GPDALMQVAV CGSLIGWRNV TRILVFTDA GFHFAGDGKL GGIVLPNDGQ 300
CHLENNMYTM SHYYDYPISIA HLQKLSENN IQTIFAVTEE PQPVYKELKN LIPKSAVGT 360
SANSNNVIQL IIDAVNSLSS EVILENGKLS EGVTSISKSY CKNGVNGTGE NGRKCSNISI 420
GDEVQFEISI TSMKCFPKDS DSKIRPLGF TEEVEVILQY ICECEQSEI IPESPKHEG 480
NGTFEGGACR CNEGRVGRHC ECSTDEVNSE DMDAYCRKEN SSEICSNNGE CVCGQCVCRK 540
RDNTNEIYSG KFCECDNFNC DRNGLICGG NGVCKCRVCE CNPNYTGSA DCSLDTSTCE 600
ASNGQICNGR GICECGVCKR TDPKFGQCT EMCQTCLGVC AEHKECVQCR AFNKGKKJDT 660
CTQECSEYFNI TKVESRDKLP QPVQPDVSH CKERDVEDCW FYFTYSVNGN NEVMVHVVEN 720
PECTPTGDI PIAGVAVAGI VLIGLALLLI WKLLMIIHDR REPAKFEKEK MNAKMDTGEN 780
PIYKSAVTTV VNPKYEGK

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Seq ID NO: 7 DNA sequence
Nucleic Acid Accession #: NM_002425
Coding sequence: 26..1453

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60
65
70
75
80

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1 11 21 31 41 51
AAAGAAGGTA AGGGCAGTGA GAATGATGCA TCTTGCAATC CTTGTGCTGT TGTGTCTGCC 60
AGTCTGCTCT GCTTATCTCT TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT 120
TGCCACAGCA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAC AGTTTAGAAG 180
AAAGGACAGT AATCTCATTT TTAATAAAT CCAAGGAATG CAGAAGTTCC TTGGGTTGGA 240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
TCTGACGTT GGTCACTTCA GCTCCTTTC TGGCATGCGG AAGTGGAGGA AAACCCACCT 360
TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTGT ATTCTGCCAT 420
TGAGAAGGCT CTGAAAGTCT GGAAGAGGTT GACTCCACTC ACATTCTCCA GGCTGTATGA 480
AGGAGAGGCT GATATAATGA TCTCTTTCGC AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA 600
TATTCACTTT GATGATGATG AAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATCTCT 660
CGTGTCTGCT CATGAACCTG GCACTCCCT GGGCTCTTT CACTCAGCCA ACACCTGAAGC 720
TTTGATGTAC CCACTCTACA ACTCATTCAC AGAGCTCGCC CAGTTCGCC TTTGCAAGA 780
TGATGTGAAT GGCATTCAGT CTCTCTACGG ACCTCCCTCT GCCTCTACTG AGGAACCCCT 840
GTTGCCACCA AAATCTGTTT CTTCGGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT 900
GTCTCTCGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTCTTTAAAG ACAGATATTT 960
TTGGCGAAGA TCCCACTGGA ACCCTGAACC TGAATTTCAAT TTGATTCTG CATTTTGGCC 1020
CTCTCTTCCA TCAATTTGG ATGTGTCATA TGAAGTTAAC AGCAGGGACA CCGTTTAT 1080
TTTTAAAGGA AATGAGTTCT GGGCCATCAG AGGAATGAG GTACAAGCAG GTTATCCAAG 1140
AGGCATCCAT AGCTGGGTT TTCTCCCAAC CATAAGGAAA ATTGATGCAG CTGTTTCTGA 1200
CAAGGAAAAG AAGAAAACAT ACTTCTTTG AGCGGACAAA TACTGGAGAT TTGATGAAA 1260
TAGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320
GCCTAAGGTT GATGCTGTAT TACAGGCATT TGGATTTTTC TACTTCTTCA GTGGATCATC 1380
ACAGTTTGGT TTTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAAGA GTAACAGCTG 1440
GTTACATTGC TAGGCGAGAT AGGGGGAAGA CAGATATGGG TGTTTTTAAT AAATCTAATA 1500
ATTATTCATC TAATGTATTA TGAGCCAAAA TGGTTAATTT TTCTGCAATG TTCTGTGACT 1560

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GAAGAAGATG AGCCTTGACG ATATCTGCAT GTGTCATGAA GAATGTTTCT GGAATTCTTC 1620
 ACTTGCTTTT GAATTGCACT GAACAGAAAT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680
 ATGTATTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCTGTTC 1740
 CTT

Seq ID NO: 8 Protein sequence
 Protein Accession #: NP_002416

1 11 21 31 41 51
 | | | | |
 MHLAFLVLLC LPVCSAYPLS GAAKEEDSNK DLAQQYLEKY YNLEKDVQKF RRDNSNLIVK 60
 KIQGMQKFLG LEVTGKLDTD TLEVMRKPRC GVPDVGHFSS FPGMPKWRKT HLTIRIVNYT 120
 PDLPRDAVDS AIEKALKVWE EVTPLTF SRL YEGEADIMIS FAVKEHGDFY SFDGPGHSLA 180
 HAYPPGPGLY GDIHPDDDEK WTEDASGTNL FLVAAHELGH SLGLFHSANT EALMYPLVNS 240
 PTELAQFRLS QDDVNGIQSL YGPPPPASTEE PLVPTKSVPS GSEMPAKCDP ALSFDAISTL 300
 RGEYLFPKDR YFNRRSHWN EPEPHLISAF WPSLPSYLD AYEVSNRDTV FIFKGNFWA 360
 IRGNEVQAGY PRGHTLGFPP PTIRKIDAAV SDKEKKTYF FAADKYWRPD ENSQSMQGF 420
 PRLIADDFPG VSPKVDVAVLQ AFGFFYFFSG SSQFEFDPNA RMVTHILKSN SNLHC

Seq ID NO: 9 DNA sequence
 Nucleic Acid Accession #: XM_058189.2
 Coding sequence: 169..774

1 11 21 31 41 51
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 GAAGACCACG TCAGCTCTTC AGTTGTTGAT CATTGTCTAT TGTTCTCCAA ACAGTAAACC 60
 AGTATTTCAC ACTGAGGATG TCGGCTGGGG GTATATTCCA ATTCCCGCTC TCCTCATGAA 120
 TATGAAGTGA AGGGCTCTGA CCTCGGAAGT GGTCTCAAGC AGGCAAAAT GGGGTCTCGG 180
 AAGTGTGGAG GCTGCTTAAG TTGTTTGCTG ATTCCGCTTG CACTTTGGAG TATAATCGTG 240
 AACATATTAT TGTATTTCCC GAATGGGCAA ACTTCTATG CATCCAGCAA TAAACTCACC 300
 AACTACGTGT GGTATTTTGA AGGAATCTGT TTCTCAGGCA TCATGATGCT TATAGTAACA 360
 ACAGTTCTTC TGGTACTGGA GAATAATAAC AACTATAAAT GTTGCAGAG TGAAACTGTC 420
 AGCAAAAAAT ATGTGACACT GCTGTCAATT ATCTTTTCTT CCTCGGAAT TGCTTTTCTT 480
 GGATACTGCC TGGTCACTC TGCTTGGGT CTGTCCAAG GGCATATTG CCGCACCTT 540
 GATGGCTGGG AGTATGCTTT TGAAGGCACT GCTGGACGTT TCCTTACAGA TTCTAGCATA 600
 TGGATTCACT GCTGGAACCC TGACATGTT GTGGAGTGG AATCATTTT ATTTTCCATT 660
 CTCATAACCC TCAGTGGGCT TCAAGTGATC ATCTGCTCA TCAGAGTAGT CATGCAACTA 720
 TCCAAGATAC TGTGTGAAG CTATTCAGTG ATCTCCAGC CTGGAATCAT TTGAATAAGG 780
 ACAAAATGTT TTCAATTATC AAGCATGGC CATCTATCTA AATATTATAT CACTGTGTA 840
 GACTTGAGGG CAATATTGAA ATGATGGTGC TTTCTGCAAT TGGTGTATT TGTAAAAA 900
 TTTGCACTCC TCACGTGACA TGCAAGTATA CCACCTTCC ATTTAGTATG TTTTAAAGT 960
 AATATGCTC AGAACTTCA GAAATACTTC TGCCCTTTGA TCAACAAT CCATTTCCTA 1020
 GAATCTGTAC TAGGGAAGTA AATAAGAATA TGAGAGAAAC CTTTATGCAA ATATGTATAT 1080
 TGCAACATTA TTTAATATTC TGGAAAATG GAAACACCCC AAAATTCTAA ACTCAGAGGA 1140
 AGGATTAAAT AAAGAGTGGT ACATACTGTA AATGTTTTCT GATATTAAAA AAAAAATTAA 1200
 ATAAAAATA AAGAGTACTA CATGGTTGTA AAA

Seq ID NO: 10 Protein sequence
 Protein Accession #: XP_058189.1

1 11 21 31 41 51
 | | | | |
 MGSRKGGCL SCILLPLALW SIIVNILLYP PNGQTSYASS NKLTNYVWYF EGICFSGIMM 60
 LIVTTVLVLV ENNNNYKCCQ SENCSSKCVT LLSIIFSSLG IAFSGYCLVI SALGLVQGFY 120
 CRTLDGWEYA FEGTAGRFLT DSSIWIQCLE PAHVVEWNII LPSILITLSG LQVLIICLIRV 180
 VMQLSKILCG SYSVIFQPGI I

Seq ID NO: 11 DNA sequence
 Nucleic Acid Accession #: NM_002421.2
 Coding sequence: 1..1409

1 11 21 31 41 51
 | | | | |
 ATGCACAGCT TTCTCCACT GCTGCTGCTG CTGTCTGGG GTGTGGTGTG ACACAGCTTC 60
 CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGA AAAA 120
 TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCAGTG 180
 GTTGAAAAAT TGAAGCAAT GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACAGAT 240
 GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCTGATGT GGTCTAGTTT 300
 GTCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAAT 360
 TACACGCCAG ATTTGOC AAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCACACTC 420
 TGGAGTAATG TCACACCTCT GACATTCAAC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
 ATATCTTTTG TCAGGGGAGA TCATCGGAGC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
 CTGTCTCATG CTTTTCAACC AGGCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTGCGGC TCATGAACCT 660
 GGCCATTCTC TTGGACTCTC CCAATTCTACT GATATCGGGG CTTTGATGTA CCTAGCTAC 720
 ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
 GGACGTTCCC AAAATCCTGT CCAGCCCATC GGGCCACAAA CCCCAGGAGT ATGTGACAGT 840
 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAGG TGATGTTCTT TAAAGACAGA 900
 TTCTACATGC GCACAAATCC CTCTACCCG GAAGTTGAGC TCAATTTTCA TTCTGTTTTC 960
 TGGCCACAA C GTCGAAATGG GCTTGAAGCT GTGCGACAG AGATGAAGTC 1020
 CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
 CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
 TTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGAGGATAT 1200
 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCTCT 1260

GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTA TTCTTTTCAT 1320
 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

5 Seq ID NO: 12 Protein sequence
 Protein Accession #: NP_002412.1

1 11 21 31 41 51
 10 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VEKLKQMGEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
 YTPDLPRADV DHAIEKAPQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAHAEL GHSGLSLHST DIGALMYPYSY 240
 15 TFSGDVQLAQ DDIDGIAIY GRSONPVQPI GPQTPKACDS KLTFDAITTI RGEVMPFKDR 300
 FYMRINPFYP EVELNPFISV WPQLPNGLEA AYEAFADRDEV RFFKGNKYWA VQGQNVLHGY 360
 PKDIYSSPGF PRTVKHIDAA LSEENTGKTY FFFVANKYWRV DEYKRSMDPG YPKMLAHDFP 420
 GIGHKVDVAV MKDGFYFFH GTRQYKDFPK TKRILTQKA NSWFNCRKN

20 Seq ID NO: 13 DNA sequence
 Nucleic Acid Accession #: NM_002421.2
 Coding sequence: 1..1409

1 11 21 31 41 51
 25 ATGCACAGCT TTCCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTC ACACAGCTTC 60
 CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA 120
 TACTACAAAC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCAGTGG 180
 GTTGAAAAAT TGAAGCAATC GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACAGAT 240
 30 GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCCTGATGT GGCCTCAGTT 300
 GTCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAA 360
 TACACGCCAG ATTTCGCCAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCACACTC 420
 TGGAGTAATG TCACACCTCT GACATTCACC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
 35 CTTGCTCATG CTTTCAACC AGGCCAGGAT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGCCCTC 660
 GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC 720
 ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
 GGACGTTCCC AAAATCCTGT CCAGCCCATC GGCCCAACAA CCCCAAAAGC ATGTGACAGT 840
 40 AAGCTAACTT TTGATGCTAT AACTACGATT CGGGGAGAAAG TGATGTTCTT TAAAGACAGA 900
 TTCTACATGC GCACAAATCC CTTCTACCGG GAAGTTGAGC TCAATTTCAT TTCTGTTTTC 960
 TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020
 OGGTTTTTCA AAGGGAAATA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
 CCAAGGACA TCTACAGCTC CTTTGGCTTC CTTAGAACTG TGAAGCATAT CGATGCTGCT 1140
 45 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200
 GATGAATATA AACGACTTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCTC 1260
 GGAATTGGCC ACAAAGTTGA TGCACTTTTC ATGAAAGATG GATTTTCTA TTCTTTTCAT 1320
 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

50 Seq ID NO: 14 Protein sequence
 Protein Accession #: NP_002412.1

1 11 21 31 41 51
 55 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VEKLKQMGEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
 YTPDLPRADV DHAIEKAPQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 60 LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAHAEL GHSGLSLHST DIGALMYPYSY 240
 TFSGDVQLAQ DDIDGIAIY GRSONPVQPI GPQTPKACDS KLTFDAITTI RGEVMPFKDR 300
 FYMRINPFYP EVELNPFISV WPQLPNGLEA AYEAFADRDEV RFFKGNKYWA VQGQNVLHGY 360
 PKDIYSSPGF PRTVKHIDAA LSEENTGKTY FFFVANKYWRV DEYKRSMDPG YPKMLAHDFP 420
 GIGHKVDVAV MKDGFYFFH GTRQYKDFPK TKRILTQKA NSWFNCRKN

65 Seq ID NO: 15 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 141..1580

1 11 21 31 41 51
 70 TCTGCGTGTG CCGGGGCTAG GGGCTGGAAG TCCTGGCTCT AGTTGCACCT CGGAAGGAAA 60
 AGGCAACACG AGGAGGGGAG GCGTCTTAGG ACTGCCTGGA TCCAGAGCAC TTTCCTGGGC 120
 CTCTACAGGC CTGTGTGCTG ATGGGTTCCT CCGCGGCCCC GGAGGGAGCG CTGGGCTAGC 180
 75 TCGCGAGTTC CACTCGCCAC TCCTCCGACG TGCTGGGCAA CCTCAACGAG CTGCGCCTGC 240
 GCGGGATCCT CACTGAGTTC ACGCTGCTGG TTGGCGGGCA ACCCTCAGA GCACACAAGG 300
 CAGTTCTCAT GGCCTGCAGT GGCCTCTTCT ATTCAATTTT CCGGGGCCGT GCGGGAGTGC 360
 GGGTGGACCT GCTCTCTCTG CCGGGGGGTC CCGAAGCGAG AGGCTTCGCC CCTCTATTGG 420
 80 ACTTCATGTA CACTTCGCGC CTGCGCCTCT CTCAGCCAC TGCACCRGCA GTCTAGCGG 480
 CCGCCACCTA TTTGCAGATG GAGCACGTGG TCCAGGCATG CCACCGCTTC ATCCAGGCCA 540
 GCTATGAACC TCTGGGCATC TCCCTGCGCC CCCTGGGAAG AGAACCCCAA ACACCCCAA 600
 CCGCCCTTCC ACCAGGTAGT CCGAGGCGCT CCGAAGGACA CCGAGACCA CTAAGTGAAT 660
 CTGGAAGCTG CAGTCAAGGC CCCCCAGCT CAGCCAGCCC TGACCCCAAG GCCTGCAACT 720
 GGAAGAAAGTA CAAGTACATC GTGCTAAACT CTCAGGCCTC CCAAGCAGGG AGCCTGGTGC 780

5 GGGAGAGAAG TTCTGGTCAA CCTTGGCCCC AAGCCAGGCT CCCAGTGA GACGAGGCCT 840
 CCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GTGAAGAAGG ACCCATTCCT GGTCCCCAGA 900
 GCAGGCTCTC TCCAACTGCT GCCACTGTGC AGTTCAAATG TGGGGCTCCA GCCAGTACCC 960
 CCTACCTCCT CACATCCCAG GCTCAAGACA CCTCTGGATC ACCCTCTGAA CGGGCTCGTC 1020
 CACTACCGGG AAGTGAATTT TTCAGCTGCC AGAACTGTGA GGCTGTGGCA GGGTGTCTAT 1080
 CGGGGCTGGA CTCCTTGGTT CCTGGGGAAG AAGACAAACC CTATAAGTGT CAGCTGTGCC 1140
 GGTCTTGGTT CGCTACAAG GGCAACCTTG CCAGTCATCG TACAGTGAC ACAGGGGAAA 1200
 AGCCTTACCA CTGCTCAATC TGGGAGGCC GTTTTAAACG GCCAGCAAA ACAGGAAACG 1260
 10 ACAGCCGCAT CCATTCCGGA GAGAAGCGT ATAAGTGTGA GACGTGCGGC TCGCGCTTTG 1320
 TACAGGTGGG ACATTCTGGG GGCACCGTGC TGATCCACAC CGGGGAGAAG CCTACCCCTT 1380
 GGCCTACCTG CGGAACCCGC TTCCGCCACC TGCAGACCTC CAAGAGCCAC GTTCGCATCC 1440
 ACACCGGAGA GAAGCCTTAC CACTGCGACC CCTGTGGCCT GCATTTCCGG CACAAGAGTC 1500
 AACTGGGGCT GCATCTGCGC CAGAAACACG GAGCTGTACT CAACACCAA GTGCACTACC 1560
 15 ACATTCTCGG GGGGCCCTAG CTGAGCGCAG GCCCAGGCC CACTTGCTTC CTGCGGGTGG 1620
 GAAAGGTGAG GCTCCAGCGG TTGCTTCCCT ATCAGGCTTG GGCATAGGGG TGTGCCAGGC 1680
 CACTTTGGTA TCAGAAATTT CCACCTCTCT AATTTCTCAC TGGGGAGAGC AGGGGTGGCA 1740
 GATCGTGGAT AGATCTGGCT CTGTTTGTCT GGTCAAACCT TCCTCCCAAC AAGCCAGATT 1800
 GTTCTGAGG AGAGAGCTAG CTAGGGGCTG GGAAGGGGA GAGATTGGAG TCCTGGTCTC 1860
 20 CCTAAGGGAA TAGCCCTCCA CCTGTGGCCC CCATTGCATT CAGTTTATCT GTAAATATAA 1920
 TTTATTGAGG CCTTTGGGTG GCACCGGGGC CTTCATTGGA TTGCAATTCC CACTCCCTCT 1980
 TTCCACAAGT GTGATTAAGA GTGACCAAGA ACACAGAAGG TGAGATCACA GCTCTGCTGG 2040
 CAGAGCTGAT TAGCCCTTAC CTCTCTGTT TGGCTTGGT ATTTTATATT ATTTCTGTCA 2100
 TAACTTTTAT CTTTAGAATT GTTCTTCTC CTGTTTGTCT GCTTGTAGT TTGTTAAAA 2160
 25 TGGAAAAAGG GGTCTCTGT GTTCTGCCCT TGAATTTCTA GGTCTGGAAC CTTTATTTGT 2220
 TCTAGGGCAG CTTCTGGGAC ATGCGGGATT GTGGAATTGG GTCAGGAACC CTCTCTGGTA 2280
 TTCTGGATGT TGTAGGTTCT CTAGCAGTCT AGAAATGGAT ACAGACATTT CTCTGTCTT 2340
 CAGGGTGTAT AGGAACCAT ATGTTGAGCC CAAAATGGAA GTAATAATA ATGCTCCTG 2400
 GAGGCTGTGG GTGTGGGGGA TTCTGTATCT GGATTCCTGA TCACTCCAAC TGGAGGCTGT 2460
 30 GGGTGTGGGG GATTCCTGTAT CTGATTCGG TATCACTCCA AGTGGAGGCT GGCAGGTTTT 2520
 TCTGCAAGAT GATTCAGGAT CTAAATGTC CCATTAATCT GGTCACTTGG GTTGTGCTCT 2580
 GCTGTATCCA TCTATAGTGG TAGAGACCCA CCAGGGCTCA AGTGGAGTCC ATCATCCTCC 2640
 CACGGGGGCC TGTCTTAGC ACTGAGTTGA TCGCTCCATG GGGGAGAGAT CAGACATTCC 2700
 TTATCAGAGA TGATGTGACC TTTCTGACT CTGCCCAGTC TCTATGAATG TTATGSCCTA 2760
 35 GGAAGAATC ATGAAACTCT TTAGCTTGAT TAGATGGTAA ACAGTGTAA CCCATCCTTT 2820
 ACTACAGAGG CATATGGGTT TGAATGTTAC CTGGGGTCT CTCTATTGAG TTGAGCCCTC 2880
 TCTTCTTTTA GTGGGTTTGG GACATCTTCT GGCAAGTGTG CAGATGCCAG AACCTTCTTT 2940
 TCCTCTGAGG GGGATGTGTC TTGTAACCT TACCTTTTAA AAGCTGGGTC TGTGACCTGG 3000
 TCTTCCCATC CTGCACTTCC TGTCTGGAAC CAGTGAATGC ATTAGAACCT TCCATAGGAA 3060
 40 AAGAAAAAGG GCTGAGTTCC ATTCTGGGTT TGCTGTAGTT TGGTTGGGAT TATGTGTGTC 3120
 ATTACAGATG TAAGAAGATT ACTAGCCCAT AGGCCAAAGG OCTGTTCTAG TTGACCAAGT 3180
 TTCAAGTAGG ATTAAGAGGT TGGTTGAGGG GTGCAGTTTC TGGTGTAGGC CAGGTAGGTA 3240
 GAAAGTGAGG AACAGGGTTG CCTCTGGCT GGGTGGAGTC TCTGAATGT TAGAAGAAGC 3300
 GCTGAAGCCT TGATTGATAG TTCTGCCCTG TGTGTCCCTG GGGCTTATCT GATTATGGGA 3360
 45 CGAGGATAGA AAGTAAGAAG CACTTTTGA TTTGTGGGTT AGAACTTCAA CAATAAGTCA 3420
 GTTCTAGTGG GTGTGCGCTG GGGACTAGTG AGAAAGCTAC TCTTCTCCCT CTCCCTCTT 3480
 TCTCCCATG GCCCCTGCTG AGAATTAAG AAGGAAGAAG GGAAGGCGGA GAGATCTATA 3540
 AGAAGGAATC ATGATTTCTA TTTAGCAGAT TGGATGGGCA GGTGAGAAT GCCTGGGGGT 3600
 50 AGAAATGTGA GATCTTGCAA CATCAGATCC TTGGAATAAA GAAGCCTCTC TGYGWRAAA 3660
 AAAAAAAAAA AAAAAA

Seq ID NO: 16 Protein sequence
 Protein Accession #: FGENESH predicted

55 1 11 21 31 41 51
 MGSPAAPEGA LGYVREFTRH SSDVLGNLNE LRLRGILTDV TLLVGGQPLR AHKAVLIACS 60
 GPFYSIPRGR AGVGVNDVLSL POGPEARQFA PLLDFMYTSR LRLSPATAPA VLAATYLMQ 120
 EHVYQACHRF IQASYEPLGI SLRPLEAEP TPPTAPPPTS PRRSEGHDPD PTERSRSCSQ 180
 60 PPSPASPDFK ACWKKYKYI VINSQASQAG SLVGERSSQG PCPQARLPSG DEASSSSSSS 240
 SSSSEBGPPI GPQSRLSPTA ATVQFKCGAF ASTPYLLTSQ AQDTSQSPSE RARPLPGSEF 300
 FSCQNCBAVA GCSGGLDSL V PGEDDKPKYC QLCRSSFRYK GNLAHRTVH TGEKPYHCSI 360
 CGARPNRPNR LKTHSRHSG EKPKYKCTCG SRFVQVAHLR AHVLIHTGEK PYPCTGCTR 420
 FRIHQTLKSH VRIHTGKPY HCDPCGLHFR HKSQRLHLR QKHGAATNTK VHYHILGGP

65 Seq ID NO: 17 DNA sequence
 Nucleic Acid Accession #: XM_039209
 Coding sequence: 1..2049

70 1 11 21 31 41 51
 ATGCTGAAGA TGCTCTCCTT TAAGCTGCTG CTGCTGGCGG TGGCTCTGGG CTTCTTTGAA 60
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 CGAGTGACA GCCCGGGGCT AGGGCGCCTG GAGAATAAGA TATTTCTGT TACCAACAAC 300
 ACAGAAATGT GGAAGTTACT GGAGGAATC AAATGTGCAC TTGCTCTCC ACATTCTCAA 360
 AGCCTGTTC ACTCACCTGA GAGAGAAGTC TTGGAAGAG ACCTAGTACT TCCTCTGCTC 420
 TGCAAGACT ATTGCAAGA ATTCTTTTAC ACTTGGCGAG GCCATATTCC AGGTTTCTCT 480
 80 CAACAACCTG CGGATGAGTT TTGCTTTTAC TATGCAAGAA AAGATGGTGG GTTGTGCTTT 540
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 GAATATGACA AAGTGAAGA GATCAGCAGA AAGCACAAC ACAACTGCTT CTGTATTGAG 660
 GAGGTTGTGA GTGGGCTCGG GCAGCCCGTT GGTGCCCTGC ATAGTGGGGA TGGCTGCA 720
 CGTCTCTTCA TCTGGAAAA AGAAGTTTAT GTGAAGATAC TTACCCCTGA AGGAGAAATT 780
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GAAAGAGGAC TGCTAAGCCT CGCATTCCAT CCCAATTACA AGAAAAATGG AAAGTTGTAT 900
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25 Seq ID NO: 18 Protein sequence
Protein Accession #: XP_039209

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SLFHSFEREV LERDVLVPLL CKDYCKEPPY TCRGHIPGFL QTDADEFCEY YARKDGGLCF 180
PDPFRKQVRG PASNYLDQME EYDKVEEISR KHKHNCFCIQ EVVSGLRQPV GALHSGDGSQ 240
RLFLEKEGY VKILTPEGEI FKEPYLDIHK LVQSGIKGGD ERGLLSLAFH PNYKXGKLY 300
VSYTTNQRW AIGPHDHLR VVEYTVSRKN PHQVDLRTAR VFLEVAELHR KHLGGQLLFG 360
PDGFLYIILG DGMITLDDME EMDGLSDFTG SVLRLLDVTG MCNVPSYIPR SNPHFNSTNG 420
PPEVFAHGLH DGRCAVDRH PTDININLTI LCGSDSNGKNR SSARILQIHK GKDYSEPSL 480
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45 Seq ID NO: 19 DNA sequence
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Coding sequence: 1..1506

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TATGGAATGT ATGCATATGC TGGCTGGTTT TACCTCAACT TTGTTACTGA AGAAGTAGAA 780
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5 TTATCTGTCA TTTTTTTTT TCACATCAGT TTGATCAGGA AAGTGATAA CACATCTTAG 2280
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Seq ID NO: 20 Protein sequence
 Protein Accession #: NP_055146.1

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 SMSVSWSARI QIFTFCKLT AILIIIVPGV MQLIKGQTON FKDAFSGRDS SITRLPLAFY 240
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 NAVAVTFPSR LLGNFSLAVP IFVALSCFSG MNGGVFAVSR LPFYVASREGH LPBILSMIHV 360
 30 RKHTPLPAVI VLHPLTMIML FSGDLDSLNL FLSPARWLFI GLAVAGLIYL RYKCPDMHRP 420
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35 Seq ID NO: 21 DNA sequence
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 Coding sequence: 64..1497

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 45 GTTGTAAAAA AATCCGAGA AATGCAGAAG TTCTTGGAT TGGAGGTGAC GGGGAGCTG 300
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 Protein Accession #: NP_002413

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 80 LHAAYAGPGV INGDHFDADD EQMTKDTTGT NLPLVAHEI GHSLGLFHSN NTEALMYFLY 240
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 TLRGEILFK DRHFWRKSLR KLEPELHLIS SFWPSLPSGV DAAYEVTSKD LVPIFKGNQF 360
 WAIRGNVRA GYPRGIHTLG FPPTVRKIDA AISKKKNKT YPFVEDKYWR FDEKRNSEMP 420
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Seq ID NO: 23 DNA sequence
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Coding sequence: 57..764

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Seq ID NO: 24 Protein sequence
Protein Accession #: NP_006519

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TCEKFFSGGC HNRNENRFP DEATCMGFCA PKKIPSPCY S PKDBGLCSAN VTRYFNPFRY 180
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Coding sequence: 1..2825

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10 Seq ID NO: 26 Protein sequence
Protein Accession #: NP_005449.1

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ERMGTIKFTQ PQDSREVIVG EYNAVADTLE IINDTIRPQG SEPPKDKTII LEQLRKISLP 480
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25 VGGMLLIDL ILICQAVDP LRRTVEKYSM EPDPAGRDIS IRPLLEHCEN THMTINLGIV 660
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FCIVALVIIF CSTITLCLVF VPKLITLRTN PDAATQNRFF QFTQNKKED SKTSTSVTSV 780
NQASTSRLEG LQSENHRLRM KITELDKDLE EVTMQLQDTP EKTTYIKQNH YQELNDILNL 840
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35 Seq ID NO: 27 DNA sequence
Nucleic Acid Accession #: NM_000450.1
Coding sequence: 117..1949

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GGTCTTACAA CACCTCCAG GAAGCTATGA CTTATGATGA GGCCAGTGCT TATTGTGAGC 240
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TATTGAGCTA TTCAACCAAGT TATTACTGGA TTGGAATCA AAAAGTCAAC AATGTGTGGG 360
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CCCTGGAATC CCCTGAGCAT GGAAGCCCTGG TTTGAGTCA CCACTGGGA AACTTCAGCT 720
50 ACAATTCTTC CTGCTCTATC AGCTGTGATA GGGGTTACCT GCCAAGCAGC ATGGAGACCA 780
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GCATTAGAAA TTAGCTGTGT GAAATACCAG TGTGTTTGT GTTTGAGTTT TATTGAGAAT 3720
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20 Seq ID NO: 28 Protein sequence
Protein Accession #: NP_000441.1

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DVGWMDERC SKKILALCTT AACINTSCSG HGECVETINN YTKCDPFGS GLKCEQIVNC 180
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240
ECDAVTNPAN GFVECFQNPQ SPPWNTTCTF DCEEGFELMG AQLQCTSSG NWDNEKPTCK 300
AVTCRAVRQ QNGSVRCSHS PAGEFTFKSS CNFTCEEFGM LQGPQVRELT TQGWTOQIP 360
VCEAPQCTAL SNPERGYMNC LPSASGSRFY GSSCEFSCEQ GFVLKSKRL CCGPTGEWEN 420
EKPTCEAVRC DAVHQPPLGL VRCASPIGE FTYKSSCAPS CEEGFELYGS TOLECTSQGQ 480
WTEEVPSQV VKCSSLAVPG KINMSCSGEP VPGTVCKFAC PEGWTLNGSA ARTCGATGHW 540
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Seq ID NO: 29 DNA sequence
Nucleic Acid Accession #: NM_007036
Coding sequence: 56..610

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TCCCTACGGC ACCTTCGGGA TGGATTGCAG AGAGACCTGC AACTGCCAGT CAGGCATCTG 420
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AGTATTTACC TGTATTTTAT TCTTGAAGTT GGCCACAGA GTTGTGAATG TGTGTGGAAG 1920
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Seq ID NO: 30 Protein sequence
Protein Accession #: NP_008967.1

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LNPR

Seq ID NO: 31 DNA sequence

Nucleic Acid Accession #: NM_000963

Coding sequence: 135..1949

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WO 03/042661

Seq ID NO: 32 Protein sequence
Protein Accession #: NP_000954

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NMMFAFFAQH FTHQFFKTDH KRGPAFTNGL GHGVDLNHIY GETLARQRKL RLPKDGKMKY 240
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VLKQEHPEWG DEQLFQTSRL ILIGETIKIV IEDYVQHLGS YHFKLKFDPE LLPNKQFQVQ 360
NRIAAEFNTL YHWHPLLPDT FOIHDQKYNQ QQPIYNNISL LEHGITQFVE SPTRQIAGRV 420
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Seq ID NO: 33 DNA sequence
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Coding sequence: 1..1361

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TGCCGCTGCT CGCTGCAGCA CGCCAACCAC GAGAAGCGCC TGCGCTTACA TGCGCACTCC 1140
ACCAACGACA GCGCCGCTT TGTGCAGCG CCGTTGCTCT TCGCGTCCCG GCGCCAGTCC 1200
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Seq ID NO: 34 Protein sequence
Protein Accession #: NP_001499.1

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55 ATLLHVLTLF FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTEYPL 180
VNVPSHGLT CNRSSTRHHE QPETSNNISIC TNLSSRWTFV QSSIFGAFVY YLVVLLSVAP 240
MCMNMQVLM KQKGLSLAGG TRPPQLRKSE SEESRTARRQ TIIFLRLIVV TLAVCWMPNQ 300
IRRIIMAAKP KHDWTRSYFR AYMILLPFSE TFFYLSSVIN PLLYTVSSSQ FRRVFVQVLC 360
60 CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEABPQ 420
SKSQSLSLSE LEPNSGAKPA NSAAENGFOE HEV

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Seq ID NO: 35 DNA sequence
Nucleic Acid Accession #: NM_006475.1
Coding sequence: 28..2538

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65      1      11      21      31      41      51
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AACAGAAGCTG CAACGGAGAG ACTCAAGATG ATTCCTTTT TACCATGTT TTCTCIACIA 60
70 TTGCTGCTTA TTGTTAACCC TATAAAGGCC AACATCATT ATGACAAGAT CTGGCTCAT 120
AGTGTATATCA GGGGTGCGGA CCAAGGCCCA AATGCTGTG CCCTTCAACA GATTTTGGGC 180
ACCAAAAGAA AATACTTCAG CACTTGTAG AACTGTGATA AAAAGTCCAT CTGTGGACAG 240
AAAACGACTG TTTTATATGA ATGTTGCCCT GGTATATGA GAATGGAAGG AATGAAAGGC 300
TGCCACGACG TTTTGGCCAT TGACCATGTT TATGGCACT TGGGCATCGT GGGAGCCACC 360
ACAACGACGC GCTATTCTGA CGCCTCAAAA CTGAGGGAGG AGATCGAGGG AAGGGGATCC 420
75 TTCACTTACT TTGCACCGAG TAATGAGGCT TGGGACAAC TGGATTCTGA TATCGTAGA 480
GGTTTGAGTA GCAACGTGAA TGTGAATTA CTGAATGCTT TACATAGTCA CATGATTAAT 540
AAGAGAAATG TGACCAAGGA CTTAAAAAT GGCAATGATTA TTCTTCAAT GTATAACAAT 600
TTGGGGCTTT TCATTAAACA TTATCTTAAT GGGGTGTGCA CTGTAAATG TGCTGGAATC 660
80 ATCCATGGGA ACCAGATTGC AACAAATGGT GTTGTCCATG TCATTGACG TGTGCTTACA 720
CAAAATTGGTA CCTCAATTCA AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTACA 780
GCAGCTGCCA TCACATCGGA CATATTGGAG GCCCTTGGAA GAGACGGTCA CTTCACACT 840
TTTGCTCCCA CCAATGAGGC TTTTGAGAAA CTTCCAGGAG GTGTCTTACA AAGGTTTCATG 900
GGAGACAAGG TGGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT 960
TCTGAGTCTA TTATGGGAGG AGCAGTCTTT GAGACGCTGG AAGGAAATAC AATTGAGATA 1020

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5 GGATGTGACG GTGACAGTAT AACAGTAAAT GGAATCAAAA TGOTGAACAA AAAGGATATT 1080
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 CAAGTTATTG AGCTGGCTGG AAAACAGCAA ACCACCTTCA CGGATCTTGT GGCCCAATTA 1200
 GGCTTGGCAT CTGCTCTGAG GCCAGATGGA GAATACACTT TGCTGGCACC TGTGAATAAT 1260
 GCATTTTCTG ATGATACTCT CAGCATGGTT CAGCGCTCC TTAAATTAAT TCTGCAGAA 1320
 CACATATTGA AAGTAAAGT TGGCCTTAAT GAGCTTTACA ACGGGCAAT ACTGGAAACC 1380
 ATCGGAGGCA AACAGCTCAG AGTCTTCGTA TATCGTACAG CTGTCTGCAT TGAAATTTCA 1440
 TGCATGGAGA AAGGGAGTAA GCAAGGAGA AACGGTGGGA TTCACATATT CCGGAGATC 1500
 10 ATCAAGCCAG CAGAGAAATC CCTCCATGAA AAGTTAAAC AAGATAAGCG CTTTAGCACC 1560
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 CTGATAAGCG CCAAAATGTC TCTTCAAAAC ATCATTCTTT ATCACTGAC ACCAGGAGTT 1740
 TTCATTGGAA AAGGATTGTA ACCTGGTGT ACTAACATT TAAAGACCAC ACAAGGAAGC 1800
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 15 TCGACATGCA TACTTGAAGC TGGTGTAAAT CATGTTGTAG ATAACTCCT CTATCCAGCA 1920
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 20 AGACTGATTA AAGAGGTGCA AACAAATACT GAAGTGATCC ATGGAGAGCC AATTATTAAA 2220
 AAATACACCA AAATCATTTG TGGAGTGCCT GTGGAATAA CTGAAAAGA GACACGAGAA 2280
 GAACGAATGA TTACAGGTCC TGAATAAAAA TACACTAGGA TTTCTACTGG AGGTGAGAGA 2340
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 25 ACACCGTGA GGAAGTTGCA AGCCAACAAA AAGTTCAAG GTTCTAGAAG ACGATTAAAG 2520
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 30 CACCTTACAC CCTTTTTCAT CTTGACATTA AAGTTCTGCG CTAACTTTGG AATCCATTAG 2820
 AGAAAAATCC TTGTCAACAG ATTCATTACA ATTCAAAATG AAGAGTTGTG AACTGTTATC 2880
 CCATTGAAA GACCGAGCCT TGTATGTATG TTATGGATAC ATAAATGCA CGCAAGCCAT 2940
 TATCTCTCCA TGGGAAGCTA AGTTATAAAA ATAGGTGCTT GGTGTACAAA ACTTTTTATA 3000
 35 TCAAAAGGCT TTGCACATTT CTATATGAGT GGGTTTACTG GTAAATATATG TTATTTTTTA 3060
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 TCTCAACGT TCAATAAAAA CCATTTTCA GATATAAGA GAATTACTTC AAATTGAGTA 3180
 ATTCAGAAA ACTCAAGATT TAAGTTAAAA AGTGGTTTGG ACTTGGGAA

Seq ID NO: 36 Protein sequence
 Protein Accession #: NP_006466.1

40
 1 11 21 31 41 51
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 45 KNWYKKSICG QKTTVLYECC PGYMRMEGMK GCPAVLPIDH VYGTGLGIVA TTTQRYSDAS 120
 KLREELBEGK SFYTFAPSNB AWDNLDSDIR RGLSENVNVE LLNALHSHMI NKRLMTKDLK 180
 NGMIIPSMYN NLGLFINHYP NGVVTVNCAR IIHGNQIATN GVVHVIDRVL TQIGTSIQDF 240
 IEAEDDLSPF RAAAITSDIL EALGRDGHFT LFAPTNEAPE KLPRGVLERP MGDKVASEAL 300
 50 MKYHILNTLQ CSESIMGGAV PETLEGNITIE IGCDDGSITV NGIKMVNKKD IVTNNGVIHL 360
 IDQVLIPDSA QKVIELAGKQ QTTPTDLVAQ LGLASALRPD GEYTLAPVN NAFSDDTLMS 420
 VORLLKLLQ NLHLKVKVGL NELVNGQILE TIGGKQLRVE VYRTAVCIEN SCMEKSGSKQG 480
 RNGAIHIFRE IIPKAEKSLH EKLKQDKRPS TPLSLLEAAD LKELLTQPGD WTLFVPTNDA 540
 FKGMTSESEKE ILIRDKNALQ NIIYLHLPFG VPIGKGFEPG VTINILKTTQG SKIFLKEVND 600
 55 TLLVNELKSK ESDIMTNGV IHVVDKLLYP ADTPVGNQDL LEILNKLIKY IQIKFVRGST 660
 FKEIPVTYVT TKIITKVVEP KIKVIEGSLQ PIKTEGPTL TKVKIEGEPB FRLIKEGETI 720
 TEVIHGEPII KKYTKIDGV PVEITEKETR KERIITGPEI KYTRISTGGG ETEETLKKLL 780
 QSEVTKVTKF IEGGDHGLFE DEIKRLQQG DTPVRKLQAN KKVQGSRRRL RBGRSQ

Seq ID NO: 37 DNA sequence
 Nucleic Acid Accession #: NM_002416
 Coding sequence: 40..417

60
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 AAGGTCGCT GTTCCTGCAT CAGCACCAC CAAGGACTA TCCACCTACA ATCTTGAAA 180
 GACCTTAAAC AATTGCCCC AAGCCCTTCC TGGGAGAAA TTGAAATCAT TGCTACACTG 240
 70 AAGAATGGAG TTCAAAACATG TCTAAACCCA GATTCAAGAG ATGTGAAGGA ACTGATTAAA 300
 AAGTGGGAGA AACAGGTCAG CCAAAAGAAA AAGCAAAAGA ATGGGAAAAA ACATCAAAAA 360
 AAGAAAGTTC TGAAAGTTGG AAAATCTCAA CGTCTCTGTC AAAAGAGAC TACATAAGAG 420
 ACCACTTCAC CAATAAGTAT TCTGTGTAA AAATGTTCTA TTTTAATTAT ACGCTATCA 480
 TTCCAAAGGA GGATGGCATA TAATACAAAG GCTTATTAAT TTGACTAGAA AATTAAAAAC 540
 ATTACTCTGA AATTGTAAC AAAGTTAGAA AGTTGATTTT AAGAAATCAA ACGTTAAGAA 600
 75 TTGTTAAAGG CTATGATTGT CTTGTCTCT CTACCAACCA CCAAGTTGAAT TTCAATCAGC 660
 TTAAGGCCAT GATTTTAGCA ATACCCATGT CTACACAGAT GTTCAACCAA CCACATCCCA 720
 CTCACAACAG CTGCTGGGAA GAGCAGCCCT AGGCTTCCAC GTACTGCGAG CTCCAGAGAG 780
 TATCTGAGGC ACATGTCAGC AAGTCTAAG CCTGTAGCA TGCTGGTGAG CCAAGCAGTT 840
 80 TGAAATGGAG CTGACCTCA CCAAGCTGCT GTGGCCATCA ACCTCTGTAT TTGAATCAGC 900
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 TTCAATCTTG CCGCTCAGG CTGACCATT TATTCTTTT TGTTCCTCTT TGCTTCAITC 1080
 AAGTCAGCTC TTCTCATATC TACCACAATG CAGTGCCTTT CTCTCTCCA GTGCACCTGT 1140
 CATATGCTCT GATTATCTG AGTCAACTCC TTTCTCATCT TGTCCCAAC ACCCCACAGA 1200

5 AGTGTCTTCT TCTCCCAATT CATCCTCACT CAGTCCAGCT TAGTTCAGT CCTGCCTCTT 1260
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 CACATGGGTG AACACTCAAT GGTAACTAA TTCTGGGTG TTTATCCTAT CTCTCCAACC 1380
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 CTAGCCTCTG GTAACCTCTT ACTTATTATC TTCAGGACAC TCACTACAGG GACCAGGGAT 1620
 GATGCAACAT CCTTGTCTTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAATAAGAA 1680
 GCACGTGCTA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG 1740
 10 AAAAAATATAT AATCTTACAA TGAAAAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC 1800
 CCAACCATAC AAAAAATCCT TTTCCCGAAG GAAAAGGGCT TTCTCAATAA GCTCAGCTT 1860
 TCTAAGATCT AACAAAGATG CCACCGAGAT CCTTATCGAA ACTCATTTTA GGCAAAATATG 1920
 AGTTTTATTG TCCGTTTACT TGTTCAGAG TTTGATTGT GATTATCAAT TACCACACCA 1980
 TCTCCCATGA AGAAAGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAGCAG CCAAGTCGGT 2040
 15 TAGTGAAGC ATGATTGGTG CCCAGTTAGC CTCGCGCAGG TGTGGAACCC TCCTCCAGG 2100
 GGAGGTTTCTG TGAATTGCTG AGGAGAGGTT GTCTGTGGCC AGAATTTAAA CCTATACTCA 2160
 CTTTCCCAAA TTGAATCACT GCTCACACTG CTGATGATT AGAGTGCTGT CCGGTGGAGA 2220
 TCCCACCCGA ACGTCTTATC TAATCATGAA ACTCCCTAGT TCCTTCATGT AACTTCCCTG 2280
 AAAAAATCTAA GTGTTTCATA AATTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG 2340
 20 GTAGACAGTA TATAACTAAC AACCAAGAGC TACATATTGT CACTGACACA CAGCTTATAA 2400
 TCAATTATCA TATATATACA TACATGCATA CACTCTCAA GCAATAAAT TTTCACTTCA 2460
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 TATCAATAAA TAGACCTTA ATCAG

25 Seq ID NO: 38 Protein sequence
 Protein Accession #: NP_002407

30 1 11 21 31 41 51
 MKKSGVLFLL GIILLVLIGV QGTFVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPSCEK 60
 IEIILATLKNQ VQTCINPDSA DVKELIKKWE KQVSQKKKQK NGKKHQKKVY LKVRKSQRSR 120
 QKKIT

35 Seq ID NO: 39 DNA sequence
 Nucleic Acid Accession #: NM_006670
 Coding sequence: 85..1347

40 1 11 21 31 41 51
 CCGGCTCGCG CCCTCCGGGC CCAGCCTCCC GAGCCTCGG AGCGGGCGCC GTCCAGCCC 60
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 GACGGGGCTC TGGCGCTGCG CGGACTAGCG CTGTACTTCC TGGGCTGGGT TCCTCGTCTC 180
 TCTCCCACTT CCTCGGCATC CTCCTTCTCC TCCTCGGCGC GGTTCCTGGC TTCGCGCGTG 240
 TCCGCCCCAGC CCGCGCTGCC GGACCACTGC CCGCGCTGT GGGAGTGCTC CGAGGCGAGG 300
 45 CGCACAGTCA AGTGGGTAA CGCAATCTG ACCGAGGTGC CCAAGGACCT GCCCGCTTAC 360
 GTGCGCAACC TCTTCTTAC CGGCAACCA GTCGCGGTGC TCCCTGCGCG CGCTTCTGCC 420
 CGCGGGCGCG CGCTGGCGGA GCTGGCGCGC CTCACCTCA GCGGCGAGCG CCTGGAGGAG 480
 GTGCGCGCGG GCGCCTTCGA GCATCTGCCC AGCCTGGCGC AGCTCGACCT CAGCCACAAC 540
 CCAGTGGCGG ACCTCAGTCC CTTCGCTTC TCGGCGAGCA ATGCCAGCGT CTCGGCCCCC 600
 50 AGTCCCTCTG TGGAACTGAT OCTGAACCA ATCGTGCCCC CTGAAGATGA GCGGCGAAGC 660
 CGGAGCTTGG AGGGCATGG GGTGGCGGCC CTGCTGGCGG GCGGTGCACT GCAGGGGCTC 720
 CGCGCTTGG AGCTGGCCAG CAACCACTTC CTTTACCTGC CGCGGGATGT GCTGGGCCAA 780
 TCGCCAGCCG TCAGGCACCT GGACTTAAGT AATAATTGCG TGGTGAGCCT GACCTAGCTG 840
 55 TCCTTCGCCA ACCTGACACA TCTAGAAAGC CTCACCTGG AGGACAATGC CCTCAAGGTC 900
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 AACAAATCCT GCGCTGCGGA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAAACA 1020
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 GTCTCTTGG AACTCAACAG TGCTGACCTG GACTGTGACC CGATTCTTCC CCTCATCCCTG 1140
 CAAACCTCTT ATGTCTTCTT GGTATTTGTT TTAGCCCTGA TAGGCGCTAT TTTCTCTCTG 1200
 60 GTTTTGTATT TGAACCGCAA GGGGATAAAA AAGTGGATGC ATAACATCAG AGATGCCTGC 1260
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 CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA 1440
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 65 TTTCTCGGTG TGTCTGTGTA ATGTAAGAGC ATGAACAGTT GTGTATAGTG TTTTACCCTC 1560
 TTCTTTTCT TGGAACTCCT CAACACGTAT GGAGGGATT TTAGGTTTC AGCATGAACA 1620
 TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680
 ACAGATAGCA TTCAACAAA GCTGCCTCAA CTTTTCGAG AAAAAACIT TATTATATAA 1740
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 70 CTGCAAGCT TAGCAGGCTC TTCAAAATAA CTCATGGTG CACAGGAGCA CCGCATCCA 1860
 AGAGCATGCT TACATTTTAC TGTCTGCTAT ATTACAAAAA ATAATTGCA ACTTCATAAC 1920
 TTCTTTGACA AAGTAAATTA CTTTTTTGAT TGCAGTTTAT ATGAAATGT ACTGATTTT 1980
 TTTTAATAAA CTGATCGAG ATCCAACCGA CTGAATTGTT AAAAAAAA AAAAAATAAG 2040
 ATTCTTAAA GAA

75 Seq ID NO: 40 Protein sequence
 Protein Accession #: NP_006661

80 1 11 21 31 41 51
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 QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLPLTG NQLAVLPAGA FARRPPLAEL 120
 AALNLSGSLR DEVRAGAFEH LPSLRQLDLS HNFLADLSPP AFSGSNASVS APSPLVELIL 180
 NHIVPPEDER QNRSFEGMVV AALLAGRALQ GLRRLRLASN HFLYLPDVL AQLPSLRHLD 240

LSNNSLVSLT YVSPRNLTSL ESHLEEDNAL KVLHNGTLAE LQGLPHIRVF LDMNFWVDC 300
 HMADMVTLK ETEVVQKDR LTCAYPEKMR NRVLLELNSA DLDCDPILPP SLQTSYVFLG 360
 IVLALIGAIF LVLVLYNRKG IKWMHNIIRD ACRDEMEGYH YRYEINADPR LTNLSNSNDV

5

Seq ID NO: 41 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..927

10 1 11 21 31 41 51
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 TTCTCCTCTC CGGCGCGGTT CCTGGCTTCC GCGGTGTCCG CCCAGCCCCC GCTGCGGGAC 180
 CAGTGCCCCG CGCTGTGCGA GTGCTCCGAG GCAGCGCGCA CAGTCAAGTG CGTTAACCGC 240
 15 AATCTGACCG AGGTGCCCCA GGACCTGCCC GCCTACGTGC GCAACCTCTT CCTTACCGGC 300
 AACCAGCTCG CCAGCAACCA CTTCCTTTAC CTGCGCGGGG ATGTGCTGGC CCAACTGCCC 360
 AGCTCAGTCA ACCTGGACTT AAGTAATAAT TCGCTGGTGA GCCTGACCTA CGTGTCTTTC 420
 CGCAACTCGA CACATCTAGA AAGCTCCAC CTGGAGGACA ATGCCCTCAA GGTCTCTCAC 480
 AATGGCACCC TGGCTAGTGT GCAAGGTCTA CCCACATTA GGGTTTTCTT GGACAACAAT 540
 20 CCTGGGTCTT GCGACTGCCA CATGGCAGAC ATGGTGACCT GGCTCAAGGA AACAGAGGTA 600
 GTGCAGGGCA AAGACCGGCT CACCTGTGCA TATCGGGAAT AAATGAGGAA TCGGGTCTTC 660
 TTGGAATCTA ACAGTGTCTG CTGGGACTGT GACCGGATTC TTCCCCCATC CCTGCAAAAC 720
 TCTTATGTCT TCTGGGTAT TGTTTTAGCC CTGATAGGCG CTATTTTCTT CTGCTTTTTC 780
 TATTTGAACC GCAAGGGGAT AAAAAAGTGG ATGCATAACA TCAGAGATGC CTGCAAGGAT 840
 25 CACATGGAAG GGTATCATT CAGATATGAA ATCAATGGGG ACCCCAGATT AACAAACCTC 900
 AGTTCCTAAC CGGATGCTCT CGAGTGA

30

Seq ID NO: 42 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
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 QCPALCBCE AARTVKVNR NLTEVPTDLP AYVRNLFITG NQLASNHPLY LPRDVLAQLP 120
 35 SLRHLDSLNN SLVSLTVVSP RNLTHLESLS LEDNALKVLH NGTLAEQLGL PHIRVFLDNN 180
 PWVDCHEMAD MVTWKETEY VQKDRILTCA YPEKMRNRVL LELNSADLDC DPILPFLSLT 240
 SYVFLGIPLA LIGAIFLLVL YLNRKGIKKW MHNIRDACRD HMEGVHYRYE INADPRLTNL 300
 SSNSDVLE

40

Seq ID NO: 43 DNA sequence
 Nucleic Acid Accession #: NM_058173
 Coding sequence: 68..340

45 1 11 21 31 41 51
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 CACCACCATG AAGTTCTTAG CAGTCTGCT ACTCTGGGA GTTTCATCTT TCTGGTCTC 120
 TGCCCAAGAT CCGACAACAG CTGCTCCAGC TGACACGTAT CCAGCTACTG GTCTCTGCTG 180
 50 TGATGAAGCC CTGATGCTG AAACCACTGC TGCTGCAACC ACTGCGACCA CTGCTGCTCC 240
 TACCACTGCA ACCACCGCTG CTCTACCACT TGCTGTAAA GACATTCAGT TTTTACCCAA 300
 ATGGGTGGGG GATCTCCCGA ATGGTAGAGT GTGTCCCTGA GATGGAATCA GCTTGAAGTCT 360
 TCTGCAATTG GGTCACAACT ATTATGCTT CCGTGTATT CATCCAATA CTTACCTTGC 420
 CTACGATATC CCTTTATCT CTATACAGT TATTTTCTTT CAAATAAAAA ATAACTATGA 480
 GCGAGCTAAC AT

55

Seq ID NO: 44 Protein sequence
 Protein Accession #: NP_477521

60 1 11 21 31 41 51
 | | | | |
 MKFLAVLVLL GVSIFLVSAQ NPTTAAPADT YPATGPADDE APDAETTAAA TTATTAAPT 60
 ATTAASTTAR KDIFVLPKW GDLNPRVCP

65

Seq ID NO: 45 DNA sequence
 Nucleic Acid Accession #: NM_000095.1
 Coding sequence: 26..2299

70 1 11 21 31 41 51
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 GCAGATGCTT CGGAACTGCG AGGAAACCAA CGCGGCGCTG CAGGACGTGC GGGACTGGCT 180
 GCGGCAGCAG GTCAAGGAGA TCACGTTCTT GAAAAACAG GTGATGGAGT GTGACGCGTG 240
 CGGATGACAG CAGTCAGTAC GCACCGGCGT ACCCAGCGTG CGGCCCCGTC TCCACTGCGC 300
 75 GCGCGGCTTC TGCTTCCCGG CGGTGGCGTG CATCCAGAGC GAGAGCGCGG GCGGCTGCGG 360
 CCGCTGCCCC GCGGGCTTCA CGGGCAACGG CTGCGACTGC ACCGACGTCA ACGAGTGCAA 420
 CGCCACCCCC TGCTTCCCGG GAGTCCGCTG TATCAACACC AGCCCGGGGT TCGCTGCGA 480
 GCGTGGCCCC CGGGGTGACA GCGGCCCCAC CCACAGGGC GTGGGGCTGG CTTTCGCCAA 540
 GGCCAAACAG CAGGTTTGCA CGACATCAA CGAGTGTGAG ACCGGGCAAC ATAAGTGGT 600
 80 CCCCACCTCC GTGTGCATCA ACACCGGGG CTCTTCCAG TCGCGCCCGT GCCAGCCCGG 660
 CTTGCTGGGC GACCAAGCGT CCGGCTGCCA GCGCGGCGCA CAGCGCTTCT GCCCGACGG 720
 CTGCGCCAGC GAGTGGCAAG AGCATGCAGA CTGCTGCTTA GAGCGCGATG GCTGCGGCTC 780
 GTGCGGTGTG CGGCTGGGCT GGGCCGCAA CGGATCCTC TGTGGTGGCG ACGTGAAGT 840
 AGACGGCTTC CCGGACGAGA AGCTGCGCTG CCGGAGCGG CAGTGGCGTA AGGACAACTG 900

CGTGACTGTG CCCAACTCAG GGCAGGAGGA TGTGGACCGC GATGGCATCG GAGACGCGTG 960
CGATCCGGAT GCCAGCGGGG ACGGGGTCCC CAATGAAAG GACAACTGCC CGCTGTGTGG 1020
GAACCCAGAC CAGCGCAACA CGGACGAGGA CAATGGGGC GATGCGTGGC ACAACTGCGG 1080
GTCCCAAGAG AACAGCGACC AAAAGGACAC AGACCGAGAC GGCGGGGGCG ATGCGTGCGA 1140
CGACGACATC GACGCGGACC GGATCCGCAA CCAGGCCGAC AACTGCCCCTA GGGTACCCAA 1200
CTCAGACCAC AAGGACAGTG ATGGCGATGG TATAGGGGAT GCGTGTGACA ACTGTCCCCA 1260
GAAGAGCAAC CCGGATCAGG CGGATGTGGA CCAGCATTTT GTGGGAGATG CTTGTGACAG 1320
CGATCAAGAC CAGGATGGAG ACGGACATCA GGACTCTCGG GACAACTGTC CCACGGTGCC 1380
TAACAGTGCC CAGGAGGACT CAGACCAAGA TGGCCAGGGT GATGCCTGCG ACGACGACGA 1440
CGACAATGAC GGAGTCCCTG ACAGTGGGGA CAATGCGCGC CTGGTGCTTA ACCCGGGCCA 1500
GGAGGACGCG GACAGGGAGC GCGTGGGCGA CGTGTGCCAG GACGACTTTG ATGCAGACAA 1560
GGTGTAGAGC AAGATCGAGC TGTGTCCGGA GAACTGTGAA GTACGCTCA CCGACTTCAG 1620
GGCCTTCAG ACAGTCGTGC TGGACCCGGA GGGTGACGCG CAGATTGACC CCAACTGGGT 1680
GGTGTCAAC CAGGGAAGGG AGATCGTGCA GACAATGAAC AGCGACCCAG GCGTGGCTGT 1740
GGGTACACT GCCTTCAATG CGGTGGACTT CGAGGGCAGC TTCCATGTGA ACACGGTCAC 1800
GGATGACGAC TATGCGGGCT TCATCTTTGG CTACGAGGAC AGCTCCAGCT TCTACGTGGT 1860
CATGTGGAAG CAGATGAGC AAACGTATG GCAGGCGAAC CCCTTCCGTG CTGTGGCGGA 1920
GCCTGGCATC CAATCAAGG CTGTGAAGTC TTCCACAGGC CCGGGGGAAC AGCTGCGGAA 1980
CGCTCTGTGG CATACAGGAG ACACAGAGTC CCAAGGTGCGG CTGCTGTGGA AGGACCGCGG 2040
AAACGTGGGT TGGAAAGACA AGAAGTCTTA TCGTTGGTTC CTGCAGCACC GGGCCCAAGT 2100
GGGCTACATC AGGATGCGAT TCTATGAGGG CCCTGAGCTG GTGGCCGACA GCAACGTGGT 2160
CTTGGACACA ACCATGCGGG GTGGCCGCGT GGGGGTCTTC TGCTTCTCCC AGGAGAACAT 2220
CATCTGGGCC AACCTGCGTT ACCGCTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA 2280
TCAGCTGCGG CAAGCTTAGG GACCAGGCTG AGGACCCGCG GGATGACAGC CACCCTCACC 2340
GCGGCTGGAT GGGGGCTCTG CACCAGCCCC AAGGGGTGGC CGTCTGTAGG GGAAGTGAG 2400
AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGACGGG

Seq ID NO: 46 Protein sequence
Protein Accession #: NP_000086.1

1 11 21 31 41 51
MVPDTACVLL LTIALAGASG QGQSPGLGSDL GPQMLRELQE TNAALQDVDR WLRQQVREIT 60
PLKNTVMEDD ACGMQQSVRT GLPSVRPLLH CAPGFCFPFV ACIQTESGGR CGPCPAGFTG 120
NGSHCTDVNE CNAHPCFPFR RCINTSPQFR CEACFPFGYS PTHQVGLAF AKANKQVCTD 180
INECBTGOHN CVFNSVCINT RGSFQCGPCQ PGFVGDQASG CQRGAQRFCP DGSPSECHEH 240
ADCVLERDGS RSCVCRVWGA GNGILCGRDT DLDGFPDEKL RCPEPQCRKD NCVTVFNSQG 300
EDVDRDGDIG ACDPDADGDD VPNEKDNCPV VRNPDQRNTD EDKMGDADCN CRSQKNDQK 360
DTDQDGRGDA CDDDDIDGDR RNQADNCPRV PMSDQKSDSG DGIQDADNMC PQKSNPDQAD 420
VDHDFVGDAC DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDQGDADADD DDDNDGVFDS 480
RDNCRVLPNP GQEDADRQGV GDVCQDDFDA DKVVDKIDVC PENAEVLTLD FRAFTQVFLD 540
PBGDAQIDPN WVVLNQGREI VQTMNSDPGL AVGYTAFNGV DFEGETFHVNT VTDDDYAGFI 600
PGYQDSSSPY VVMWKGMBQT YWQANPFRV AEPGIQLKAV KSSTGPGEQL RNALWHTGDT 660
ESQVRLWKD PRNVGKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDTMRGG 720
RLGVFCPSQE NIWNLRYR CNDTIPEDYE THQLRQA

Seq ID NO: 47 DNA sequence
Nucleic Acid Accession #: NM_001565.1
Coding sequence: 67..363

1 11 21 31 41 51
GAGACATTC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCCAGTCTC 60
AGCACCATGA ATCAAACTGC GATTCTGATT TGCTGCCTTA TCTTCTGAC TCTAAGTGGC 120
ATTCAAGGAG TACCTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180
CCTGTTAATC CAAGGTCTTT AGAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA 240
CGTGTGAGA TCAATGCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA 300
TCGAAGGCCA TCAAGAATT ACTGAAAGCA GTTAGCAAGG AAATGTCTTA AAGATCTCCT 360
TAAAACCGAG GGGGAGCAAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG 420
CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTT TTAGTTTGCA 480
GTTACACTAA AAGGTGACCA ATGATGGTCA CCAAATCAGC TGCTACTACT CCTGTAGGAA 540
GGTTAATGTT CATCATCTTA AGCTATTGAG TAATAACTCT ACCCTGGCAC TATAATGTAA 600
GCTCTACTGA GGTGCTATGT TCTTAGTGGA TGTCTGACC CTGCTTCAA TATTTCCTC 660
ACCTTTCCCA TCTTCCAAGG GTACTAAGGA ATCTTCTGCG TTGGGGGTTT ATCAGAAATC 720
TCGAATCTC AAATAACTAA AAGGTATGCA ATCAAACTCG CTTTAAAG AATGCTCTT 780
ACTTCATGGA CTTCCTGTC CATCTCCCA AGGGGCCCAA ATCTTTCAG TGGCTACCTA 840
CATACATTC CAAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAATATT 900
CTTATTTAAT GAAAGACTGT ACAAAGTATA AGTCTTAGAT GTATATATTT CCTATATGTT 960
TTTCAGTGA CATGGAATAA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020
TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG 1080
TTTTCAATA AAAATGAGGT ACTCTCCTGG AAATATTAAG

Seq ID NO: 48 Protein sequence
Protein Accession #: NP_001556.1

1 11 21 31 41 51
MNQTAILICC LIFLTLGSIQ GVPLSRTVRC TCISISNPQV NPSLEKLEI IPASQFCPRV 60
EIIATMKKKK EKRCINPESK AIKNLLKAVS KEMSKRSP

Seq ID NO: 49 DNA sequence
Nucleic Acid Accession #: XM_057014
Coding sequence: 143..874

1 11 21 31 41 51
 5 GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCCTCGGAG 60
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 CGCTGCCCGG CAGCGGGGAG CCATGCGACC CCAGGGCCCC GCCCGCTCCC CGCAGCGGCT 180
 CGCGGCGCTC CTGCTGCTCC TGCTGCTGCA GCTGCCGCG CGTTCGAGCG CCTCTGAGAT 240
 CCCCAGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG 300
 AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG 360
 10 CATTCCGGGT ACACCTGGGA TCCCAGGTCC GGATGGATTG AAAGSAGAAA AGGGGGAATG 420
 TCTGAGGGAA AGCTTTGAGG AGTCTCGAC ACCCAACTAC AAGCAGTGT CATGGAGTTC 480
 ATTGAATTAT GGCATAGATC TTGGGAAAAT TGCGGAGTGT ACATTTACAA AGATGCGTTC 540
 AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACCTCGG CTAATAATGCA GAAATGCATG 600
 CTGTACGGT TGGTATTTCA CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCAATTGA 660
 15 AGCTATAATT TATTTGGACC AAGGAAGCCC TGAATGAAT TCAACAATTA ATATTCAATG 720
 CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTTGCTAT 780
 CTGGGTGGCG ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCACT 840
 TTCTCGTATC ATTATTGAAG AACTACCAAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900
 TTTTTCATAT ATGCTTGGGA ATGTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA 960
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 TTTAAATCTA GCATTATTTCA TTTTGCCTCA ATCAAAAGTG GTTTCATAT TTTTTCATG 1080
 TGGTTAGAAAT ACTTCTCTCA TAGTCACATT CTCTCAACCT ATAATTGGGA ATATTGTTGT 1140
 GGTCTTTTGT TTTTCTCTT AGTATAGCAT TTTTAAAAAA ATATAAAGC TACCAATCTT 1200
 TGTACAATTT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA 1260
 25 CAACCTTAAA AAAAAAAAAA AAAA

Seq ID NO: 50 Protein sequence
 Protein Accession #: XP_057014

1 11 21 31 41 51
 30 MRPQGPAAAP QRLRLGLLLL LLQLPAPSSA SEIPKKGKKA QLRQREVVDL YNGMCLQGPA 60
 GVPGRDGGSPG ANGIPGTPI PGRDGFKEGK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120
 GKIAECTPTK MRSNALSRLV FSGSLRLKCR NACQQRWYFT FNGAECGSLP PLEAIILYLDQ 180
 35 GSPEMNSTIN IHRTSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIEE 240
 LPK

Seq ID NO: 51 DNA sequence
 Nucleic Acid Accession #: NM_020974
 Coding sequence: 81..3080

1 11 21 31 41 51
 40 GGGCTCCCGG CACACCTCCC CGCGCGCGCG CGGCCACCGC CCGCACTCCG CCGCTCTGCG 60
 45 CCGCAACCGC TGAGCCATCC ATGGGGGTG CGGGCGCGCA CCGTCCCGG CGCGCTCCG 120
 CGGTGCTGCT GCTGCTGCTG CTGCTGCGC CACTGCTGCT GCTGCGCGGG GCCGTCCCCG 180
 CGGGTCCGGG CCGTCCCGCG GGGCGCGCAG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240
 ATGACTGCCA TGCCGACGCC CTGTGTGAGA ACACACCCAC CTCCTACAAG TGCTCTGCA 300
 AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT GATGAATGT GGAATGAGC 360
 50 TCAATGAGAG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATCTG TGCACCTGTT 420
 TTGATGGCTT CATGTTGGCT CATGACGCTC ATAAATGTCT TGATGTGAC GAGTGCTCG 480
 AGAACCAATG CGGCTGCCAG CATACTGTG TCAAGTCTAT GGGGAGCTAT GAGTGTCTGT 540
 GCAAGAGAGG GTTTTCTCTG AGTGACAATC AGCACACCTG CATTCAACCG TCAGGAGAGG 600
 GCCTGAGCTG CATGAATAAG GATCACGCTG GTAGTCACAT CTGCAAGGAG GCCCAAGGG 660
 55 CGAGCGTCCG CTGTGAGTGC AGGCCTGGTT TTGAGCTGGC CAAGAACCGG AGAGACTGCA 720
 TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCGGATG 780
 GCCCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCTCTG 840
 AGCGAGAGGA CACTGTCTCT GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG 900
 ATAAACGGGT GAAACGGCGG CTGCTCATGG AAACGTGTGC TGTCAACAT GGAAGCTGTG 960
 60 ACCGCACCTG TAAGGATACT TCGACAGGTG TCCACTGCGA TTGTCTGTGT GGATTCACTC 1020
 TCCAGTTGGA TGGGAAGACA TGTAAAGATA TTGATGAGTG CCAGACCGCG AATGGAGGTT 1080
 GTGATCATTT CTGCAAAAC ATCGTGGGCA GTTTTGACTG CGGCTGCAAG AAAGGATTTA 1140
 AATTATTAAC AGATGAGAAG TCTTGCCAAG ATGTGGATGA GTGCTCTTTG GATAGGACCT 1200
 65 GTGACCACAG CTGCATCAAC CACCTGGCA CATTGCTTG TGCTTGCAAC CGAGGTGACA 1260
 CCTGTATGG CTTCACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGGAGGCT 1320
 GTCAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CCAGTGCCAC CCTGGGTACA 1380
 AGCTCCACTG GAATAAAAA GACTGTGTGG AAGTGAAGGG GCTCTGCCC ACAAGTGTGT 1440
 CACCCGTTGT GTCCCTGCAC TGCGGTAAGA GTGGTGGAGG AGACGGGTGC TTCTCAGAT 1500
 GTCACCTGCG CATTACCTTC TCTTCAGATG TCACCAACAT CAGGACAGT GTAACCTTTA 1560
 70 AGCTAAATGA AGGCAAGTGT AGTTTGAAAA ATGCTGAGCT GTTCCCGAG GGTCTGCGAC 1620
 CAGCACTACC AGAGAAGCAC AGCTCAGTAA AAGAGAGCTT CCGCTACGTA AACCTTACAT 1680
 GCAGCTCTGG CAAGCAAGTC CCAGGAGCCC CTGGCGGACC AAGCAACCCCT AAGGAAATGT 1740
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 75 TGAGCTGCAT CGTAAAGCGA ACOGAGAAGC GGCTCCGTAA AGCCATCCGC ACGCTCAGAA 1860
 AGGCGGTCCA CAGGGAGCAG TTTCACTTCC AGCTCTCAGG CATGAACCTC GACGTGGCTA 1920
 AAAAGCCTCC CAGAACATCT GAACGCCAGG CAGAGTCTGT TGGAGTGGGC CAGGCTCATG 1980
 CAGAAAACCA ATGTGTCACT TGCAGGGCTG GGACCTATTA TGATGGAGCA CGAGAAACCT 2040
 80 GCATCTATG TCCAAATGGA ACCCTTCAAA ATGAGGAAGG ACAATGACT TGTGAACCAT 2100
 GCCCAAGACC AGGAAATCTT GGGGCCCTGA AGACCCCAAG AGCTTGAAT ATGTCTGAAT 2160
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 GTGCGCTGGG CACGTTCCAG CCGTGAAGCTG GTGCAACTTC CTGCTTCCCC TGTGGAGGAG 2280
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 CATACAGGCC TGAATTTGGA AAAATAATT GTGTTTCTTG CCCAGGAAAT ACTACGACTG 2460
 ACTTTGATGG CTCACAAAC ATAACCCAGT GTAAAAACAG AAGATGTGGA GGGGAGCTGG 2520

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GAGATTTCAC TGGGTACATT GAATCCCCAA ACTACCCAGG CAATTACCCA GCCAACACCG 2580
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TCTTCCTGCC CATAGAGGAC GACTGTGGGG ACTATCTGGT GATGCGGAAA ACCTCTTCAT 2700
CCAATTCTGT GACAACATAT GAAACCTGCC AGACCTACGA ACGCCCATC GCCTTCACCT 2760
CCAGGTCAAA GAAGCTGTGG ATTCAATTCA AGTCCAATGA AGGGAACAGC GCTAGAGGGT 2820
TCCAGTCCC ATACGTGACA TATGATGAGG ACTACCAGGA ACTCATTGAA GACATAGTTC 2880
GAGATGCGAG GCTCTATGCA TCTGAGAAC ATCAGGAAAT ACTTAAGGAT AAGAAACTTA 2940
TCAAGGCTCT GTTTGATGTC CTGGCCCATC CCCAGAACTA TTTCAAGTAC ACAGCCAGG 3000
AGTCCCGAGA GATGTTTCCA AGATCGTTCA TCCGATTGCT ACGTTCCAAA GTGTCCAGGT 3060
TTTGTAGACC TTACAAATGA CTCAGCCAC GTGCCACTCA ATACAAATGT TCTGCTATAG 3120
GGTTGGTGGG ACAGAGCTGT CTTCCTTCTG CATGTTCAGCA CAGTCGGGTA TTGCTGCCTC 3180
CCGTATCAGT GACTCATTAG AGTTCAATTT TTATAGATAA TACAGATAAT TTGTAAAT 3240
GAACTTGGTT TTTCTTTCCC AGCATGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT 3300
CAGCTTCTCA CTGCTGTGGG CGATGTCTT GGATAGATCA CGGCTGGCT GAGCTGGACT 3360
TTGGTCAGCC TAGGTGAGAC TCACCTGTCC TTCTATTCTG AAACCTCAGC TTCTCTAGC 3420
TGATGTGAAA AGGAGGCCAC AGAATAAGCT GCTTATTCTG AAACCTCAGC TTCTCTAGC 3480
CCGGCCCTCT CTAAGGAGC CCTCTGACT CGTGTGCAGG CTCTGACCAG GCAGAACAGG 3540
CAAGAGGGGA GGAAGGAGA CCCCTGCAGG CTCCTCCAC CCACTTGAG ACCTGGGAGG 3600
ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGATCC CAGGAACCTG 3660
AGTTCTAAGC AGTGTCTGTG AAAAAAATAA GCAGAAAGAA TTAGAAATAA ATAAAACTA 3720
AGCACTTCTG GAGACAT

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Seq ID NO: 52 Protein sequence
Protein Accession #: NP_066025

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1 11 21 31 41 51
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LCQNTPTSYK CSCRPYQGE GRQCEDIDEK GNELNGGCVH DCLNIPGNR CTCTFDGFLA 120
HDGHNICDND ECLENNGGCG HTCVNVMGSY ECCCKEGFFL SDNQHTCIHR SEBGLSCMNK 180
DHGCSHICKE APRGSVACEC RPFELAKNQ RDCILTQNHG NGGQCHSCDD TADGPBSCSH 240
PQYKMHDTGR SCLEREDTVL EVTESNTISV VDGDKRVKRR LLMETCAVNN GCDRTCKDT 300
STGVHCSCPV GFTLQLDGKT CKDIDECQTR NGGCDHFCNK IVGSFDCGCK KGFLLTDEK 360
SQQDVDECSL DRTCDHSCIN HPGTAFACAN RGYTLYGFTH CGDTNECSIN NGGQCVQVNV 420
TVGSYECQCH PGYKLHWNKK DCVEVKGLLP TSVSPRVSLH CGKSGGGDGC FLRCHSGIHL 480
SSDVTITRTS VTFKLNKGK SLKNAELPPE GLRPALEPKH SSVKESPRYV NLTCSSGKQV 540
PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCDLSCIIVK TEKRLKRAIR TLRKAVHRE 600
FHLQLSGMNL DVAKKPPTS BRQAESCQVG QGHAENQCVS CRAGTYDGA RERCILCPNG 660
TFQNEEQMT CEPCEPRPNS GALKTPBAWN MSECGLQCP GEYSADGFAP CQLCALGTFQ 720
PEAGRTSCFP CGGLATKHQ GATSPQDCET RVQCSFGHFY NTTHRCIRC PVGTYPPEFG 780
KNKCVSCPEN TTDFDGSTN ITQCKNRRCG GELGDFGTGI ESPNYPGNYP ANTECTWTIN 840
PPPKRILIV VPEIFLPIED DCGDYLVMRK TSSNSVTTY ETCQTYERPI APTSRSKKLN 900
IQPKSNEGNS ARGFQVYVVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLIALFDV 960
LAHPQNYFKY TAQESREMPF RSPFIRLLRSK VSRFLRPYK

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Seq ID NO: 53 DNA sequence
Nucleic Acid Accession #: NM_014211
Coding sequence: 157..1479

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1 11 21 31 41 51
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GTCCTGCTCG TAGGCTGAAA GGACTTGCCC TAACAGAGCC TCAACAACTA CCTGGTGAAT 120
CCTACTTCAG CCCCTTGCTG TGAGCAGCTT CTCAACATGA ACTACAGCCT CCACCTGGCC 180
TTCTGTGCTC TGAGTCTCTT CACTGAGAGG ATGTGCATCC AGGGGAGTCA GTTCAACGTC 240
GAGGTGGGCA GAAGTGACAA GCTTTCCTCG CCTGGCTTTG AGAACCTCAC AGCAGGATAT 300
AACAATTTTC TCAGGCCCAA TTTTGGTGGG GAACCCGTAC AGATAGCGCT GACTCTGGAC 360
ATTGCAAGTA TCTCTAGCAT TTCAGAGAGT AACATGGACT ACACAGCCAC CATATACCTC 420
CGACAGCGCT GGATGGACCA CGGCTGTGTG TTGTAAGGCA ACACAGCCTT CACTCTGGAT 480
GCGCGCTCG TGAGTCTCTT CTGGGTGCCA GATACTTACA TTGTGGAGTC CAAGAAGTCC 540
TTCTCCATG AGTCACTGT GGAACACAGG CTCATCCGCC TCTCTCCAA TGGCACGGTC 600
CTGTATGCC TCAGAACTAC GACAACCTGT GCATGTAACA TGGATCTGTC TAAATACCCC 660
ATGGACACAC AGACATGCAA GTTGCAAGCT GAAAGCTGGG GCTATGATGG AAATGATGTG 720
GAGTTCACTT GGTGAGAGG GAACGACTCT GTGCGTGGAC TGGAACACCT GCGGCTTGCT 780
CAGTACACCA TAGAGCGGTA TTTCACTTTA GTCAACAGAT CGCAGCAGGA GACAGGAAAT 840
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GTCAGTATTA CTAATATCAT CAACAGCTCC ATCTCCAGCT TTAACAGGAA GATCACTTT 1260
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GACAAGTTCA AGTTTGTCTT CGAGAAAAG ATGGGACGGA TTGTTGATTA TTTCACAAAT 1380
CAAAACCCCA GTAATGTGTA TCACTATTCC AAACACTGT TTCTTTGAT TTTTATGCTA 1440
GCCAATGTAT TTTACTGGGC ATACTACATG TATTTTGTAG TCAATGTTAA ATTTCTTGCA 1500
TGCCATAGGT CTTCAACAGG ACAAGATAAT GATGTAATG GTATTTTAGG CCAAGTGTGC 1560
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ATGAAGCTCC AACCATGTTT CTAAGCTGTG TAGAAGTCTT AGCATTATAG GATCTGTGTA 1680
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AAGAATGGGA AGGAGACCAT TGGGTAACCC TCAAGTGTCA GAAGTGTGTT CTAAAGTAAC 1860
TATACATGTT TTTTACTAAA TCTCTGAGT GCTTATAAAA TACATTGTG CTAATTGAGG 1920
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CTTTTCCCAT TATACTTCTC ACAATTCAGT TTCTATGAGT TTGATCACTT GATTTTTTTA 3060
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TATGAGCCAA TCATATTGTT GATTTTTTAA AAAAAGTTTA AAAGGAAATA TCTGTTCTGA 3180
AACCCCACTT AAGCATGTGT TTTATATAAA AACATGATA AAGATGTGAA CTGTGAAATA 3240
AATATACCAT ATTAGTACC CACC
  
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 Seq ID NO: 54 Protein sequence
 Protein Accession #: NP_055026

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VQIALTLIDIA SISSISESNM DYTATIYLRQ RMDQRLVFE GNKSFTLDAR LVEFLWVPDT 120
YIVSEKSKFL HEVTVGNRLI RLFNSGTVLV ALRITTTVAC NMDLSKYPMD TQTCRLQLES 180
WGYDGNDSVR TWLRGNDVSR GLEHLRLAQY TIERYFTLV T RSQOETGNYT RLVLPQELRR 240
NVLYFILETY VPSTFLVVLV WVSFWISLDS VPARTCIGVT TVLSMTTLM I GSRTSLPNTN 300
CFIKALDVYL GICFSFVFGA LLEYAVAHYS SLQQMAADR GTTKEVEEVS ITNIINSSIS 360
SFKRKISFAS IEISSDNVDY SDLTMKTSBK FKFPVREKMG RIVDYFTIQN PSNVHDYHKL 420
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 Seq ID NO: 55 DNA sequence
 Nucleic Acid Accession #: XM_084007
 Coding sequence: 138..2405

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CGCGAGACGA AGGCGCAATG CGCAGGAAGT TATCTGTAAT CTTGATCCTG ACCTTTGGCC 180
TCTCTGTAC AAATCCCTT CATGAACATA AAGCAGCTGC TTTCCGCCAG ACCACTGAGA 240
AAATTAGTCC GAATTGGGAA TCTGGCATTG ATGTTGACTT GGCAATTTC ACACGGCAAT 300
ATCATCTACA ACAGCTTTTC TACGCTATG GAGAAAAATA TCTTTGTGCA GTTGAAGGGT 360
TCAGAAAAAT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG 420
ACCAAGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCA CACAGACCATG 480
AGCATCACTC AGACCAAGAG CATCACTCTG ACCATGATCA TCACTCCAC CATAATCATG 540
CTGCTTCTG TAAAAATAAG CGAAAAGCTC TTTGCCCAGA CCACTGACTG GATAGTTTCAG 600
GTAAGATATC TAGAAACAGC CAGGGGAAAG GAGCTCACCG ACCAGAACAT GCCAGTGGTA 660
GAAGGAATGT AGAGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACTG 720
TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACCTCTTC 780
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GAAACACAAA TGAATATCCG CAGGAGTGTG TCAATGCATC AAAGCTACTG ACATCTCATG 960
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TTCTTGTGTA ACATGTCCTC ACATTGATCA AACAAATTA AGATAAGAAG AAAAAGAATC 1500
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Protein Accession #: XP_084007

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Seq ID NO: 58 Protein sequence
 Protein Accession #: NP_056234.1

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 AGGCATTCAA TAAATGCACA ACGCCCAAG GAAATAAAT CCTATCTAAT CCTACTCTCC 2520
 ACTACACAGA GGAATCACT ATTAGTATTT TGGCATATTA TTCTCCAGGT GTTGTCTTAT 2580
 GCACCTATAA AATGATTTGA ACAAATAAAA CTAGGAACCT GTATACATGT GTTTCATAAC 2640
 CTGCTCTCTT TGCTTGGCCC TTTATTGAGA TAAGTTTTC TGTCAGAAA GCAAGAAACA 2700
 80 TCTCATTTCT AACAGCTGTG TTATATTCCA TAGTATGCAT TACTCAACAA ACTGTTGTGC 2760
 TATTGGATAC TTAGGTGGTT TCTTCACTGA CAATACTGAA TAAACATCTC ACCGGAATTC

Seq ID NO: 64 Protein sequence

Protein Accession #: NP_003005.1

1 11 21 31 41 51

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MPLSILVALC	LMLHLALGVR	GAPCEAVRIP	MCRHMPWNIT	RMPNHLHST	QENAILAIEQ	60
YBELVDVNC	AVLRFFFCAM	YAPICTLEFL	HDIPIKPKSV	CQRARDDCEP	LMKMYNHSWP	120
ESLACDELFP	YDRGVCISPE	AIVTDLPELV	KWIDITPDM	VQERPLDVDC	KRLSPDRCKC	180
KKVKPTLATY	LSKNYSYVIH	AKIKAVQRSG	CNEVITTVVDV	KEIFKSSSPI	PRTQVPLITN	240
SSQCCHILP	HQDVLIMCYE	WRSRMMLLEN	CLVEKWRDQL	SKRSIQWEER	LQEQRRTVQD	300
KKKTAGRTSR	SNPPKPKGKP	PAPKPASPKK	NIKTRSAQRR	TNPKRV		

Seq ID NO: 65 DNA sequence
 Nucleic Acid Accession #: BC010423
 Coding sequence: 248..1780

1 11 21 31 41 51
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CACAGCGTGG	GAAGCAGCTC	TGGGGGAGCT	CGGAGCTCCC	GATCAAGGCT	TCTTGGGGGT	60
AGCTACGGCT	GGGTGTGTAG	AACGGGGCCG	GGGCTGGGGC	TGGGTCCCTT	AGTGGAGACC	120
CAAGTGCAG	AGGCAAGAAC	TCTGCAGCTT	CCTGCCTTCT	GGGTCACTTC	CTTATTCAAG	180
TCTGCAGCGG	GCTCCAGGGG	AGATCTCGGT	GGAACCTTCAG	AAACGCTGGG	CAGTCTGCCT	240
TTCAACCATG	CCCCTGTCCC	TGGGAGCCGA	GATGTGGGGG	CCTGAGGCGT	GGCTGTCTGT	300
GCTGCTACTG	CTGCATCAT	TTACAGGCCG	GTGCCCGCGG	GGTGAGCTGG	AGACCTCAGA	360
CGTGGTAACT	GTGGTGTCTG	GCCAGGACCG	AAAACCTCCC	TGCTTCTACC	GAGGGGACTC	420
CGGCGAGCAA	GTGGGGCAAG	TGGCATGGGC	TGGGTGGGAC	GCGGGCGAAG	GCGCCCAAGG	480
ACTAGCGCTA	CTGCACTCCA	AATACGGGCT	TCACTGTGAGC	CGGCTTACG	AGGGCCCGCT	540
GGAGCAGCCG	CGGCCCCAC	GCAACCCCTT	GGACGGCTCA	GTGCTCTGCG	GCAACGCAGT	600
GCAGGCGGAT	GAGGGCGAGT	ACGAGTGGCG	GGTCAGCACC	TTCCCGCGCG	GCAGCTTCCA	660
GGCGCGGCTG	CGGCTCCGAG	TGCTGGTGCC	TCCCTGCGCC	TCACTGAATC	CTGGTCCAGC	720
ACTAGAAGAG	GGCCAGGGCC	TGACCTTGCC	AGCCTCTGCG	ACAGCTGAGG	GCAGCCAGC	780
CCCCAGGTG	ACCTGGGACA	CGGAGGTCAA	AGGCACAACG	TCCAGCCGTT	CCTTCAAGCA	840
CTCCCGCTCT	GCTGCGTGCA	CCTCAGAGTT	CCACTTGGTG	CCTAGCCGCA	GCATGAATGG	900
GCAGCCACTG	ACTTGTGTGG	TGTCCCATCC	TGGCTGTCTC	CAGGACCAAA	GGATCACCCA	960
CATCTCCAC	GTGCTCTTCC	TTGCTGAGCG	CTCTGTGAGG	GGCCTTGAAG	ACCAAAATCT	1020
GTGGCAGATT	GGCAGAGAAG	GAGCTATGCT	CAAGTGCCCTG	AGTGAAGGGC	AGCCCCCTCC	1080
CTCATACAA	TGGACACGGC	TGGATGGGCC	TCTGCCAGGT	GGGGTACGAG	TGGATGGGGA	1140
CACCTTGGGC	TTTCCCCAC	TGACCACTGA	GCACAGCGCG	ATCTACGCTC	GCCATGTCTG	1200
CAATGAGTTC	TCCTCAAGGG	ATTCTCAGGT	CACGTGGGAT	GTTCTTGACC	CCCAGGAAGA	1260
CTCTGGGAAG	CAGGTGGACC	TAGTGTGAGC	CTCGGTGGTG	GTGGTGGGTG	TGATCGCGCG	1320
ACTCTGTGTC	TGCTTCTTGG	TGGTGGTGGT	GGTGCTCATG	TCCCGATACC	ATCGGGCGAA	1380
GGCCAGCAG	ATGACCCAGA	AATATGAGGA	GGAGCTGACC	CTGACCAGGG	AGAACTCCAT	1440
CGGAGGCTG	CATTCCCATC	ACACGGACCC	CAGGAGCCAG	CGGAGGAGA	GTGTAGGGCT	1500
GAGAGCCGAG	GGCCACCTTG	ACTCCACGCT	GACCAACGCT	AGGGAGATAG	AAACACAGAC	1560
AGAGCCCGAG	GGCGCAGGTT	CTGGGCGGGC	CGAGGAGGAG	GAAGATCAGG	ATGAAGGCAT	1620
TGAAGTCTG	TCTCCAGGCT	CTGGGCGGGC	CGAGGAGGAG	GAAGATCAGG	ATGAAGGCAT	1680
CAAAACGGCC	ATGAACCAAT	TTGTTTCAAG	GAATGGGACC	CTACGGGCCA	AGCCCCCGGG	1740
CAATGGCATC	TACATCAATG	GGCGGGGACA	CCTGGTCTGA	CCAGGCGCTG	CCTCCCTTCC	1800
CTAGGCGCTG	CTCCTTCTGT	TGACATGGGA	GATTTTAGCT	CATCTTGGGG	GCCTCCTTAA	1860
ACACCCCCAT	TTCTTGGCGA	AGATGCTCCC	CATCCCACTG	ACTGCTTGAC	CTTTACCTCC	1920
AACCTTCTG	TTTATCGGGA	GGGCTCCACC	AATTGAGTCT	CTCCACCAT	GCATGCAAGT	1980
CACCTGTGTG	GTGCATGTGT	GCCTGTGTGA	GTGTTGACTG	ACTGTGTGTG	TGTGGAGGGG	2040
TGACTGTCCG	TGGAGGGGTG	ACTGTGTCCG	TGGTGTGTAT	TATGCTGTCA	TATCAGAGTC	2100
AAGTGAAGTC	TGGTGTATGT	GCCACGGGAT	TTGAGTGGTT	GGGTGGGCAA	CACTGTGAGG	2160
GGTGGCGTG	TGTGTCTATG	GGCTGTGTGT	GACCTCTGCC	TGAAAAGCA	GGTATTTTCT	2220
CAGACCCAG	AGCAGTATTA	ATGATGCAGA	GATTGGAGGA	GAGAGGTGGA	GACTGTGGCT	2280
CAGACCCAGG	TGTGCGGCA	TAGCTGGAGC	TGGAATCTGC	CTCCGGTGTG	AGGGAACCTG	2340
TCTCTACCA	CTTCCGAGCC	ATGGGGGCAA	GTGTGAAGCA	GCCAGTCCCT	GGGTGAGCCA	2400
GAGGCTTGAA	CTTGTACAGA	AGCCCTCTGC	CCTCTGGTGG	CCTCTGGGCG	TGCTGCATGT	2460
ACATATTTTC	TGTAAATATA	CATGCGCGCG	GAGCTTCTTG	CAGGAATACT	GCTCCGAATC	2520
ACTTTTAATT	TTTTTCTTTT	TTTTTCTTTT	CCCTTCCCAT	TAGTTGTATT	TTTTATTAT	2580
TTTTATTATT	ATTTTCTTTT	AGAGTTTGAG	TCCAGCGCTG	ACGATATAGC	CAGACCTGTT	2640
CTGTAAAAAA	ACCAAAACCC	AAAAAAAATA	AAAAAAAATA			

Seq ID NO: 66 Protein sequence
 Protein Accession #: AAH10423

65
 70
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MPLSLGAEMW	GPEAWLLLLL	LLASFTGRCP	AGELETSQDV	TVVLGQDAKL	PCFYRGDSGE	60
QVGQVAVARV	DAGEGAQELA	LLHSKYGLHV	SPAYEGRVEQ	PPPPRNFLDG	SVLLRNAVQA	120
DEGEYECRV	TFPAGSFQAR	LRLRLVLPPL	PSLNFGPALE	BQGLTLAAS	CTAEGSPAPS	180
VTWDTEVKGT	TSSRSFKHSR	SAAVTSBFLH	VPSRSMNGQP	LTCVVSHPGL	LQDQRITRIL	240
HVSFLAEASV	RGLEDQNLWE	IGREGAMKLC	LSEGGPPPSY	NWTRLDGFLP	SGVRVGDGTL	300
GFPLTTTEHS	GIYVCHVSNE	FSSRDSQVTV	DVLDPQEDSG	RQVDLVASV	VVVGVIAALL	360
FCLLVVVVVL	MSRYHRRKAQ	QMTQKYREEL	TLTRENISRR	LSSHETDPRS	QPEBSVGLRA	420
EGHPDSLKON	SSCSVMSEEP	EGRSYSTLT	VREISTQTEL	LSPGSGRAEE	EEDQDEGIQK	480
AMNHFVQENG	TLRAKPTGNG	IYINGRHLV				

Seq ID NO: 67 DNA sequence
 Nucleic Acid Accession #: NM_001203
 Coding sequence: 274..1782

1	11	21	31	41	51	
CGCGGGGCGC	GGAGTCCGGG	GGGCTCGCG	GGAOCGGGCG	AGTGGGAGA	CGCGGGCGCT	60
GAGGACGCGG	GAGCCCGGAG	CGCACGCGCG	GGGTGGAGTT	CAGCCTACTC	TTTCTTAGAT	120
GTGAAGAGAA	AGGAAGATCA	TTTCATGCCT	TGTTGATAAA	GGTTCAGACT	TCTGCTGATT	180

5 CATAACCAATT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240
 TGGCATAAGT GAGAGACAAA CTTCCTTGAT AACATGCTTT TGGAAAGTGC AGGAAAATTA 300
 AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGGCC CCACCCCCCG TCCAAAGGTC 360
 TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420
 GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTGCGCTGT GGTCACTTCT 480
 GGTTGCGTAG GACTAGAAGG CTCAGATTTT CAGTGTGCGG ACACCTCCAT TCCTCATCAA 540
 AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCTTACA 600
 CTGCTCCAT TGAAAAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCTTTACTT 660
 10 ATATCTGTGA CTGTCTGTAG TTGCTCTTG GTCCTTATCA TATTATTTTG TTACTTCCGG 720
 TATAAAAGAC AAGAAACACG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAACCTTAC 780
 ATTCTCTCTG GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAAGTGA 840
 TCAGGCTCC CTCTGCTGGT CCAAGGACT ATAGCTAAGC AGATTGAGT GGTGAACAG 900
 ATTGAAAAG GTGCTATGG GGAAGTTTG ATGGGAAAGT GCGCTGGCGA AAGGTAGCT 960
 15 GTGAAAGTGT TCTTACCAC AGAGGAAGCC AGCTGGTTC GAGAGACAGA AATATATCAG 1020
 ACAGTGTATG AAGAACATGA AACATTTTG GGTTCATTG CTGCAGATAT CAAGGGGACA 1080
 GGGTCTCGGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140
 TATCTGAAGT CCACCACTCT AGACGCTAAA TCAATGCTGA AGTTAGCTTA CTCTCTGTCT 1200
 AGTGGCTTAT GTCAATTACA CACAGAAATC TTTAGTACTC AAGGCAACCC AGCAATTGCC 1260
 CATCGAGATC TGAAAAGTAA AACATTTCTG GTGAAGAAA ATGGAACCTG CTGTATTGCT 1320
 20 GACCTGGGCC TTGCTGTTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380
 AATCGAGTTG GCACCAACAG CTATATGCTC CCAGAAGTGT TGGACGAGAG CTTGAACAGA 1440
 AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCTCAT CCTTTGGGAG 1500
 GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAA ACCAGCTTCC TTATCATGAC 1560
 25 CTAGTGCCCA GTGACCCCTT TTATGAGGAC ATGAGGGAGA TTGTGTGAT CAAGAAGTTA 1620
 CGCCCTCAT TCCCAACCG GTGGAGCAGT GATGAGTGT TAAGGCAGAT GGGAAAATC 1680
 ATGACAGATG GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTAAAGAAA 1740
 ACACCTTGCA AATGTCTAGA GTCCAGGAC ATTAACTCT GATAGGAGAG GAAAAGTAAG 1800
 CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860
 30 TAAGCATCCA CAGTACAAGC CTTGAACATC GTCTGCTTC CCAGTGGGTT CAGACCTCAC 1920
 TTTTCAGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980
 TCTGTTTGA GCGGAGAAA CCGTTGGGTA ACTGTTCAA GATATGATGC AT

Seq ID NO: 68 Protein sequence

Protein Accession #: NP_001194

35 1 11 21 31 41 51
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 40 MLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHHCPE DSVNNICSTD GYCPTMIEED 60
 DSGLPVVTSG CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECKNDLHPTL PPLKNRDFVD 120
 GPIHHRALLI SVTVCSLLLV LIILFCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180
 EQSSQSSGSGS GLPLLQVQRTI AKQIQMVQKI GKRGYGEVVM GKWRGEKVAV KVFFTTBEAS 240
 WFRTEYIQT VMRRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTLDAKS 300
 MLKLAYSVS GLCHLHTEIF STQKPAIAH RDLKSKNIV KKGTCCTIAD LGLAVKFISD 360
 45 TNEVDIPFNT RVGTRKYMPP EVLDESILNRN HFQSYIMADM YSPGLILWEV ARRCVSGGIV 420
 EYQLPYHDL VPSDFSYEDM REIVCIKKLR PSFPNRSWSD ECLRQMGKLM TECWAHNPAS 480
 RLTLALRVKKT LAHMSBSQDI KL

Seq ID NO: 69 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 166..1737

50 1 11 21 31 41 51
 | | | | |
 55 TTGGGGGTTT ATTCTCTTCC CTTCTAACTT GACAGGGTCT TGCTCTGTCA TTCAGGCAAG 60
 AGTGCAGTAG TGTGACTACT TCTTACTGCC GCCTCAAGCT TCCAGCCTCA ACTCAAGCAA 120
 TCTCCACACC TCAGCCACCC AAGTGGCTGG GACTACAGAT TAAGAAATGAC CCAAAATAAA 180
 TTAAGCTTTT GTTCCAAGAG CAATGTGTAT ACTGAAGTGC CTGATGGAGG ATGGGGCTGG 240
 GCGGTAGCTG TTTCAATTTT CTTGTTGAA GTCTTCACTT ACGGCATCAT CAAGACATT 300
 60 GGTGTCTTCT TTAATGACTT AATGGACAGT TTAATGAAT CCAATAGCAG GATCTCATGG 360
 ATAATCTCAA TCTGTGTGTT TGTCTTAACA TTTTCAGCTC CCCTGCGCAC AGTCTTGAGC 420
 AATCGTTTCG GACACCGTCT GGTAGTATG TTGGGGGGGC TACTTGTGAG CACCGGGATG 480
 GTGGCGCGCT CTTCTCACA AGAGGTTTCT CATATGTACG TCGCCATCGG CATCATCTCT 540
 GGTCTGGGAT ACTGCTTTAG TTTTCTCCCA ACTGTAACCA TCCTATCACA ATATTTTGGC 600
 65 AAAAGACGTT CCATAGTCAC TGCAGTGTCT TCCACAGGAG AATGTTTCOG TGTGTTTGCT 660
 TTGCGACACG CAATCATGGC TCTGAAGGAG CGCATTGGCT GGAGATACAG CCTCCTCTTC 720
 GTGGGCTTAC TACAGTTAAA CATGTTCATC TTCGGAGCAC TGCTCAGACC CATCTTTATC 780
 AGAGGACACG CGTCACCGAA AATAGTCATC CAGGAAAATC GGAAGAAGC GCAGTATATG 840
 CTTGAAAATG AGAAAACACG AACCTCAATA GACTCCATTG ACTCAGGAGT AGAATAACT 900
 70 ACCTCACCTA AAAATGTGCC TACTCACACT AACCTGGAAC TGGAGCGGAA GGCOCGACATG 960
 CAGCAGGTCC TGGTGAAGAC CAGCCCCAGG CCAAGCGAAA AGAAAGCCCC GCTATTAGAC 1020
 TTCTCCATTT TGAAGAGAGAA AAGTTTATAT TGTATGATAT TATTGTGCTT CTTTGAACAA 1080
 CTGGGATTTT TTGCACTTTC CTTGTACATC ATTCTCTGG GCATTAGTCT GGGCATTGAC 1140
 CAGGACCGCG CTGCTTTTTT ATTATCTACG ATGGCCATTG CAGAAGTTTT CGGAAGGATC 1200
 75 GGAGCTGGTT TTGTCCTCAA CAGGGAGCCC ATTGTGAAGA TTTACATTGA GCTCATCTGC 1260
 GTCATCTTAT TGACTGTGTC TCTGTTTGGC TTTACTTTTG CTACTGAAT CTGGGGTCTA 1320
 ATGTATGCA GCATATTTTT TGGGTTTATG GTTGAACAA TAGGAGGGAC TCACATTCCA 1380
 CTGCTTGTCT AGGATGATGT CGTGGGCAIT GAGAAGATGT CTTCTGCAGC TGGGCTCTAC 1440
 ATCTTCATTG AGAGCATAGC AGGACTGGCT GGACCGCCCC TTGCAGGTTT GTTGGTGGAC 1500
 80 CAAAGTAAGA TCTACAGCAG GGCCTTCTAC TCCTGCGCAG CTGGCATGGC CCGGCTGCT 1560
 GTGTGCTGCG CCTGTGTGAG ACCGTGTAAG ATGGGACTGT GCCAGCATCA TCACCTCAGT 1620
 GAAACAAAGG TAGTGAGCCA TCGTGGGAAG ACTTACAGG ACATACCTGA AGACTTTCTG 1680
 GAARTGATC TTGCAAAAAA TGAGCACAGA GTTCACTGTC AAATGGAGCC GGTATGACAC 1740
 ACTTTCTTAC AACCAACAGC ACTGTGTTGG CTGGAGAGGG ATGGGGTGGG CCAACCGGGG 1800
 ACACAAGGAG GCAGAGGAGC TAACCCCTCT ACTCCACTTT CAAAACCTACA TTTTAAAGGG 1860

AATGTGTATG TGAAGAGCAC TACCAACATC GCTTTTGTGT TGTTTTGTGT TGTTTTAAGC 1920
 TTTTTTTTTT TGCTTGTGTT TAAAGCCAAA ACACAAAAACA ACCAAGCACT CTTCATATA 1980
 TAAATCTGGC TGTATTCACT AGCAATACAA GAGATATGTA GAAAGACTCT TTGGTTCACA 2040
 TTCCGATATT AAAATAGTGA CATGAACATG CAAAGTGGTT TTAAGAGCTT TCACGTGGGA 2100
 TAAATGATT TCTTTTTTCT TTTCTTTCT TCTATGGTC TTGCTGAAT AAACACTCT 2160
 CCTGAATAAA ACACATCCA ACCCAGGTCA TTGAATGAA ATTGCCAGT C

Seq ID NO: 70 Protein sequence
 Protein Accession #: Bos sequence

1 11 21 31 41 51
 MTQNKLKLS KANVYTEVPD GGWGNVAVS FFFVEVFTYG IIKTFGVFFN DLMDSFNESN 60
 SRISWIISIC VFVLTFAPL ATVLNRFHG RLVMVLGGLL VSTMVAASF SQEVSHMYVA 120
 IGIISGLGYC FSFLPTVIL SQYFGKRRSI VTAVASTGEC FAVFAPAPAI MALKERIGWR 180
 YSLLFVGLLQ LNIIVFGALL RPIFIRGPAS PKIVIQENRK EAQVMLENEK TRTSIDSIDS 240
 GVELTTSFKN VPTHNLELE PKADMQQVLV KTSRPPSEKK APLLDPSILK EKSFIYALF 300
 GLFATLGFFA PSLYIIPGLI SLGIDQDRAA FLSTMAIAE VFGRIGAGFV LNREPIRKIY 360
 IELICVILLT VSLFAPTFAT EFWGLMSCSI FFGFMVGTIG GTHIPLLAED DVVGIEKMSS 420
 AAGVYIFIQS IAGLAGPPLA GLLVDSKIY SRAFYSCAAG MALAAVLAL VPRCKMGLCQ 480
 HHSGETKVV SHRGKTLQDI PEDFLEMDLA KNEHRVHVQM EPV

Seq ID NO: 71 DNA sequence
 Nucleic Acid Accession #: NM_004694
 Coding sequence: 166..1737

1 11 21 31 41 51
 TTGGGGGTTT ATTCTCTCC CTCTAACTT GACAGGGTCT TGCTCTGTCA TTCAGGCAAG 60
 AGTGCACTAG TGTGATCACT TCTTACTGCC GCTCAAGCT TCCAGCCTCA ACTCAAGCAA 120
 TCCTCCACC TCAGCCACCC AAGTGGCTGG GACTACAGAT TAAGAAATGAC CCACAAATAA 180
 TTAAGACTTT GTTCCAAAGC CAATGTGTAT ACTGAAGTGC CTGATGGAGG ATGGGGCTGG 240
 GCGGTAGCTG TTTTCATTTT CTTCGTGAA GTCTTCACT ACAGCATCAT CAAGACATTT 300
 GGTGTCTTCT TTAATGACTT AATGGACAGT TTAATGAAT CCAATAGCAG GATCTCATGG 360
 ATAATCTCAA TCTGTGTGTT TGTCTTAACA TTTTCAGCTC CCTCGCCAC AGTCTGAGC 420
 AATCGTTTCG GACACCGTCT GGTAGTGTAT TTGGGGGGG TACTTGTGAG CACCGGGATG 480
 GTGGCGCCTT CTTTCTCACA AGAGGTTTCT CATATGTACG TCGCCATCGG CATCATCTCT 540
 GGTCTGGGAT ACTGCTTTAG TTTTCTCCA ACTGTAACCA TCCATCACA ATATTTTGGC 600
 AAAAGACGTT CCAATAGTGC TGCAGTTGCT TCCACAGGAG AATGTTTCGC TGTGTTTGGT 660
 TTCGCACCAT CAATCATGGC TCTGAAGGAG CGCATTGGCT GGAGATACAG CCTCCTCTTC 720
 GTGGGCTAC TACAGTTAAA CATGTCTATC TTGGGAGCAC TGCTCAGACC CATCATATTC 780
 AGAGGACGAG CGTCAACGAA AATAGTCATC CAGGAAATC GGAAAGAAGC GCAGTATATG 840
 CTTGAAATG AGAAACACAG AACCTCAATA GACTCCATTG ACTCAGAGT AGAACTAACT 900
 ACCTCACCTA AAAATGTGCC TACTCACACT AACCTGGAAC TGGAGCCGAA GGCCGACATG 960
 CAGCAGGTCC TGGTGAAGAC CAGCCCCAGG CCAAGCGAAA AGAAAGCCCC GCTATTAGAC 1020
 TTCTCCATTT TGAAGAGAAA AAGTTTATT TGTATGATC TATTGTGCT CTTTGCAACA 1080
 CTGGGATTTT TTGACCTTTC CTTGTATACG ATTCTCTGG GCATTAGTCT GGGCATTGAC 1140
 CAGGACCGCG CTGCTTTTAT ATTATCTAAG ATGGCCATTG CAGAAGTTT CGGAAGGATC 1200
 GGAGCTGGTT TTGTCTCAA CAGGAGAGCC ATTCGTAAGA TTTACATTGA GCTCATCTGC 1260
 50 ATGTCATGCA GCATATTTT TGGGTTATG GTTGAACAA TAGGAGGACT CACATTCCAC 1320
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 ATCTTCATTC AGAGCATAGC AGGACTGGCT GGACCGCCCC TTGCAGGTTT GTTGGTGGAC 1440
 CAAAGTAAGA TCTACAGCAG GGCCTTCTAC TCTCGCCAG CTGGCAGTGC CCGCTGCTCT 1500
 55 GTGTGCTCG CCTGTGTGAG ACCGTGTAAG ATGGGACTGT GCCAGCGTCA TCACTCAGGT 1560
 GAAACAAAGG TAGTGAGCCA TCGTGGGAAG ACTTTACAGG ACATACCTGA AGACTTTCTG 1620
 GAAATGGATC TTGCAAAAAA TGAGCACAGA GTTCACTGTC AAATGGAGCC GGTATGACAC 1680
 ACTTTCTTAC AACCAACAGC ACTGTGTTGG CTGGAGAGGG ATGGGGTGGG CCCAACGGGG 1740
 ACACAAAGGAG GCAGAGGAGC TAACCCCTCT ACTCCACTTT CAAAACCTACA TTTTAAAGGG 1800
 AATGTGTATG TGAAGAGCAC TACCAACATC GCTTTTGTGT TGTTTTGTGT TGTTTTAAGC 1860
 60 TTTTTTTTTT TGCTTGTGTT TAAAGCCAAA ACACAAAAACA ACCAAGCACT CTTCATATA 1920
 TAAATCTGGC TGTATTCACT AGCAATACAA GAGATATGTA GAAAGACTCT TTGGTTCACA 1980
 TTCCGATATT AAAATAGTGA CATGAACATG CAAAGTGGTT TTAAGAGCTT TCACGTGGGA 2040
 TAAATGATT TCTTTTTTCT TTTCTTTCT TCTATGGTC TTGCTGAAT AAACACTCT 2100
 65 CCTGAATAAA ACACATCCA ACCCAGGTCA TTGAATGAA ATTGCCAGT C

Seq ID NO: 72 Protein sequence
 Protein Accession #: NP_004685

1 11 21 31 41 51
 MTQNKLKLS KANVYTEVED GGWGNVAVS FFFVEVFTYG IIKTFGVFFN DLMDSFNESN 60
 SRISWIISIC VFVLTFAPL ATVLNRFHG RLVMVLGGLL VSTMVAASF SQEVSHMYVA 120
 IGIISGLGYC FSFLPTVIL SQYFGKRRSI VTAVASTGEC FAVFAPAPAI MALKERIGWR 180
 YSLLFVGLLQ LNIIVFGALL RPIIIRGPAS PKIVIQENRK EAQVMLENEK TRTSIDSIDS 240
 GVELTTSFKN VPTHNLELE PKADMQQVLV KTSRPPSEKK APLLDPSILK EKSFIYALF 300
 GLFATLGFFA PSLYIIPGLI SLGIDQDRAA FLSTMAIAE VFGRIGAGFV LNREPIRKIY 360
 IELICVILLT VSLFAPTFAT EFWGLMSCSI FFGFMVGTIG GLTTHCLLM MSWALQKMSS 420
 AAGVYIFIQS IAGLAGPPLA GLLVDSKIY SRAFYSCAAG MALAAVLAL VPRCKMGLCQ 480
 RHSGETKVV SHRGKTLQDI PEDFLEMDLA KNEHRVHVQM EPV

Seq ID NO: 73 DNA sequence
 Nucleic Acid Accession #: NM_002184.1
 Coding sequence: 256..3012

1 11 21 31 41 51
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 GAGCAGCCAA AAGGCCCGCG GAGTCGCGCT GGGCGCGCCC GGCGCAGCTG AACCGGGGGC 60
 CGCGCCTGCC AGGCCGACGG GTCTGGCCCA GCCTGGCGCC AAGGGGTTGG TGCGCTGTGG 120
 5 AGACGGCGGAG GGTGCGAGCG GCGCGGCGCT AGTGAAACCC AATGGAAGAA GCATGACATT 180
 TAGAAGTAGA AGACTTAGCT TCAATCCCTG ACTCCTTCAC TTACTAATTT TGTGATTGTT 240
 AAATATCCGC GCAAGATGTT GACGTTGCAG ACTTGGGTAG TGCAAGCCTT GTTTATTTTC 300
 CTCACCATG AATCTACAGG TGAACITCTA GATCCATGTG GTTATATCAG TCCTGAATCT 360
 CCAGTTGTAC AACTTCATT TAAITTCACT GCAOTTTGTG TGCTAAAGGA AAAATGTATG 420
 10 GATTATTTTC ATGTAAATGC TAATTACATT GTCTGGAAAA CAAACCATTT TACTATTCTT 480
 AAGGAGCAAT ATACTATCAT AAACAGAAAC GCATCCAGTG TCACCTTTAC AGATATAGCT 540
 TCATTAAATA TTCAGCTCAC TTGCAACATT CTTACATTG GACAGCTTGA ACAGAATGTT 600
 TATGGAATCA CAATAATTTT AGGCTTGCCCT CCAGAAAAAC CTAATAATTT GAGTTGCATT 660
 GTGAAGGAGG GGAAGAAAAAT GAGGTGTGAG TCGGATGGTG GAAGGGAAC ACACCTGGAG 720
 15 GTCAACTTCA CTTTAAAAAT TGAATGGGCA ACACACAAGT TTGCTGATTG CAAAGCAAAA 780
 CGTGACACCC CCACCTCATG CACTGTTGAT TATTCTACTG TGTATTTTGT CAACATTGAA 840
 GTCTGGGTAG AAGCAGAGAA TGCCCTTGGG AAGGTTACAT CAGATCATAT CAATTTTGTAT 900
 CCTGTATATA AAGTGAAGCC CAATCCGCCA CATATTTAT CAGTGATCAA CTCAGAGGAA 960
 CTGTCTAGTA TCTTAAAAAT GACATGGACC AACCCAAGTA TTAAGAGTGT TATAATACTA 1020
 20 AAATATAACA TTCAATATAG GACCAAGAT GCCTCAACTT GGAGCCAGAT TCCTCTTGAA 1080
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Seq ID NO: 74 Protein sequence
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75 Seq ID NO: 76 Protein sequence
 Protein Accession #: NP_071414

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Seq ID NO: 77 DNA sequence

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Seq ID NO: 78 Protein sequence

Protein Accession #: Eos sequence

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Seq ID NO: 79 DNA sequence
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 Coding sequence: 39..1358

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Seq ID NO: 81 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..2070

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15 Seq ID NO: 82 Protein sequence
 Protein Accession #: FGENSEH predicted

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35 Seq ID NO: 83 DNA sequence
 Nucleic Acid Accession #: NM_005264.1
 Coding sequence: 557..1954

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Seq ID NO: 84 Protein sequence
 Protein Accession #: NM_005264.1

1 11 21 31 41 51
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 YEPVNSRLSD IFRVVPFISD VFQQVEHIPK GNNCLDAKA CNLDDICKY RSAYITPCTT 180
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Seq ID NO: 85 DNA sequence
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Seq ID NO: 86 Protein sequence
 Protein Accession #: XP_027172.1

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55 Seq ID NO: 87 DNA sequence
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 80 GGTTCGCGGC CGGGGCTGGG GATCCCTCGG GGTCTCCAG ACCAGCAGGA AGTCAGGCAC 1200
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 ACCAGAGAGC AGGGGCAGGA GAGGCCCTTC TGGCAGAGCA GCGTGGGAAG ACAAGGGAGG 1320
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 GGAGGAGGT GAGAGGAGGT GCTTGAAGGA GGCAGAGGT AGGAAAGCCC ATCTGTTTAG 1440
 GGCATGACGA TTAGGCTGGA GTCTGGTACC TCCCTCCAT TATAGCTCTC TCCTGCTCTT 1500

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	TCATTTTGGT	ACTAAAAACC	AGAGTCCTAG	GCGGGGGCTG	TATTTGAGCC	CAACGTCATG	1560
	TAAGACTTAG	GAGGTAAAC	CAGGACTGGA	GGCCAGATCT	CCTGGCTCCT	GGGGCCCCAC	1620
	CTGAGCCTAG	CACAGGCTG	GACCACTATG	CCTGGAGGA	GTCCCGGTCT	GCTGTGGTGT	1680
	TGGGAGGTTT	GGAGGATGCA	GAGGGGTTGG	GGCTGGGTGG	GCACCGTCA	GGCTGACCAG	1740
5	AAGGTGCCTG	CAGGCCATCC	GGCGTTTCGA	GGAGTGCTGT	GAGGCCAGC	AGCACTGGAA	1800
	GCAGTCCAC	CACATGTGCT	ACTGGGAGCT	GATGTGGTGC	TTCACTTACA	AGGGCCAGTG	1860
	GAAGATGTCC	TACTTCTAGC	CCGACCTGCT	CAGCAAGGAG	AACTGCTGGT	CCAAGGTGGG	1920
	CTGATGCCAC	GTGTTAGGGG	CATGGGTGA	CCAGGGCTGA	CTGTGTGCTT	CCAGACCACG	1980
	GGCCAAATCC	CTAACTGAAC	ACAGATGTCT	CAGCTGGAAT	CTAAACATAA	CCTTAAATTC	2040
10	TAATAGGACT	CAGGCTTGA	AGGAACATAA	GACCACAAGA	GAAACTTCTG	AACCACAATG	2100
	TGTACAAAG	AGATTTCTAG	TCACAAAGGA	CAGAAACATG	GCTCCCTCTG	TCCAGTAGAA	2160
	CTGTTTCTGT	GGTAGAAATG	TTCTACTTAT	GCATGCCCCA	AATATGGTAG	TCACCAGCCA	2220
	CATGTGCACA	CTGAGCACAT	GAAATGTGCC	TAGTGCAACT	GGGAACTGAA	TTGTTTTCAG	2280
	TTTATTATTA	TTTAAATGTA	AAATTAATA	GCCATGTAGG	GCTTGTGGCC		2340
15	ACTATATTGG	ACTATGCAGG	TCCAAAACAC	AAAAGSCTCA	TATAACTGAA	CATTCTTGGC	2400
	ACATCCGACT	TCAGGTAGGG	CTGGATCCAG	GAATTCAAAT	GATGTGCTCT	GGCTTGGTCT	2460
	TTCCATTGT	GGCTGTGCTC	TCTCCTATGA	CATCTTTGTT	TCTGCTGCAT	CTTTGCAGGA	2520
	AGGTTCTCTC	CATGTGCATC	GCAAGGTGGC	CACGGGCTGC	TTCTACTCAT	ATCCTCCCTT	2580
	TGGTTTCAAC	CAGAGTCCCA	CAGTTTGAGC	CTCACTGGTC	TGACTTGTCA	CCTGCCAATG	2640
20	CCTGGAACAG	AGGGGTGGGA	AGATTCTCTA	TGGGCTGAGA	GTAGGAGAGG	GGTGGTCCCA	2700
	CAGAAGAAA	TGATGCACCC	AGAAATAGTG	GAGGGATTAA	CAAGATGCCA	TACAGGCAAA	2760
	ACAAAGCCAA	ACAGATGCCC	GCCTACCAAA	GATGAAATTT	ATCATGGTAA	GTATTGAAAT	2820
	AAGTGTATAG	TTGTACCATC	ATAGTAATGA	TAGTGCAGAA	ATTGGAACCA	AGAGTCTTAC	2880
25	AACCACTTAG	CTCAGCAAA	GTCTAATCTG	TTATTGTAA	ATACACAGGA	CATGTGTCTT	2940
	CATGGCTTCA	TCCCTCGCCC	ATGGCAGACA	TTGCTAATCA	ATCCTCTGCC	ATGAGCCTAG	3000
	CTGTGACCTT	AGATACCTTC	CCTGCAAAAGC	TCCAGGCAGC	CGTTAGAACT	GACCCACATT	3060
	GGCACCCTGT	AGGAGACCTG	TCATCTGCAT	CTGGTCCCTC	CCCTCCTCT	GCATGGAGGT	3120
	CTCTTCCGTA	GCCTCTGCTG	GGGACCAAGC	TGAAGGGGAA	TTCTCTGGGT	CTGGGGCAGG	3180
30	TGGGGCTGGG	GAGGGGAGCA	GGCTCTTACT	GAGCTCTCAA	CATGCTGGGC	ACCTGTCTATG	3240
	TCCTCCACAC	CACACCCAGT	GAGGAGAAGT	TATTATCTCC	ATTGGGCACA	TGAGGGCCAC	3300
	TGATGCTAAG	CGAGGACTGT	GACTTTCCCA	CCCACATGGC	TGTTGGTGAC	AGACACCGGA	3360
	TTTGAGGACA	GTCTGTGTG	ACTCAGAGGC	CTCTGCTTCT	CTCTTGTCTC	TAGAGTCTCT	3420
	CTGAGGATGG	GGGGCTTGCC	CTGAGCCCAT	CCTGCTGTTG	AAGSTGCTTC	CTCAGGCCCA	3480
	GCTCCCATGG	CCCCACACCC	CCCTCCTCAT	CACCTCCTAC	TCCCAAAAG	GACAAAGCCT	3540
35	CAGGGAACCT	TTTTTCTTTT	TTTAGAGAGC	GGGTCTTGCT	ATGTTGGTCA	GGCTGGTCTT	3600
	GAACCTCTGG	GCCACAGCAA	TCTTCCCGCC	TCTGCTCCTT	AAAGTGTGG	GATTCTGGGC	3660
	CTTAGGGAAC	CTTTTGAAC	TGAAAGTGAC	GCTCGAAGCC	TTCTCTGTAGA	GTGAGGTGGG	3720
	TGGCTGGGGC	TAAACATATG	GGGAAGGAGA	GACCTGTGTG	GGGCACACAG	CTGCTATATA	3780
	GAGGAACAGA	AGGTGGGCCA	GGCTCCCGAC	CTGTGAGGAA	ATCTGGCTCA	GTCCCCAGAC	3840
40	CGCTGTGTGG	CTTTGGGGTG	GCCAGTCCCT	CTCTCTCTGC	AACACTCTCC	TCATGAGGAC	3900
	TTCTGTGAAA	AATGGGGGTT	GTAAACCTCT	GAGTCTGGG	GGCCACCCCA	TTTCTAATCT	3960
	CCAGAACTTG	GCCACCAACG	ACTCCACCAA	CTTCTAGTCC	TGGGACCTGG	GCCTCTGGCC	4020
	ATTGCCATAG	GCACCACTGT	CTCTGTGAG	GCAGGCGCCC	CCTCTGCCAG	GATCCTCCGA	4080
	GGTCAGCTGC	TGGGTCTGAC	CCGAGAGCCC	TGGCTGAGCG	ACGGATGAAC	GGAGTATGCA	4140
45	GACACAGGCT	TGCTTGTGAG	CAGATGGGGG	ACCCTGCGCA	GAGTCAGCAG	CGGCCCCCAT	4200
	AAGCCTGCCA	CGCTTGCATT	TATTTAGTAC	AGATGTAATG	ACAAAGGCCT	AAAGCAAACT	4260
	CCATTTGTGG	GTAAATTAACA	TTGTGCGCCC	CCCAGAAAGA	GCAGTCTCTC	GCATGATGAT	4320
	TAAAGGCCAG	GTTCGGAGGC	CTAAGTAAAC	CAACTTATCT	AGATCAATTC	CCTTACTTCT	4380
	TGTTATCTAC	TCTGAGAGAA	TTAGCTGCC	TTAGCCAAA	TCCTTTCCCG	AAGCTTTTGC	4440
50	AAAACCTCCG	AGGCTTCCAA	GGTTTGTCTC	TTTCTGTAAT	TTTTCTCACC	ACCTGACCT	4500
	ATCTCTGCA	GTACGCGCTG	TGGAGGCCTT	TGTTTTCOC	CCAGTGTCTG	CAGCCTAGAG	4560
	GCTGAGATGG	CCAGAAACAA	GGTGGTGACA	GTGGCGTGTG	CAGGCGTTGG	GAAACCCAG	4620
	GAGCTAAGG	CATGCCCAGG	CAACCAAGGA	GGACAGGAAG	GCTTCTGAGG	AGAGACCTCT	4680
	GAGGTGGGTC	TTGAGAGGGA	AGGACTTAGG	GAGGCAGAGT	GGAGGAAGTG	AGAGGACACC	4740
55	CCAAGCCAG	AGGGCGGCAG	GACCAAGGC	TCAGAAGCCA	GGGCGCTGCA	GAGGGGCTGT	4800
	GTGCCACAGG	GTGAAGAGTT	TGTGTGCGAG	AAGGGCAGGG	GGCTTGCATC	AGGGGTGACA	4860
	GCTGCTCTTT	TGTCCCAAGC	TAGCCCTCTG	ACATCCCTGG	AGAGTGGGCT	GTCCTGTGGC	4920
	TCTAAGTCAC	AGCCCCCATC	CTAACCTTGG	TGGTGCAGTG	AGGGTGGAGT	GTCCTGTGGC	4980
	AGGAGGGAAG	ACTCTTGGAG	ATGAGCCTGG	TGAAGGGATA	ATGGCATCCC	GGGCGGAGGA	5040
60	GCAGCACAGG	CAGAGGCTTG	GGGAGAGTTT	AAGGAGTGTA	GGGGAGGAAA	TGGCAGAAGA	5100
	TGAGCCAGAA	AAAGAAAGGT	TAGGCGAGGT	CCTGGAGGAC	ATGAGTGGCT	GTTTGGGCTT	5160
	TATCCAGCAG	TGGGGGAGCC	TTGGCAGGCT	TGTGGCTTAG	ATAGGTGCTT	TAGAAAGCCC	5220
	ACCAGCAGTT	GCTGGGCCAC	CCGCTGGCT	GGGTCTCTGT	CTAAGGCAGG	AAATACAGAA	5280
	ATGAGCAGGA	AAAGACCCCC	TCAAGGCTCA	CGTCTAGTGT	GGGAGACAG	AAACACAGAT	5340
65	GGGCAATATA	ACACGATGTC	TGGTTCAGT	AAGTGCAGTG	AAGAACAAGC	GAGGCTGGAT	5400
	GCAGGGAGTG	ATGGGAGGGG	CTTTGTAAAG	GGAGGTGCGG	GGAGGCTGT	CTCAGAGGAC	5460
	ACCAGAAATG	AGCGCAGGAG	CAGCACGTGG	CAGTCACATG	GCAGGCGGTT	AGGGCAGAGG	5520
	GAGCTGGGCA	GGGCACAGCA	GGGCAGGAGT	GTGTTTATG	TGTCTGGGA	ACCGCCTGGA	5580
	GGCGTCTGT	TGGCTGGAGT	GCTGCAGGTC	TCAAGGAAAT	TGTAGGAGAT	GTCTCTGAG	5640
70	TGTGATGGAA	TATAACCAAG	TTTCCAGAA	GAACCTGACAT	GATCTGACTT	AAAAAGGTCA	5700
	GTGTGGGAAA	TGGCTTGACG	GGGACAGGAG	TGGGAGCAGG	GAGATAGGAG	ACAATGTGTA	5760
	CCAGGACAGC	AGAAAGACAT	CCCGGGTAGC	CTGGAACAGG	GAGACCGGTT	GGAGTGGTGT	5820
	GCAGTCCGAT	AATGAGAGCC	GTAGGGCAAG	GCCAGCAGGA	TCCTAGAGTG	AGACGGGAGG	5880
	TAAAGTCACC	GGGACTTGGT	GTCTCCACGT	CAGGGGCAGG	GGAAAGGGAG	AGGACAAGGG	5940
75	TGACCGGGGA	GGTTAAAGAT	GGGACCGGGG	CCAGACGCGAG	TGGCTCATGC	CTGTAATCCT	6000
	AGCACTTTGG	GAGGCTGAGG	CGGGCGGATG	GCTTGAAGTC	AGGAGTTTGA	AACCGGCTCT	6060
	GCCAACATGG	TGAACCCCGG	TCTCTACTAA	AATATACAAA	AATTAGCCTG	GCGTGGTGGT	6120
	GCATGCCCTG	AGTCCAGACT	ATTCAGGAGG	CTGAGGCGAC	AAGAATCGCT	TGAACCTGGG	6180
80	AGGCGGAGGT	TGCAGTGAGC	CGAGATCGCG	CCATAGCACT	CCAGCCTTAG	CCTGGGCGAC	6240
	AGAGCGAGAC	CACATC					

Seq ID NO: 88 Protein sequence
Protein Accession #: BAA32297.1

1 11 21 31 41 51
5 VETPPQGSVH SGHLGSSVVD PHTGTGNAGE RGRGRGARV LALDSGGMDS SPSLFLIRTP 60
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ILLAGNMKE AQMLCQRHRR KSSVTDSPSS LVNRPTLGQF TEEBIHAIEVC YAECLLQRAA 180
LTFLLQSSSHG GAVRPRLHHD PSHACSCPPG PGRQHLFLQ DENMVSPIKG GIKVRNSYQT 240
YKELDSLQVS SQYCKGENHP HPEGGVKLG VAFNLTLML PTRILRLLEF VGFSGNKDYG 300
LLQLEBGASG HSPRSVLCVM LLLCYHTFLT FVLGTGNVNI EEAEKLLKPY LNRYPKGAIF 360
10 LFPAGRIEVI KGNIDAVSDG GPRGWGSLG VSQTSRKSQT CDILDRIDRW GRGGGPRENQ 420
PESRRRRGFS GRAAWEDKGG GGICGANDPD WEI

Seq ID NO: 89 DNA sequence

Nucleic Acid Accession #: AF007170

Coding sequence: 73..1725

1 11 21 31 41 51
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AGCTACCTCA AGCCCAAGAAC CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC 180
CTGGAGATGC AGGCCATGAT GACCTTTGAC CCTCAGGACA TOCTGCTTGC CGGCAACATG 240
ATGAAGGAGG CACAGATGCT GTGTGAGAGG CACCGGAGGA AGTCTTCTGT AACAGATTCC 300
TTCAGCAGCC TGTGTAACCG CCCACGCTG GGCCAAATCA CTGAAGAAGA AATCCACGCT 360
25 GAGGTCTGCT ATGCAGAGTG CCTGCTGCAG CGAGCAGCCC TGACCTTCTC GCAGGACGAG 420
AACATGTTGA GCTTCATCAA AGCGGCGATC AAAGTTGCAA ACAGCTACCA GACCTACAAAG 480
GAGCTGGACA GCTTTGTTCA GTCTTCACAA TACTGCAAGG GTGAGAACCA CCGCACTTT 540
GAAGGAGGAG TGAAGCTTGG TGTAGGGGCC TTCAACCTGA CACTGTCCAT GCTTCTACT 600
AGGATCTTGA GGCTGTTGGA GTTTGTGGGG TTTTCAGGAA ACAAGGACTA TGGGCTGCTG 660
30 CAGCTGAGAG AGGGAGCGTC AGGGCACAGC TTCGCTCTG TGCTCTGTGT CATGCTCTG 720
CTGTGCTACC ACACCTTCTC CACCTTCTGT CTGCTACTG GGAACGTCAA CATCGAGGAG 780
GCCGAGGAGC TCTTGAAGCC CTACCTGAAC CGGTACCCCTA AGGGTGCCAT CTTCCTGTT 840
TTTGACGAGG GATTGAAGT CATTAAAGGC AACATTGATG CAGCCATCCG GCGTTTCGAG 900
GAGTGCTGTG AGGCCCAGCA GCATGGAAG CAGTTTCACC ACATGTGCTA CTGGGAGCTG 960
35 ATGTGTGTCT TCACCTACAA GGGCCAGTGG AAGATGTCTT ACTTCTACGC CGACCTGCTC 1020
AGCAAGGAGA ACTGTCTGTC CAAGGCCACC TACATTACA TGAAGGCCGC CTACCTCAGC 1080
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GTGCCAGGCC TGAAGCTCAA GATTGCTGGG AAATCTCTAC CCACAGAGAA GTTTGCCATC 1200
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40 ATGATGTACA TCTGGAACGG CTACGCGGTG ATTGGGAAGC AGCCGAAACT CACGGATGGG 1320
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45 TATGACCACT ACTTGATCCC AAAGCCCTCT CTGGAGCTGG CCTGTCTGCT TATGGAGCAA 1560
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50 CCCCCCTGCC TGCCCTGCTT TTGGGGTCCA CGGCACTCC AGTTGGATGG CACAACATAG 1860
TGTATCCGCT TCTGGAACCG GCTGGCATT TCACCACTGT AGCCAAAGGC CTTTGCCAAG 1920
GGCAGAGCAG GTGGAGCCCT CTGCTGCCC TATCACACT ACGGGTACTT GCTTTTCACT 1980
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55 TCAGCAAGTT CTGAGCTTGT GTGACGGAAG GTCTTCAGA GGACCTGAGG AATGCTGGG 2220
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CCACTACCTT ACTACTACA CTTCAATTCA CTCCTTTTGT AAATTTCCAA TTTAAAAATC 2340
AAGCAGCTCT TTTTAGTGAG ATAAATCTG AGCTCTTCTG TAGAAAAATC AATCTCTACC 2400
AGTAGAAAT GCCAGGGCTT GATGGAAGAG CTGTGTAGCC CTTTCTATGC CAAAGCCAGG 2460
60 AAATTTGGGG GGCAGGAGGA GGTTCCTAGA ATCCAGTCTG TATCTTTGCT GTATGCCAAA 2520
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Seq ID NO: 90 Protein sequence

Protein Accession #: AAC39582.1

1 11 21 31 41 51
70 KEAASGKSDR RTPESSLHEA LDQOMTALDL FLTNQFSEAL SYLKPRTKES MYHSLTYATI 60
LEMQAMMTFD PODILLAGNM MKEAQMLQOR HRRKSSVTD SSSLVNRPTL GQFTTEEIHA 120
EVCYAECLLQ RAALTFLQDE NMVSFIKGGI KVRNSYQTYK ELDSLQSSQ YCKGENHPHP 180
EGGVKLGVGA FNLTLSMLPT RILRLLEFVG FSGNKDYGLL QLEEGASGHS PRSVLCVMLL 240
75 LCYHTFLTFF LGTGNVNIIE AEKLLKPYLN RYPKGAIFLP FAGRIEVIKG NIDAAIRRFE 300
ECCBAQGHKQ QFHMCYVWL MWCPTYKQSW KMSFYADLL SKENCWSKAT YIYMKAAYLS 360
MFGKEDIKPP GDDEVELFRA VPGLKLKLAG KSLPTEKFAI RKERRYFSSN PISLFPVPALE 420
MMYIWNQYAV IGKQPKLTDG ILEIITRAEE MLEKGFENEY SVDDECLVKL LKGLCLKYLG 480
RVQBAENFR SISANEKKIK YDHYLIPNAL LELALLLMEQ DRNEEAIKLL ESAKQNYKNY 540
80 SMESRTHFRI QAATLQAKSS LENSRRSMVS SVSL

Seq ID NO: 91 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 31..906

1 11 21 31 41 51
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 GACTGCGTAC TGCAGTGGGA AGAGCAGAAC TGCTCTGGGG GCGCTCTGAA TCACTTCCGC 180
 TCCGCGCCAGC CAATCTACAT GAGTCTAGCA GGCTGGACCT GTGCGGACGA CTGTAAATAT 240
 GAGTGTATGT GGGTCACCGT TGGGCTCTAC CTCCAGGAAG GTACAAAGT GCCTCAGTTC 300
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 10 TCGTTTCTCA ATGGCTTGGC CAGCCTGGTG ATGCTCTGCC GCTACCGCAC CTTCGTGCCA 420
 GCCTCTCTCC CCATGTACCA CACCTGTGTG GCCTTCGCCT GGGTGTCCCT CAATGCATGG 480
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 GACTATGGCT ACAACCTGGT GGCACACGTG GCTATTGGCC TGGTCAACGT GGTGTGGTGG 660
 15 CTGGCCTGGT GCCTGTGGAA CCAGCGGCGG CTGCTCACG TGGCAAGTG CGTGGTGGTG 720
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 AGCTTCTTGG AAGATGACAG CTTGTACCTG CTGAAGGAAT CAGAGGACAA GTTCAAGCTG 900
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 20 CCCTTCTCCC CTCAACCTTT GAGATGATTT TCTCTTTTCA ACTTCTTGA CTGGACATG 1020
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 25 GCCTCTGTG TACCTGGGAG ACCAGGGACC ACAGGCCCTTA GGGATACAGG GGTCTCCCTT 1320
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 35 TAATCACTTG TGGAGCGCCA CTTGGCCCAA GAGCCACCT GGGCGGACAG CAGGAGCTCT 1920
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 40 TTTGGGGAG AGGAAGGGG GATTGAGGG AGAAGGGGAG AAAGCTTATG GCTGGGTCTG 2220
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 45 GAGGGGAGCT ATGCTAGGAC TCCAACTCA GGAAGTGGG TGGCCTGGCG TAGCTTCTT 2520
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 AAGCCTCAA AAAAAAAAA AAAAAAAAA AAAAA

Seq ID NO: 92 Protein sequence
 Protein Accession #: Bos sequence

1 11 21 31 41 51
 55 MAGLAARLVL LAGAAALASG SQGDREPVYR DVLQCEBQN CSGALNHRF SRQPIYMSLA 60
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 MLCRYRTFVP ASSPMYHTCV AFANVSLNAW FWTVPFTRD TDLTEKMDYF CASTVILHSI 180
 YLCCVTVLGL QHPAVVSAPR ALLLLMLTVH VSYLSLIRFD YGYNLVANVA IGLNVVWVWL 240
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Seq ID NO: 93 DNA sequence
 Nucleic Acid Accession #: NM_033419.1
 Coding sequence: 18..980

1 11 21 31 41 51
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 70 TCTACATGAG TCTAGCAGGC TGGACCTGTC GGAAGAGTTC TAAATATGAG TGTATGTGG 240
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 CCTCTCCCG GTTCTGTTC TTCAAGAGC CGGCATCGGC CGTGGCTCG TTTCTCAATG 360
 GCCTGGCCAG CTTGGTGTG CTCTGCGCT ACAGCACCTT CGTGCCAGCC TCCTCCCCA 420
 TGTACACAC CTGTGTGGCC TGGCCTGGG TGTCCCTCAA TGCATGTTT TGGTCCACAG 480
 75 TTTTCCACAC CAGGACACT GACCTCACAG AGAAATGGA CTACTTCTGT GCTCCACTG 540
 TCATCTTACA CTCAATCTAC CTGTGCTGCG TCAGGACCGT GGGGCTGCG CACCCAGCTG 600
 TGGTCACTGC CTTCGGGCT CTCTGCTGC TCACTGTGAC CGTGCACGTC TCCTACCTGA 660
 GCCTCATCCG CTTGACTAT GGCTACAACC TGGTGGCCAA CGTGGCTATT GGCCTGGTCA 720
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 80 AGTGGTGTG GGTGGTCTG CTGCTGCGG GGTGTGCTT GCTGAGCTG CTTGACTTCC 840
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 5 CAGGGGGTCC CTTTCTGTTA CCACCCCCA CCTCTCTCCA GGACACCACT AGGTGGTGTCT 1440
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 10 TGTGCTGCTG TCTGTTGAG AGCTGCCAC CGTGTGTCG GAGTGTGGC CAGCTGAGT 1680
 GCATAGGTGA CAGGGCCGTG AGCATGGCC TGGGTGTGTG TGAGCTCAGG CCTAGGTGCG 1740
 CAGTGTGGAG ACGGGTGTGT TCGGGGAAGA GGTGTGGCTT CAAAGTGTGT GTGTGCAGG 1800
 GGTTGGGTGT TTAGCTGGG TTAGGGGAAC GTGTGTGCG GTGTGTGGT GCATGTGAGA 1860
 TGAGTGACTG CCGGTGAATG TGTCCACAGT TGAGAGGTTG GAGCAGGATG AGGGAATCCT 1920
 15 GTCACCATCA ATAATCACTT GTGGAGCGCC AGCTCTGCC AAGCGGCCAC CTGGGCGGAC 1980
 AGCCAGGAGC TTATCATGGC CAGGCTGCC GTGTGCATGT TCCCTGTCTG GTGCCCTTT 2040
 GCGCCCTCC TGCACACCTC ACAGGGTCCC CACACACAG TGCCCTCCAG AAGCAGCCCC 2100
 TCGGAGGCGA TGAAGGAAA ATGGGATGG CTGGGGCTCT CTCCATCCTC CTTTCTCT 2160
 TGCCCTGCGA TGGCTGGCTT TCCCTCCAA AACCTCCATT CCCCCTGCTC CAGCCCCCTT 2220
 20 GCCATAGCCT GATTTTGGGG AGGAGGAAG GCGGATTGA GGGAGAGGG GAGAAAGCTT 2280
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 CGAGCGAGG GCCACACTAT GCCTGCGCCC TGTAAAGGT GACCCCTGCC ATTTACCAGC 2400
 AGCCCTGGCA TGTCTCTGCG CCACAGGAAT AGAATGGAGG GAGCTCCAGA AACTTCCAT 2460
 CCCAAAGGCA GTCTCGTGG TTGAAGCAGA CTGGATTITT GCTCTGCCCC TGACCCCTTG 2520
 25 TCCCTCTTGG AGGAGGGGA GCTATGCTAG GACTCCAACC TCAGGACTC GGTGGCGCTG 2580
 CGCTAGCTTC TTTGATACT GAAAACCTTT AAGGTGGAG GGTGGCAAGG GATGTGCTTA 2640
 ATAAATCAAT TCCAGCCTC AAAAAAAAAA AAAAAAAAAA AA

Seq ID NO: 94 Protein sequence
 Protein Accession #: NP_219487.1

30 1 11 21 31 41 51
 MKDVGPESCG QPTPCWPSA LESVLGKASQ HLGLESGQPL YLLELNWGGT ECALSSSTGRT 60
 AACFLPISLL PTSPAALWLP EALCLPGRPG TTGLRDTGGP LLLPPPTLLQ DTRRWCHMLV 120
 35 LWPAKVHGDG PHGILRDQAA GIGKEFHPDH CPSQVPRRPH HTPFQGGSS KPRARILCCC 180
 LVESLPFCVG SVGQAEICGD RAVSMGLGVC ELRPRCAVWR RVLGSKRGCF KVCVCRGWVC

Seq ID NO: 95 DNA sequence
 Nucleic Acid Accession #: XM_090469
 Coding sequence:

40 1 11 21 31 41 51
 ATGGGGTTTG GAGACCAGGG AACGGTGGAA GGGAGCCTAG GAAAGTGGAA AGATAGCTCC 60
 45 TGCCCGGTGC TGGACAGGAC GCAGGTGAAC AAGCCCTGCC TGCTGGAGGC TGCCAAGCAC 120
 AGCCACACACC CCTTGCATGG ACAGTCGGTC AACAGCCACC CATCAGGTGC TCATCAGAAA 180
 CCACCTGAAG TGAATAATGTT TGGAGCCAGT CAAGGTTTGC TGACAAATGA AACAAACCAG 240
 TCCCTGGCAC AAGGCACAGG CTGCTCAGTG TGCTGGAGG TGAACGGCCC AGGGTTGGAA 300
 50 ATGTCTCTTC CTGGAGTGT CAGTGTCTAT GCTGGCCAGG TGGAGCACAG AAGACAAATG 360
 AACTCGCAG ATACTGACTG GGAAGTCTAG GAGGGACAG GAAGTCTAGA TTTCCCGGTG 420
 GCTGCCACAC AGGAAGACAC TTTCTTTTTC AAAGACATCA AGCACACAAG TACGTTCCAG 480
 CAATCAGTTC AGCAGCAGAA TTGCATTAC AGCCCCAGAG AAAAAACCTG TGGGAATGTC 540
 AGGGACCTTT GCGGCCACAC AAGGCAGAG GCGCCGCTTG CCTCAGCAG GCCCTGGGG 600
 55 CTCAGCGCGA GCGCGCGGCC GTCCCCAGT ACACCCATGG CGCCCTTCCC GACCTCTGAC 660
 CGCAGCTAG ACGCGCCAGG CCGCCCCCCC GGGCTGGGGA GCTCGGCAGC AGCCCTCAC 720
 TGCCTGCCCG CGGCTCCAGA AGCCACAGAA CTCTTCTTCC TGCTGCCCTT TTATCCAGAT 780
 GGCAGCCAC CACCTAAGGA CATCTTCAG ACGCTCCAG ACAAGGCACC TGGGAAGAGA 840
 CTGCATCAAG AATCACCAGG TTCAATTCCA ATAGGTTTAT GTAACAGAAC AGCTGAACCA 900
 60 TGTATCAAG GGGCTCTGGG TGTGGCTGCT GAAGCAGCAT TTCCTTACA GTTTTCCAGT 960
 GAATGA

Seq ID NO: 96 Protein sequence
 Protein Accession #: XP_090469

65 1 11 21 31 41 51
 MGFDQGTVE GSLGTSKDS CRVLDRTOVN KPCLEAAKH SPHPLHGQSV NSHPSGAHQK 60
 PFEVKMFGAS QSLTMTETNQ SLAQGTGCSV CWFVNGPGLS MSLPGVLSAD AGQVEHRRM 120
 NSADTDWGT EGPGLDFAV AAHQEDTFFL KDIKHTSTFR QSVQQNCIY SPREKPGNV 180
 70 RAPCAPPRRE APLALSRPWR LSRSPAPSPR TPMAPPTSD RELDARGPPP GLRSSAAAPH 240
 CLPAAPFAQK LFFLLPLYPD GSPFPKDILO TLQHKAPGRK LQESPGSPF IGLCNRTAEP 300
 CIKGAIGVAA EAPFHLQFS E

Seq ID NO: 97 DNA sequence
 Nucleic Acid Accession #: NM_003474.2
 Coding sequence: 37..3036

75 1 11 21 31 41 51
 80 CACTAAGCT CTCTCTAGTC CCGGGGCCAA CTGGACAGT TTGCTCATTT ATTGCAACGG 60
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 CTTTITTAATA ATGAAAGGC TAGAAGAGCT CAGCGCGCGC GCGGGCGGTG CGGAGGGGCT 180
 CCGGAGCTGA CTCGCGGAGG CAGGAAATCC CTCGGTCCG GACGCGCGGC CCGCTCGGC 240
 GCCCGGTGG GATGCTGAG CGCTGCGCGC CCGGCGCGAG AGCTGCTGCA CTGAAGGCG 300

	GCGACGATGG	CAGCGCGCCC	GCTGCCCGTG	TCCCCCGCCC	GCGCCCTCCT	GCTCGCCCTG	360
	GCCGGTGCTC	TGCTCGCGCC	CTGCGAGGCC	CGAGGGGTGA	GCTTATGGAA	CGAAGGAAGA	420
	GCTGATGAAG	TGTGCACTGC	CTCTGTTGCG	AGTGGGGACC	TCTGGATCCC	AGTGAAGAGC	480
5	TTCGACTCCA	AGAATCATCC	AGAAGTGCTG	AATATTGCGA	TACAAOCGGA	AAGCAAAAGAA	540
	CTGATCATAA	ATCTGSAAG	AAATGAAGGT	CTCATTGCCA	GCAAGTTTCA	GGAAACCCAC	600
	TATCTGCAAG	ACGGTACTGA	TGTCTCCCTC	GCTCGAAATT	ACACGGTAAT	TCTGGGTAC	660
	TGTTACTACC	ATGGACATGT	ACGGGGATAT	TCTGATTTCAG	CAGTCAGTCT	CAGCACGTGT	720
	TCTGGTCTCA	GGGGACTTAT	TGTGTTTGAA	AATGAAAGCT	ATGCTCTAGA	ACCAATGAAA	780
10	AGTGCAACCA	ACAGATACAA	ACTCTTCCCA	CGCAAGAAAGC	TGAAAAGCGT	CCGGGGATCA	840
	TGTGGATCAC	ATCACACAC	ACCAAACCTC	GCTGCAAAGA	ATGTGTTTCC	ACCACCTCT	900
	CAGACATGGG	CAAGAAAGCA	TAAAAGAGAG	ACCCTCAAGG	CAACTAAGTA	TGTGGAGCTG	960
	GTGATCGTGG	CAGACAAACG	AGAGTTTCAG	AGGCAAGGAA	AAGATCTGGA	AAAAGTTAAG	1020
	CAGCGATTAA	TAGAGATTGC	TAATCACGTT	GACAAGTTT	ACAGACCACT	GAACATTCCG	1080
15	ATCGTGTGG	TAGGCGTGGG	AGTGTGGAAT	GACATGGACA	AATGCTCTGT	AAGTCAGGAC	1140
	CCATTACCA	ATGOGCAGCT	TGTGAGTGGG	GTATTATTCC	AAGGGACCA	CATCGGCATG	1200
	TCCCATGACA	ATGOGCAGCT	TGTGAGTGGG	GTATTATTCC	AAGGGACCA	CATCGGCATG	1260
	GCCCCAATCA	TGAGCATGTG	CACGGCAGAC	CAGTCTGGGG	GAATTGTCT	GGACCATTC	1320
	GACAATCCCC	TGGGTGACG	CGTGACCTCG	GCACATGAGC	TGGGCCACAA	TTTCGGGATG	1380
20	AATCATGACA	CATGAGACAG	GGGCTGTAGC	TGTCAAATGG	CGGTGTAGAA	AGGAGGCTGC	1440
	ATCATGAAGC	CTTCCACCGG	GTACCCATT	CCCATGGTGT	TCAGCAGTTG	CAGCAGGAAG	1500
	GACTTGGAGA	CCAGCCTGGA	GAAGGAATG	GGGCTGTGCC	TGTTTAACT	GCCGGAAGTC	1560
	AGGGAGTCTT	TCGGGGGCCA	GAAGTGTGGG	AACAGATTG	TGGAAGAAGG	AGAGGAGTGT	1620
	GACTGTGGGG	AGCCAGAGGA	ATGTATGAAT	CGCTGTGCA	ATGCCACCA	CTGTACCTCG	1680
25	AAGCCGAGCG	CTGTGTGCGC	ACATGGGCTG	TGCTGTGAAG	ACTGCCAGCT	GAAGCCTGCA	1740
	GGAAACAGCG	CGAGGACTCT	CAGCAACTCC	TGTGACCTCC	CAGAGTTCTG	CACAGGGGCC	1800
	AGCCCTCACT	GCCAGCCCAA	CGTGTACTCG	CAOGATGGGC	ACTCATGTCA	GGATGTGGAC	1860
	GGCTACTGCT	ACAATGCGAT	CTGCCAGACT	CAOGAGCAGC	AGTGTGTCTC	ACTCTGGGGA	1920
	CCAGGTGCTA	AACCTGCCCC	TGGGATCTGC	TTTGAGAGAG	TCAATTCTGC	AGGTGATCCT	1980
30	TATGCAACT	GTGGCAAAGT	CTCGAAGAGT	TCCTTTGCCA	AATGCGAGAT	GAGAGATGCT	2040
	AAATGTGGAA	AAATCCAGTG	TCAAGGAGGT	GCCAGCCGGC	CAGTCATTGG	TACCAATGCC	2100
	GTTCCTCATG	AAACAAACAT	CCCCCTGCA	CAAGGAGGCC	GGATTCTGTG	CCGGGGGACC	2160
	CACGTGTACT	TGGGCGATGA	CATGCGCGAC	CCAGGGCTTG	TGCTTGCAAG	CACAAAGTGT	2220
	GCAGATGGAA	AAATCTGCTT	GAATCGTCAA	TGTCAAATA	TGATGTCTT	TGGGTTTCA	2280
35	GAGTGTGCAA	TGCAGTGCCA	CGCGAGAGGG	GTGTGCAACA	ACAGGAAGAA	CTGCCACTGC	2340
	GAGGCCCACT	GGGCACCTCC	CTTCTGTGAC	AAGTTTGGCT	TTGGAGGAAG	CACAGACAGC	2400
	GGCCCCATCC	GGCAAGCAGA	TAAACCAAGT	TTAACCATAG	GAATTCCTGT	GACCATCCTG	2460
	TGTTCTTCTG	CTGCCGATT	TGTGTTTAT	CTCAAAAGGA	AGACCTGTAT	ACGACTGCTG	2520
	TTTACAAATA	AGAAGACCA	CATTGAAAAA	CTAAGGTGTG	TGCGCCCTTC	CCGGCCACCC	2580
40	CGTGGCTTCC	AACCTGTGCA	GGCTCACCTC	GGCCACCTTG	GAAGGCGCT	GATGAGGAAG	2640
	CCGCCAGATT	CCTACCCACC	GAAGGACAA	CCCAGGAGAT	TGCTGCAGTG	TCAGAATGTT	2700
	GACATCAGCA	GACCCCTCAA	CGGCTGAAT	GTCCCTCAGC	CCCAGTCAAC	TCAGCGAGTG	2760
	CTTCTTCCCC	TCCACCGGGC	CCCACTGTGA	CCTAGGCTCC	CTGCCAGACC	CCTGCCAGCC	2820
	AAGCCTGCAC	TTAGGCAGGC	CCAGGGGACC	TGTAAGCCAA	ACCCCTTCA	GAAGCCTCTG	2880
45	CCTGCAGATC	CTCTGGCCAG	AACAACCTGG	CTCACTCATG	CCCTTGGCCAG	GACCCACAGG	2940
	CAATGGGAGA	CTGGGCTCCG	CCTGGCACCC	CTCAGACCTG	CTCCACAATA	TCCACACCAA	3000
	GTGCCCAGAT	CCACCCACAC	CGCCTATATT	AAGTGAGAAG	CCGACACCTT	TTTTCAACAG	3060
	TGAAGACAGA	AGTTTGCACT	ATCTTTCAGC	TCCAGTTGGA	GTTTTGTGTA	CCAACCTTTA	3120
	GGATTTTCTT	TAATGTTTAA	AACATCATTA	CTATAAGAAC	TTTGAGCTAC	TGCCCTCAGT	3180
50	GCTGTGCTGT	GCTATGCTGC	TCTGTCTACT	TGCACAGGTA	CTTGTAATAT	ATTAATTTAT	3240
	GCAGAATGTT	GATTACAGTG	CAGTGGGCTG	TAGTAGGCAT	TTTTACCATC	ACTGAGTTT	3300
	CCATGGCAGG	AAGGCTTGT	GTGCTTTTAG	TATTTTAGTG	AACTTGAAT	ATCCTGCTTG	3360
	ATGGGATTCT	GGACAGGATG	TGTTTGCTTT	CTGATCAAGG	CCTTAITGGA	AAGCAGTCCC	3420
	CCAACTACCC	CCAGCTGTGC	TTATGGTACC	AGATGCAAGT	CAAGAGATCC	CAAGTAGAAT	3480
55	CTCAGTTGAT	TTCTGCGATT	CCCCATCTCA	GGCCAGAGCC	AAGGGGCTTC	AGGTCCAGGC	3540
	TGTGTTTGGC	TTTCAGGGAG	GCCCTGTGCC	CCTTGACAAC	TGGCAGGCAG	GCTCCCAGGG	3600
	ACACCTGGGA	GAATCTGGC	TTCTGGCCAG	GAAGCTTGG	TGAGAACCTG	GGTTGCAGAC	3660
	AGGAATCTTA	AGGTGTAGCC	ACACCAGGAT	AGAGACTGGA	ACACTAGACA	AGCCAGAACT	3720
	TGACCTCTGAG	CTGACCAGCC	GTTAGCATGT	TTGGAAGGGG	TCTGTAGTGT	CACTCAAGGC	3780
60	GGTGCTTGAT	AGAAATGCCA	AGCACTTCTT	TTTCTCGCTG	TCCTTCTTAG	AGCACTGCCA	3840
	CCAGTAGGTT	ATTAGCTTGG	GGAAAGGTGG	TGTTTCTGTA	AGAAACCTAC	TGCCCAGGCA	3900
	CTGCAAACCG	CCACCTCCCT	ATACTGCTTG	GAGCTGAGCA	AATCACCACA	AACTGTAAAT	3960
	CAATGATCCT	GTATTCAGAC	AGATGAGGAC	TTTCCATGGG	ACCACAATA	TTTTCAGATG	4020
	TGAACCATTA	ACCAGATCTA	GTCAATCAAG	TCTGTTTACT	GCAAGGTTCA	ACTTATTAAC	4080
65	AATTAGGCAG	ACTCTTTATG	CTTGCAAAAA	CTACAACCAA	TGGAATGTGA	TGTTTATGGG	4140
	TATAGTTTAT	GTCTGCTATC	ATTATTCGTA	GATATTGGAC	AAAGAACCTT	CTCTATGGGG	4200
	CATCCTCTTT	TTCCAACCTG	GCTGCAGGAA	TCITTTAAAG	ATGCTTTTAA	CAGAGTCTGA	4260
	ACCTATTCTT	TAAACACTTG	CAACCTACCT	GTTGAGCATC	ACAGAAATGT	ATAAGGAAT	4320
	CAACTTGCTT	ATCAACTTCC	TAAATATTAT	GAGATGTGGC	TTGGGCGACA	TCCCTTGAA	4380
70	CTCTTCACTC	TTCAATATGC	TGACTAGGGA	GCCATGTTTC	ACAAGGTCTT	TAAAGTGACT	4440
	AATGGCATGA	GAATACAAA	AATACTCAGA	TAAGGTAAAA	TGCCATGATG	CCTCTGTCTT	4500
	CTGGACCTGT	TTTCACATTA	GAAGCAAAAT	GACAACAGTT	ACATAATTCA	CTCTGAGTGT	4560
	TTTATGAGAA	AGCTTCTT	TGGGGTCAAC	AGTTTTCCTA	TGCTTTGAAA	CAGAAAAATA	4620
	TGTACCAAGA	ATCTTGGTTT	GCCTTCCAGA	AAACAAAAC	GCAATTCAC	TTCCCGGTGT	4680
75	TCCCACTGT	ATCTAGGCAA	CATAGTATTC	ATGACTATGG	ATAAACTAAA	CAGTGACAC	4740
	AAACACACAC	AAAAGGGAAC	CCAGCTCTAA	TACATTCCAA	CTCGTATAGC	ATGCATCTGT	4800
	TATTTCTATA	GTTATTAAAT	TCTTTAAAT	GTAAGCCAT	GCTGGAAAT	AATAGTCTG	4860
	AGATACATAT	AGAATTACTG	TAACTGATTA	CACTTGTGTA	TTGTACTAAA	GCCAAACATA	4920
	TATATACAT	TAAAAGGTT	TACGAATTT	TATGGTGCAT	TACGTGGGCA	TTGTCTTTT	4980
80	AGATGCCAA	ATCCTTAGAT	CTGGCATGTT	AGCCCTCCT	CCAATTATA	GAGGATATGA	5040
	ACCAAAAAA	AAAAAAA	AA				

Seq ID NO: 98 Protein sequence
Protein Accession #: NP_003465

1 11 21 31 41 51
 5 MAARPLPVSP ARALLLALAG ALLAPCEARG VSLWNEGRAD EVVSASVRSR DLWIPVKSPD 60
 SKNHPVVLNI RLQRESKELI INLERNEGLI ASSFTETHYL QDGTDVSLAR NYTVILGHYCY 120
 YHGHVRGYSD SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRVYKLPAP KLKSVRGSOG 180
 SHENTPNLAA KNVFPPPSQT WARRHKRETL KATKYVELVI VADNREFORQ GKDLKVKQR 240
 LIRIANHVDK FYRPLNIRIV LVGVEVWDM DKCSVSQDPP TSLHEFLDNR KMKLLPRKSH 300
 DNAQLVSGVY FQGTITIGMAP IMSMCTADQS GGIVMDHSDN PLGAAVTLAR ELGHNFGMNH 360
 10 DTLDRGCSQ MAVKGGCICM NASTGYPPFM VPSSCSRKDL ETSLEKMGV CLFNLPEVRE 420
 SPGGQKQGNR FVEGESEDC GEPEBOMNRC CNATTCTLKP DAVCAHGLCC EDCQLKPAQT 480
 ACRDSSNSCD LPEFCTGASP HCPANVYLHD GHSCQDQVDGY CYNGICQTHE QQCVTLMGPG 540
 AKPAPGICFE RVNSAGDPYG NCGKVSKESS AKCEMRDAKC GKIQCQGGAS RPIVGTNAVS 600
 IETNIPLOQG GRILCRGTHV YLGDDMPDPG LVLAGTKCAD GKI CLNRQCC NISVFGVHEC 660
 15 AMQCHGRVC NNRKNCHCEA HWAPPFCDKF GFGGSTDSGP IRQADNQGLT IGLVLTILCL 720
 LAAGFVVYLK RKTILIRLLPT NKKTITIEKLR CVRPSRPPRG PQPQAHGLH LGKGLMRKPP 780
 DSYPPKDNFR RLLQCCNVDI SRPLNGLNVP QPQSTQRVLP PLHRAPRAPS VPARPLPAKP 840
 ALRQAGQTCR PNPPQKPLPA DPLARTTLT HALARTPGQM ETGLRLAPLR PAPQYPHQVP 900
 RSTHTAYIK

20 Seq ID NO: 99 DNA sequence
 Nucleic Acid Accession #: NM_003714
 Coding sequence: 135..1043

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 TAATACCAAG AACCATGTGT GCGAGCGGCG TGGGCCAGTT CATGACCCCTG GCTTTGGTGT 180
 30 TGGCCACCTT TGACCGGCGC CGGGGGACCG ACGCCACCAA CCCACCGGAG GGTCCCAAG 240
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 ATGCCACGG CAAGTCATTC ATCAAAGACG CCTTGAATG TAAGGCCAC GCTCTCGGCG 480
 ACAGGTTCGG CTGCATAAGC CGGAAGTGCC CGGCCATCAG GGAAATGTGT TCCAGTTCG 540
 35 AGCGGGAATG CTACCTCAAG CACGACCTGT GCGCGGCTGC CCAGGAGAAC ACCCGGGTGA 600
 TAGTGGAGAT GATCCATTTC AAGGACTTGC TGCTGCAGGA ACCCTACGTG GACCTCGTGA 660
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 40 GGGCCCCACA CGGGGAAGCA GGACATCACC TCCAGAGGCC CAGCAGTAGG GAGACTGGCC 900
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 45 GTCCATTTC TTATCTATGG ACATTCCAAA ACATTTCACA TTAGAGAGGG GGGATGTAC 1140
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 50 GCAGCAGCCT CTGGTGTGT CTGCGGGA GTCAGGGCG CTGGATTCCA GGACAGGAGT 1500
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 55 TGTCTGGCT GGGGGGGACA CTGTCCAAG GAGTGGCCCC TATGAGTTTA TATTTTAAOC 1740
 ACTGCTTCAA ATCTCGATT CACTTTTTT ATTTATCCAG TTATATCTAC ATATCTGTCA 1800
 TCTAAATAAA TGGCTTTCAA ACAAGCAAC TGGGTCAAT AAACCACTC AAAGGGGGT 1860
 TAAAAAATAA AAAACCAAGC CATCCTTTGA GGCTGATTIT TCTTTTTTT AAGTTCTATT 1920
 TTAAGAGCTA TCAACAGCG ACATAGCCAT ACATCTGACT GCCTGACATG GACTCCTGCC 1980
 60 CACTTGGGG AAACCTTATA CCCAGAGGAA AATACACACC TGGGGAGTAC ATTTGACAAA 2040
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 GAAGAAGAG AATGAAGACT ACTTAGTAAT TCCCATCAGG AAATGCTGAC CTTTACATA 2220
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 65 TTTAGCAATA AGGAGAGGAG TCCAAGGGGA CAAATAAAG CAGAGAGAGA GAGAGAGAGA 2340
 GGGAGAGGAA GAAAGAGAG AGAGAAAAGA GCCTCGTGCC

Seq ID NO: 100 Protein sequence
 Protein Accession #: NP_003705

70 1 11 21 31 41 51
 MCAERLQFM TLALVLATPD PARGTDATNP PEGPQDRSSQ QKGRSLQNT AEIQHCLVNA 60
 GDVCGGVFEC PENNSCEIRG LHGICMTFLH NAGKFDAGK SFIKDALCKC AHALRRHFGC 120
 75 ISRKCPAIRE MVSQQLRECY LKHDLCARAAQ ENTRVIVEMI HFKDLLLHEP YVDLVNLLLT 180
 CGEEVKRAIT HSVQVQCEQN NGSLSILSF CTSIAIQKPT APPERQPOVD RTKLSSRAHFG 240
 EAGHHLPEPS SRETGRGAKG ERGSKSHFNA HARGRVGGLG AQGPSGSSEW EDEQSEYSIDI 300
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80 Seq ID NO: 101 DNA sequence
 Nucleic Acid Accession #: NM_005940
 Coding sequence: 23..1489

1 11 21 31 41 51

5
10
15
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35
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CGCCCTCTG CCCCGATGCT TGCTGCTGCT GCTCCAGCG CGCCGCTGC TGGCCCGGCG 120
TCTGCGCGG GACGTCCACC ACCTCCATGC CGAGAGGAGG GGGCCACAGC CCTGGCATGC 180
AGCCCTGCC AGTAGCCCGG CACCTGCCCC TGCCACGCGA GAAGCCCCCG GGCTGCCAG 240
CAGCCTCAGS CTTCCCGCT GTGGCGTGCC CGACCCATCT GATGGGCTGA GTGCCCGCAA 300
CCGACAGAAG AGGTTCTGTC TTCTGGCGG GCGCTGGGAG AAGACGAGCC TCACCTACAG 360
GATCCTTCGG TTCCCATGGC AGTTGGTGCA GGAGCAGGTG CGGCAGACGA TGGCAGAGGC 420
CCTAAAGGTA TGGAGCGATG TGACGCCACT CACCTTTACT GAGGTGCAGG AGGCCCTGTC 480
TGACATCATG ATCGACTTCG CCAGGTACTG GCATGGGGAC GACCTGCCGT TTGATGGGCC 540
TGGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC CGAGAAGGGG ATGTCCACTT 600
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CATTGGTTC TTCCAAAGTG CTCAGTACTG GGTGTACGAG GTCCATGCTG CCTTGGTCTG 1200
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ATGCCCTCAG GGTGTCTGAC CCCTGCCAGG CCAAGAATAT CAGGCTAGAG ACCCATGGCC 1620
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AGCGACTGTC TCAGACTGGG CAGGGAGGCT TTGCGATGAC TTAAGAGGAA GGGCAGTCTT 1800
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GTTACAGTGC AAATGGGAG GGGTATTCTT CATGCAGGAG ACCCCAGGCC CTGAGGCTGT 2160
CAACATACCT CAATCTGTC CCAGGCCGGA TCCTCTGTAA GCCCTTTTTC CAGCACTGCT 2220
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Seq ID NO: 102 Protein sequence
Protein Accession #: NP_005931

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1 11 21 31 41 51
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LVQEQVRQTM AEALKVHSDV TPLTFTEVHE GRADIMIDFA RYWHGDDLPF DPGGILAH 180
FFPKTHREGD VHFVDYDETWT IGDDQGTDL LQVAHEFHVH LGLQHTTAAK AIMSAPYTFR 240
YPLSLSPDDC RGVLHLYGQFP WPTVTSRTPA LSPQAGIDTN EIAPLEPDAP PDACEASFDA 300
VSTLRGLRFF FKAGFVWRLR GQQLQPGYPA LASRHQWGLF SPVDAAPEDA QGHIWFFQGA 360
QYVWYDGEKP VLGPAPLTEL GLVRFVPHAA LVWGPENKI YFPRGRDYWR FHPSTRRVD 420
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Seq ID NO: 103 DNA sequence
Nucleic Acid Accession #: NM_033151.2
Coding sequence: 351..4499

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 Protein Accession #: NP_149163.2

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 PILIIPKILE YSEBQLGNVV HGVGLCFALF LSECVKSLSF SSSWIINQRT AIRFRAAVSS 240
 70 FAFELKIQFK SVIHITSGBA ISFPTGDVNY LFBGVCYGPL VLITCASLVI CSISSYPIIG 300
 YTAFAIALCY LLVFPPLAVFM TRMAVKAQHH TSEVSDQRI RVTSEVLTCIK LIKMYTWKFP 360
 FAKIIEDLRR KERKLEKCG LVQSLTSITL FIIPVTAVAT VWLIHTSLKL KLTASMAFSM 420
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 LSAVDAHVGK HIPEECIKKT LRKTVVLVT HQLQYLEFCG QIILLENGRI CBNTHSELM 720
 QKRGYKQLI QRMKEATSD MLQDTAKIAE KPKVBSQALA TSLESLSNGN AVPEHQLTQE 780
 EEMEESLSW RVVHHYIQA GGYMVSCIIF FPFVVLVFLT IFSFWLSYV LEQSGTNS 840
 80 RESNGTMADL GNIADNPQLS FYQLVYGLNA LLLICVGVCS SGIFTKVTRK ASTALHNKLF 900
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 YILLMGAIM VICPIYMMF KKAIGVFKRL ENYSRSLPLS HILNLSQLGS SIHYGKTED 1020
 FISQFRLTD AQNNYLLPL SSTRWMLRL EIMTNLVTIA VALPVAFGIS STPYSPKMA 1080
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 IIPQDHYMKY RDNTPTVLHG INLTIRGHEV VGIVGRTGSG KSLGLMALFR LVEPMAGRIL 1200

IDGVDICISIG LEDLRSLSV IPQDPVLLSG TIRFNLDPPD RHTDQIWDIA LERTFLTKAI 1260
 SKFPKLIHTD VVENGNNFSV GERQLLCIAR AVLRNSKIIL IDEATASIDM ETDLIQRTI 1320
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Seq ID NO: 105 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..4043

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TGGGGGAAGT	ATGATGCTGC	CTTGAGAAC	ATGATTCCCT	TCCGTCCCAA	GCCGAGGTTT	240
CTGCCCCCCC	AGCCCCTGGA	CAATGCTGGC	CTGTTCTCCT	ACCTCACCGT	GTCATGGCTC	300
ACCCCGCTCA	TGATCCAAAG	CTTACGGAGT	CGCTTAGATG	AGAACACCAT	CCCTCCACTG	360
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ACCGTGCTTC	ACGGCATCAA	CCTGACCATC	CGCGGCCACG	AAGTGGTGGG	CATCGTGGGA	3420
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Seq ID NO: 106 Protein sequence
 Protein Accession #: Eos sequence

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	SVHDASDKNV	QRHRLWEESE	VSRREGIEKAS	VLLVMLRFQR	TRLIFDALLG	ICPCIASVLG	180
	PILIIIPKILE	YSEDLGNVNV	HGVGLCPALF	LSECVKSLSF	SSSWIINQRT	AIRFRAAVSS	240
	FAPEKLIQFK	SVIHITSGBA	ISPFITGDVNY	LFEGVCYGPL	VLITCASLVI	CSISSYFIIG	300
	YTAPIAILCY	LLVPLAVFPM	TRMAVKAQHH	TSEVSDQIR	VTSEVLTCIK	LIKMYTWEKP	360
10	FAKIIIEGMES	LTPCSKPGDG	MAPSMLASLN	LLRLSVFPVP	IAVKGLTNSK	SAVMRPFKKPF	420
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	PREEGNSLGP	ELHKINLVVS	KGMMLGVCGN	TGSGKSSLLS	AILEMHILLE	GSVGVOGSLA	540
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	SQALATSLRE	SLNGNAVPEH	QLTQSEEMEE	GSLSWRVYHH	YIQAAGGYMV	SCIIFFPVVL	780
	IVFLTIFPSW	WLSYWLBOQS	GTNSSRESNG	TMADLGNIA	NPQLSFYQLV	YGLNALLLIC	840
	VGVCCSGIFT	KVTRKASTAL	HNKLFNKVFR	CPMSFFDTIP	IGRLNCFAG	DLEQLDQLLP	900
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	LVTLAVALPV	AFGISSTPYS	PKVMAVINVL	QLASSPQATA	RIGLEBAQF	TAVERILQYM	1080
	KMCVSEAPLH	MEGTSCPDGW	PQHGEIIFQD	YHMKYRDNT	TVLHGINTLI	RGHEVVGIVG	1140
	RTSGSGKSLG	MALFRLVEPM	AGRILIDGVD	ICSIGLEDLR	SKLSVIPQDP	VLLSGTIRFN	1200
	LDPFDRHTDQ	QIWALERTF	LTKALSFKPK	KLHTDVVENG	GNFVSVERQL	LCIARAVLRN	1260
25	SKILLIDEAT	ASIDMETDTL	IQRTIREAFQ	GCTVLVIAHR	VTTVLNCDHI	LVMGNGKVVE	1320
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Seq ID NO: 107 DNA sequence

Nucleic Acid Accession #: NM_024022

Coding sequence: 202..1563

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	AGAGGTCCGT	AAATAGTCAC	CATGGGGGAA	AATGATCCGC	CTGCTGTGTA	AGCCCCCTTC	240
	TCATTCCGAT	CGCTTTTGGG	CCTTGATGAT	TTGAAAATAA	GTCTGTGTGC	ACCATGATGCA	300
	GATGCTGTGT	CTGCACAGAT	CCTGTCACTG	CTGCCAATGA	AGTTTTTTCC	AATCATCGTC	360
	ATTGGGATCA	TGCAATTGAT	ATTAGCACTG	GCCATTGTGC	TGGGCATCCA	CTTCGACTGC	420
40	TCAGGGAAGT	ACAGATGTCT	CTCATCCTTT	AAGTGTATCG	AGCTGATAGC	TCGATGTGAC	480
	GGAGTCTCGG	ATTCGAAAGA	CGGGGAGGAC	GAGTACCGCT	GTGTCCGGGT	GGGTGTGTGAG	540
	AATGCCGTGC	TCCAGGTGTT	CACAGCTGCT	TCGTGGAAGA	CCATGTGTCTC	CGATGACTGG	600
	AAGGGTCACT	AGCCTAATGT	TGCCGTGTCC	CAACTGGGTT	TCCCAAGCTA	TGTGAGTTCA	660
45	GATAACCTCA	GAGTGAGCTC	GCTGGAGGGG	CAGTTCGGGG	AGGAGTTTGT	GTCCATCGAT	720
	CACCTCTTGC	CAGATGACAA	GGTGACTGCA	TTACACCACT	CAGTATATGT	GAGGGAGGGA	780
	TGTGCTCTCG	GCCACGTGGT	TACCTTGACG	TGCACAGCCT	GTGGTCATAG	AAGGGGCTAC	840
	AGCTCACGCA	TGCTGGGTGG	AAACATGTCC	TTGCTCTGCG	AGTGGCCCTG	GCAGGCCAGC	900
	CTTCAGTTCC	AGGGCTACCA	CCTGTGCGGG	GGCTCTGTCA	TCACGCCCTC	GTGGATCATC	960
50	ACTGCTGCAC	ACTGTGTTTA	TGACTTGTAC	CTCCCAAGT	CATGGACCAT	CCAGGTGGGT	1020
	CTAGTTTCCC	TGTTGGACAA	TCCAGCCCCA	TCCCACTTGG	TGGAGAAGAT	TGCTACCAAC	1080
	AGCAAGTACA	AGCCAAAGAG	GCTGGGCAAT	GACATCGCCC	TTATGAAGCT	GGCCGGGCCA	1140
	CTCAGCTTCA	ATGAATGAT	CCAGCCTGTG	TGCTGCCCCA	ACTCTGAAGA	GAACCTCCCC	1200
	GATGGAAAAG	TGTGTGGGAC	GTCAAGATGG	GGGCGCACAG	AGGATGGAGG	TGACGCTTCC	1260
55	CCTGTCTCTGA	ACCACCGCGC	CGTCCCTTTG	ATTTCACAAC	AGATCTGCAA	CCACAGGGAC	1320
	GTGTACGGTG	GCATCATCTC	CCCTCCATG	CTCTGCGCGG	GCTACCTGAC	GGGTGGCGTG	1380
	GACAGCTGCC	AGGGGGACAG	CGGGGGCCCC	CTGTGTGTGC	AAGAGAGGAG	GCTGTGGGAG	1440
	TTAGTGGGAG	CGACCACTTT	TGGCATCGGC	TGCGCAGAGG	TGAACAAGCC	TGGGGTGTAC	1500
	ACCCGTGTCA	CCTCCTTCTC	GGACTGTGAT	CAOAGACAGA	TGGAGAGAGA	CCTAAAAACC	1560
60	TGAAGAGGAA	GGGACAAAGT	AGCCACCTGA	GTTCTTGAGG	TGATGAAGAC	AGCCCGATCC	1620
	TCCCTGGGAC	TCCGTGTGAT	GAACCTGCAC	ACGAGCAGAC	ACCCCTTGAG	CTCTGAGTTC	1680
	CGGCACCACT	AGCAGGCCCG	AAAGAGGCAC	CCTTCCATCT	GATTCCAGCA	CAACCTTCAA	1740
	GCTGCTTTT	GTTTTGTGTT	TTTTTGAGGT	GGAGTCTCGC	TCTGTGTCCC	AGGCTGGAGT	1800
	GCAGTGGGGA	AATCCCTGCT	CACTGCAGCC	TCCGCTTCCC	TGGTTCAGAC	GATTCTCTTG	1860
65	CCTCAGCTTC	CCAGTAGACT	GGGACCAAG	GTGCCCCCA	CCACACCCAA	CTAATTTTGT	1920
	TATTTTATAGT	AGAGACAGGG	TTTCAACATG	TTGGCCAGGC	TGCTCTCAAA	CCCTGACCT	1980
	CAAATGATGT	GCCTGCTTCA	GCCTCCCA	GTGCTGGGAT	TACAGGCATG	GGCCACCAAG	2040
	CCTAGCCTCA	CGCTCCTTTC	TGATCTTCAC	TAAGAACAAC	AGAAGCAGCA	ACTTGCAAGG	2100
	GCGGCCCTTC	CCACTGGTCC	ATCTGGTTTT	CTCTCCAGGG	GTCTTGCAAA	ATTCTGACG	2160
70	AGATAAGCAA	TATGTGTACC	TCACGTGCAA	AGCCACCAAC	AGCCACTCAG	AAAAGACGCA	2220
	CCAGCCCAAG	AGTGACAGAC	TGCAGTCACT	GCAAGTTTTT	ATCTCTAGGG	ACCAGAACCA	2280
	AACCCACCTT	TTCTACTTCC	AAGACTTATT	TTACATGTG	GGGAGGTIAA	TCTAGGAATG	2340
	ACTCGTTTAA	GGCCTATTTC	CATGATTTC	TTGTAGCAIT	TGTTGCTTGA	CGTATTATTG	2400
75	TCCTTTGATT	CCAAATAATA	TGTTTCTTTC	CCTCAAAAAA	AAAAAAAAAA	AAAAAAAAAA	2460
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Seq ID NO: 108 Protein sequence

Protein Accession #: NP_076927

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	TAASWKTMCS	DMWKGHYANV	ACAQLGPPSY	VSSDNLRVSS	LEGQFREEFV	SIDHLLPDDK	180
	VTALHHSVYV	REGCASGRHV	TLQCTACGHR	RGYSSRIVGG	NMSLLSQNPW	QASLQPGGYH	240

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 LGNDIALMKL AGPLTFNEMI QPVCLPNSSE NFPDGVKVCWT SGWGATEDGG DASPVLNHAA 360
 VPLISNKICN HRDVGIIIS PSMLCAGYLT GGVDSCQGDS GGFLVCQERR LWKLVGATSF 420
 GIGCAEVNKP GYVTRVTSFL DWIHBQMERD LKT

Seq ID NO: 109 DNA sequence
 Nucleic Acid Accession #: NM_000493.2
 Coding sequence: 97..2139

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 ACAGGCATAA AAGGCCACT ACCTCAACACC AAGACACAGT TCTTCATTCC CTACACCATA 240
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 CGGGCTGGAA TTTCTGTGCC AGGAAACCT GGACCAACAG GACCCACAGG AGCCCAAGGA 600
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 CCAGGTCCCC AAGGCCCTCC TGGGGAACGA GGGCCAGGAG GCATTGGAAA GCCAGGAGCT 900
 GCTGGAGCCC CAGGCCACCC AGGGATTCCA GGAAACAAAG GTCTCCCTGG GGCTCCAGGA 960
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 GAAAGAGGAC CTGCTGGCCT TCCTGGGGGT CAGGGTGCCA AAGGGGAACA AGGCCAGCA 1080
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 AAAGGTGATC CTGAGTTGG AGGACCTCTC GTCTCTCCAG GCGCTGTGGG CCCAGCAGGA 1380
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 CCCAAATAT TGAAGTTCAT CTGAAATGCA AGGTGCTTTC ATCAATGAAC CTTTCAAAA 2820
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 GACCTATCT TATTAGTTA ACACAAGTG GATTAAATTG ATTTCTTTAA TTCCTTATTG 2940
 AATCTTATG GATATGATT TCTGGATTG CAGAACATTA GCACATGTAC CTTGTGCTC 3000
 CCATTCAGT GAAGTTATA TTTACACTGA GGGTTTCAA ATTGACTAG AAGTGGAGAT 3060
 ATATTATTTA TTTATGCACT GTACTGTATT TTTATTTGC TGTTTAAAC TTTTAAAGCT 3120
 TGCTCACTT ATTAAGCAC AAAATGTTT ACCTACTCT TATTACGAC ACAATAAAT 3180
 AACATCAATA GATTTTATAG CTGAATTAAT TTGAAAGCAG CAATTGCTG TTTCAACCA 3240
 TTCTTTCAAG GCTTTTCTT CGACCAATA AAATAACATC AATAG

Seq ID NO: 110 Protein sequence
 Protein Accession #: NP_000484.2

1 11 21 31 41 51
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 GPYGPKGIDV PAGLPGRGP PGPPGIPGPA GISVPGKPGQ QGPTGAPGR GPPGKGPAG 180
 VPGMNGKGE MGYGAPRGP ERGLPGPQGP TGPSPGPPGVG KRGENGVPGQ PGIKGRDGP 240
 GEMGPIGPPG PQGPPIGPGP EGIGKPGAAG APGQPGIPGT KGLPGAPGIA GPPGPPGPGK 300
 PGLPGLKGER GPAGLPGGP AGKBPQAGL PGKPLGTGP GNMGPQPGK IPGSHGLPG 360
 KGETGPAGPA GYPGAKGERG SPGSDGKPGY PGKPLDGPX GNPGLPGPK DPGVGGPPGL 420
 PGVPGAGAK GMPGNGEAG PRGAPGIPGT RGPPIGPIG GPPGPPQAV MPEGFIKAG RPSLSGTPLV 480
 ATKGLNGPTG PPGPPGPRGH SGEPGLPGPP GPPGPPQAV MPEGFIKAG RPSLSGTPLV 540
 SANQVGTMP VSAFTVILSK AYPALGTPIP FDKILYMRQ HYDPRGTGIFT QIPGIYYS 600
 YHVHVKGTHV WVGLYKNGTP VMYTYDEYTK GYLDQASGSA IIDLTENDQV WLQLPNAESN 660
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Seq ID NO: 111 DNA sequence
Nucleic Acid Accession #: NM_000949
Coding sequence: 285..2153

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ATGTCTCTGT	GCAGGAAGTA	CTCATCGACT	GATGTGGCAG	ACTTTGCTCC	CTGACAAAAC	180
TAAAGAACTC	TCTATTTCAT	GGAGGCGAAC	ACTGAAGATG	CTTCCACAT	GAACCTGAA	240
GTGAACCTCT	GATACATTTT	CTGCAGCAAG	AGAAGGCAGC	CAACATGAAG	GAAAATGTGG	300
CATCTGCAAC	CGTTTTCACT	CTGCTACTTT	TTCTCAACAC	CTGCCTTCTG	AATGGACAGT	360
TACCTCTGGG	AAAACCTGAG	ATCTTTAAAT	GTGTTCTCC	CAATAAGGAA	ACATTCACTT	420
GCTGGTGGAG	GCTTGGGACA	GATGGAGGAC	TTCCTACCAA	TTATTCACTG	ACTTACCACT	480
GGGAAGGAGA	GACACTCATG	CATGAATGTC	CAGACTACAT	AACCGTGGGC	CCCACTCCTT	540
GCCACTTTGG	CAAGCAGTAC	ACCTCCATGT	GGAGGACATA	CATCATGATG	GTCAATGCCA	600
CTAACCCAGT	GGGAAGCAGT	TTCTCGGATG	AACCTTATGT	GGACGTGACT	TACATAGTTC	660
AGCCAGACCC	TCTTTGGGAG	CTGGCTGTGG	AAGTAAACAA	GCCAGAGAC	AGAAAAACCTT	720
ACCTGTGGAT	TAAATGCTCT	CCACCTACCC	TGATTGACTT	AAAAAATCGT	TGGTTCACGC	780
TCTGTATGTA	AATTCGATTA	AAACCCGAGA	AAGCAGCTGA	GTGGGAGATC	CATTTTGCTG	840
GGCAGCAAA	AGAGTTTAA	ATTCTCAGCC	TACATCCAGG	ACAGAAATAC	CTTGTCCAGG	900
TTGCTGCAAC	ACCAGACCAT	GGATCTGGA	GTGCATGGAG	TCCAGCGACC	TTTATTGAGA	960
TACCTGCTCC	TCTTCCCATG	AATGATACAA	CCGTTGGGAT	CTCTGTGGCT	GTCTTTCTTG	1020
CTGTCTATCT	TTTGATTATT	GTCTGGGCG	TGGCTTTGAA	GGGCTATAGC	ATGGTGACCT	1080
GCATCTTTCC	GCCAGTTCCT	GGGCCAAAA	TAAAGGATT	TGATGCTCAT	CTGTTGGAGA	1140
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ACTATGAGGA	CTGTCTGGTG	GAGTATTAG	AAGTAGATGA	TAGTGAGGAC	CAGCATCTAA	1260
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ACACTGACTC	AGGCCGGGGG	AGCTGTGACA	GCCCTTCCTT	TTTGTCTGAA	AAGTGTGAGG	1380
AACCCGAGGC	CAATCCCTCC	ACATTCTATG	ATCCTGAGGT	CATTGAGAAG	CCAGAGAATC	1440
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CCAGATCTCT	TATCCACAT	ATTACTGATG	TGTGTGAGCT	GGCTGTGGGC	CCTGCAGGTG	1620
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CTAAAAACGT	GGCTTGCTTT	GAAGAATCAG	CCAAAGAGGC	CCCACCATCA	CTTGAACACA	2040
ATCAAGCTGA	GAAAGCCCTG	GCCAACTTCA	CTGCAACATC	AAGCAAGTGC	AGGCTCCAGC	2100
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ACTAATGGAA	TGATTGGTTA	AAATGTGATT	TTTCTTCAGG	TAACTACTAC	GAGTACGTGA	2220
AATGCTCAAG	AATGTAGTCA	GACTGACACT	ACTAAAGCTC	CCAGCTCCTT	TCATGCTCCA	2280
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AAAAGCAGCA	TGCTTAGTAT	TCTTGGAGGA	CAATGCCAAT	AGGTATATCC	TCTGGAAGAA	2460
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AAGATGACAA	AAGAAAATT	TCCACATAGG	AAAATGCCAT	GAAAATTGCT	TTTGAAGAAC	2580
AACTGCATAA	CCTTTACACT	CCTCGTCCAT	TTTATTAGGA	TTACCCAAAT	ATAACCATTT	2640
AAAGAAAGAA	TGCATTCCAG	AACAAATTGT	TTACATAAGT	TCCTATACCT	TACTGACACA	2700
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Seq ID NO: 112 Protein sequence
Protein Accession #: NP_000940

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VTYIVQPDPP	LELAVEVKQP	EDRKPYLWIK	WSPPTLIDLK	TGWFLLLYEI	RLKPERAAEW	180
EHFAGQQTE	FKILSLHPGQ	KYLQVVRCKP	DHGYVSAWSP	ATFIQIPSDF	TMNDTIVWIS	240
VAVLSAVICL	IIWVAVALKG	YSMVTCTFPF	VPGPKIKGFD	AHLLEKGSSE	ELLSALGQD	300
FPPTSDYEDL	LVEYLEVDD	EDQHLSVSHS	KEHPSQGMKP	TYLDPDTDSG	RGSCTSPSLL	360
SEKCEPQAN	PSTFYDPEVI	EKPENPETTH	TWDPQCISME	GKIPYFHAGG	SKCSTWPLPQ	420
PSQHNPRSSY	HNITDVCELA	VGPAGAPATL	LNEAGKDALK	SSQTIKSRE	GRATQQREVE	480
SFHSETDQDT	PWLLPQEKTP	FGSAKPLDYV	ELHKVNDGKA	LSLLPKQREN	SGKPKKPGTP	540
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Seq ID NO: 113 DNA sequence
Nucleic Acid Accession #: XM_062811
Coding sequence: 1..888

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GGCGAGCCCA	CCATCTGCTG	CGGCAGCTGC	GCGTTGCGCT	ACTGCTGCTC	CAGCGCGGAG	240
GCGCGCTGG	ACCAAGGGGG	CTGCGACAAT	GACCGCCAGC	AGGGCGCTGG	CGAGCTTGGC	300
CGGCGGACAA	AAGACGGCCC	CGACGGCTCG	GCAATGCCCA	TCTAGTGGCC	GTTCCTCATT	360
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10 Seq ID NO: 114 Protein sequence
 Protein Accession #: XP_062811

1 11 21 31 41 51
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 Coding sequence: 223..1512

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 TTTGATAAAC TTTATAACAC TTTAAAAAAA CAGTTTCCTG CTATGGCCCT GAAGATTCTCT 240
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 CAGAAAAAAA TAGTTCTCAA CAGAAAAGAG CAAAAACATA TTATGGCTGA ACGTAATGTG 660
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 ACTGAACTT CTATTTGTGT GAATATATTC AAATATGAT AACTAGTCCC TCATTTTAT 1620
 ATGTAATGAT GAAACTATG AAAAAATGTA TTTCTTCTA TGTGCAAGAA AAATAGGGCA 1680
 TTTCAAAGAG CTGTTTGTAT TAAATTTAT ATTCTGTGTT AATAAGCTTA TTTTAAACA 1740
 ATTTAAAGC TATTATCTCT AGCATTAACC TATTTTAAA GAAACCTTTT TTGCTATTGA 1800
 CTGTTTTTC CTTCTAAGTT TACATAACA TCTACCCAAG ATAGACTGTT TTTTAACTG 1860
 CAATTTCACT TCAGCTAACA TATATTAATA CCTTTGTAAC TCTTTGCTAT GGCTTTTGT 1920
 ATCACACCAA AACTATGCAA TTGGTACATG GTTGTTTAAG AAGAAACCGT ATTTTCCAT 1980
 GATAATCAC TGTTTGAAAT ATTTGGTTCA TGGTATGATC GAAATGTAAA AGCATAATTA 2040
 ACACATGGC TGCTAGTTAA CAATTGGAAT AACTTTATTC TGCAGATCAT TTAAGAAGTA 2100
 ACAGGCCGGG CGCGGTGGCT CACGCTGTGA ATCCAGCAC TTTGGGAGGC TGAGGCGGGC 2160
 AGATCACCTG AGGTGAGGAG TTGGAGACCA GCCTGACCAA CATGGACAAA CCCGCTCTCT 2220
 ACTAAAAATA CAAATTTGTC AGGGTGTGTT GGCACATGCC TATAATCCCA GCTACTTGGG 2280
 AGGCTAAGGC AGGAGATCG CTTGAACCGG GGAGCGGAG GTTGCACTGA GCCAGATCG 2340
 CACCATGCA CTCCTGCTG GGCACACAGA GTGAACTCC ATCTCCAAAA A

70 Seq ID NO: 116 Protein sequence
 Protein Accession #: NP_037389

1 11 21 31 41 51
 75 MALKIPAKRI PGDNFDPDFI KQRAGLNEF IQNLVRYPEL YNHPDVRAFL QMDSPKHQSD 60
 PSEDEDERSS QKLHSTSONI NLGPGSNPHA KPTDPDLKV IGKGSFGKVL LAKRKLDGKF 120
 YAVKVLQKKI VLNRKEQKHI MAERNVLLKN VKHPLVLGLH YSFQTEKLY FVLDPVNGGE 180
 LFFHLQREES FPEHRARFYA ABASALGYL HSIKIVYRDL KPENILLDSV GHVLTDFGL 240
 CKEGIAISDT TTTFCGTPEY LAPEVIRKQP YDNTVDWNL GAVLYEMLYG LPFFYCRDVA 300
 EMYDNLKPK LSLRPGVSLT AWSILEELLE KDRQNLGAK EDFLEIQNH FFEISLWADL 360
 VQKKIPFFFN PNVAFPDDR NFDTAFTET VPYSVCVSSD YSIVNASVLE ADDAFVGFPSY 420
 APPSEDLFL

Seq ID NO: 117 DNA sequence
 Nucleic Acid Accession #: NM_004004.1

Coding sequence: 1..681

1 11 21 31 41 51
5 ATGGATTGGG GCAAGCTGCA GAAGATCCTG GGGGGTGTGA ACAAACATC CACCAGCATT 60
GGAAAGATCT GGCCTACCGT CCTCTTCATT TTTGSCATTA TGATCCTCGT TGTGGCTGCA 120
AAGGAGGTGT GGGGAGATGA GCAGGCCGAC TTTGTCTGCA ACACCTTGCA GCCAGGCTGC 180
AAGAACGTGT GCTACGATCA CTACTTCCCC ATCTCCACA TCCGGCTATG GGCCTGTCAG 240
CTGATCTTCG TGTCCAGCCC AGCGTCCTTA GTGGCCATGC ACGTGGCCTA CCGGAGACAT 300
10 GAGAAGAAGA GGAAGTTCAT CAAGGGGGAG ATAAAGAGTG AATTAAAGGA CATOGAGGAG 360
ATCAAAACCC AGAAGGTCCG CATCGAAGGC TCCCTGTGGT GGACCTACAC AAGCAGCATC 420
TTCTTCCGGG TCATCTTCGA AGCCGCTTC ATGTACGTCT TCTATGTCTAT GTACGACGGC 480
TTCTCCATGC AGCGGCTGGT GAAGTGCAAC GCCTGGCCTT GTCCCAACAC TGTGGACTGC 540
15 TTTGTGTCCC GGGCCACGGA GAAGACTGTC TTCACAGTGT TCATGATTGC AGTGTCTGGA 600
ATTGTGATCC TGTGAATGT CACTGAATTG TGTATTGTG TAATTAGATA TTGTCTGGG 660
AAGTCAAAAA AGCCAGTTTA A

Seq ID NO: 118 Protein sequence
Protein Accession #: NP_003995.1

20 1 11 21 31 41 51
MDWGLTLQTL GGVNKHSTSI GKWLTVLFI FRIMILVVAA KEVWGDEQAD FVCNTLQPGC 60
KNVCYDHYFP ISHLRLWALQ LIPVSSPALL VAMHVAYRRH EKKRKFIKGB IKSEFKDIEE 120
25 IKTKVRIEGB SLNWTYSSSI PFRVIFEAAP MYVIFYVMYDG FSMQRLVKCN ANPCPNTVDC 180
FVSRPTEKTV FTFVMIASVG ICILLNVTEL CYLLIRYCSG KSKKPV

Seq ID NO: 119 DNA sequence
Nucleic Acid Accession #: XM_061091.1
Coding sequence: 1..2481

1 11 21 31 41 51
35 ATGCCAAATA CTTACAGAAC AACCAGGATT GAAATTGGC TTCTCCAAGA GCGCCCCGGG 60
CACCGAGCGC TGGTCCGCGC TCTCCTTCCG GTGAGTCCCA GCCCGAGATT GGCTCTGGCG 120
CCCGGGTACC CGCCAGTGCC GGCTGCCGAT GACCGATTCA CGCTCCCGAT GATTGAGGT 180
CAGATGCATG GTGAGAAAGT AGATCTCTGG AGCCTTGGTG TTCTTTTGCTA TGAATTTTFA 240
GTGGGGAAGC CTCCTTTTGA GGCAAAACGAA GTCCATGTAA GCAAAAGAAC CATCGGGAAG 300
40 ATTTTCAGCTG CCAGCAAAT GATGTGGTGC TGGCTGCAG TGGACATCAT GTTCTGTGTA 360
GATGGGTCTA ACAGCGTCGG GAAAGGGAGC TTTGAAAGT CCAAGCATT TGCCATCACA 420
GTCTGTGACG GTCTGGACAT CAGCCCCGAG AGGGTCAGAG TGGAGCATT CCAGTTCAGT 480
TCCACTCCTC ATCTGGAATT CCGCTTGGAT TCATTTTCAA CCCAACAGGA AGTGAAGGCA 540
AGAATCAAGA GATGTGTTT CAAAGGAGGG CGCACGGAGA CGGAACCTGC TCTGAAATAC 600
45 CTTCTGCACA GAGGGTTGCC TGGAGGAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC 660
GTCACTGATG GGAAGTCCCA GGGGGATGTG GCACTGCCAT CCAAGCAGCT GAAGGAAAGG 720
GGTGTCACTG TGTTTGCTGT GGGGGTCAGG TTTCCAGGT GGGAGGAGCT GCATGCACTG 780
GCCAGCGAGC CTAGAGGGCA GCACGTGCTG TTGGCTGAGC AGGTGGAGGA TGCCACCAAC 840
GGCCTCTTCA GCACCTCAG CAGCTCGGCC ATCTGCTCCA GCGCCACGCC AGCTGGGAGC 900
50 CCGAGCTTG TCTTCATGGA GCGGTTAATG GSCATCTCTC TGATAGGCCC CTGTGACTCG 960
CAGCCCTGCC AGAATGGAGG CACATGTGTT CCAGAAGGAC TGGACGGCTA CCAATGCCTC 1020
TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG 1080
GTGACCTCC TCTTCTGCTG GGACAGCTCT GCGGGCACCA CTCTGGACGG CTCTCTGCGG 1140
GCCAAGTCT TCGTGAAGCG GTTTGTGCGG GCGGTGCTGA GCGAGGACTC TCGGGCCCCG 1200
55 GTGGGTGTGG CCACATACAG CAGGAGCTG CTGGTGGCGG TGCTGTGGG GAGATACCA 1260
GATGTGCTCT ACCTGTGCTG GAGCCTCGAT GGCATTCCCT TCCGTGTGTG CCCCACTCTG 1320
ACGGGCACTG CCTTTGGGCA GGCGGCAGAG CGTGGCTTGG GGAGCGCCAC CAGGACAGGC 1380
CAGGACCGGC CAGTGAAGT GGTGGTTTGG CTCACTGAGT CACACTCGA GGATGAGGTT 1440
GCGGGCCGCA GCGGTCAAGC AAGGGCGCGA GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG 1500
60 GCGGTGCGGG CAGAGCTGGA GGAGATCACA GGCAGCCCAA AGCATGTGAT GGTCTACTCG 1560
GATCCTCAGG ATCTGTTCAA CCAATCCCT GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG 1620
CGGCCAGGGT GCGGACACA AGCCCTGGAC CTCGTCTTCA TGTGGACAC CTCTGCCTCA 1680
GTAGGCGCGG AGAATTTTGC TCAGATGCAG AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT 1740
GAGGTGAACC CTGACGTGAC ACAGGTGCGC CTGGTGTGT ATGGCAGCCA GGTGCAGACT 1800
65 GCCTTGGGGC TGGACACCAA ACCCACCAGG GCTGCGATGC TGCGGGCCAT TAGCCAGGCC 1860
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ATGACCGTCC AGAGGGGTGC CCGGCTGTGT GTCCCCAAG CTGTGTGTGT GCTCACAGGC 1980
GGGAGAGGCG CAGAGGATGC AGCGTTCCT GCCCAGAAAG TGAGGAACAA TGGCATCTCT 2040
70 GTCTTGTGTG TGGCGTGGG GCCTGTCTTA AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC 2100
CGGGATTCCC TGATCCAGT GGCAGCTTAC GCGACCTGC GGTACCAACA GGACGTGCTC 2160
ATTGAGTGGC TGTGTGAGA AGCCAAGCAG CCAATCAACC TCTGCAAAAC CAGCCCGTGC 2220
ATGAATGAGG GCAGCTCGT CCTGCAGAA GTGAGCTACC GCTGCAAGTG TCGGATGGC 2280
TGGGAGGGCC CCCACTGCGA GAAACGTGAG TGGAGCTCTT GCTCTGTATG TGTGAGCCAG 2340
75 GGATGGAATC TTGAGAGGCC CCTGAGGCAC ATGGCTCCCG TGACGAGGGG CAGCAGCGGT 2400
ACCCCTCCCA GCAACTACAG AGAAGCCCTG GGCAGTAAA TGGTGCCTAC CTCTCTGGAAT 2460
GTCTGTGCCC CAGGTCTCTA G

Seq ID NO: 120 Protein sequence
Protein Accession #: XP_061091.1

80 1 11 21 31 41 51
MPNTSGITRI EIWLLQEPGP HRLVAALLP VSPSPALALA PGYFPVPAAD DRFTLPMIGG 60
QMHGKVDLW SLGLVLCYEFV VGRKPPPEANE VHSVKETIGK ISAAKRMWMC SAAVDIMFLL 120

5 DGSNSVKGGS FERSKHFAIT VCDGLDISPE RVRVGAFQFS STPHLEFPLD SFSTQQEVKA 180
 RIKRMVFKGG RTETELALKY LLHRGLFPGGR NASVPQILII VTDGKSQGDV ALPSKQLKER 240
 GVTVFAVGVR FPRWHEELHAL ASEPRGQHV LAEQVEDATN GLFSTLSSSA ICSSATPAGS 300
 PELVFMERLM GISLIGPCDS QPCQNGGTCV PEGLDGVQCL CPLAFGGGAN CALKLSLECR 360
 10 VDLLFLDSS AGTTLDGFLR AKVFKRFRVR AVLSSEDSRAR VGVATYSREL LVAVFVGEVQ 420
 DVFDLWVSLD GIPFRGGPTL TGSALRQAAE RGFGSATRTG QDRPRRVVVL LTESHSEDEV 480
 AGPARHARAR ELLLLGVGSE AVRAELEIIT GSPKHMVVS DPQDLFNQIF ELQKLCRSRQ 540
 RFGCRTQALD LVFMLDTSAS VGPENFAQMQ SFVRSCALQF EVNPDVTQVQ LVVYGSQVQT 600
 15 AFGLDTKPTR AMLRAISQA PYLGGVGSAG TALLHIYDKV MTVQRGARPG VPKAVVVLTG 660
 GRGAEDAAVP AQKLRNNGIS VLVVGVGPVL SEGLRLRAGP RDSLIHVAAY ADLRYHQDVL 720
 IEWLCGEAKQ PVNLCKPSPC MNEGSCVLQN GSYRCKCRDG WEGPHCENRE WSSCSVCVQS 780
 GWILETPLRH MAPVQEGSSR TFPNSYREGL GTEMVPTFWN VCAPGP

Seq ID NO: 121 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..2424

20 1 11 21 31 41 51
 ATGCCCCCTT TCCTGTTGCT GGAGGCCGTC TGTGTTTTCC TGTITTCAG AGTGCCCCCA 60
 TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC 120
 AGCAAAATGA TGTGGTGTCTC GGCTGCAGTG GACATCATGT TCTGTTAGA TGGGTCTAAC 180
 AGCGTCGGGA AAGGGAGCTT TGAAGGTCC AAGCACTTG CCATCAGCT CTGTGACGGT 240
 25 CTGGACATCA GCCCGAGAG GGTCAAGATG GGAGCATTC AGTTCAGTTC CACTCCTCAT 300
 CTGGAATTCC CTTGGATTTC ATTTTCAACC CAACAGGAAG TGAAGCAAG AATCAAGAGG 360
 ATGGTTTTCA AAGGAGGGCG CACGAGAGCG GAACCTGTCT TGAATACCT TCTGCACAGA 420
 GGGTTCGCTG GAGGCAGAAA TGCTTCTGTG CCCAGATCC TCATCATCGT CACTGATGGG 480
 AAGTCCAGG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCACTGTG 540
 30 TTTGCTGTGG GGGTCAGGTT TCCCAAGTGG GAGGAGCTGC ATGCACTGGC CAGCAGAGCT 600
 AGAGGGCAGC ACGTGTCTGT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC 660
 ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT C3AGGCTCAG 720
 CCTGTGAGC ACAGGACGCT GGAGATGGTC CGGGAGTTG CTGGCAATGC CCCATGCTGG 780
 AGAGGATCGC GCGGACCCCT TGCGGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG 840
 AGAGTGTTC TAACCCACCC TGCCACCTGC TACAGGACCA CCTGCCCAGG CCCCTGTGAC 900
 35 TCGCAGCCCT GCCAGAATGG AGGCACATGT GTTCCAGAAG GACTGGACGG CTACCAAGTC 960
 CTCTGCCCGC TGGCCTTTGG AGGGGAGGCT AACTGTGCCC TGAAGCTGAG CCTGGAATGC 1020
 AGGTCAGACC TCTCTTCTCT GCTGGACAGC TCTGCGGGCA CCACTCTGGA CGGCTTCCTG 1080
 CGGGCCAAAG TCTTCGTGAA GCGGTTTGTG CGGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140
 CGAGTGGGTG TGCCACATA CAGCAGGGAG CTGCTGGTGG CGGTGCTGTG GGGGGAGTAC 1200
 40 CAGGATGTGC CTGACCTGGT CTGGAGCCCTC GATGGCATTG CCTTCGTGG TGGCCCCACC 1260
 CTGACGGGCA GTGCCCTGGG GCAGCGCGCA GAGCGTGGCT TCGGGAGCGC CACCAAGACA 1320
 GGCCAGGAGC GGCCACGTAG AGTGTGTTT TTGCTCACTG AGTCACACTC CGAGGATGAG 1380
 GTTGCGGGCC CAGCGCTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT 1440
 GAGGCGGTGC GGGCAGAGCT GGAGGAGATC ACAGGCAGCC CAAAGCATGT GATGCTCTAC 1500
 45 TCGGATCCTC AGGATCTGTT CAACCAAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCGCC 1560
 CAGCGGCCAG GGTGCGCGAC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CACCTCTGCC 1620
 TCAGTAGGCG CCGAGAATTT TGCTCAGATG CAGAGCTTTG TGAAGAGCTG TGCCCTCCAG 1680
 TTTGAGGTGA ACCCTGAAGT GACACAGGTC GGCCTGGTGG TGTATGGCAG CCAGGTGCAG 1740
 50 ACTGCCCTCG GGCTGGACAC CAAACCCACC CGGGCTGCGA TGCTGCGGGC CATTAGCCAG 1800
 GCCCCTTACC TAGGTGGGTG GGGCTCAGCG GGCACCGCCC TGCTGCACAT CTATGACAAA 1860
 GTGATGACCG TCCAGAGGGG TGCCCGGCCCT GGTGTCCCA AAGCTGTGGT GGTGCTCACA 1920
 GCGCGAGAGC GGCAGAGGGA TGCAAGCGTT CCTGCCAGA AGCTGAGGAA CAATGGCATC 1980
 TCTGTCTTGG TCGTGGGCGT GGGCCCTGTC CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT 2040
 55 CCCCGGATT CCCTGATCCA CGTGGCAGCT TACGCGGACC TGCGGTACCA CCAGGACGTG 2100
 CTCAATTGAGT GGCTGTGTGG AGAAGCCAA GACGAGCTCA ACCTCTGCAA ACCCAGCCCG 2160
 TGCATGAATG AGGGCAGCTG CGTCTGCAAG AATGGGAGCT ACCGCTGCAA GTGTGCGGAT 2220
 GGCTGGGAGG GCGCCCACTG CGAGAACCGT GAGTGGAGCT CTTGCTCTGT ATGTGTGAGC 2280
 CAGGGATGGA TTCTTGAGAC GCCCCTGAGG CACATGGCTC CCGTGCAAGA GGGCAGCAGC 2340
 60 CGTACCCCTC CCAGCAACTA CAGAGAAGGC CTGGGCACTG AAATGGTGCC TACCTTCTGG 2400
 AATGTCTGTG CCCCAGGTCC TTAG

Seq ID NO: 122 Protein sequence
 Protein Accession #: Eos sequence

65 1 11 21 31 41 51
 MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLDGSN 60
 SVKGGSFERS KFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
 70 MVFKGGRTST ELALKYLLHR GLPGRNASV PQILLIIVTDG KSQGDVALPS KQLKRGVTV 180
 FAVGVRFPRW BELHALASEP RQGHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
 PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPPYSWK RVFLTHPATC YRTTCRPGCD 300
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDSS SAGTTLDGFL 360
 RAKVFKRFRV RAVLSSEDSRA RGVATYSRE LLVAVFVGEY QDVFDLWVSL DGIPFRGGPT 420
 75 LTGSALRQAA ERGFGSATRT QDRPRRVVVL LTESHSEDE VAGPARHARA RELLLGVGS 480
 EAVRAELEI TSPKHMVVS SDPDLFNQI PELQKLCRSR RRPGRCTQAL DLVFMMLDTSA 540
 SVGPENFAQM QSFVRSCALQ FEVNPDTQV GLVYGSQVQ TAPGLDTPKT RAAMLRAISQ 600
 APYLGGVGS A TALLHIYDK VMTVQRGARP GVPKAVVVL T GGRGAEDAAV PAQKLRNNGI 660
 SVLVVGVGPV LSEGLRLRAG PRDSLIHVA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP 720
 80 MNEGSCVLQ NGSYRCKCRD WEGPHCENR WSSCSVCVQS QGWILETPLR EMAPVQEGSS 780
 RTPPSNYREG LGTEMVPTFW NVCAPGP

Seq ID NO: 123 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 89..2356

1 11 21 31 41 51
 5 G C C C C C T G G C C O G A G C C G G C C C G G G T C T G T A G T A G A G C G C C C G G G C A C O G A G C G C T G 60
 G T C G C G C G C T C T C T C T C C G T T A T A T C A A C A T G C C C C C T T C C T G T G C T G G A A G C C G T C T G 120
 T G T T T T C C T G T T T T C C A G A G T G C C C C C A T C T C T C C C T C C C A G G A G T C C A T G T A A G C A A 180
 A G A A A C C A T C G G A A G A T T T C A G C T G C C A G C A A A A T G A T G T G T G C T C G G T G G T G G A C T G C A G T G G A 240
 C A T C A T G T T T C T G T T A G A T G G G T C T A A C A G C G T C G G G A A G G G A G C T T T G A A G G T C C A A 300
 G C A C T T T G C C A T C A C A G T C T G T G A C G G T C T G A C A T C A G C C C G A G A G G T C A G A G T G G G 360
 10 A G C A T T C C A G T T C A G T C T C T C A T C T G G A A T T C C C C T T G A T T C A T T T C A A C C C A 420
 A C A G A A G T G A A G G C A A G A T C A A G A G G A T G G T T T T C A A A G A G G G C G C A C G A G A C G G A 480
 A C T T G C T C T G A A T A C C T T C T G C A G A G G T T G C C T G G A G G C A G A A A T G C T T C T G T G C C 540
 C C A G A T C C T C A T C A T C G T C A C T G A T G G G A A G T C C C A G G G G G A T G T G G C A C T G C C A T C C A A 600
 G C A G C T G A A G A A G G G G T G T C A C T G T G T T T G C T G T G G G G T C A G G T T T C C A G G T G G G A 660
 15 G G A G C T G C A T G C A C T G G C C A G C A G C C T A G A G G C A G C A C G T G C T G T G T G G T C A G A G C A G G T 720
 G G A G G A T G C C A C C A A C G G C C T C T C A G C A C C C T C A G C A G C T C G G C C A T C T G C T C A G C G C 780
 C A C G C C A T C T G C A G G G T G A G C T C A C C C C T G T G A G A C A G G A G A C G C T G G A G A T G G T C C G 840
 G G A G T T C G C T G G C A A T G C C C C A T G C T G G A G A G A T C G C G G C G G A C C C T T G C G T G C T G G C 900
 T G C A C A T G C T C C C T C T A C A G T G A A G A G A G T T T C C T A A C C A C C C T G C A C C T G C T A 960
 20 C A G G A C C A C C T G C C C A G G C C C T G T G A C T C G A G C C C T G C A G A A T G G A G C A C A T G T G T 1020
 T C C A G A A G G A C T G A C G G C T A C C A G T G C C T C T G C C G C T G C C T T T G G A G G G A G G C T A A 1080
 C T G T G C T C T G A A T A C C T T C T G A A T G C A G G T G C A C C T C T C T C C T G C T G G A C A G C T C 1140
 T G C G G G C A C C A C T C T G G A C G C T C C T G C G G C C A A G A A G T C T T C G T A A G C G G T T G T G C G 1200
 G C C C T G C T G A C G C A G G A C T C T G G G C C C G A G T G G T G T G C C A C A T A C A G C A G G A G C T 1260
 25 G C T G T G G C G G T G C C T G T G G G G G A G T A C C A G G A T G C C T G C T G C T G G A G C C T G C T G A 1320
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 G C G T G G C T T C G C A G C G C C A C C A G G A C A G G C C A G G A C C G G C C A C G T A G A G T G T G T T T 1440
 G C T C A C T G A T C A C A C T C C G A G G A T G A G T T G C G G G C C C A G C G C T C A C G C A A G G G C G C G 1500
 A G A G A C T G C T G C T G T G G G T A G G C A G T G A G G C C C G T G C G G G C A G A G C A T C A C 1560
 30 A G G C A G C C C A A A G C A T G T G A T G G T C T A C T C G A T C C C A G A T C T G T C A A C A A A T C C C 1620
 T G A G A C T G C A G G G A A G C T G T G C A G C C G C C A G C G C C A G G T G C C G A C A A A G C C T G G A 1680
 C C T C G T C T C A T G T T G G A C A C C T C G C C T C A G T A G G G C C C G A G A A T T T T G C T C A G A T G C A 1740
 G A G C T T T G T G A A A G C T G T G C C C T C A G T T G A G G T G A A C C T G A C G T G A C A C A G G T C G G 1800
 C C T G T G T G T G T A T G C G A G C C A G G T G C A G A C T G C C T T C G G G C T G G A C A C C A A A C C C A C C G 1860
 35 G G C T G C G A T G T G C G G G C C A T T A G C C A G G C C C C T A C C T A G G T G G G G T G G C T C A G C C G G 1920
 C A C C G C C C T G C T C A C A T C T A T G A C A A A G T G A T G A C C G T C A G A G G G G T G C C C G C C T G G 1980
 T G T C C C A A A G C T G T G G T G G T G C T C A C A G G C G G G A G A G G C G C A G A G A T G C A G C C G T T C C 2040
 T G C C C A A A G C T G A G A A C A A T G C A T C T C T G T C T T G G T C G T G G G C G T G G G C C T G T C C T 2100
 40 A A G T G A G G T T G C G G A G G C T T G C A G G T C C C C G G A T T C C C T A T C C A C G T G G C A G T T A 2160
 C G C C A C C T G C G T A C C A C C A G G A C G T G C T C A T T A G T G G C T G T G T G G A G A A G C C A A G C A 2220
 T C C A G T C A A C C T C T G C A A A C C A G C C C G T G C A T G A A T G A G G C A G C T G C G T C C T G C A G A A 2280
 T G G A G C T A C C G T G C A A G T G T G G G A T G G C T G G G A G G G C C C C A C T G C G A G A A C C G A T T 2340
 C T T G A G A C G C C C C T A G G C A C A T G G C T C C C G T G C A G G G C A G C A G C C G T A C C C C T C C C 2400
 45 A G C A C T A C A G A A A G C C C T G G C A C T G A A A T G T G C C T A C C T C T G A A T G T C T G T G C C 2460
 C A G G T C C T T A G A A T G T C T G C T T C C C G C C G T G G C C A G G A C C A C T A T T C T C A C T G A G G A G 2520
 G A G G A T G T C C A A C T G C A G C C A T G C T G C T A G A G A C A A G A A G C A G C T G A T G T C A C C C A C 2580
 A A A C G A T G T T G T T G A A A A G T T T G A T G T G T A A G T A A A T A C C C A C T T C T G T A C C T G C T G T 2640
 G C C T T G T T G A G G C T A T G T C A T G T C A C T G C C A C C T T T C C C T T G A G A T A A A C A A G G G T C C T G A A 2700
 50 G A C T T A A A T T A G C G C G C C T G A C G T T C C T T T G C A C A C A A T C A A T G C T G C C A G A A T G T T G T 2760
 T G A C A C A G T A T G C C C A G C A G A G C C T T T A C T A G A G C A T C C T T T G A C G G

Seq ID NO: 124 Protein sequence
 Protein Accession #: Eos sequence

55 1 11 21 31 41 51
 M P F F L L L E A V C V F L P S R V P P S L P L Q E V H V S K E T I G K I S A A S K M M W C S A A V D I M F L L D G S N 60
 S V K G S F P E R S K H P A I T V C D G L D I S P E R V R V G A P Q F S S T P H L E F P L D S F S T Q Q E V K A R I K R 120
 60 M V F K G S R T E T E L A L K Y L L H R G L P G R N A S V P Q I L I I V T D G K S Q G D V A L P S K Q L K E R G V T V 180
 F A V G V R F P R W E E L H A L A S E P R G Q H V L L A E Q V E D A T N G L F S T L S S S A I C S S A T P D C R V E A H 240
 P C E H R T L E M V R E F A G N A P C W R G S R R T L A V L A A H C P F Y S W K R V F L T H P A T C Y R T T C P G P C D 300
 S Q P C Q N G T F C V P E G L D G Y Q C L C P L A F G G E A N C A L K L S L E C R V D L L F L L D S S A G T T L D G F L 360
 R A K V F V K R F V R A V L S E D S R A R V G V A T Y S R E L L V A V P V G E Y Q D V P D L V N S L D G I P F R G G P T 420
 65 L T G S A L R Q A A E R G F G S A T R T Q D R P R R V V V L L T E S H S E D E V A G P A R H A R A R E L L L L G V G S 480
 E A V R A E L E E I T G S P K H V M V Y S D P Q D L F N Q I P E L Q G K L C S R Q R P G C R T Q A L D L V F M L D T S A 540
 S V G P E N F A Q M Q S F V R S C A L Q F E V N P D V T Q V G L V V Y G S Q V Q T A P G L D T K P T R A A M L R A I S Q 600
 A P Y L G G V G S A G T A L L H I Y D K V M T V Q R G A R P G V P K A V V V L T G G R G A E D A A V P A Q K L R N N G I 660
 S V L V V G V G P V L S E G L R R L A G P R D S L I H V A A Y A D L R Y H Q D V L I E M L C G E A K Q P V N L C K P S P 720
 70 C M N E G S C V L Q N G S Y R C K C R D G W E G P H C E N R F L R R P

Seq ID NO: 125 DNA sequence
 Nucleic Acid Accession #: NM_031942.1
 Coding sequence: 145..1260

75 1 11 21 31 41 51
 C C C G A G C C C C G C C C C T C G G C G C C G G G T G C G C G C C C C A G C T G C C A G C C G C G C T G C T G C 60
 T G C T C C T C C T G C T G T G G G A C C G C T G A C C G C G C G C G C T C T C C C C C G C T C C A A G C G 120
 C G A T C T G G G C A C C C G C C A C C A G C A T G G A C G C T C G C G C G T G C G C A G A A A G A T C T C A G A 180
 80 G T A A A G A A G A A C T T A A A G A A A T T C A G A T A T G T G A A G T T G A T T T C C A T G G A A A C C T C G T C A 240
 T C C T C T G A T A C A G T T G T G A C A G C T T G C T C T G A T A A T T T T G C A A A C A C G A G G C T G C A G 300
 T C A G T T C G G G A A G G C T G T A G G A C C C G C A G C A G T G C A G G C A C T C T G G A C C T C A G G G T G 360
 G G A T G A A G T T T C A G C G C G G A G T A C C A G G G A G C A C C A A C A A A A A A G C A G A G T C C C G C 420
 C A G C C C T C A G A G A A T T C T G T G A C T G A T T C C A A C T C G A T T C A G A A G A T G A A G T G G A A T G 480

5 AATTTTTTGG AGAAAAGGGC TTTAAATATA AAGCAAAACA AAGCAATGCT TGCAAAACTC 540
 ATGTCGAAT TAGAAAAGCTT CCCTGGCTCG TTCGTGGAA GACATCCCTC CCCAGGCTCC 600
 GACTCACAAT CAAGGAGACC GCGAAGGCGT ACATTCCTCG GTGTGCTTC CAGGAGAAAC 660
 CCGAAGCGGA GAGCTCGTCC TCTTACCAGG TCAAGGTCCC GGATCCTCGG GTCCCTTGAC 720
 GCTCTACCCA TGGAGGAGGA GGAGGAAGAG GATAAGTACA TGTTGGTGAG AAAGAGGAAG 780
 ACCGTGGATG GCTACATGAA TGAAGATGAC CTGCCAGAA GCCGTGCTC CAGATCATCC 840
 GTGACCTTGC CGCATATAAT TCGCCAGTG GAAGAAATTA CAGAGGAGGA GTTGAGAAC 900
 GTCTGCAGCA ATTCTCGAGA GAAGATATAT AACCGTTCAC TGGGCTCTAC TTGTATCAA 960
 10 TGCCGTAGCA AGACTATTGA TACCAAAACA AACTGCAGAA ACCCAGACTG CTGGGGCGTT 1020
 CGAGGCCAGT TCTGTGCCCC CTGCCCTCGA AACCGTTATG GTGAAGAGGT CAGGGATGCT 1080
 CTGCTGGATC CGAACTGGCA TTGCCCGCCT TGTGAGGAA TCTGCAACTG CAGTTTCTGC 1140
 CGGCAGCGAG ATGAGACGGTG TGGACTGGG GTCCTTGTGT ATTTAGCCAA ATATCATGGC 1200
 TTTGGGAATG TGCATGCTTA CTGAAAGAGC CTGAAACAGG AATTGAAAT GCAAGCATAA 1260
 15 TATCTGAAA ATTTGCTGCC TGCTTCTAC TTCTCAATC TTCTTGTAA AAGTTTCCAA 1320
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 20 GAAACACAA ATAGTATTA ACTAACTAGA TCTATTGAAT TTCAGAGAAG AGCCTTCTAA 1680
 CTGTGTTACA CAAAACGAG TATGATTAG CACTCATACT AGTTGAAATT TTTAATAGAA 1740
 TCAAGGCACA AAAGTCTTAA AACCATGTGG AAAAATTAGG TAATTATTGC AGATTGATGT 1800
 CTCTCAATCC CATGTATGTC GCTTATGTTA CAAGTGTGT TCACAGTTGA GACTTAATTT 1860
 25 CTCTTAATTT CTCTGCCCC AAGGGTAAGT GGTGCGTCCA GCTTACAGA TCATAATTCA 1920
 AAGGTGTGAG GCAATGTAA TACTTAATTA AAATAATGAT GGAAGAGCTA TCTGGAGATT 1980
 ATGAGTAAGC TGATTGAAAT TTTCACTATA AAACCTTAGT ATAATTGTAG TTTGCAAGT 2040
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 TTGATATTAA AAACAGTCT GTGGTCTCTT GCAGTTCTT GTAAATTTAT AAACAGGCA 2160
 30 CAAGATILGS GTTTAGATT TAAACACTTT TATAACAATG ATAAGTGCTT TTTTGGAGAT 2220
 GTAACTTTAA GCAGTTTGT AACCTGACAT CTCTGCCAGT CTAGTTTCTG GGCAGGTTTC 2280
 CTGTGTCAGT ATTCCCCCTC CTCTTTGCAT TAATCAAGGT ATTTGGTAGA GGTGGAATCT 2340
 AAGTGTGTTG ATGTCCAATT TACTTGCATA TGTAACCAT TGCTGTGCCA TTCAATGTTT 2400
 GATGCATAAT TGGACCTTGA ATCGATAAGT GTAAATACAG CTTTTGATCT GTAATGCTTT 2460
 35 TATACAAAG TTTATTTTAA TAATAAAATG TTTGTTCTAA AAAAAAATAA

Seq ID NO: 126 Protein sequence
 Protein Accession #: NP_114148.1

40 1 11 21 31 41 51
 MDARRVPQKD LRVKKNLKKF RYVKLISMET SSSSDSDSCDS FASDNFANTR LQSVREGCRT 60
 RSQCRHSGFL RVAMKFPARS TRGATNKKAE SRQPSSESVT DSNDSSEDES GNMFLKRAL 120
 NIKQNKAMLA KLMSELESFP GSFRGREPLP GSDSQRRPR RRTFPGVASR RNPERRARPL 180
 45 TRSRILIGS LDALPMEEBE EEDKYLVRK RKTVDGYMNE DDLFRSRRSR SSVTLPHIIR 240
 PVEEITEEEL ENVCNSRREK IYNRSLGSTC HQCRQKTIDT KTNCRNPDCW GVRGQPCGPC 300
 LRNRYGEEVR DALLDPNWHC PPCRGICNCS FCRQRDGRCA TGVLVYLAKY HGFNVHAYL 360
 KSLKQEFEMQ A

50 Seq ID NO: 127 DNA sequence
 Nucleic Acid Accession #: AF305616.1
 Coding sequence: 1..863

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 ATGCACCGCT TGATGGGGGT CAACAGCACC GCGGCGCGCG CGGCGGGGCA GCCCAATGTC 60
 TCCTGCAAGT GCAACTGCAA ACGCTCTTTG TTCAGAGCA TGGAGATCAC GGAGCTGGAG 120
 TTTGTTTACA TCATCATCAT CGTGGTGGTG ATGATGGTGA TGGTGGTGGT GATCACTGTC 180
 CTGCTGAGCC ACTACAAGCT GTCTGCACGG TCCTTCATCA GCGGCGACAG CCAGGGGCGG 240
 60 AGGAGAGAAAG ATGCCCTGTC CTCAGAAGGA TGCCGTGTGG CCTCGGAGAG CACAGTGTCA 300
 GGCACCGGAA TCCAGAGGCC GCAGGTCTAC GCCCGGCTC GGCCCAACGA CCGCTGGGCC 360
 GTGCCGCCCT TGCCCGAGCG GGAGCGCTTC CACCGCTTCC AGCCCACTTA TCCGTACCTG 420
 CAGCACGAGA TCGACCTGCC ACCCACCATC TCGCTGTGAG ACGGGGAGGA GCCCCACCC 480
 TACCAGGGCC CTGCAACCTT CCAGCTTCGG GACCCGAGC AGCAGCTGGA ACTGAACCGG 540
 65 GAGTCGGTGC GCGCAACCCC AAACAGAAAC ATCTTCGACA GTGACCTGAT GGATAGTGCC 600
 AGGCTGGGCG GCCCTGCCCC CCCCAGCAGT AACTCGGSCA TCAGCGCCAC GTGCTACGGC 660
 AGCGGCGGGC GCATGAGGGG GCGCGCGCCC ACCTACAGCG AGGTCTATCG CCACTACCGG 720
 GGGTCTCTCT TCCAGCACCA GCAGAGCAGT GGGCGGCGCT CCTTGTCTGA GGGGACCCGG 780
 70 TCCACACACA CACACATGCG GCCCTAGAG AGCGAGGCCA TCTGGAGCAA AGAGAAGGAT 840
 AAACAGAAAG GACACCTCT CTAG

Seq ID NO: 128 Protein sequence
 Protein Accession #: AAL09357.1

75 1 11 21 31 41 51
 MHRIMGVNST AAAAGQPNV SCTCNCKRSL FQSMETILE FVQIIIVVV MMVWVVITC 60
 LLSHYKLSAR SPISRHSQGR RREDALSSEG CLWPSESTVS GNGIPEQVY APPRPTDLRA 120
 VPPFAQRERF HRFQPTYFYL QHEIDLPTTI SLSDGEEPPP YQGPCTLQLR DPEQLELNR 180
 80 ESVRAPPPNRT IPDSILMDSA RLGGPCPPSS NSGISATCYG SGRMBEGPPP TYSEVIGHYP 240
 GSSFQHQSS GPFSLEGT RLRHTIAPLE SAAINSKEKD KQKGHPL

Seq ID NO: 129 DNA sequence
 Nucleic Acid Accession #: NM_004952.1

Coding sequence: 1..718

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5 1 11 21 31 41 51
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CTGGCCCAAG GGCCCGGAGG GGCGCTGGGA AACCGSCATG CGGTGTACTG GAACAGCTCC 120
AACCAGCACC TGCCGCGAGA GGGCTACACC GTGCAGGTGA ACGTGAAAGA CTATCTGGAT 180
ATTACTGCC CGCACTACAA CAGCTCGGGG GTGGGCCCCG GGGCGGACC GGGGCCCGGA 240
GGCGGGGAG AGCAGTACGT GCTGTACATG GTGAGCCGCA ACGGCTACCG CACCTGCAAC 300
GCCAGCCAGG GCTTCAAGCG CTGGGAGTGC AACCGGCCCG ACGCCCGCA CAGCCCATC 360
AAGTTCTCGG AGAAGTTCCA GCGCTACAGC GCCTTCTCTC TGGGCTACGA GTTCCACGCC 420
GGCCACGAGT ACTACTACAT CTCCAGCCCC ACTCACAACC TGCACTGGAA GTGTCTGAGG 480
ATGAAGGTGT TGTCTGCTG CGCTCCACA TCGCACTCCG GGGAGAAGCC GGTCCCACT 540
CTCCCCAGT TCACCATGGG CCCCATGTG AAGATCAACG TGCTGGAAGA CTTTGAGGGA 600
GAGAACCCCT AGGTGCCCAA GCTTGAGAAG AGCATCAGCG GGACCAAGCC CAAACGGGAA 660
CACCTGCCCT TGCCGCTGGG CATGCCCTTC TTCTCATGA CGTCTTGCC CTCTTAG

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Seq ID NO: 130 Protein sequence
Protein Accession #: NP_004943.1

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20 1 11 21 31 41 51
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MAAAPLLLLL LLVPVPLPL LAQPGGALG NRHAVYMNSS NQHLRREGYT VQVMVNDYLD 60
IYCPHYNSSG VGPAGPQPG GGAEQYVLYM VSRNGYRTCN ASQGFKEWEC NRPHAPHSPI 120
KFSEKFRYS APSLGYEFA GREYYYISTP THNLHWKCLR MKVFCVCAST SHSGEKFPVT 180
LPQFTMGPNV KINVLEDPEG ENPOVPKLEK SISGTSKPRE HLPLAVGLAF FLMTPLAS

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Seq ID NO: 131 DNA sequence
Nucleic Acid Accession #: NM_012445.1
Coding sequence: 276..1271

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35 1 11 21 31 41 51
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GCGGCAGCCC CGCGCGCCCC CGCAGCCCCT TCTCTCTCTT TCTCCACGCT CCTATCTGCC 120
TCTCTCTGGA GGCCAGGCGG TGCAAGCATCG AAGACAGGAG GAACTGGAGC CTCAITGGCC 180
GGCCCGGGGG GCGCGCTCGG GGCCTAAATA GGAGCTCCGG GCTCTGGCTG GGACCGGACC 240
GCTGCCGCGC GCGCTCCCGC TGCTCTGCGC GGGTGTGGA AAACCCAGC CCGGCGCGCG 300
CCCTGGGCAA GGCCCTCTGC GCTCTCTCTC TGGCCACTCT CGGCGCGCGC GGCCAGCCTC 360
TTGGGGGAGA GTCCATCTGT TCGCCAGAGC CCGCGGCCAA ATACAGCATC ACCTTACAGC 420
GCAAGTGGAG CCAGACGGCC TTCCCAAGC AGTACCCCTT GTTCCGCCCC CTTGGCAGT 480
GGTCTTCTGT GCTGGGGGCC GCGCATAGCT CCGACTACAG CATGTGGAGG AAGAACCAGT 540
ACGTAGTAA CCGGCTGCGC GACTTTGCGG AGCGCGGCGA GGCTGGGCG CTGTGTAAGG 600
AGATCGAGGC GCGCGGGGAG GCGCTGCAGA GCGTGACGCG GGTGTTTTTG GCGCCGCGCG 660
TCCCGCAGGG CACCGGGGAG ACGTCGGCGG AGCTGGAGGT GCAGCGCAGG CACTCGCTGG 720
TCTCGTTTGT GGTGCGCATC GTGCCAGGCC CCGACTGGTT CGTGGGCGTG GACAGCCTGG 780
ACCTGTGGGA CCGGACCGGT TGGCGGGAAC AGCGCGCGCT GGACCTGTAC CCTACGAGC 840
CGGGGACGGA CAGCGGCTTC ACCTTCTCTT CCCCCAATT CGCCACCATC CCGCAGGACA 900
CGGTGACGGA GATAACGTCC TCCTCTCCCA GCCACCGGCG CAACTCTTTC TACTACCGCC 960
GGCTGAAGGC CTGCTCTCCC ATCGCCAGGG TGACACTGGT GCGGCTGCGA CAGAGCCCCA 1020
GGCCCTTCTAT CCTCCCGGCC CCACTCTCTG CCAGCAGGGA CAATGAGATT GTAGACAGCG 1080
CCTCAGTTC AGAAACGCCG CTGGACTGCG AGGTCTCCCT GTGGTCTGCT TGGGGACTGT 1140
GCGAGGCGCA CTGTGGGAGG CTCGGGACCA AGAGCAGGAC TCGCTACGCT CCGGTCCAGC 1200
CCGCCAACAA CGGAGGCCCC TGCCCCGAGC TCGAAGAAGA GCGTGAAGTG GTCCCTGATA 1260
ACTGCTCTTA AGACAGAGC CCGCAGGCC CTGGGGCCCC CGGAGCCATG GGGTGTGGGG 1320
GGCTCTCTGT CAGGCTCATG CTGCAGGCGG CCGAGGCACA GGGGGTTTCG CGCTGCTCTC 1380
GACCGCGGTG AGCGCGCGCC GACCATCTCT GCACTGAAGG GCCTCTGCT GCGCGGCAGC 1440
GGCAITGGGA AACAGCCTCC TCCTTCTCCA ACCTTCTCTC TTAGGGGCCC CCGTGTCCCG 1500
TCTGCTCTCA GCCTCTCTCT CCGCAGGAT AAGTCTATCC CCAAGGCTCC AGCTACTCTA 1560
AATTATGGTC TCCTTATAAG TTATTGCTGC TCCAGGAGAT TGCTCTCAT CGTCCAGGGG 1620
CTTGCTCCC ACGTGGTTGC AGATACTCTA GACCTGGTGC TCTAGGCTGT GCTGAGCCCA 1680
CTCTCCCGAG GCGCATCCA AGCGGGGGCC ACTTGAGAAG TGAATAAATG GGGCGGTTTC 1740
GGAAGCGTCA GTGTTTCCAT GTTATGGATC TCTCTGCTT TGAATAAAGA CTATCTCTGT 1800
TGCTCAC

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Seq ID NO: 132 Protein sequence
Protein Accession #: NP_036577.1

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70 1 11 21 31 41 51
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MENPSPAAL GKALCALLLA TLGAAGQPLG GESICARAP AKYSITFTGK WSQTAFPKQY 60
PLFRPAQWS SLLGAHSSD YSMWRKNQYV SNGLRDPFAER GEANALMKRI EAAGEALQSV 120
HAVPSAPAVP SGTGQTSBEL EVQRRLSLVS FVVRIVPSPD WFGVDSLDL CDGDRWREQA 180
ALDLYPYDAG TDSGTFPSSP NFATIPQDTV TEITSSSPSH PANSFYFPLR KALPFIARVT 240
LVRLRQSPRA FIPPAFVLPS RDNEIVDSAS VPETPLDCEV SLWSSWGLCG GHCEGLGTSK 300
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Seq ID NO: 133 DNA sequence
Nucleic Acid Accession #: NM_019894
Coding sequence: 1..1314

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80 1 11 21 31 41 51
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AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
CTGAGCCTGG CGAGTATCAT CATTTGGTTT GTCCTCATCA AGGTGATTCT GGATAAATAC 180
TACTTCTCTT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
CTGGACTGTC CCTTGGGGGA GGACGAGSAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
GCAGTGGCAG TCCGCTCTCT CAAGGACCGA TCCACACTGC AGGTGCTGGA CTGGGCCACA 360
GGGAACCTGT TCTCTGCTGT TTTGACAAAC TTCACAGAAG CTCTGCTGTA GACAGCCTGT 420
AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTGCAATGCG GAACTCAAGT 540
GGGCCCTGTC TCTCAGGCTC CTTGGTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
AGCATCCAGT ACAGACAAAC GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC 720
CTCAGCGCAG CCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
GGCTCAGACA AACTGGGCAG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840
TTCACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
GCCACCCAC TCTGGATCAT TGGATGGGG TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
GACATCTGTC TGACGGCTGT AGTCCAGGTC ATTGACAGCA CACGCTGCAA TGCAGACGAT 1080
GCGTACCAGG GGGAGATCAC CGAGAAGATG ATGTGTGACG GCATCCCGGA AGGGGGTGTG 1140
GACACCTGCC AGSGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
GTGGGCATCG TTAGTGGGG CTATGGCTGC GGGGGCCCGA GCACCCACAG AGTATACACC 1260
AAGGTCTCAG CCTATCTCAA CTGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

Seq ID NO: 134 Protein sequence

Protein Accession #: NP_063947.1

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1 11 21 31 41 51
MLQDPDSQDP LNSLDVKPLR KFRIPMETFR KVGIPILIAL LSLASIIIV VLIRVILDKY 60
YFLCQQLPHF IPRKQLCDGE LDCPLGEDDE HCVKSPFEGP AVAVRLSKDR STLQVLDSAT 120
GNWFACFDN FTEALAEATC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRMNS 180
GPCLSGSLVS LHCLACGKSL KTRPVVGGEE ASVDSWPQV SIQYDKQHVC GGSILDPEHW 240
LTAHRCFRKH TDVFNWKVRA GSKLGSFSPS LAVAKIIIE FNPMPKND IALMKLQFPL 300
TFSGTVRPIR LPFFDEELTP ATPLWIIWVG FTQNGGKMS DILLQASVQV IDSTRCNADD 360
AYQGEVTEKM MCAGIPBGGV DTCQDSSGP LMYQSDQWHV VGVISWVGVC GGPSTPGVYT 420

Seq ID NO: 135 DNA sequence

Nucleic Acid Accession #: NM_003045

Coding sequence: 148..2037

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75
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1 11 21 31 41 51
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CTGAGACATC TTTGCTGCAA GATCGAGGCT GTCCTCTGGT GAGAAGGTGG TGAGGCTTCC 120
CGTCATATTG CAGCTCTGAA CAGCAACATG GGGTGCAAG TCCTGCTCAA CATTGGGCAG 180
CAGATGCTGC GCGCGAAGGT GGTGGACTGT AGCCGGGAGG AGACGCGGCT GTCTCGCTGC 240
CTGAACACTT TTGATCTGGT GGCCTCGGG GTGGGCAGCA CACTGGGTGC TTGTGTCTAC 300
GTCCTGGCTG GAGCTGTGGC CGGTGAGAA GCAGGCCCTG CCATTGTGAT CTCTTCCTG 360
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CCCAAGACGG GCTCAGCTTA CCTCTACAGC TATGTCAACG TTGGAGAGCT CTGGGCCCTC 480
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ATGACTCTGA ACGCCCCCG CGTGTGGCT GAAAACCCCG ACATATTGCG AGTGATCATA 660
ATTCTCATCT TGACAGAGCT TTAACTCTT GGTGTGAAAG AGTCGGCCAT GGTCAACAAA 720
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TGTTTGAACA ATGACACAAA AGAAGGGAAG CCGGTGTGTT GTGGATTTCAT GCCCTTCGGG 900
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ATCGCCACA CAGGTGAAGA GGTGAAGAAC CCACAGAAGG CCATCCCGGT GGGGATCGTG 1020
GGTCCCTCT TGAATGCTT CATCGCCTAC TTTGGGGTGT CGGCTGCCCT CACGCTCATG 1080
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TGGGAAGGT CCAAGTACGC AGTGGCCGTG GGCTCCTCTT CGGCTCTTTC CGCCAGTCTT 1200
CTAGGTTCGA TGTTCCTCAT GCCTCGGGTT ATCTATGCCA TGGCTGAGGA TGGACTGCTA 1260
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TGGGTGCGC TTGCTGCTGT GATGGCTTC CTCTTGACC TGAAGGACTT GGTGGACCTC 1380
ATGTCCATTG GCATCTCTCT GGCTTACTCG TTGTGTGCTG CTGTGTGTTT GGTCTTACGG 1440
TACCAGCCAG AGCAGCCTAA CCTGGTATAC CAGATGGCCA GTACTTCCGA CGAGTTAGAT 1500
CGACGAGACC AAAATGAATT GGCAAGCACC AATGATTCCC AGCTGGGTTT TTTACAGAG 1560
CGAGAGATGT TCTCTTTGAA AACCACTACT TCACCCAAAA ACATGGAGCC TTCCAAAATC 1620
TCTGGGCTAA TTGTGAACAT TTCAACAGC CTTATAGCTG TTCTCATCAT CACCTTCTGC 1680
ATTGTGACCG TGCTTGAAG GGAGGCTCTC ACCAAGGGG CGCTGTGGGC AGTCTTCTG 1740
CTCGCAGGGT CTGCCCTCTT CTGTGCCGTG GTACGCGGCG TCATCTGGAG GCAGCCCGAG 1800
AGCAAGACCA AGCTCTCATT TAAGGTTCCC TTCTGCGGAC TGCTCCCAT CTTGAGCATC 1860
TTGTGTGAGC TCTATCTCAT GATGACGCTG GACCAAGGCA CCTGGGTCCG GTTGTCTGTG 1920
TGGATGCTGA TAGGCTTCAT CATCTACTTT GGCTATGGCC TGTGGCAGC CGAGGAGGCG 1980
TCCCTGGATG CCGACCAAGC AAGGACTCCT GACGCAACT TGGACCAATG CAAGTACGCG 2040
ACAGCCCCGC CCCCCGAGG TGGCAGCAG CCGAGGGAC GCCCCAGAG GACCGGAGG 2100
CACCCACACC TCCCCACCAG TGCAACAGAA ACCACTGCG TCCACACCT CACTGCA

Seq ID NO: 136 Protein sequence

Protein Accession #: NM_003045

1 11 21 31 41 51
| | | | | |
1003

5 MGCKVLLNIG QQMLRRKVVD CSRESTRLSR CLNTFDLVAL GVGSTLGAHV YVLGAVARE 60
 NAGPAIVISF LIAALASVLA GLCYGEFGAR VPKTGSAYLY SYVTGELWA FITGWNILIS 120
 YIIGTSSVAR AWSATFDELI GRPIGEFSRT HMTLNAPGVL AENPDIFAVI IILILTGLLT 180
 LGVKESAMVN KIFTCTINVLV LGFIMVSGFV KGSVKRWQLT EEDFGNTSGR LCLNNDTKEG 240
 KPGVGGPMFP GPSGVLSGAA TCFYAFVGF D CIATTGSEVK NPQKAIPVGI VASLLICPIA 300
 YFGVSAALTL MPPYFCLDMN SPLPDAFKHV GWEGAKYAVA VGLCALASAS LLGSMFFMPR 360
 VIYAMAEDGL LFKFLANVND RTKTPIIATL ASGAVAAVMA FLFDLKLVD LMSIGTLLAY 420
 10 SLVAACVLVL RYQPEQPNLV YQMASTSEDL DPADQNELAS TNDSQLGLPLF EAMFSLKTI 480
 LSPKNMEPSK ISGLIVNIST SLIAVLIITF CIVTVLGRE A LTKGALMAVF LLAGSALLCA 540
 VVTGVINRQP ESKTKLSFKV PFLPVLPILS IFNVVYLMQ LDQGTWVRFA VWMIGTFIY 600
 FGYGLMHSEE ASLDADQART PDGNLDQCK

15 Seq ID NO: 137 DNA sequence
 Nucleic Acid Accession #: NM_032044.1
 Coding sequence: 182..658

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40 Seq ID NO: 138 Protein sequence
 Protein Accession #: NP_114433.1

45 1 MASRSMRLLL LLSCLAKTGV LGDIIMRPSK APGWPHYKSN CYGYFRKLKN WSDAELEQCS 60
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50 Seq ID NO: 139 DNA sequence
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70 Seq ID NO: 140 Protein sequence
 Protein Accession #: XP_051860.2

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5 SEYPGSYLTK NDNWLVRHPD CINVDPWRGA ICSGCAQMY IQAYKTENLR MKIIRKNDFPS 660
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10 Seq ID NO: 141 DNA sequence
 Nucleic Acid Accession #: Bos sequence
 Coding sequence: 261..2861

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Seq ID NO: 142 Protein sequence
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Seq ID NO: 144 NP Protein sequence

Protein Accession #: NP_006008.1

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Seq ID NO: 146 Protein sequence

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 45 PCMCRCCKNC GGENHQKQKE NGPFLRKCFA ISLLVICIII SIGIFYGFVA NHQVRIKIR 180
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 50 YDSYWLGLGL VICSLTLIV IFYVLGLLGG VGVDRHATP TTRGCVSNTG GVFLMVGVL 480
 SFLPCMLIMI IVLVTFVFGA NVEKLICBPY TSKELFRVLD TPYLINEDWE YVLGKLFNK 540
 SKMKLTFEQV YSDCKKNRGT YGTLHLQNSF NISEHLNINE HTGSISSLE SLKVMNLNIFL 600
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 55 NTSSVIIEST KKYGRITIGY FEHYLQWIEF SISEKVASCK PVATALDTAV DVFLCSYIID 780
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Seq ID NO: 149 DNA sequence
 Nucleic Acid Accession #: NM_033049.1
 Coding sequence: 28..1566

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 70 ACACATAGTT CCTCCACAT TCCTATACCT ACTGCTGCAG ACAGTGAGTC AACCACAAAT 360
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Seq ID NO: 150 Protein sequence
 Protein Accession #: NP_149038.1

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 40 LHSEITSLFK DVFQTSVYQG TVLLTVSTSL SPRSEMRADD KFNVTIVTII LAETTSNEK 300
 TVTEKINKAI RSSSNFLNY DLTLLRCDYD CNOTADDCLN GLACDCSDSL QRPNPQSPFC 360
 VASSLKCPDA CNAQHKQLI KXSGGAPECA CVPGYQEDAN GNCQKCAFYG SGLDCDKFKQ 420
 LILTIVGTIA GIVILSMIIA LIVTARSNK TKHIERENLI DEDFQNLKLR STGFTNLGAE 480
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Seq ID NO: 151 DNA sequence
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 65 AATGGGCTTT CATTTGTGTC CCTATGTGT CCTCTGTG TGCCAACAAG AAATCATCAG 900
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 70 TAAACTTTGT CATATGGTAC AAATATTCCC TGCCCCCTG CAGTTTCCCA TTTGTCTTTC 1140
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40 Seq ID NO: 152 Protein sequence
Protein Accession #: Eos sequence

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1 MGAPHWWDQL QAGSSEVDWC EDNYTIVPAI AEFYNTISNV LFFILPPICM CLFRQYATCF 60
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DRGRFVKVVS VLSAVTTCLA FVKPAINNIS LMTLGVPCTA LLIAELKRCR NMRVFKLGLF 180
SGLWNTLALF CWISDRACE LLSSPNFPYL HCMWHILICL AAYLGVCVCPA YFDAASEIPE 240
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50 Seq ID NO: 153 DNA sequence
Nucleic Acid Accession #: NM_001432.1
Coding sequence: 167..676

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Seq ID NO: 154 Protein sequence
 Protein Accession #: NP_001423.1

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 LTVILILFL ITVVGSTYYF CRWYRNRSK EFKKEYERVV SGDPQLPQV

Seq ID NO: 155 DNA sequence
 Nucleic Acid Accession #: NM_013282.2
 Coding sequence: 85..2466

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 ACCACACCGG TGGACTCGCT GTCCAGGCTG ACCAAGGTGG AGGAGCTGAG GCGGAAGATC 180
 CAGGAGCTGT TCCACGTGGA GCCAGGCTGT CAGAGGCTGT TCTACAGGGG CAAACAGATG 240
 70 GAGGACGCGC ATACCTCTT OGAATACGAG GTCCGCTGTA ATGACACCAT CCAGCTCCTG 300
 GTCCGCCAGA GCCTCTGTCT CCCCCACAGC ACCAAGGAGC GGGACTCGA GCTCTCCGAC 360
 ACCGACTCCG GCTGCTGCCT GGGCCAGAGT GAGTCAGACA AGTCTCCAC CCAAGGCGAG 420
 GCGGCGCGCG AGACTGACAG CAGGCCAGCC GATGAGGACA TGTGGGATGA GACGGAATTG 480
 GGGCTGTACA AGGCTCAATG GTACGTGAT GCTCGGACA CGAACATGGG GCGGTGGTTT 540
 75 GAGGCGCAGG TGTGAGGGT GACGCGAAG GCCCCTCCC GGGACGAGCC CTGAGCTCC 600
 AGTCCAGGC CGGCGCTGGA GGAGGACGTC ATTTACCAGC TGAATAACGA CGACTACCG 660
 GAGAAGCGCG TGTCTCAGAT GAATCCAGG GAGTCCGAG CGGCGCCCG CACCATCATC 720
 AAGTGGCAGG ACCTGGAGGT GGGCCAGGTG GTCATGCTCA ACTACAAACC CGACAAACCC 780
 80 AAGGAGCGGG GCTTCTGGTA CGACGCGGAG ATCTCCAGGA AGCGCGAGAC CAGGACGCG 840
 CGGAACTCT ACGCCAAGT GGTGCTGGGG GATGATTCTT TGAACGACTG TCGGATCATC 900
 TTGTGGAGC AAGTCTTCAA GATTGAGCGG CCGGTGGAAG GAGCCCAT GGTGTGACAC 960
 TCCATGAGAC GGAAGAGCGG CCGTCTCTGC AAGCACTGCA AGGACGAGCT GAACAGACTC 1020
 TGCGGGTCT GCGCCTGCCA CCTGTGCGGG GCGCGGAGG ACCCGACAA CGAGCTCATG 1080
 TGGATGAGT GCGACATGCG CTTCCACATC TACTGCTGG ACCCGCCCT CAGCAGTGT 1140

5	5	10	15	20	25	30	35	40	45
CCCAGCAGG	ACGAGTGGTA	CTGCCCTGAG	TGCCGGAATG	ATGCCAGGGA	GGTGGTACTG	1200			
GCGGAGAGC	GGCTGAGAGA	GAGCAAGAAG	AAGGCGAAGA	TGGCTCGGC	CACATCGTCC	1260			
TCACAGCGGG	ACTGGGGCAA	GGGCATGGCC	TGTGTGGGCC	GCACCAAGGA	ATGTACCATC	1320			
GTCCCGTCCA	ACCACTACGG	ACCCATCCCC	GGGATCCCCG	TGGGCACCAT	GTGGCGGTTC	1380			
CGAGTCCAGG	TCAGCGAGTC	GGGTGTCCAT	CGGCCCCACG	TGGCTGGCAT	ACACGGCGGG	1440			
AGCAACGACG	GAGCGTACTC	CCTAGTCCCTG	GCGGGGGGCT	ATGAGGATGA	CGTGGACCAT	1500			
GGGAATTTTT	TCACATACAC	GGGTAGTGGT	GGTCGAGATC	TTTCGGGCAA	CAAGAGGACC	1560			
GCGGAACAGT	CTTGTGATCA	GAAACTCACC	AACACCAACA	GGGCGCTGGC	TCTCAACTGC	1620			
TTTGCTCCCA	TCAATGACCA	AGAAGGGGCC	GAGGCCAAGG	ACTGGCGGTC	GGGGAAGCGG	1680			
GTCAGGGTGG	TGCGCAATGT	CAAGGGTGGC	AAQAATAGCA	AGTACGCCCC	CGCTGAGGGC	1740			
AACCGCTACG	ATGCGATCTA	CAAGGTGTGT	AAATACTGGC	CCGAGAAGGG	GAAGTCCGGG	1800			
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CGGCGACAG	TGTTTACAGT	CCCTGCTGTC	CGCTACGACC	TGGGCGCGAG	CTATGCCATG	2400			
CAGGTGAACC	AGCCTCTGCA	GACCGTCTTC	AACCGCTCT	TCCCCGGCTA	CGGCAATGGC	2460			
CGGTGATCTC	CAAGCACTTC	TCGACAGGCG	TTTGTCTGAA	AACTGTTCGG	AGGGCTCGTT	2520			
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CCTAAATAGT	TTTGTCTTCC	TTTTTTTTTA	TTTTTATTTT	TCAATCTAT	ACATTITCAG	2640			
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CATAAAGGCC	TGCAATTTCT	CGACAAAACA	ACACAAGATT	TTTTAAAGAT	GGAATCAGAA	2760			
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CAACTCTTTA	AGAAGGCGAC	AGGATCAGTC	CTTCTCTAGG	GTTCTGGCCC	CCAAGGTCA	2880			
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CACGCGAATA	TGGCTCTAAG	GGGACTCTGC	TCCACGTGGG	GCCAGGCGTG	TGACTGAOCG	3180			
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GTCAACCGGA	TTCTAGAAAC	TGCGGTCACT	CAGTTCTTCC	TGACACCGGA	TGGGTGCTTG	3360			
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GAGCAATGTT	ATTTTTTAA	GGTTTTTTTC	ACCTCCTTAT	TCTTAGATTA	TTAATGTATT	3720			
AGGGAAGAAT	GAGACAAATT	TGTTAGGCT	TTTTCTAAAG	TCCAGTACTT	TGTCAGATT	3780			
TTAGATTCTC	AGAATAAATG	TTTTTCACAG	ATTGAAAAAA	AAAAAAA					

Seq ID NO: 156 Protein sequence
Protein Accession #: NP_037414.2

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	YEVRLADTIQ	LLVRQSLVLP	HSTKERDSEL	SDTDSGCCLG	QSESDKSSTH	GEAAAEATDSR	120
	PADEDMDET	ELGLYKNEY	VDARDTNGA	WFEAQVVRVT	RKAPSRDEPC	SSTSRPALBE	180
55	DVIYHVXKDD	YPENGVVQNM	SRDVRARAR	IIKWQDLEVG	QVVMNLNYPD	NPKERGFWD	240
	AEISRKRETR	TARELYANV	LGDDSLNDCR	IIFVDEVFKI	BRPGEKSPMV	DNPMRRKSGP	300
	SCXKCKDDVN	RLCRVCACHL	CGGRQDFDKQ	LMCDECDMAF	HIYCLDPFSL	SVPSSEBNYC	360
	PECRNDASEV	VLAGERLRES	KKKAKMASAT	SSSQRDWKGK	MACVGRTEKC	TIVPSNHYGP	420
	IPGIFVGTMW	RFRVQVSESG	VHRPHVAGIH	GRSNDGAYSL	VLAGGYEDDV	DHGNFFTYTG	480
60	SGGRDLGSKN	RTAEQSCDQK	LTNTNRALAL	NCFAPINDQR	GABAKDWRSG	KPVVRVENVK	540
	GGKNSKYAPA	EGNRYDGIYK	VVKYWPBKPK	SGFLVWRYLL	RRDDDEPGPW	TGEGKDRIKK	600
	LGLTMQYPEG	YLBALNRER	EKENSKREEE	BQBGGFASP	RTGKGKWKRK	SAGGGPSRAG	660
	SPRRTSEKTK	VEPYSLTAQ	SSLIREKSN	AKLWNEVLAS	LKDRPASGSP	FQLFLSKVEE	720
65	TFQCICCCQL	VFRPITTVQ	BNVCKDCLDR	SFRAQVPSCP	ACRYDLGRSY	AMQVNPQLQT	

Seq ID NO: 157 DNA sequence
Nucleic Acid Accession #: NM_000756.1
Coding sequence: 186..776

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	TCTCTGCAGA	GAGGCGGCAG	CACCCGCTC	ACCTGCGAAG	CGCCTGGGAA	GCGAGTGCCC	180
75	CTAACATGCG	GCTGCCGCTG	CTTGTGTCCG	CGGGAGTCCCT	GCTGGTGGCT	CTCCTGCCCT	240
	GCCCGCATCG	CAGGCGGCTC	CTGAGCCGCG	GGCCGGTCCC	GGGAGCTCGG	CAGGCGCGCG	300
	AGCACCTCA	GCCCTTGGAT	TTCTTCCAGC	CGCCGCGCA	GTCGAGCAG	CCCCAGCAGC	360
	CGCAGGCTCG	GCGGGTCCCT	CTCCGATGCG	GAGAGGAGTA	CTTCTCCGCG	CTGGGGAACC	420
	TCAACAGAG	CCCGGCGGCT	CCCTTTCCG	CGCCTCTCT	GCTCTCGCG	GGAGGCGAGC	480
80	GCAGCGCGCC	TTCCGCGGAA	CAGGCGACCG	CCAACTTTTT	CGCGGTGTTG	CTGCAGCAGC	540
	TGCTGTCTCG	TCCGCGCTCG	CTCGACAGCC	CGCGGCTCT	CGCGAGCGCG	GGCGCTAGGA	600
	ATGCCCTCGG	CGCCACCCAG	GAGGCACCGG	AGAGAGAAAG	GCGGTCCGAG	GAGCCTCCCA	660
	TCTCCCTGGA	TCTCACCTTC	CACCTCTCTC	GGGAAGTCTT	GGAAATGGCC	AGGGCGAGC	720
	AGTTAGCACA	GCAAGCTCAG	AGCAACAGGA	AACTCATGGA	GATTATTGGG	AAATAAAAGC	780

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GTGCGTTTGG CCAAAAAGAA TCTGCATTTA GCACAAAAAA AATTAAAAAA AATACAGTAT 840
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GGGAGAGAGG GAGAGAGCCT ATACCCCTTA CTAGCATGCG ACAAAGTGTA TTCACGTGCA 960
GCAGCAACAC AATGTTATTC GTTTTGTCTA CTTTAGTTT CCGTTTCCAG GTGTTTATAG 1020
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AGTCACTCAA TGTGTTTTGT TGTGCTCTGA GCCAAAGAGA ATGCCATTCT CTTGGGTGGG 1140
TAAGACTAAA TCTGTAAGCT CTTTGAAACA ACTTTCCTCT GTAAACGTTT CAGTAATAAA 1200
ACATCTTTCC AGTCCTTGCT CAGTTTGGTT GTGTAAGAGA ATGTTGAATA CTTATATTTT 1260
TAATAAAAGT TGCAAAGGT

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Seq ID NO: 158 Protein sequence
Protein Accession #: NP_000747.1

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LPRRLSDSPA ALAERGARNA LGGHQEAPER ERRSEEPPI SLDLTFHLLRE VLEMARAEQL 180
AQAHSNRKL MEIIGK

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Nucleic Acid Accession #: NM_001200.1
Coding sequence: 325..1514

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GAGAAGGAGG AGGCAAGAA AAGGAACGGA CATTCGCTCC TTGCGCCAGG TCCTTTGACC 240
AGAGTTTTC CATTGTGGAG CTCTTCAAT GGAAGTGTCC CCGCTGTCTT CTAGACGGA 300
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TTCCCGAGGT CTTCTGGGCG GCGCGGCGCT GCCTCGTTCC GGAGCTGGGC CGCAGGAAGT 420
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CGGTGCTGCC CCGCTACATG CTAGACCTGT ATCGCAGGCA CTCAGGTGAG CCGGCTCAC 600
CCGCCCCAGA CCACCGGTTG GAGAGGCGAG CCAGCGAGC CAACACTGTG CGCAGCTTCC 660
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TGGAGGAGAA ACAAGGTGTG TCCAAGAGAC ATGTTAGGAT AAGCAGGTCT TTGCACCAAG 1080
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ACTCTAAGAT TCCTAAGGCA TGCTGTGCTC GCACAGAACT CAGTGTCTAT TCGATGCTGT 1440
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GTGGGTGCTG CTAGTACAGC AAAATTAAAT ACATAAATAT ATATATA

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Seq ID NO: 160 Protein sequence
Protein Accession #: NP_001191.1

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FGLKQRPTPS RDAVVPYML DLYRRHSGQP GSPAPDRLLE RAASRANTVR SFPHHEESLE 120
LEPESGKTTR RFFNLSISIP TEEFITSABL QVFREQMQDA LGNNSSFHHR INIYBIKPA 180
TANSKFPVTR LLDLT

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Seq ID NO: 161 DNA sequence
Nucleic Acid Accession #: NM_001999.2
Coding sequence: 1..8736

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CAGCCGCGCG CGCAACAGGT TCGGTCCGCT ACAGCAGGCT CTGAAGGCGG GTTCTTAGCG 180
CCCGAGTATC GCGAGGAGGG TGCCGAGTGG GCCAGCCGCG TCCGCGCGCG AGGACAGCAG 240
GACGTGCTCC GAGGGCCCAA CGTGTGCGGC TCCAGATTCT ACTCTACTG CTGCCCTGGA 300
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GATGGAATTT GTTCCCGTCC TAACATGTGT ACTTGTTCCT GTGGGCAAAAT ATCATCAACC 420
TGTGATCAA AATCAATTCG GCAGTGCAGT GTGAGATGCA TGAATGGTGG GACCTGTGCA 480
GATGACCACT GCGAGTGCCA GAAAGGATAT ATTGGAACCT ATTGTGGACA ACCTGTCTGT 540
GAAAATGGAT GTCAGAATGG TGGACGTTGC ATGCCCAAC CGTGTGCTTG TGTATTGGG 600
TTCACTGGTC CACAGTGTGA AAGAGATTAC AGGACAGGCC CGTGTTCAC TCAGGTCAAC 660
AACCAGATGT GCAAGAGGCA GCTGACAGGC ATTGTCTGCA CGAAGACTCT GTGCTGTGCC 720
ACCACTGACG GGGCGTGGGG CCATCCCTGT GAGATGTGTC CAGCCCAAGC TCAGCCCTGC 780
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	TTTTGTGTTT	TTCCACGTGG	ATATGTAACC	TCAACAGATG	GCTCTCGATG	CATCGATCAG	1080
5	AGAACAGGCA	TGTGTTTCTC	GGGCTCTGGT	AATGGCCGCT	GTGCACAGA	GCTCCCGGGG	1140
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	CCTGAAGCCT	GTCCTGTCTG	AGGTTCTGAG	GAATATGCGA	GACTTTGCAT	GGATGGACTT	1260
	CCAAATGGAG	GAATTCAGG	GAGTGTGGT	TCCAGACCTG	GAGGCACTGG	GGGAAATGGC	1320
	TTTGCCCAAA	GTGGCAATGG	CAATGGCTAT	GGCCACAGAG	GGACAGGCTT	CATCCCCATC	1380
10	CCTGAGAGCA	ATGGCTTTTC	TCTGGCGTT	GGGGAGCCG	GTGTGGGGGC	CGGGGACAG	1440
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Seq ID NO: 162 Protein sequence
 Protein Accession #: NP_001990.1

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Seq ID NO: 163 DNA sequence

Nucleic Acid Accession #: NM_013372.1

Coding sequence: 63..617

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 Protein Accession #: NP_037504.1

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 GAGGATATCC GAGCCGAGC AGACACCTT ATGTTGAGG GTCACGACAC AACATCCAGT 1080
 80 GGGATCTCTT GGATGCTGTT CAATTTGGCA AAGTATCCGG AATACCGGA GAAATGCGA 1140
 GAAGAGATTC AGGAAGTCAT GAAAGGCGG GAGCTGGAGG AGCTGGAGTG GGACGATCTG 1200
 ACTGCTGTC CTTTACAACT TATGTGCATT AAGGAGAGCC TGCGCCAGTA CCCACTGTC 1260
 ACTCTTGTCT CTGCGCAATG CACGAGGAC ATCAAGCTCC CAGATGGGCG CATCATCCCC 1320
 AAGGAATCA TCTGCTTGGT CAGCATCTAT GGAACCCACC ACAACCCAC AGTGTGGCCT 1380
 GACTCCAAGG TGTACAACCC CTACCGCTTT GACCCGACA ACCACAGCA GCGCTCTCCA 1440

CTGGCCTATG TGCCCTTCTC TGCAGGACCC AGGAATTGCA TCGACAGAG CTTCGCCATG 1500
 GCGAGTTCG GCGTGGTGT GGCCTAACA CTGCTAOGTT TCGGCTGAG CGTGGACCGA 1560
 ACGCGCAAGG TCGGCGCGAA GCGGAGCTC ATACTGCGCA GCGAGAACGG GCTCTGGCTC 1620
 AAGGTGGAGC CGCTGCTCC GCGGGCTGA

Seq ID NO: 167 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 | | | | |
 MPPLPSRMSR GPSLVTGRML PITDRLLHLL GLEKTAFRY AVSTLLFL FFLPRLRLRF 60
 LRLCRSPYIT CRRLRCFPQP PRRNWLLGHL GMYLPNEAGL QDEKKVLDNM HHVLLVMMGP 120
 VLPFLVLVHP DYIKPLLGAS AALAPKDDLF YGFLKPWLDG GLLLSRGDKM SRHRRLLTPA 180
 PHFDILKPYM KIFNQSDIM HAKWRHLAEG SAVSLDMFEH ISLMTLDSLQ KCVFSYNSNC 240
 QEKMSDYISA IIELSALSVR RQYRLHHYLD FIYYSADGR RFRQACDMVH HFTTEVIQER 300
 RRALRQQGAE AWLKAQKQKT LDFIDVLLLA RDEDGKELSD EDIRAEADTF MFBGHDTTSS 360
 GISWMLFNLA KYPEYQEKCR EBIQEVMKGR ELELEWDDL TQLPFTTMC I KESLRQYPPV 420
 TLVSRQCTED IKLPDGRIP KGIICLVSIY GTHNPTVWP DSKVYNPYRF DFDNPQQRSP 480
 LAYVPSFAGP RNCIQQSPAM ASLRVVVALT LLRFRLSVDR TRKVRKPEL ILRTENGLWL 540
 KVEPLPFRA

Seq ID NO: 168 DNA sequence
 Nucleic Acid Accession #: AK058088.1
 Coding sequence: 252..1772

1 11 21 31 41 51
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 AGGAAACCAA GGCAAGCTCC CCCTGTCAAA GCACCTTGGC CCATAAGAAG AAAAGGGGGA 60
 GCCCCAGATG TGATGAGCGC TTCCAGGCTT CAGGCTCAGA AGGCGCCCCC AGCTCTCCTG 120
 TAACCTCAGG GCGCAGTGTG TGGGAGTTCC TCCACTCAGC ACACCTCCCC TGTAACACAG 180
 CCTGTGGTGG GCAAAGAGGC TTGGGAACGG TTGCTTGTCT TTCTCTCTCT GCGTAATTTC 240
 CACTTTTATT CATGATAATG TCGAACACGC ACAAAGCTCG GCTGGAAACG CCGGTCACTG 300
 GCTCAACCAA CCGGTGGGCT TTGCCCAAC AGCCTTCTC TGGGGACCTG CTCTCACTTT 360
 CCCAGATGTG CAAGGCTCTG AGCATAGACT TTGAGGAAGC TTTGAGGAAC CCAGACAGGT 420
 TATGCTTTTC ACAATCCAG AAGTTTTTCT TTGAGAATTT CAAGAACAAG GACATCCAAA 480
 TGGGGGAAGC AGATGTGATT CTGAGTGCCT TGGGCTTCAA ATGGGAGCTC CATCAGCCCC 540
 GGCTTTTTCG GTCTGAGACC TTGGCCAAGC TCTACCTGAA AGCCTGGCG CAGGGCAACA 600
 CACACCCCTT GAGGGAGCTG GAGGAGCTTC TCGAGCTCA ATCACCTAAG AAGACCAAG 660
 AAAAATCCCC TGCAAGAGG ATCATCATTT CCTTGAAGAT CAATGACCCA CTGGTCACTA 720
 AAGTGCCTCT CGCCAGCGCC CTGAAGAACC TCTACATGAG TGAGGTGGAG ATTAACCTGG 780
 AAGACCTACT GGGAGTGTCT GCTTCGCCCC ACATCCTCCA GTTCAGTGGC CTGTTTCAAA 840
 GGTGGGTGGA TGTGATGATA GCCAGACTCA AGCCAAGCAC CATCAAGAAA TTCTACGAGG 900
 CCGGCTGCAA GTACAAGGAA GAGCAGCTCA CCACCGGCTG CGAGAAGTGG CTGGAATGA 960
 ACTTGGTTCC TCTAGGGGGG ACGCAGATCC ACCTCCACAA AATCCACAG GACCTGCTCC 1020
 ACAAGTGTCT GAAGTCCCCC AGGTATTATTA CCTTTAGTGA ATTCCATCTT CTGAAAACAA 1080
 TGTCTTTGTG GGTCTTCTTG CAACTGAATC ACAAGATTCA GGCATTTCCG ACTTATGAAA 1140
 CCGTATGATC ATTTTAAAG AGCTTCTCTG AGAAGCTGTG CTCTCTGGAC CGGGACATAG 1200
 GACGAGCTTT GAGGCGCTC TTCTCTGCTT TGGCTCTGCA CGGCATCACC AAAGGCAAGG 1260
 ATCTGGAGGT GCTGCGGAC CTTAACTTCT TCCAGAGTCT ATGGCTCGAG CAGTTTACAG 1320
 TCAACCATTA CCAAGCAGCT GAGAAATGGG GCGACATGTT CCACCTGAAA GATCTTAAAC 1380
 CCCAGGCTGT GAGATTGGG CTGCTCTTTA ACCAGGAGAA TACAATTAT TOGAAAACGA 1440
 TTGCTCTATA TGGATTCTTC TTAAAGATAA AGGAGCTCAA ACATGATACT ACCTCTTATA 1500
 GTTTTTCAT CAGAGAATA AAGCACAGC ACCTGGAATC TCCTCTGCG GTCTACGAGC 1560
 ACAACCAAGT CAGCTTGGGA GGGCACGCC TGGTGAAGTA TGAGATCAGA GCAGAGGCC 1620
 TGGTTGACGG CAAGTGGCAG GAGTTCAGGA CAACACAGAT CAAGCAGAAG TTTGGGTGA 1680
 CCACTCATCT CTGCAAAAGC CATACTTGA AAATCCAAAC TGTGGGCATC CCAATCTATG 1740
 TAAGTTTTCG ATTCATCTTC CCAGCATCTT GACAGTTTCC AGAAGAATCT ATGGGATTTT 1800
 CCCCCCACTG GTCTGCATAA AAGAAAATAA AATGACATRA AAGGGAGC

Seq ID NO: 169 Protein sequence
 Protein Accession #: BAB1658.1

1 11 21 31 41 51
 | | | | |
 MIMSNTKAR LERRVTGSTN RWRLPKQPPS GDLLSLSQMC KALSIDFEEA LRNPDRLCIS 60
 QIQKFFPENF KNKDIQSGEA DVILECLGFK WELHQPRLFQ SETLAKLYLK ALAQGTTHPL 120
 RELEELLRAQ SPKKTKKSP AKRIIISLKI NDPLVTKVAF ATALKNLYMS EVBINLEDLL 180
 GVLAHAHLQ FSLGFORCVD VMIAHLKPSI IKKPYEAGCK YKEBQUTTG EKWLEMLVP 240
 LGGTQIHLHK IPQDLHLKVL KSPRLFTFSE FHLLKTMLLW VFLQLNYKIQ AIPTYETVMT 300
 FPKSPFENCC FLORDIGRSL RPLFLCLRHL GITKKGDLSE LRHLNFPFES WLDQVTNVHY 360
 HALENGGDMV HLKDLNTQAV RFGLLFNQEN TTVSKTIALY GPPFKIKGLK HDTTTSYSFYM 420
 QRIKHTLES PSAVYENHEV SLRAARLVKY BIRAEALVDG KMQEPRTNQI KQKFGLTSS 480
 CKSHTLKIQT VGPIIYVSPA FIPPAS

Seq ID NO: 170 DNA sequence
 Nucleic Acid Accession #: NM_007000.1
 Coding sequence: 1...777

1 11 21 31 41 51
 | | | | |
 ATGGCGTCTG CGGCAGCAGC GGAGGCCGAG AAGGGATCTC CAGTTGTGGT GGGCGTCTA 60
 GTTGTGGGCA ATATCATTAT TCTGCTGTCA GGCGTGTCCC TGTTTGCTGA GACCATATG 120
 GTGACAGCCG ACCAGTACCG TGTATACCCA CTGATGGGAG TCTCAGGCAA GGATGAGCTC 180
 TTGCTGTGTG CCTGATTGTC CATCTTCTGC GGCTTCTCCT TCTTCATGCT AGCCAGTTTT 240

5
10
Seq ID NO: 171 Protein sequence
Protein Accession #: NP_008931.1

15
20
1 11 21 31 41 51
MASAAAAEAR KQSPVVVGLL VVGNIIILLS GLSLFARTIN VTADQYRVYP LMGVSGKIDV 60
FAGAWIAIPC GFSFFMVASF VGGAALCRRR SMVLTYLVLM LIVYIFECAS CITSYTHRDY 120
MVSNSPLITK QMLTFYSADT DQGELETRLM DRVMIQECC GTSGPMDWVN FTSAFRAATP 180
EVVFPWPFLC CRRTGNFIPL NEBGCRIGHM DYLPFKGCFE HIGHAIDSYT WGISWFGFAI 240
LMWTLFVMLI AMYFPTML

25
Seq ID NO: 172 DNA sequence
Nucleic Acid Accession #: NM_006760.1
Coding sequence: 39..593

30
35
40
1 11 21 31 41 51
GAAAGCCTGC CAGCACCTAT TCCACCTCCC AGCCAGCAT GGCACCCCTG CTGCCCATCC 60
GGACCTTGCC CTGTATCCTG ATTCTGCTGG CTCTGCTGTC CCCAGGGGCT GCAGACTTCA 120
ACATCTCAAG CCTCTCTGGT CTGCTGTCCC CGGCGCTAAC GGAGAGCCCTG CTGGTTGCCT 180
TGCCCCCTGT TCACCTCACA GGAGGCAATG CCACACTGAT GGTCCGGAGA GCCAATGACA 240
GCAAAAGTGGT GACGTCCAGC TTTGTGGTGC TCCTCGTCCC TGGGCGCAGG GAAGTGGTGA 300
GTGTGGTGA CAGTGGTGCT GGCTTCACAG TCACTGGGCT CAGTGCATAC CAGGTGACAA 360
ACCTCGTGCC AGGAACCAAA TTCTACATT CTACCTAGT GAAGAAGGGG ACAGCCACTG 420
AGTCCAGCAG AGAGATCCCA ATGTCCACAC TCCTCGAAG GAACATGGAA TCCATTGGGC 480
TGGGTATGGC CCGCACAGGG GGCACTGGTG TCATCACGGT GCTGCTCTCT GTCGCCATGT 540
TCCTGTGGT GCTGGGCTTC ATCATTTGCC TGGCACTGGG CTCCCGCAAG TAAGGAGGTC 600
TGCCCCGAGC AGCAGCTTCT CCAGGAAGCC CAGGGCAGCA TCCAGCTCCC CAGCCCACCT 660
GCTCCAGAGC CCGAGGCTCT TGGCTCCCTT GGTGCCCTCG CCTCCTCTTC CTGCCCTCCT 720
CTCCCCTAGA GCCTCTCTCT CCTCTGTCC CTCTCTCTGC CCCCAGTGCC TCACCTTCCA 780
ACACTCCATT ATTCCTCTCA CCCCCTCCT GTCAGAGTTG ACTTCTCTCC CATTTTACCA 840
CTTTAAACAC CCCATAACA ATTCCCCAT CCTTCAGTGA ACTAAGTCCC TATAATAAAG 900
GCTGAGGCTG CATCTGCCAA AAAAAA AAAA

45
Seq ID NO: 173 Protein sequence
Protein Accession #: NP_006751.1

50
1 11 21 31 41 51
MAPLLPIRTL PLILILLALL SPGAADFNIS SLSGLLSPAL TESLLVALPP CHLTGGNATL 60
MVRANDSKV VTSSEFVPPC RGRRELVSUV DSGAGFTVTR LSAYQVNLV PGTFKYISYL 120
VKKGATATESS RBIPMSTLPR RMESIGLGM ARTGGMVVIT VLLSVAMFLV VLGFIIALAL 180
GSRK

55
Seq ID NO: 174 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2733

60
65
70
75
80
1 11 21 31 41 51
ATGAAAGTTG GAGTGCTGTG GCTCATTICT TTCCTCACCT TCACTGACGG CCACGGTGGC 60
TTCCTGGGGA AAAATGATGG CATCAAAACA AAAAAAGAAC TCATTGTGAA TAAGAAAAAA 120
CATCTAGGCC CAGTCGAAGA ATATCAGCTG CTGCTTCAGG TGACCTATAG AGATTCCAAG 180
GAGAAAAGAG ATTTGAGAAA TTTTCTGAAG CTCCTGAAGC CTCATTATT ATGGTCACAT 240
GGGCTAATTA GAATATCAG AGCAAAAGCT ACCACAGACT GCAACAGCCT GAATGGAGTC 300
CTGCAGTGA CCTGTGAAGA CAGCTACACC TGGTTCCCTC CCTCATGCCCT TGATCCCCAG 360
AACTGCTACC TTCACACGGC TGGAGCACTC CCAAGCTGTG AATGTCATCT CAACAACCTC 420
AGCCAGAGTG TCAATTTCTG TGAGAGAACA AAGATTGGG GCATTTCAC AATTAAATGAA 480
AGGTTTACAA ATGACCTTTT GAATTCATCT TCTGCTATAT ACTCCAATA TGCAAAATGGA 540
ATTGAAATTC AACTTAAAAA AGCATATGAA AGAATTCAAG GTTTTGAGTC GGTTCAGGTC 600
ACCCAATTTC GAAATGGAAG CATCGTTGCT GGGTATGAAG TTGTTGGCTC CAGCAGTGCA 660
TCTGAATGTC TGTACGCCAT TGAACATGTT GCGGAGAAGG CTAAGACAGC CCTTCACAAG 720
CTGTTTCCAT TAGAAGACGG CTCCTTCAGA GTGTTCCGAA AAGCCCAAGT TAATGACATT 780
GTCTTTGAT TTGGGTCCAA GGATGATGAA TATACCTCG CCTGCAGCAG TGGCTACAGG 840
GGAAACATCA CAGCCAGTGT TGAGTCTCTT GGTGGCAGG TCATCAGGGA GACTTGTGTG 900
CTCTCTCTGC TTGAAGAATC GAACAAGAAT TTCAGTATGA TTGTAGGCAA TGCCACTGCA 960
GCAGCTGTGT CATCTCTGTT GCAAAATCTT TCTGTATCA TTGGGCAAAA CCACTCAACC 1020
ACAGTGGGGA ATCTGGCTTC GGTGGGTGCG ATTCTGAGCA ATATTTCATC TCTGTCACTG 1080
GCCAGCCATT TCAGGGTGTG CAATTCAACA ATGGAGGATG TCATCAGTAT AGCTGACAAT 1140
ATCCTTAATT CAGCCCTCAGT AACCAACTGG ACAGCTTAC TGCGGGAAGA AAGATATGCC 1200
AGCTCAACGT TACTAGAGAC ATTAGAAAAC ATCAGCACTC TGGTGCCCTC GACAGCTCTT 1260
CCTCTGAATT TTTCTGGGAA ATTCAATGAC TGGAAAGGGA TTCCAGTGAA CAAAGCCAA 1320
CTCAAAAGGG GTTACAGCTA TCAGATTAAA ATGTGTCCCC AAAATACATC TATTCCCATC 1380
AGAGGCCGTG TGTTAATTGG GTCAGACCAA TTCCAGAGAT CCCTTCAGA AACTATTATC 1440

5 AGCATGGCCT CGTTGACTCT GGGGAACATT CTACCCGTTT CCAAAATG G 1500
 GTCAATGGAC CTGTGATATC CACGTTTATT CAAAACATTT CCATAAATGA AGTTTTCCTA 1560
 TTTTITTTTCCA AGATAGAGTC AAACCTGAGC CAGCCTCAIT GTGTGTTTGG GGATTTCAGT 1620
 CATTTCGAGT GGAACGATGC AGGCTGCCAC CTAGTGAATG AAACCTCAAGA CATCGTGACG 1680
 TGCCAATGTA CTCACITGAC CTCCTTCTCC ATATTGATGT CACCTTTTGT CCCCTCTACA 1740
 ATCTTCCCCG TTGTAATAATG GATCACCTAT GTGGGACTGG GTATCTCCAT TGGAAAGTCTC 1800
 ATTTTATGCC TGATCATCGA GGCTTTGTTT TGGAAAGCAGA TTAATAAAAG CCAAACTCT 1860
 CACACACGTC GTATTGTCAT GGTGAACATA GCCCTGTCCC TCTTGATTGC TGAATGCTGG 1920
 10 TTTATTTGTT GTGCCACAGT GGACACCAAG GTGAACCCCT CTGGAGTCTG CACAGCTGCT 1980
 GTGTTCTTTA CACACTTCTT CTACCTCTCT TGTGTTCTCT GGATGCTCAT GCTTGGCATC 2040
 CTGCTGGCTT ACCGGATCAT CCTGTGTTTC CATCACATGG CCCAGCATTT GATGATGGCT 2100
 GTTGATTTT GCCTGGGTTA TGGGTGCCCT CTCATTATAT CTGTCAATAC CATTGCTGTC 2160
 ACGCAACCTA GCAATACCTA CAAAAGGAAA GATGTGTGTT GGCTTAACGT GTCCAATGGA 2220
 15 AGCAAAACCA TCCTGGCTTT TGTGTGCCCT GCACCTGGCTA TTGTGGCTGT GAACCTCGTT 2280
 GTGGTGTGTC TAGTTCTCAC AAAGCTCTGG AGGCGGACTG TTGGGGAAAG ACTGAGTCGG 2340
 GATGACAAGG CCACCATCAT CCGCGTGGGG AAGAGCCTCC TCATTCTGAC CCTCTGCTA 2400
 GGGCTCACCT GGGGCTTTGG AATAGGAACA ATAGTGGACA GCCAGAATCT GGCTTGGCAT 2460
 GTTATTTTGG CTTTACTCAG TCATTCCAG GGATTTTTTA TCTTATGCTT TGAATACTC 2520
 20 TTGGACAGTA AGCTGCGACA ACTTCTGTTT AACAAAGTTG CTGCCCTAAG TTCTTGGAA 2580
 CAAACAGAAA AGCAAACTC ATCAGATTTA TCTGCCAAAC CCAAAATCTC AAAGCCTTTC 2640
 AACCCACTGC AAAACAAAGG CCATTATGCA TTTTCTCATA CTGGAGATTC CTCGACAAC 2700
 ATCATGCTAA CTCAGTTTGT CTCAAATGAA TAA

25 Seq ID NO: 175 Protein sequence
 Protein Accession #: Eos sequence

30 1 11 21 31 41 51
 MKVGVLWLIS FFFPTDGHGG FLGKNDGIKT KKLIVNKKK HLGPEVEYQL LLQVITYRDSK 60
 EKRDLRNPLK LLKPLLHSH GLIRIIRAKA TIDCNLSNGV LQCTCEDSYT WFFPSCILDPO 120
 NCYLHTAGAL PSCECHLNLQ SQSVNFCERT KINGTFPKINE RFTNDLNLSS SAIYSKYANG 180
 IEIQLKKAYE RIGQFESVQV TQFRNGSIVA GYEVVGSSEA SELLSAIEHV AEKAKTALHK 240
 LFPLEDGSFR VFGKAQCNDI VFGFGSKDDE YTLPCSSGYR GNITAKCESS GNQVIRETCV 300
 35 LSLLEELNKN FSMIVGNATE AAVSSPVQNL SVIIRQNPST TVGNLASVVS ILSNLSLSL 360
 ASHFRVSNST MEDVISIADN ILNSASVTNW TVLLREKEYA SSRLLLETLEN ISTLVPTAL 420
 PLNFRSKFID KWDIPVKNKSL LKRGYSYQIK MCPQNTSIP RGRVLIGSDQ FQRSLPETII 480
 SMASLTGNI LPVSKNGNAQ VNGPVIISTVI QNYSINEVFL PFSKIESNLS QPHCVFWDPS 540
 HLQWMDAGSR LVNETQDIVT CQCHLTSTFS ILMSPFVPST IFFVVKMITY VGLGISIGSL 600
 40 ILCLILEALF WKQIKKSQTS HTRRICMVNI ALSLLIADVW FIVGATVDIT VNP9GVCTAA 660
 VPFTHFFYLS LFFWMLMLGI LLAYRIILVF HMAQHLMA VGFCGLYGCP LIISVITIAV 720
 TQPSNTYKRK DVCWLWNSNG SKPLLAFVVP ALAIVAVNFP VLLVLVTKLM RPTVGERLSR 780
 DDKATIIIRVG KSLIILTPLL GLTWGFGIGT IVDSONLAWH VIFALLNAFO GFFILCFGIL 840
 LSKLRQLLF NKLIALSSWK QTEKQNSSDL SAKFKPSKPP NPLQNKGHYA PSHTGDSSEN 900
 45 IMLTQFVSNB

Seq ID NO: 176 DNA sequence
 Nucleic Acid Accession #: AB035089.1
 Coding sequence: 9845..10219

50 1 11 21 31 41 51
 GGCATGCGAG CCATCGGGGA AAATCCATAG TGCAGATAAA GCAAGGAGGA AGAAGAGGGA 60
 CAGTTCTAGT AAAAGGGAGA ACATCAATAT AGGATGTTTC TTAGCAATAG AAAAGAGAGG 120
 55 CCAAGAGGAA TTAGGGAGAG AGTTATAAGA GATCAGCAAG GGGACAGGGT TAGATTGGT 180
 TTGGTTTGAA AGCATACAGT AAATATGATG TCTGTCCCTG GCAGTGTGCG CAGAGTAGGA 240
 AGGAGGAAGG GAGGCAAGAG ATAATATCAT TTTCTCTGTG CTCCAACCTG ACTTACATAT 300
 GAGACTATTT CCTCTCTGTC TTTTCAAACC TTAATGGAGT TGTITTCCTC CATGAAAACC 360
 AAGAAGAGAA AGCTAGTTAG TCTTGTCTG AGGTGTGTCA ATGTATACAT ATCTATATCT 420
 60 GTAGACAGAA TCCTTGGGAA TACAGTAATT GACATATATT CTGTTATTTG ATGCTTGAAA 480
 AATCTCCTCC ACTAACCAGT TTCCCTATAG ATTGCCACAA GCACATAATA AGAAACAATA 540
 AATAAAATGT TCTCTTGACT TTGTTACTTA ACAATGCTGA GAAAACCTTA CAGCCTTCAT 600
 AAGGAAGTGA GGTCCAGGAA AATCTAGGAG ATATTCTTCT ACCAATCTAT AAAGGCATTA 660
 65 GTAATGACAG GATATTTCCT GAAAGTGTAA TTTCCCATG AGGATTTGTT TTTAATTCTT 720
 GGATTCCTGG AGCCAATGAA GTTGGTGTAT GTTTATGAAA TATCAAGAGA CATAAGTTGG 780
 CAAGTGTTC TATGCAAAAA CTCTTGGGAA TTTCTGAGIT CTCTGTGGCA ATATATGACA 840
 TCAGGATATG TCCAGTCTCA CACACCAGGA TATGTCTCTT CTAGCCTGTC TATCACATGC 900
 TAGGAGAACT ATTAGGAAC AGAAAAAAT GCCTGAAATG ATTTCTCAT TGAACCTCATC 960
 70 CAAGCTTCT CTAAATTTAA GCAAACTCCT GGTCTTTTTC AGTTAGTACC TTTCTTAA 1020
 TTCAACCTTC AGGCAAAACC TCCGTGCCCT AGACGTTTAG CCATAGTCTG AAATTCTCTT 1080
 CCATAGATTG GTCCCTGTGA ACCCGGTTT GTCTCAGCTT GTTATCCTGT TTTTCTCTC 1140
 CCTCCATTCC CAGGATGAGC TTGTGTCTTC TGTCTATGA GACATTAGAT TCCTTTTCTT 1200
 TGGTACCGGA GTAATCCAT CCTACTCCAA TAGAGGAAGG TCCATTTTTG TCTTATAGCG 1260
 CTGGATGCAG ACTCAGCTGA GAAGACCAIT ATTCTTTT GGAATCTTCT ATCTCAGATA 1320
 75 TTTCTCTTTC TTTCTTTTTC TTCTATCTTT GGATTTTATG TCCATCAACG CCCCATTAGT 1380
 CTATTCCCGG ACTTCAATCA GGGAACTTAT ACCTCTTAAA CTCATTGAGA GACTCAAAAC 1440
 ATATATATGT ATACAGGAGA CCTAAGAAGA GCATGTCTTG GGGGTTGAGG AAACAGGCAG 1500
 GTGAGAAATT TCAGATTTGG AAACACAGCT TCCTTTCTCC CATCCAGCCC CTACTTTCAG 1560
 CCTAIGTGT TCTGGCACCT TGTGTAGAT AAATCTCCCT TGACTTTGTG ATGTGCTGAG 1620
 80 AAAACAAACT CAGGCTGTGT GTTAAAAAGG GCCCATGACA ATACCAAGTG TTGGGGAGAA 1680
 TGTGGAGAAA TCAGAACTCT ATTCAAGGTC GGTGGGAATG CACACTTGTG CAGAATTCTA 1740
 TGGAGAAGAG TCTGGCATTCT CCTCAAAATG TTAACCTGGA TTTACCATAT GACCCAGOGA 1800
 TTTCTATTAT AGGTTTATAC TCAAAAGAAA TGAAGAAATA TGCCATGCAA AAAAATGTAC 1860
 ATGAAGAGTC ACAACATCAT TATTCTAAT AGTAAAGGA TGGAAACAAC ACAAATGTCC 1920
 ATCAACTTAT GATTAAAGAA AATCTGGTCT ATTCATAGAA TGGAAATATTA TTGACCACA 1980

	AAAAGGAATG	ATGTACTGAT	CCATGCAATG	ATGTGGACAA	ACCATGAAA	TAACACTAGA	2040
	TTAAAGAAGC	CAGTCACAAA	AGGACTTACT	GTATGATTCC	ATTACCTGA	AATGTTTGA	2100
	ATAGGCAAT	CCATAGAAAC	AGGAGGTAGA	TTCTGGTTT	CCAGGGTCTC	CAGGAAGGGA	2160
	AGAATGAAGT	ACAAGATTTC	TTTTGGAGGT	AGTGAAATTG	TTGTGGAATG	AGATCATGAT	2220
5	GATGATAGCA	CAACTTTGTG	AATATAATA	AATCATTGAA	TTGTACAGTT	GAATTTATGG	2280
	TATATAAAT	ATATGTTAAT	AAAAAGGGG	TCCACAAAAC	AAACAGCCCC	CCACTCTGGT	2340
	TGTCAGGGAG	ATATTGGATT	AAATGGCCTT	GGACAACAAC	CCCTCTCCCT	GGCCACAGAC	2400
	ATTCTTCAGA	TTACAAGATA	TTCCAGGGGA	AACACTGGAA	TGAGTCTGAA	GCCAGGTGCT	2460
	AAACAGAAGG	ACCATTGAGA	AATGTTGTGA	TCCTGACAGG	TCAAGCAATT	TATTTTTCGG	2520
10	CTTCATTTTT	AAATGTAAAA	TTAGAAAGCT	GCCATTTAAA	ATGGCCCGTC	TGTTTCAATT	2580
	GCTCTTCTCA	GTGTGAGCCT	GTTAACTCAA	TGTGTTAGTC	TGTTTTCATG	CTGCTGATAA	2640
	AAACATACTT	GAGACTGGCA	AGAAAAAGAG	GTTTAAATTG	GCTTAGAGTT	CCACGTGATT	2700
	GGGAGGGCCT	CAGAATCACA	GTAGGAGGCA	AAAGTTATTC	TTACATGGTG	GCTGCAAGAG	2760
	AAGATGAGGA	AGAAGCAAAA	GAAGAAACCC	CTGATAAAC	CATCGATCT	CCTGAGGCTT	2820
15	ATTAACATATC	ATGAGAATAG	CACAAGAAAG	ACCGGCCCCC	ATGATTCAAT	TACCTCTACC	2880
	TGGTCCCTCT	CAATAACATG	TGGAATTTCT	GGTAGATACA	ATTCAGTTG	AGATTGSGT	2940
	GGGAACACAG	CAAAACCATG	TCACTCAGCA	AGGCAGATAA	CTTCTCACT	GAGCCTATGC	3000
	AACAGAAAC	CATCTGGGAT	GGTTGTAAGG	GGCAGAGGAA	GTGACTGGTA	GGATCACTGC	3060
	CAAGCTGAG	CACCTCAGAG	AAGGCAATAG	AATCCTATT	TCCATAGTAT	GCTATAAGAT	3120
20	ACTGAAGTAC	ACTTCTTAC	TATCTCTTTC	GACTTAGAAT	TAGCACTACA	TTCCCTGTGA	3180
	TACAGAAAA	TTACTAAGGA	AATTCATAGG	ATGACAAAA	CTTTCAGAAC	TGAAAAACAG	3240
	GAAATGTAA	CTTTTATGTT	CTTTGTTATT	CGAAGTATGC	CTAAAAGACA	ATGCAAAATC	3300
	CAAGAAAAGA	ATGGTGGGTT	TTTTGTTTGT	TTGGTTTGTG	TTTTGTTTGA	CAGCTGGAGT	3360
	AGAATACAAA	GGGATGGAGT	TGAAACAAAT	GAGAGGAAAT	TGGAATTTCTA	AACCTATTCT	3420
25	CATTGGCATT	AGAAAGGCAC	CTACATGTAT	TTCACTGAG	CCGGTGACTG	CTGACTTGCA	3480
	TTCTTATTTT	TTCCCTATAG	ATTAAGAAAG	AGGTACAATG	GTAGAACTGT	AATCCTGTCC	3540
	TTTGTATATA	ATTTTCATAT	TCATAAAGGT	GAGTGTATGC	CCGCTTGTGA	AATCTGAAAT	3600
	TGAGTAACTT	CAATACTATA	CCACAGAGGG	AAAGGCAGCA	AGAGGAGAGG	CATAAATTTA	3660
	GGATCTCACC	CTTCATTCCA	CAGACACACA	CAGCCTCTCT	GCCCACCTCT	GCTTCTCTTA	3720
30	GGACACAGG	TAAGAGCTTC	AAGCCTCTCC	AGCTTAATAA	CATGAATTAT	TTTTTGAAAT	3780
	AATAATGATA	CTGTGTTCTA	TATCATGCAT	CTCCTGCAAT	CTGCTGATT	ATATTTTACT	3840
	TATTCTGCCA	GAGCAAAAT	AAAATACCTA	TTTCATCTGA	TTTGTCTTT	ATCTAAATG	3900
	CTTAGTTCCA	AGTAAACCAA	GGCACTTTTA	GGAAACAGCA	GGGAGAGTGC	CTTGACGCCA	3960
	GAGAGTCTTG	AAGGAGATGT	CAGGGACGCA	TCTTAACAGC	TGGTTGGATG	TGATCCACAT	4020
35	AGGTCTCCTG	TTAGCATTTA	TTGTAAAGCC	ATCCTACCTA	GCTCTAGTGT	AACCAAGAT	4080
	GAAAGAAAGA	TAAAGAGGTT	CGATTACTTA	TTTACAATAG	TCTTTAAAAA	CGTAGTTTGG	4140
	TAAGCCTTCT	AATTAGGACA	TTAATATATT	TAATATATGC	ACATTGTAGA	AAGATTGAAG	4200
	CGTTAAAAAT	AAGAGAAAAA	CTTTAAATGT	CAAAATCTCA	CAACCCAGAT	ATATCAATTC	4260
	TTTAAGAAAA	TTGTACTACA	AAATACCAT	CCATTTTATA	AGTCATTCT	GACAGGAATC	4320
40	TGATGCTTTT	CCAGGAGTTC	CAGATCAGAT	CGAGTTTACC	ATGAATTCAC	TCAGTGAAGC	4380
	CAACACCAAG	TTCATGTTTC	ATCTGTTCCA	ACAGTTTACA	AAATCAAAAG	AGAACAACAT	4440
	CTTCTATTCC	CTTATGACGA	TCACATCAGC	ATTAGGGATG	GTCCCTCTAG	GAGCCAAAGA	4500
	CAACACTGCA	CAACAAATTA	GCAAGGTAGC	TATCAGCATC	ATTAAGTTGT	CCTGTGTCAG	4560
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	CCTCAGAGCA	TAGGTCTGGA	TCAGGATAGG	CTGGGTTTCA	ACTCCAGCTT	TGCTCTTAC	5040
	AAATGATGAA	TAGAGGAGG	ACACAACATG	TOGGAGTCCC	AGTGACCTCA	TOCCAGAAAA	5100
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	CAAAAACAAA	GATCAGAAAC	ATCATGGTTA	AAATTACTGG	AGAGAAGTCT	GAGAAGCAAT	6660
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Seq ID NO: 177 Protein sequence
 Protein Accession #: BAB21525.1

80

1 11 21 31 41 51
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5 DAIKKFYQTS VESTDFANAP EESRKKINSW VESQTNKIK NLPFDGTIGN DTTLLVLVNAI 180
YFKGQWENKF KKGNTKEEF WPNKNTYKSV QMMRQYNSEF FALLEDVQAK VLEIPYKGD 240
LSMIVLLPNE IDGLQKLEEK LTAELKMENT SLQNMRETCV DLHLPRFKME ESYDLKDTLR 300
TMGMVNIFNG DADLSGMTWS HGLSVSKVLH KAFVEVTEEG VEAATAAVV VVELSSPSTN 360
BEPCNHPFL PFRQNKTNIS ILFYGRFSSP

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50 Seq ID NO: 179 Protein sequence
Protein Accession #: NP_001901.1

55 1 11 21 31 41 51
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60 PPSGLNVVVP TKQAYWQIAL DNIQVGGTVM FCSBGCQAIV DTGSLITGP SDKIKQLQNA 300
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65 Seq ID NO: 180 DNA sequence
Nucleic Acid Accession #: NM_018058.1
Coding sequence: 319..1575

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Seq ID NO: 181 Protein sequence
 Protein Accession #: NP_060528.1

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Seq ID NO: 182 DNA sequence
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 Coding sequence: 1..1962

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Seq ID NO: 183 Protein sequence
Protein Accession #: CAC08451

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Seq ID NO: 184 DNA sequence
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Coding sequence: 1..4794

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 Protein Accession #: FGENESH

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5 Seq ID NO: 187 Protein sequence
 Protein Accession #: NP_000575.1

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 Protein Accession #: NP_055267.1

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 TGQVLTCDCR PAGTYVSEHC TMTSLRVCSS CFPVGTPTRE NGIEKCHDCS QPCWPWMIK 120
 LPCAALTDBRE CTCPPQMFQS NATCAPHTVC FVGWGVKKG TETEDVRCKQ CARGTFSDVP 180
 SSVNKKCKAYT DCLSONLVVI KPGTKETDNV CGTLSPFSSS TSPSPGTAIF PRPEHMETHE 240
 VPSSTYVPKO MNSTENSSA SVRPKVLSSI QBGTVPDNTS SARGKEDVNK TLPNLQVNVH 300
 QQGPHEHRL KLLPSMEATG GEKSSTPIK PKRGHPQNL HKHFDINEHL PMMIVLPLLL 360
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 VLVVIVVCSI KSSRTLLKKG PRQDPSAIVE KAGLKSMTP TQNRKWIYY CNHGIDILK 420
 LVAAQVGSOW KDIYQFLCNA SEREVAAPSN GYTADHERAY AALQHWITIR PEASLAQLIS 480
 ALRQHRNRDV VEKIRGLMED TTQLETDKLA LPMSPSPSLP SPIPSFNAKL ENSALLTVEP 540
 SPQDKNKGFF VDESEPLLRC DSTSSGSSAL SRNGSFITKE KKDTVLQRVR LDPCLQPIF 600
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 DDMHLFINPE ELRVIEBIPQ AEDKLDRLFE IIGVKSQEAS QTLSDSVYSH LPDLL

30
 Seq ID NO: 192 DNA sequence
 Nucleic Acid Accession #: XM_044533
 Coding sequence: 238..2751

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 1 11 21 31 41 51
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 AGTCCGCGCG AGCCACCTGA GCCCCGAGCG CGGGACACCG TCCTCTCTCG TCTCCGAATG 240
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 CGGCCACGCG TGCTGCTGCT CTTGCTGCTG CTGCTCTGCG TGCAAGCGCC GCCTCCGACC 360
 TGGGCGCTCA GCCCCCGGAT CAGCCTGCCT CTGGGCTCTG AAGAGCGGCC ATTCTCTAGA 420
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 AGCGCGAGTC ACCTGTTTAC CTGTGGCACA GCAGCCTTCA GCCCATGTG TACCTACATC 720
 AACATGGAGA ACTTCAACCT GGCAGAGGAC GAGAAGGGGA ATGTCTCTCT GGAAGATGGC 780
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 GCCTCAGGCT ACATTCTCTG GAGCCTGGGC AGCTTGCAAG GCGATGATGA CAAGATCTAC 1020
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 TTTTCTTCA GCGAGACTGG CCAGGAATTT GAGTTCTTTG AGAACACCAT TGTGTCCCGC 1080
 ATTGCCCCGA GTGCTCAGGG CGATGAGGGT GGAGAGCGGG TGCTACAGCA GCGCTGAGAC 1140
 TCCTTCTCTA AGGCCAGCT GCTGTGCTCA CGGCCGACG ATGGCTTCCC CTTCAAAGTG 1200
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 ACCAGGCGGT GGATCCAGGA CATCGAGGGA GCGAGCGCCA AGGACCTTTG CAGCGCGCT 1980
 TCGGTTGTGT CCGCGTCTTT GTTACCAACA GGGGAGAAGC CATGTGAGCA AGTCCAGTTC 2040
 CAGCCCAACA CAGTGAACAC TTTGGCCTGC CGCTCTCTCT CCAACCTGGC GACCCGACTC 2100
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 GGCTTCCAGC AGCTGGTAGC CAGCTACTGC CCAGAGGTGG TGAGAGACGG GGTGGCAGAC 2280
 CAAACAGATG AGGGTGGCAG GTTACCCGTC ATTATCAGCA CATCGCGTGT GAGTGACCA 2340
 GCTGGTGGCA AGGCCAGCTG GGGTGAGAC AGGTCTTACT GGAAGGAGTT CTTGTGTATG 2400
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 CTGATCACC GAGGTACCCA GTCCCTGTCA GACAGCCCCC CGGGGTCCCG AGTCTTCACT 2640
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 GGCCAGCTGG CCTGCTGCTC TCCAGTCAAG TAGCGAAGCT CCTACCACCC AGACACCCAA 2940
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 TGCTCCTTAT GTAAACTGAG CCCTTTGTTT AAAAAACAA TCCAAATGTG AAATAGAAAT 3060
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 GGGGTGCTGG GATGCAATC AAAGTGGTTG TCTGAGACAG AGTTGGAAC CCTCACCAAC 3180

5 TGGCCTCTTC ACCTTCCACA TTATCCCCTG GCCACCGGCT GCCCTGTCTC ACTGCAGATT 3240
 CAGGACCAGC TTGGGCTGGG TGGGTTCTGC CTTGCCAGTC AGCCGAGGAT GTAGTTGTGG 3300
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 CAGGGAAGAG ACTGTGCGCT GCCTTCTCC GTTGTGCGT GAGAACCCGT GTGCCCTTTC 3540
 CCACCATATC CACCTCGCT CCATCTTGA ACTCAACAC GAGGAACATA CTGACCCCTG 3600
 GTCTCTCCC CAGTCCCAAG TTCACCTCC ATCCCTCAC TTCTCCACT CTAAGGGATA 3660
 10 TCAACACTGC CAGACACAGG GGCCTGAAT TTATGTGGT TTTATACAT TTTAATAAG 3720
 ATGCACTTTA TGTCATTTT TAATAAAGT TGAAGAATTA CTGTTT

Seq ID NO: 193 Protein sequence
 Protein Accession #: XP_044533.3

15 1 11 21 31 41 51
 MLRTAMGLRS WLAAPWALP PRPPLLLLL LLLLLQPPP TWALSPRISL PLGSEERPFL 60
 RFEAHISNY TALLLSRDGR TLYVGARAL FALSSNLSFL PGGEYQELLW GADAEEKQQC 120
 SFKGRDFQRD QNYIKILLP LSGSHLPTCG TAAPSPMCTY INMENFTLAR DEKGNVLLED 180
 20 GKGRCPDFPN FKSTALVVDG ELYTGTVSSF QGNPDAISRS QSLRPTKTES SLNWLQDPAF 240
 VASAYIPESL GSLQDDDDKI YFFFSETQGE FEFFENTIVS RIARICKGDE GSERVLQQRW 300
 TSFLKAGLLC SRPDDGFFFN VLQDVFTLSP SPQDWRDTLF YGVFTSQWHR GTTBGSVAVC 360
 FTMKDVRQVF SCLYKEVNRRE TQQWYTVTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL 420
 NPLKDHFLMD GQVRSRMLLL QPQARYQVRA VHRVPLGHT YDVLPLGTGD GRLHKAVSVG 480
 25 PRVHIIIEELQ IFSSGQPVQN LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD 540
 PYCAWSGSSC KHVSLYQPOL ATRPWIQDIE GASAKDLCSA SSVVSPSFVP TGEKPCBQVQ 600
 PQFNTVNTLA CPLLNLAIR LHLRNGAPVN ASASCHVLPD GDLLLVGTQQ LGEPQCSLE 660
 EGFQQLVASY CPEVVEDGVA DQTDGGSVP VIISTSRVSA PAGGKASWGA DRSYNKEFLV 720
 MCTLFVLAVL LPVLFLLYRH RNSMKVFLKQ GECASVHPKT CPVILFPETR PLNGLGPFST 780
 30 PLDHRGQSL SDSPGSRVP TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSV

Seq ID NO: 194 DNA sequence
 Nucleic Acid Accession #: NM_022819.1
 Coding sequence: 1..635

35 1 11 21 31 41 51
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 40 AGCCTGGGTA TGAAGAAGTT CTTACCCGTG GCATCCTTTC CTGGCAGCGT TCTGTCCACA 180
 GCTCAGCGCA GCCTGCTCAA CCTGAAGGCC ATGTTGGAGG CCGTCACAGG GAGGAGCGCC 240
 ATCTGTCTCT TCGTGGGCTA CGGTGCTAC TGTGGGCTGG GGGCCGCTGG CCAGCCCAAG 300
 GATGAGGTGG ACTGTGCTG CCACGCCAC GACTGCTGCT ACCAGGAAT CTTTGACCAA 360
 GGCTGTACCC CTTATGTGGA CCACTATGAT CACACCATG AGAACACAC TGATAGATGC 420
 45 TGCAATGACC TCAACAAGAC AGAGTGTGAC AAGCAGACAT GCATGTGTGA CAAGAACATG 480
 GTTCTGTGCG TCAATGAACA GACGTACCGA GAGGAGTACC GTGGCTTCCT CAATGTCTAC 540
 TGCCAGGGCC CCAGCCCAAA CTGCAGCATC TATGAACCGC CCCCTGAGGA GGTCACTGCG 600
 AGTACCAAT CCCACGCC CCCTGCCCT CCCTAG

Seq ID NO: 195 Protein sequence
 Protein Accession #: NP_073730

55 1 11 21 31 41 51
 MADGAKANPK GPKKKVLDRC FSGWRGPRFG ASCPSRTSRS SLGMKKFTV AILAGSVLST 60
 AHGSLNLKA MVEAVTGRSA ILSFVGYGCT CGLGGRGQPK DEVDWCCHAH DCCYQELFDQ 120
 GCHPYVDHY HTIENITEIV CSDLNKTECD KQTCMDKMN VLCLMNQTYR BEYRGFLNVY 180
 CQGPFPNCIS YEPPEEVTCT SHQSPAPPAP P

Seq ID NO: 196 DNA sequence
 Nucleic Acid Accession #: XM_028196.1
 Coding sequence: 1315..1791

65 1 11 21 31 41 51
 GGCAATGATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT 60
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 AGACTGGGGG GCTGCAGAGG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCGATGGG 180
 70 ATGGCCTGGG CTGGGCCCTT GAGGCCAGGC TGACTTGGAC ATGGCAAGAG GGGTCCCAAG 240
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 CTGCTCTCTG GAGCGGGTGG AGTCAGGGAA GAGCTGAGCT GGGGAGTCAC CCTGGGCTG 360
 GGGTCAAGCT AGGCCCAATG TAGCACCTG GTTCCCTGCT CTGTAGGTGA CAGGAGCCAG 420
 CCAGGCCAGG TGTGTCCCT CCCAGGCCCT TAGGACGGCG GGTACAGGGG CCAGCAGCTG 480
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 75 GAGTCCAGGC AGCGGCTGAG TCAGTGTGTG TGAATGTTC TGGCGCTCC CAGCTGCACC 600
 CTGCCCTTAC CTGCCACAC CTAACCTTCA TCTTCAGGCG CTGCGGCCCT GAGCCCTGCT 660
 CAGGAATGCA CTTTATAGCC AGGCTGTCTC AGTGAGCTCC GCGCAGACCC AGCCCTGCTC 720
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 80 ATGCTCCACC TGATGGCTG GCAAAACATG GTGGGCCCCA GCTGTGGTGC GTGCTGGGGT 840
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 AGGCAGGGCC CAGGCTCCAG GGCCAGGAG AGAGAAGCAG GAGAGGAGAG AGCTTCTCTG 960
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 AGGCTGCCCA GGCCTGCTC GCTTGGCTGG GGTGGGGGCG TGCTGGGAGG TGGCTGGGAG 1080
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CTTCTGCTG CACAGAACCC TGGCCCTGG CCACCCCGTG CTGCTCTCTT GCGCTGGCAG 1200
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CACCCACCAG TCTCTCCAG TGGCCCGGCC CCAGCTGGCA CCACAGCTAT ACCTGGGCTT 1380
ATTCCAGACC TTGTGCGCGG GACCCCTGT GAGTTGTGGG ATTCCTCAAG GGGGTGTGGG 1440
GATAACCCAG CCAAGTGGGG GCTGCAGCTG TCCACAGATG CACTCAGCCT GGCTCTACC 1500
CCAGGCCCCC GCTGGGCTCT CATTCGCGGC GCCCTTGGCG CGGGCGTCTT CCTGCTCTCC 1560
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GTCAGCGTCT CCACCCAGGC CGGACACAGA CATGAGACAA AAGTGACCCG AGGCACGCTC 2460
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GCTGGGTGGG CCTGAGCTAG GGCAGCAGGG CCTGGCTCAC GCGCTGCCT CAGATCCCGC 2640
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GGCATGAGCC CCTGGGTGAG CTCCGCTGTC CACTGGGCAC CGTGGATCTG CAGCATGTTT 2760
TGGAGCACTG GTACCTGCTG GGCOCGCGCG CTGCCACTCA GGTGAGGTGC TGGTCACCAAG 2820
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CTGGTGCCCT TCAGCCAGGT CCAGAATGTG GACCTGTGTC TGGCTGTCTG GGACCGCAGC 3240
CTGCCCTCC GAATGAGCC GTAGGCAAG GTGCACTGG GTGCCCGGGC CTCGGGGCAG 3300
CCCTGACAGC ACTGGGCAGA CATGCTGGCC CACGCCCGGC GGCCCAITGC CCAGCGGCAC 3360
CCCTGCGGCG CAGCCAGGGA GTTGGACCGC ATGCTGGCCC TGACGCCCCG CTTGCGCTG 3420
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Seq ID NO: 197 Protein sequence
 Protein Accession #: XP_028196.1

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1 11 21 31 41 51
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STPGPRWALI AGALAAAGVLL VSCLLCAACC CRRHRKPKPR DKESVGLGSA RGTITTHLVR 120
SGSLLTQSPRE GLKRLQSPG QRGEFSPRDG LTPTEAGR
  
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Seq ID NO: 198 DNA sequence
 Nucleic Acid Accession #: NM_000612.2
 Coding sequence: 553..1095

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CTCTGCCCCC CTCTATCCTT GATACACAG CTGACCTCAT TTCCCGATAC CTTTTCCTCC 300
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CAGACGAAT CTCCCCCCC CCCCCAAAAA AAAAGCCATC CCCCCGCTCT GCGCCGTGCG 420
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CTGGCCCTCC TGGAGAGSTA CTGTGCTACC CCGCCAAAT CCGAGAGGGA CGTGTGAC 840
CCTCCGACCC TGCTTCGGA CACTTCCCG AGATACCCG TGGGCAAGTT CTTCATATAT 900
GACACCTGGA AGCAGTCCAC CCAGGCGCTG CGCAGGGGCC TGCTTGCCTT CTGCGTGCC 960
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CCCTGATTG CTCTACCCAC CCAAGACCCC GCGCCCGGGG GCGCCCCCCC AGAGATGGCC 1080
AGCAATCGGA AGTGAACAA ACTGCGCNA GTCTGCAGCC CGGCGCCACC ATCTGACAGC 1140
CTCTCTCTGA CCACGACGT TTCCATCAGG TTCCATCCCG AAAATCTCTC GGTTCACAGT 1200
CCCCCTGGGG TTCTCTCTGA CCCAGTCCCC GTGCCCGGCC TCCCGAAAC AGGCTACTCT 1260
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GATTGGCTTT AAACACCCTT CACATACCCT CCCCC
  
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Seq ID NO: 199 Protein sequence
 Protein Accession #: NP_000603.1

1 11 21 31 41 51

MGIPMKXSM L VLLTFLAFAS CCIAAYRPSE TLGGELVDT LQFVCGDRGF YFSRPASRVS 60
RRSRGIVEEC CFSRCDLALL ETYCATPAKS ERDVSTPPTV LPDNFPRYPV GKFFQYDTWK 120
QSTQRLRRGL PALLRRARRH VLAKELEAFR EAKRHRPLIA LPTQDPAHGG APPENASNRK

Seq ID NO: 200 DNA sequence
Nucleic Acid Accession #: AK057131.1
Coding sequence: 61..1146

1 11 21 31 41 51
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ACCGTCTCCA GATCGATGGG CCCGAGGAGC GGGGAGCATC AAAGGGCGTC GCGAATCCCT 180
TCTCAGTTCA GCAAAGAGGA ACGGTGCGC ATGAAAGAGG CGCTGAAAGG TGCCATCCAG 240
ATTCCAACAG TGACTTTTAG CTCTGAGAAG TCCAATACTA CAGCCCTGGC TGAGTTGCGA 300
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CTGCTGATGG CTCACITTTGA TGTGGTGCCT GCCCCTGAAG AAGGCTGGGA GGTGCCCCCA 480
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TGATCTTTGG ATGATTTTCAT TCCTAACTTC AAGAAGCCCA TCGCCTTGAT TGCACTCTCA 780
GAGAAGGGTT CCATGAACCT CATGCTGCAA GTAAACATGA CTTCAGGCCA CTCTTCAGCT 840
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CCAATGCTTA TCATATTGGA AAGCGGACCA GTGGTGAAGT TATTGCAGCA ACTGGCAAA 960
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CATATTCAAA GCAGGGGTCA AGTTCAATGT CATCCCCCA GTGGCCAGG CCACTGCTCA 1080
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GGAAGTCAAT ATTACTGCCC CAGTTACTTC TATTGCAAC ACAGACAGCC GATTCTTTAC 1320
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ACGCATCCAT GGAGTCAACG AGAAATCTC AGTCCAAGCC TATGAGACCC AAGTGAAT 1440
CATCTTTGAG TTGATTGAGA ATGCTGACAC AGACCAGGAG CCACTTTCTC ACCTGCACAA 1500
ACTGTGAGGT CAAGGGGCTT GCTGGGTTAG GCATGCCGGA CCGCGGACA GGAATAACCC 1560
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ATCTGTCTTG CTCACTCTTA AACTCTCCCA AGAACAAGGC CGGGTAAAG TAAAGTCAGC 1680
AGAAATCTGG CTCTCCCTTT CCTCCGACA CTCGATCCC TTGATCCACT GGCATTGTCT 1740
GCCCTCTGTT CCCTTATCTG TCTTATGCTG GTTATTTCAC TGCTTCACCT TCAGGCTTG 1800
ACTTAACAAA TGTAGATTG AGAAATCTCA ACCAGTTGTT ACCTGATAGG AGCTTTAAT 1860
TTAGGGCACT CTGCTGGGGA TGCTTTCTCC AGAGCTTATA TATTCTCTCT TACTAGAACT 1920
TTCTTCCCC TTATTATCCC CTCTCTCTCT GGAATCATGA GCTGTCTCTT CATCTCTCT 1980
CTCTCTCTG CATCTCTCCC CTTACTCTTC AATTATTCT ACTTCTGGAC CTGGAATAC 2040
CCAACTGTTG ATACTACCAT AATTGTCACC ATATCAGTC AAATAAGTG ATCTGTGCAT 2100
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Seq ID NO: 201 Protein sequence
Protein Accession #: BAB71368.1

1 11 21 31 41 51
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LLMAHFVIVP APEBGEWVFP FSGLERDGI VYWGTLDDKN SVMALLQALE LLLIRKYIPR 180
RSFPISLGHD ESSSGTAQR ISALLQSRGV QLAFLVDEGG FILDDFIPNF KPPIALIAVS 240
EKGSNMILMQ VNMISGHSSA PPKETSIGIL AAASRLQET PMPIIFGSGT VVTVLQQLAN 300
EYGEKSLNQ CNNQDHGTH HIQSRGQVQC HPPSGPGHSQ LPDSFWTDSR RGRPTHEHC 360
G

Seq ID NO: 202 DNA sequence
Nucleic Acid Accession #: NM_004217.1
Coding sequence: 58..1092

1 11 21 31 41 51
GGCGGGGAGA GTAGCAGTGC CTGAGACCCC AGCTCTCTCT CCCCTTTCTC TCTAAGGATG 60
GCCAGAAGG AGAAGTCTTA CCCCTGSCCC TAAGGCGGAC AGACGGCTCC ATCTGGCCTG 120
AGCACCTGTC CCCAGCGAGT CCTCCGGAAA GAGCCTGTCA CCCCATCTGC ACTTGTCTCT 180
ATGAGCGGCT CCAATGTCCA GCGCCAGCT GCGCCTGGCC AGAAGGTGAT GGAGAATAGC 240
AGTGGGACAC CCGACATCTT AACGCGGCAC TTCACAATTG ATGACTTTGA GATTGGCGGT 300
CCTCTGGGCA AAGGCAAGTT TGGAAACGTG TACTTGGCTC GGGAGAAGAA AAGCCATTTC 360
ATGTTGGGCG TCAAGTCTCT CTTCAGTCC CAGATAGAGA AGGAGGGGCT GGAGCATCAG 420
CTGCGCAGAG AGATCGAAAT CCAGGCCCCC CTGACCATC CCAACATCTT CGGTCTCTAC 480
AATCATTTTT ATGACCGGAG GAGGATCTAC TTGATTTCTG AGTATGCCCC CCGCGGGGAG 540
CTCTACAAGG AGCTGCAGAA GAGCTGCACA TTTGACGAGC AGCGAACAGC CAGATCATG 600
GAGGAGTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTGATTCA CAGAGACATA 660
AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGCTGA CTTCGGCTGG 720
TCTGTGATG CGCCCTCCCT GAGGAGGAAG ACAATGTGTG GCACCCCTGA CTACCTGCC 780
CCAGAGATGA TTGAGGGGCG CATGCACAT GAGAAGGTGG ATCTGTGGTG CATTGGAGTG 840
CTTTGCTATG AGCTGCTGGT GGGGAACCCA CCCTTTGAGA GTGCATCACA CAAGAGAGC 900
TATGCGCGCA TCGTCAAGGT GGACCTAAG TTCCCGCTT CTGTGCCAC GGGAGCCAG 960
GACCTCATCT CCAACTGCT CAGGCATAAC CCTCGGAAC GGCTGCCCTT GGCCAGGTC 1020

TCAGCCACC CTTGGGTCGG GCCCACTCT CGGAGGGTGC TGCCTCCTC TGCCTTCAA 1080
 TCTGTCCCT GATGGTCCCT GTCACTTACT CGGTTGCGTG TGTTTGTATG TCTGTGTATG 1140
 TATAGGGGAA AGAAGGGATC CCTAATGTT CCCTTATCTG TTTTCTACT CTCTCTTTGT 1200
 TTAATAAAGG CTGAAGCTTT TTGT

5

Seq ID NO: 203 Protein sequence
 Protein Accession #: NP_004208

10 1 11 21 31 41 51
 MAQKENSYPW FYGRQTAPSG LSTLPQRVLR KEPVTPSALV LMSRSNVQPT AAPGQKVMEN 60
 SSGTDPILTR HFTIDDPFEG RPLGKGKPGN VYLAREKSH FIVALKVLFK SQIEKGVVEH 120
 QLRREIBIQA HLHHNPILRL YNYFYDRRI YLILEYAPRG ELYKELQKSC TFDEQRTATI 180
 MEELADALMY CHGKVIHRD IKPENLLGL KGBLKIADFG WSVHAPSLRR KTMCGTLDYL 240
 15 PFEMIEGRMH NEKVDLWCIG VLCYELLVGN PPFESASHNE TYRRIVKVDL KFPASVPTGA 300
 QDLISKLRH NPSERLPLAQ VSAHPWVRAN SRRVLPPSAL QSVA

20 Seq ID NO: 204 DNA sequence
 Nucleic Acid Accession #: AK055663
 Coding sequence: 38..1423

25 1 11 21 31 41 51
 AGAACGGCTT CCGGCGGGAG CTGTGCAGCT CCTATCATG GGGACAATTC ATCTCTTTGG 60
 AAAACCAACA AGATCCTTTT TTGGCAAGTT GTTACGGGAA TTTAGACTTG TAGCAGCTGA 120
 COGAAGGTCC TGAAGATAC TGCTCTTTGG TGAATAAAC TTGATATGTA CTGGCTTCCT 180
 GCTTATGTGG TGCAGTTCTA CTAATAGTAT AGCTTTAACT GCCTATACTT ACCTGACCAT 240
 TTTTATCTTT TTTAGTTTAA TGACATGTTT AATAAGTTAC TGGGTAACTT TGAGGAAACC 300
 TAGCCCTGTC TATTCAATTG GGTTTGAAAG ATTAGAAGTC CTGGCTGTAT TTGCTCCAC 360
 30 AGTCTTGCCA CAGTTGGGAG CTCTCTTTAT ATTAAAGAA AGTGACAGAC GCTTTTGGGA 420
 ACAGGCCGAG ATACACACGG GAAGATTATT AGTTGGTACT TTTGTGGCTC TTTGTTTCAA 480
 CTTGTTACAG ATGCTTTCTA TTGGGAATAA ACCTTTTGCT TATGTCTCAG AAGCTGCTAG 540
 TAGCAGCTGG CTCAAGAGC ATGTGTCAGA TCTTAGTCTG AGCTTGTGTG GAATTATTCC 600
 GGGACTTAGC AGTATCTTCC TTCCCGAAT GAATCCATT GTTTTGATTG ATCTGTCTGG 660
 35 AGCATTGTCT CTTTGTATTA CATATATGCT CATTTGAAAT AATAATTATT TTGCGTAGA 720
 CACTGCCTCT GCTATAGCTA TTGCCCTGAT GACATTGGC ACTATGTATC CCATGAGTGT 780
 GTACAGTGGG AAAGTCTTAC TCCAGACAAC ACCACCCCAT GTTATTGGTC AGTTGGACAA 840
 ACTCATCAGA GAGGTATCTA CCTTAGATGG AGTTTAAAG GTCCGAAATG AACATTTTTG 900
 GACCCTAGT TTTGGCTCAT TGGCTGGATC AGTGCATGTA AGAATTCGAC GAGATGCCAA 960
 40 TGAACAATG GTTCTTGCTC ATGTGACCAA CAGGCTGTAC ACTCTAGTGT CTACTCTAAC 1020
 TGTTCAAAT TTCAAGGATG ACTGGATTAG GCCTGCCCTA TTGTCTGGGC CTGTGTCAGC 1080
 CAATGTCTTA AACTTTTCTAG ATCATCACTG AATCCCAATG CCTCTTTTAA AGGGTACTGA 1140
 TGATTTGAAC CCAGTTACAT CAACTCCAGC TAAACCTAGT AGTCCACCTC CAGAATTTTC 1200
 ATTAACTACT CCTGGGAAAA ATGTGAACCC AGTTATTCTT CTAAACACAC AAACAAGGCC 1260
 45 TTATGTTTGT GGTCTCAATC ATGGACACAC ACCTTACAGC AGCATGCTTA ATCAAGGACT 1320
 TGGAGTTCCA GGAATTTGGG CAACTCAAGG ATTGAGGACT GGTTTTACAA ATATACCAAG 1380
 TAGATATGGA ACTAATAATA GAATTGGACA ACCAAGACCA TGATAGACTC TAACTTATTT 1440
 TTATAAGGAA TATTGACTCC TTGGCTTCCA ATTTATTAG TAATCCAAC TTGCATTGAC 1500
 TGTTTAACT TTTACTCTAA ATGTTAGATA ATAGTAGTCT TGTTCACAT TCATGAAACC 1560
 50 TATGAACTA TATTTTGTGA AAATGTATTT GTGACAGTGA AATCTCTGTA AATGTTAAAG 1620
 GCTTTAAATA GGCTTCTTTT AGAAAATGTG TTTCTTTAAA TTTGGATTTT GGTATCTTTG 1680
 GTTTTGTAGT TGACTGCACT GTGATGTGAC CTTACCTTTA TAAGAGCCAC TTGATGGAGT 1740
 AGATCTGTCA CATTTACTAG ATACGATATT TCTTTTCTTT TCCGAGACCG AGTCTTGCTC 1800
 55 TGCCACTGTG CCGGCCAAT ACATTATTAT TAACTTAAGG CTGTACTTTA TTAAGGCTTC 1860
 CTTAGTTTTT GTTTTGTGTT GTTTTGTGAG ATGGAGTCTC ACTCTGTGCG CCAGGCTGGA 1920
 ATGCAGTGGC ATGATCTCAG CTCAGTCAA CCTCTGCTCT CTGAGTTCAA ATGATTCTCC 1980
 TGCCCTCAGC TCCCGAGTAG CTGGGATTAC AGGCACCTGC CACCACGCC AGCTAATTTT 2040
 TGTATTTTTA GTAAAGACCG GGGATTTCAC CATGTTGGCC AGGCTGTGCT TGAACCTCTG 2100
 60 ACCTCATGAT CCACCCACT TAGCTCCCA AAGTGTGGG ATTAGGTGTG AGCCACCGCA 2160
 CCTGGCCGAT ATTTTCTTTA ATGAAATTTA TAAATATGCT TCTTGAATAA TACACATTTT 2220
 GGGAAAGGGA AAAATGTCTG TTCAAAAGT AAAGGTCTCT TTTATAGCTT TTCCAAACTT 2280
 AATTGCTAAA TTTTCTTTG AGGTCTCTCT GAATTATGTC TTACAACTA AAAGCAAAAA 2340
 TTTTATGACG AAAATTTTGA ATACATTCTA TCTAGCACA TTTGAATTTT TAATTATCAA 2400
 65 GATTTTGTGT AAAGTTTCTC TCCTTAAAA ATTTTAGTAC ATTTGTAAAT

Seq ID NO: 205 Protein sequence
 Protein Accession #: BAB70980.1

70 1 11 21 31 41 51
 MGTIHLFRKP QRSFFGKLLR EPRLVAAARR SWKILLFGVI NLICTGFLLM WCSSTNSIAL 60
 TAYTYLTIFD LFSLMTCLIS YWVTLRKPSV VYSPGFERLE VLAVPASTVL AQLGALFILK 120
 ESAERFLEQP EIHTGRLLVG TFVALCPNLF TMLSRNKPF AYVSEASTS WLQEHVADLS 180
 RSLCGIIRGL SSIFLPRMNP FVLIDLAGAF ALCITYMLIE INNYFAVDTA SAIAIALMTF 240
 75 GTMYPMVSYS GKVLQTTTP HVIGQLDKLI REVSTLDGVL EVRNEHFWTL GPGSLAGSVH 300
 VRIRRDANEQ MVLARVNTNL YTLVSTLTQV IPKDWIRPA LLSGPVAANV LNPSDEHVIP 360
 MFLKGTDDL NFVTSTPAKP SSPPPPEFSFN TPGKNVNPVI LLNTQTRPYG PGLNHGHTPY 420
 SSMLNQGLGV PGIGATQGLR TGFTNIPSRV GTNNRIGQPR P

80 Seq ID NO: 206 DNA sequence
 Nucleic Acid Accession #: NM_016361.1
 Coding sequence: 397..1662

1 11 21 31 41 51

5
10
15
20
25
30

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GGAAGTCAGG GCCGGCTCCT GTTCCTTCAA GAGTGTCTGA GGCCAACTT GAAATACAAG 60
TTTAATGTTC CTGTCGGGC AAAAGATAAG GATCOGATCT CCCCCGGCCC GGTGTGCAGC 120
AGGAGCGACC AACCCCGACC CGGGTTAAAA CTCCAGGGA CTCTTCGTG CTGCCACCTC 180
TTGTTCTCTC CCCCGTTCCC ACTCGGGTC TCCCTCAGGG CCGGAGGCA CAGCGGTCCC 240
TGCTTGCTGA AGGGGTGGAT GTACGCATCC GCAGGTTCCC GCGGACTGG GGGCGCCCGC 300
CGAGCCCGG CGCCCGCAGA AGACTTGTGT TTGCCTCCTG CAGCCTCAAC CCGGAGGCAG 360
CGAGGGCCTA CCACCATGAT CACTGGTGTG TTCAGCATGC GCTTGTGGAC CCCAGTGGGC 420
GTCCTGACCT CGCTGGGTA CTGCCTGCAC CAGCGGCGGG TGGCCCTGGC CGAGTGCAG 480
GAGGCGCATG TCCAGGTGCC GGTGACCCG AGCCTGCTGA AGTTGAAAAT GGTGCAGGTC 540
GTGTTTGCAC ACGGGGCTCG GAGTCTCTC AAGCGCTCC CGCTGGAGGA GCAGGTAGAG 600
TGAACCCCC AGCTATTAGA GGTCCCAACC CAACTCAGT TTGATTACAC AGTCACCAAT 660
CTAGCTGGTG GTCCGAAACC ATATTCTCT TACGACTCTC AATACCATGA GACCACCTG 720
AAGGGGGCA TGTTTGTGG GCAGCTGACC AAGGTGGCA TGCAGAAAT GTTTGCCTTG 780
GGAGAGAGAC TGAGGAAGAA CTATGTGGA GACATTCCT TTCTTCACC AACCTTCAAC 840
CCACAGGAGG TCTTTATTGC TTCCACTAAC ATTTTTCGGA ATCTGGAGTC CACCGCTGT 900
TTGCTGGCTG GGCTTTTCCA GTGTCAGAAA GAAGGACCCA TCATCATCCA CACTGATGAA 960
GCAGATTGAG AAGTCTTGT TCCCAACTAC CAAAGCTGCT GAGCCTGAG GCAGAGAACC 1020
AGAGGCGCGA GGCAGACTGC CTCTTACAG CCAGGAATCT CAGAGGATT GAAAAGGTG 1080
AAGGACAGGA TGGGCATTGA CAGTAGTGAT AAAGTGGACT TCTTCATCCT CTGGACAAC 1140
GTGGCTGCGC AGCAGGCACA CAACCTCCA AGCTGCCCCA TGCTGAAGAG ATTTGCACGG 1200
ATGATCGAAC AGAGAGCTGT GGACACATCC TTGTACATAC TGCCCAAGGA AGACAGGGA 1260
AGTCTTCAGA TGGCAGTAGG CCATTTCTC CACATCCTAG AGAGCAACT GCTGAAAGCC 1320
ATGGACTCTG CCACTGCCCC CGACAAGATC AGAAAGCTGT ATCTCTATGC GGCTCATGAT 1380
GTGACCTTCA TACCGCTCTT AATGACCTG GGGATTTTG ACCACAAATG GCCACGTTT 1440
CTGTGTTGACC TGACCATGGA ACTTTACCAG CACCTGGAAT CTAAGAGAGT GTTTGTGAG 1500
CTCTATTACC ACGGGAAGGA GCAGGTGCGC AGAGGTTGCC CTGATGGGCT CTGCCGCTG 1560
GACATGTTCT TGAATGCCAT GTCAATTTAT ACCTTAAGCC CAGAAAATA TAAAGCACTC 1620
TGCTCTCAA CTCAGTGAT GGAAGTTGGA AATGAAGAGT AACTGATTTA TAAAGCAGG 1680
ATGTGTGAT TTTAAATAA AGTGCCTTA TACAAAAA AAAAAA A

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Seq ID NO: 207 Protein sequence
Protein Accession #: NP_057445.1

35
40
45

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1 11 21 31 41 51
MRLWTPVGV L TSLAYCLHR RVALAELQEA DGQCPVDRSL LKLMQVQVVF RHGARSPLKP 60
LPLEBQVEMN PQLLEVPPQT QFDYTVNLN GGPKYSPYD SQYHETTLKG GMFAGQLTKV 120
GMQMQFALGE RLRLKMYVEDI PFLSPTFNPQ EVFIRSTNIF RNLESTRCLL AGLFQCQKEG 180
PIIIHTDEAD SEVLVFNYS CWSLRQRTRG RRQTASLQPG ISEDLKKVKD RMGIDSSDKV 240
DFFILLDNVA ASQAHNLPSC PMLKRFARMI EQRVDTSLY ILPKEDRESL QMAVGPFLHI 300
LESNLLKAMD SATAPDKIRK LYLAAHDVT FIPLLMTLGI FDHKWPPFAV DLTMLYQHL 360
ESKEHFVQLY YHGKEQVPRG CPDGLCLPDM FLNAMSIVTL SPEKHALCS QTVMEVNGE 420
E

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Seq ID NO: 208 DNA sequence
Nucleic Acid Accession #: CAT cluster

50
55
60

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1 11 21 31 41 51
TTTGAGGGGG TGGTGGGGG AGTTTAATTC ATAAAGAAGC CTCCTGATCA GAAAGGGGCC 60
TAACAGCCTG CCCTTGGAGA GAAGTCCTTC CTGAGGATA AGGCCTCCCA GGGGAGGAGG 120
TGCTGGGGGC CAGTGTAGG CTTGAGGCA TCCCTGGAGG CCAGTCTGT GCTCAGCAAG 180
TAGTGGCAGA GCCTGGAGTG ATGAGTGGGA TGGCCTTCTC AGGTACAGGA CTGTGCTGCT 240
TCTGGCTGCT CTGTCATTG CATTTGCCAC TCAGAACTGC CGCATCCCA GCAATGGCCA 300
GGAGCCCTCC GCAGATCAGT CCGCTCAGCT GCAGGTTTT CCAGTCATAG TAGAAGGGAT 360
CGTCTTTATG GCAAAATGG TCATTGGCTT CCAAGGCAGT CAGGCCAAT GTGTGACTCT 420
GCAGGTTCTC CACTGCTCCT TCACCAAGT CTTGCCAGGT CACCTTGGCG AGGCTCACC 480
TGAGCTGGCA GCGCAG

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Seq ID NO: 209 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..564

65
70
75
80

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1 11 21 31 41 51
ATGGAGCCCT GGGCGTGGCT GCAGGGTTTA AAGAGCCGAC CCACTGCCCC AGCAGCCTCC 60
TCAGATCOGT TCTCTGCGCT GCCAGCTCAG GACTCTGGT AAGGAGCAGT GAGGAACTCT 120
CAGAGTCACA CAGTGGGCT GACTGCCTTG GAAGCCAATG ACCATTTCG CAATAAGAC 180
GATCCCTTCT ACTATGACTG GAAAAACCTG CAGCTGAGCG GACTGATCTG CCGAGGCTC 240
CTGGCCATTG CTGGGATGCG GGCAGTCTG AGTGGCAAT GCAAAATGCA GAGCAGCCAG 300
AAGCAGCACA GTCCCTGTACC TGAGAAGGCC ATCCCACTCA TCACTCCAGG CAGATTTCTC 360
ACCTTGGCCA AATCAATAA ACCTTTATCT CCAAGCACTT TTGCTTGGT GTTTGGCATC 420
AGCTACACAT CAGTCTTCCG AGTGCTCTT TCTGCTGCC TGTACCCTGC CATTCTGGT 480
GATGCTGCTG CCTCACATC AGGCCATCCA AGCATGAGA ACATAAGCAT GCAGAACACT 540
GGAACGAAGG GCTGTACCTA ATGA

```

Seq ID NO: 210 Protein sequence
Protein Accession #: FGENESH predicted

80

```

1 11 21 31 41 51
MEPWANLQGL KSRPTCPAAS SDPFSALPAQ DTGEGAVRNL QSHIVGLTAL EANDPFANKD 60
DPFYDWNKLN QLSGLICGGL LAIAGIAAVL SGKCKCKSSQ KQHSVPVEKA IPLITPGRFL 120

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TLAKSNKPLS PSTFVLVFGI SYTSVFRVPL SASLYPAIPG DAAALTSGHP SMQNISMQNT 180
GTRGCT

Seq ID NO: 211 DNA sequence

Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..318

1 11 21 31 41 51
10 | | | | |
ATGCCCGGCC ACCCGGCTCTG TGAAGTGAGG AGCACCTCTG CCGGGCTGCC CCGTCTGGGA 60
AGTGAGGAGC GCCTCTGCCG GGCTGCCACC CCGTCTGTGA GTGCCTGCTG CGCTGGGCCC 120
AGGCCGCGCC TGCCTTGCCA GGCCCTCGGG CCCCCACCT TCCACCCAGG GGCTGCTCC 180
TCACCCAGG GTTCCATCTC CTTAGTTTCC ACCAGAGACT GGGTCTTCAT TCTCACCCTG 240
15 CTACACAGCC CCTACCAGAA CGTTCTGAAA TGCAAACTA ACAACTGTCT CACCCAGCA 300
GGAAACTCCC CAGGGTCCCG GGCCCCCTGC GGGGTTCAG GCCTCACTCT TCGCGCCCAT 360
CCCTCGCGCT TGACCGCCCT GAGCTCGCCC CCAAGTCTGG CCGTTCAGT CAGTTATCC 420
CTCCAGCCT CCAAGGTCCC CGTTACCGAA GACCGCCACC ATCAGACAT AGCGCAGCAC 480
ATATGGGACA CTGTGTGAAG AGCAGTGAGG AACCTGCAGA GTCCACAGT TGGCTGACT 540
20 GCCTTGAAG CCAATGACCC ATTTGCCAAT AAAGACGATC CCTTCTACTA TGAAGTGA 600
AAGCTGCAGC TGAGCGGACT GATCTCGGGA GGGCTCTGG CCAATGTCTG GATCGCGCA 660
GTCTGAGT GCAAATGCAT ATGCAAGAGC AGCCAGAAAG AGCAGTCC TGTACTGAG 720
AAGGCCATCC CACTCATCAC TCCAGCAGA TTCTCACT TGGCCAAATC AAATAAACC 780
TTATCTCAA GCACCTTTGT CTGTGTGTTT GGCATCAGT ACACATCAGT CTTCGAGTG 840
25 CCTCTTCTG CTTCCCTGTA CCGTCCCAT CCGTGTGATG CTGTGCCCT CACATCAGG 900
CATCCAGCA TGCAGAACAT AAGCATGCAG AACACTGGAA CGAAGGGCTG TACCTAA

Seq ID NO: 212 Protein sequence

Protein Accession #: FGENESH predicted

1 11 21 31 41 51
30 | | | | |
MPGHFVCEVR STSARLPRLG SEERLCPAAT PSVSACCAGP RPFVPCQALR PPTFHPRACS 60
SPQGISLVS TRDWVFILTL LHSPYQNLK CKPNCLTPA GNSPGSRAPC GVAGLTILRAH 120
35 PSALTALSSP FVLALHVLQS LPASKVPVTE DRHHEDIAQH IMDTGEAVR NLQSHTVGLT 180
ALEANDPFAN KDDPFYDVK NLQLSGLIC GLLAIAGIAA VLSGKCKCKS SQKHSPVPE 240
KAIFLITPGR FLTLAKSNKP LSPSTFVLVF GISYTSVFRV PLSASLYPAI PGDAAALTSG 300
HPSMQNISMQ NTGTRGCT

Seq ID NO: 213 DNA sequence

Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..1758

1 11 21 31 41 51
45 | | | | |
ATGATGGGGT CTCATGTTGC CCAGGCTGGT CTGAACTCC TGGGCTCGAG TGACCCCTCT 60
GCCTTGGCCT CCGAAAGTGC TGGGATTACA GGAAGTTTAT TACAGGAATC CATAACACTG 120
GAGGATGTGG CTGTGGACTT CACTTGGGAG GAGTGGCAAC TCCTGGGCGC TGCTCAGAA 180
GACCTGTACC GGGATGTGAT GTTGGAGAAC TACAGCAACC TGGTGGCAGT GGGGTATCAA 240
50 GCCAGCAAAC CGAGTGCACT CTTCAAGTTG GAACAAGGAG AACAACTGTG GACAATTGAA 300
GATGGAATCC ACAGTGGAGC CTGTTCAGGT TCTCCAAAGG TCCCGTCTCT CATTTTCTCA 360
TCTGTGCCCT TCACCTCTCA AAATGCGCTT CATTCTAACA TATGGAAGT TGATCATGTG 420
CTGGAGGCGT TGCAGAGTGA AAGCCTGGTG AACAGAAGGA AACCATGTCA TGAACATGAT 480
GCATTTGAAA ATATTGTTCA TTGCAGCAAA AGTCAGTTTC TGTTAGGGCA AAATCATGAT 540
ATATTGACT TACGTGGAAA AAGTTTGAAA TCCAATTAA CTTTAGTTAA CCAGAGCAAA 600
55 GGCTATGAAA TAAAGAACTC TGTGTAGTTT ACTGGAATG GGGACTCCTT TCTTCATGCT 660
AACCATGAAC GACTTCATAC TGCAATTAAA TTCCCTGCAA GTCAAAAAC CATCAGCACT 720
AAGTCCCAAT TCATCAGTCC CAAGCATCAG AAAACACGAA AATTAGAGAA GCATCATGTG 780
TGCAATGAAT GTGGGAAGAG CTTTCATCAG AAGTCTTGGC TAACTGATCA CCAGGTAATG 840
60 CATACAGGAG AGAAACCCCA CAGATGTAGT CTATGTGAGA AAGCCTTCTC CAGAAAGTTC 900
ATGCTTACTG AACATCAGCG AACTCATACA GGAGAAAAC CTTATGAATG CCTGAATGT 960
GGCAAGCCTT TTCTCAAGAA ATCAGGCTC AACATACATC AGAAAACACA TACCGAGAG 1020
AAACCCATATA TATGAGTGA ATGTGGAATA GGCTTCATCC AGAAAGGAAA TCTCATTTGA 1080
CACCAGCGAA TTCATACAGG TGAGAAACCT TATATATGCA ATGAATGTGG AAAAGGCTTC 1140
65 ATTCAGAAGA CGTGTCTCAT AGCACATCAG AGATTTCACA CAGGAAAGAC GCCCTTTGTG 1200
TGCAATGAAT GTGGAAAATC CTGTCTCAG AAATCAGGTC TCATTAAACA TCAAAGAAAT 1260
CACACAGGAG AGAAACCCCT TGAATGTAGT GAATGTGGGA AAGCCTTTAG CACAAAGCAA 1320
AAGCTCATTT TCCATCAAAG GACTCATACA GGAGAGAGAC CCTATGGCTG TAACGAGTGT 1380
GGGAAAGCGT TTGCGTATAT GTGCTGTCTG GTTAAGCATA AGAGAATACA CACAGGGGAG 1440
70 AAACAAGAGG CAGCCAGGT GGAATACTCT CCTGCAGAGA GGCACAGCTC ATTACACACC 1500
AGTATGTCA TGCAGGAGAA AAATCTGTCT AACGGGGCGA CTACACAGT GCCTTCTGTG 1560
GCCCTCAGA CATCATTAAC CATCAGCGGC CTCCTGCAAC ACAGGAACGT AGTCCTTGTG 1620
GGACAGCCAG TGGTCAGATG TGCAGCCTCA GGAGATAACA GAGGATTGTC ACAGGACAGA 1680
AACCTTGTGA ATGCAGTGAA TGTGTTGTG CTTCCGTGA TCAATTATGT CTTATTTAT 1740
75 GTTACAGAAA ACCCATAG

Seq ID NO: 214 Protein sequence

Protein Accession #: FGENESH predicted

1 11 21 31 41 51
80 | | | | |
MMGEVAQAG LELLGSSDPP ALASESAGIT GLLQESITL EDVAVDPTWE EQQLLGAQK 60
DLYRDMKLEN YSNLVAVGQY ASKPDALFKL EQGEQIMTIE DQIHSGACSG SPKVPPSIPS 120
SVPTTLQNC LHSNIWKVDHV LERLQSESLV NRRKPCEHD AFENIVHCK SQFLGQNH 180
IPDLRGRSLK SNLTLVNQSK GYEIKNSVEP TGNQDSPLHA NHERLHTAIK FPASQXLIST 240

5 KSPFISPKHQ KTRKLEKHHV CSECGKAFIK KSWLTDHQM HTGEKPHRCS LCEKAFSRKF 300
 MLTEHQRTHT GEKPYECPEC GKAFLLKXSL NIHQKHTGE KPYICSECGK GFIQKGNLIV 360
 HQRIHTGEKP YICNECGKGF IQKCLIAHQ RPHTKTFFV CSECGKSCSQ KSLIKHQRI 420
 HTGEKPFECs ECGKAFSTKQ KLIVHQRTHT GERPYGCNEC GKAFAYMSCL VKHKRIHRE 480
 KQEAARKVENP PAERHSSLHT SDVMOEKNSA NGATTQVPSV APQTSINISG LLANRNVVLV 540
 GQPVVRCAS GDNRGFAQDR NLVNAVNVVV PSVINYVLFY VTENP

10 Seq ID NO: 215 DNA sequence
 Nucleic Acid Accession #: NM_032190.1
 Coding sequence: 502..1332

1 11 21 31 41 51
 15 GATTCCGTGT TCTTGGCCAT GTTAGCCATA ATATCCTGTG CAGTATGTTT TTCTGTGCA 60
 GAGGCAAAA CATATTGGGC ATATGTTCCG AAGCCCCAG CAGTATGACC CATACTTTGG 120
 AGTGACACTC CTCTAAGAT TTATCATGAT TAAGGAGCAT GGGCTCCAGG ACCCTTAACT 180
 CCACCTGACA TAGAACAGTT AGACTCTCAG AATAATGTCA TTAATTATAC CGCTCCATTG 240
 GAAGGACTTC CTTTGTGTGT CACCACAAAG ACATCACTCA GCCATAGCTG TCTTACAGTT 300
 20 CAAGCTCACA CATGGTTGAG TCACATGCGG AAAATCATGT ACTTATTAAAG TCTTGGTTAT 360
 ATTAATGTAA CCGGTGTGCT AACCAACCAT TCCTGGCCCA ATCGCCTTCA TGTGTCTGAC 420
 TATACAGAAT GGATTCCTCT CAATAGTTC TACCCCTCTC CATAGACCCA GTGTCTTGGC 480
 CCACTGGCTA GAAAACAATC TATGTTAACT GGAGACATTG TGGATTGGGG ACCTAAAGGC 540
 CAATTAGATG GAAAAGAAGA AAATCAGAAA TCGTGGCACA AACTTTGCTG GCATTGGTGG 600
 25 CAAGCTTTTA ATGCTTCTTC TTTATATAAC ACTGGGATCC AATCCAGTC GGCCGCCAG 660
 ATTGCTTGGC ATGGAGCAGG CTTTAGCCCG CCTCTTCTC AGTGGCATTG TCTAGGGAGG 720
 AAAGGACCAA TTCAAAAGAT GATATGGAAG GCAGCATTCC CATTATGAA TGGCAACATC 780
 TGGGTGCGCA TAATACTATC CAATAATAGC AATAGTAAGC AACACAGTCT TAATGTTACA 840
 TTTGTAAGA ATATCACCAC TCAATTTACA GTTGTGTGTT TTAATCCTTA TGTGTTTTG 900
 GCAGCTAAGA AGGACCAGCT CCAGGTAAC AATACCCAAT TGACCTGTAA ATCTTGGCAG 960
 30 TTATATACTG GCATTAATCA TAGCACATTG CAAACACATA ATATCTCTAC TTTGATGATT 1020
 TTAGGTTGCA TCCCTGGGCT ATGGATTCTT GTTAATCTGT CTGAGCCATG GGCTGCCACA 1080
 ATTGCTTTAC ATTTTGTGAA ACTTCTCTA ACTCAGTTTA CTCATTGTGT CCGTAGAGGC 1140
 TTAGGCATGA TAATTTTTCG TATTGTTTAC TTGCTCACAC TAATAATTTC TGTGTGATG 1200
 TCCTCTGTAG CTTTGCATAG TTCTATTCAA ACAGCTCAGT ATGTGGAGAA CTGAGACAGC 1260
 35 ACAGTCAACC AAGGGTGGCT ACTTGAGAT AAAATTAACA CTGAGTTACA AACTGAAGTG 1320
 GCAGTGTAT ATTCACGAT TCTATGTTA GGGGAACAG TACAAGCTT GCAATTGCAG 1380
 CAGTAATGT GTTGTCAATT TAATCAGCT CATATTGTG TAACCAACTT AGAATATAAC 1440
 CAAAGTGAGT ATCCATGGGA TCTTGTGAAA GCCCATTTCG AGGGAGCTTT CACATCCGAC 1500
 40 ATCACCCTTG ATATTGGTGA ATTACAAAAC AAAATTCTTG ATTTAAATAA ACAAAITCCA 1560
 GAGTTTCAGC CTTCTTTAGA AGACTGGACT GAATTCCAGC AAGGCTGGA GAGCGTCAAC 1620
 CCTTGGACCT ATCTAAAGCA CCACATTAAC ATCTTATATA TAGTCTTGG AATAATGTG 1680
 TTTTGTCTCT GTCTTCTGTT TACATCTTT CACTTAATAC ATAAACAAGA AGGGGAAAT 1800
 45 AAAGCTACCC AGCCTGGCCT TACATCTTT CACTTAATAC ATAAACAAGA AGGGGAAAT 1860
 GTTGGGAGCC AAAAGGCCA AAGGGATGGT GACCAACTCA GCATTCCATG GGAGGCTACA 1920
 TGATCAAAAG GCAAACTGTT TATCATGAAT ACAGAATGTG GGCAAACTCG CTCTCTGTGC 1980
 TGCCCAAGAG GTTGTCTGAG GGCCATGCT CCCTGGCCCC GGCTCCTGA GTTATCTAC 2040
 TGGGACATCT AGAGCCTATT GTTCGAGGAA TGCAGTCTTG CAAGCCTACT CTGGACCGAG 2100
 CAGCTGACCT CTTCTTCCAC ACCCTTCTC ACTATCTCT TTGCTAATA AATATGGAGG 2160
 50 GCTGTGTAAA GCTCAGGGCC CTTGTCCACT AGAGGCAAGG TGTCCCTGA CCCTTCTTCC
 AAACAT

Seq ID NO: 216 Protein sequence
 Protein Accession #: NP_115566.1

55 1 11 21 31 41 51
 MLTGDIVDMG PKGQLDGKEE NQKSWHLKW HWQAFNASS LYNTGIQSQS AAQIAWHGAG 60
 FSPPLPQWHY LGRKGPIQKM IWKAAPFPMN GNIWVAILL NNSNSKQHSI NVTFVKNIIT 120
 60 QPTVCVNPY VFLAAKQDL QVNNLTQCK SCQLYHCINH STLQTHNIST LMILGCIPLG 180
 WIFVNLSEFP AATIALHPVK LLLTQFTHCV RRGLGMIIPA IYLVTLIIS VVMSSVALHS 240
 SIQTQYVEN WRTVNGQWL LENKINTELQ TEVAVL

65 Seq ID NO: 217 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..1566

1 11 21 31 41 51
 70 ATGGTGAACC CCAATCCAC TTCTCCCTC TTCAGGTTAT GTTTTTGTCT CCTGAGGAGT 60
 CAGAACCTGT GGGTTGAAGA GCAAAATCAA TGCAAAAACA TATTGGGCAT ATGTTCCCAA 120
 TCCCCAGCA GTATGGCCTA TACTTTGGAG CTCACCTCTC CTGAGATTTA TCAGATCAG 180
 GGAGAGTGGG CTCACGGAAC CTAACCTCC CGTGACATAG AAAAGTTAGA CTCTCAGAAC 240
 AATGTCATTA ATTATACCAC TCCACTGGAA GGACTCCCTT TGTTTATCAC CACAAGACG 300
 75 TCGTCAGCC ATAGCTGTCT TGCAATTCAR GCTCAACAT GGTGAGTCA CTATGGAAAA 360
 ATTATGTAAT TATTAGTCT TGGTTCTATT AATGTAACAT GTGTGCTAAC CAATCATTC 420
 CAGTCCAGTC ACCCTAATG TGCTGATTAT ACAGAATGGA TTCCATTCAA TAGTTCCTAC 480
 CCACTCTGT GGACCCAGTG TCTTGATCCA CTGGCTAGTA AACAATATAT GTCAACTGAA 540
 GACACTGTGG ATTGGGAACC TAAAGGTCAA TTAGATGGAA AAGGTGAAG TCAGAAATCA 600
 80 TGGCACAAC TTCCTGGCA TTGGCGGCAA GCTTTAATG CTTCTCTTT ATACAACAGC 660
 AGAATCCAAT CCAAGTCTGC TGCTCAGATT GCTTGGCATG GAGCAGGCTT TAGCCCACT 720
 CTCTCTCAGT TGCATTATCT GGGGAGGAAA GGACCAATTC AAGAAACTAT ATGGAAGGCA 780
 GCACTCCCAT TTATGAATGG CAACATCTGG ATTGGAACAC TGTCTAATA TAGCAATAGT 840
 AAGCAACACA GTCCTAATGT TGCAATTGTA AAGAATATCA CCATCAGTT TACAGTTTGT 900
 GTTTTAATC CTTATGCCTT TTTGGCAGCT AAGAAGAACC AGCTTCAGGT GGAGAACTGG 960

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ACACGCACAG CTGACCAAGC GAGGCTACTT CAGAATAAAA TTAACACTGA GTTACAAACT 1020
GAAGTGGCAA TGTTGAAATC CATGGTTCTG TGGTTAGGAG AACAGGTACA AAGCTTGACG 1080
TTGCAGCAGC AATTGCGTCA TCATTTTAAT CACATTGATA TTGCGTAAC TAACTCAGAA 1140
TATAACCAAA GTAGATATCC GTGGGACCTT GTGAAAGCCC ATTTGCAAGG AGCTTTCACA 1200
TCCAACATCA CCTTTGATAT TGGTGAATTA CAAAACAAAA TTATTGATT AAATAGGCAG 1260
ACTCAAGAAT TTCAGCCTTC TTAGAAGAC TGGACCGAAT TCCAGGAAGG CCTGGAGAGC 1320
CTCAACCTT GGACCTATCT AAGGCACCAC ATTAACATCT TATATGTAGT TCTTGAATA 1380
ATGTTGTTTT GTCTCTGTCT TCGGTTTATA GTCTGTAAAA TCGGATGGAC CACCAATTGG 1440
AGAATGAGAG CCTCCAGCC CAGCCTTACA TTCTTTCAAT TAATACATAA ACAGAAAGGG 1500
GGATATGCGG GGAGCCAAAG GCCTGTGGGA CGTGACCAAC TCAGCATCTT GCTGGAGGCT 1560
ATATGA

Seq ID NO: 218 Protein sequence

Protein Accession #: FGENESH predicted

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1 11 21 31 41 51
MVNPKSTSSL FRLCFLLLRS QNLWVEBQIQ CKNILGICSQ SPSSMAYTLE LTPPEIYHDQ 60
GEWAPGLPTP RDIEKLDQSN NVINYTTPL GLPLFITTKT SLSSHCLAIQ AQTWLSHYGK 120
IMYLLGLGSI NVTGVLTNHS QSSHPNCADY TEWIPFNSSY PTLWTQCLDP LASKQVMSTE 180
DVTVDWPKQG LDGKESQKS WHKLHWHWRQ AFNASSLYNS RIQSQSAAQI ANHGAGFSPP 240
LPQLHYLGRK GPIQETINKA ALPFMNGNIW IGTLSNNSNS KQHSLLVAFV KNITTQFTVC 300
VFNPAFLAA KGNQLQVENW TRTADQARLL QNKINTELQT EVAMLSKMWL WLGEQVQSLQ 360
LQQQLRRHFN HHICVTNSE YNQSEYFWDL VKAHLQGAFT SNITFDIGEL QNKIIDLNKQ 420
TQEFQPSLED WTEFQEGLES LNPWTYLRHH INILYVVLGI MLPCLCLRFI VCKIGWTTNW 480
RMRASQPSLT FFLQIHKKQG GYAGSQRPVG RDQLSILLEA I

Seq ID NO: 219 DNA sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 1..900

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ATGCCGCGCG GGGAGCTGAG CGAGGCGGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60
CCGCGGCGCG GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGTCTGT GGGCGACGCG 120
GCCGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
CGGCCCACTG CGCTGGACAC CTCTCTCTGT ACGTACGTTT AATCGCCCGT GCGGCGCGCT 240
GGCTGCGCGG GGGCTGTGCA CCGGGGAGCT GGGGCGGGCG TCTCGGCGGG AGGGCGCAGA 300
GGACCCCGGG GAGGAGACTG GAGCAGGCCC CGAGGTGCGG CTGGTGGCGG CCAGGACGCT 360
CTTCCTAACT CAGGCTCTCC CGCCCCCGCC CCGTCACTGC AAGTCTGTGT GGATGGAGCT 420
CCGCTGCGCA TTGAGCTCTG GGACACAGCG GGACAGGAGG ATTTTGACCG ACTTCGTTC 480
CTTTGCTACC CGGATACCGA TGTCTTCTGT GCGTGTCTCA GCGTGGTGCA GCCCAGCTCC 540
TTTCAAAACA TCACAGAGAA ATGGCTGCCC GAGATCCGCA CGCACAAACC CCAGCGCGCT 600
GTGCTGCTGG TGGGCACCCA GCGCGACCTG AGGGACGATG TCAACGTACT AATTCAGCTG 660
GACCAAGGGG GCGGGGAGGG CCGCGTGCCC CAACCCGAGG CTCAGGGTCT GCGCGAGAAG 720
ATCCAGGCTG GCTGCTACCT TGAGTGCTCA GCCTTGACGC AGAAGAACTT GAAGGAAGTA 780
TTTGACTCGG CTATTCTCAG TGCCATTGAG CACAAAGCCC GCGTGGAGAA GAAACTGAAT 840
GCCAAAGGTG TGCGCACCTT CTCCCGCTGC CGCTGGAAGA AGTCTCTCTG CTTGTTTGA

Seq ID NO: 220 Protein sequence

Protein Accession #: FGENESH predicted

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1 11 21 31 41 51
MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60
RPTALDTFSG TYVQSPVRPR GCGGAVHRGA GAGVSAGRR GPRGGDWSRP RGGAGAAQDA 120
LPNSGSPRPA PAVQVLVDGA FVRIELWDTA GQEDFDRLRS LCYPDTDVFL ACFSVVQPSS 180
PQNIETKWL P BIRTHNPQAP VLLVGTQADL RDDVNVLIQL DQGGREGEVP QPOAQGLAEK 240
IRACCYLECS ALTQKNLKEV FDSAILSAB HKARLEKXIN AKGVRTLSRC RWKKPFPCPV

Seq ID NO: 221 DNA sequence

Nucleic Acid Accession #: XM_063832.2

Coding sequence: 1..711

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ATGCCGCGCG GGGAGCTGAG CGAGGCGGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60
CCGCGGCGCG GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGTCTGT GGGCGACGCG 120
GCCGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
CGGCCCACTG CGCTGGACAC CTCTCTCTGT CAAGTCTTGG TGGATGGAGC TCGGTGGCGC 240
ATTGAGCTCT GGGACACAGC GGGACAGGAG GATTITGACC GACTTCGTTC CTTTGTCTAC 300
CGGATACCG ATGTCTTCTT GCGTGTCTTC AGCGTGGTGC AGCCAGCTTC CTTTCAAAAC 360
ATCACAGAGA AATGCTGCTG CGAGATCCGC AGCACAACC CCCAGGCGCC TGTGCTGCTG 420
GTGGGACCCC AGGCGGACCT GAGGGACGAT GTCAAGTAC TAATTCAGCT GGACCAAGGG 480
GGCCGCGGAG GCGCGGTGCC CCAACCCGAG GCTCAGGGTC TGGCGAGAAA GATCCGAGCC 540
TGCTGCTACC TTGAGTGTCT AGCCTTGACG CAGAAGAACT TGAAGGAAGT ATTTGACTCG 600
GCTATTCTCA GTGCCATTGA GCACAAAGCC CGCTGGAGA AGAAACTGAA TGCCAAAGGT 660
GTGCGCACCC TCTCCCGCTG CCGCTGGAAG AAGTCTTCTT GCTTCGTTTG A

Seq ID NO: 222 Protein sequence

Protein Accession #: XP_063832.1

1 11 21 31 41 51

MPPRELSEAE PFPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSSLIVS YTCNGYPARY 60
 RPTALDTFVS QVLVDGAPVR IELWDTAGQE DFDRLRLSLCY PDTDVFLACF SVVQPSFSQON 120
 ITEKWLPEIR THNPQAPVLL VGTQADLRDD VNVLIQLDDQ GREGVPVQPO AQGLAEKIRA 180
 CCYLECSALT QKNLKEVFDS AILSAIEHKA RLEKKLNAGK VRTLSRCRWK KFFCFV

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Seq ID NO: 223 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1161

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1 11 21 31 41 51
 ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAAATAG ACAAGAAGAA CTGCTGTGTG 60
 TTCCGAGATG ACTTCATTGC CAAGGTGTG CGCCCGGTGT TGGGGCTGGA GTTTATCTTT 120
 GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCCCTGGAAA 180
 TCCAGCCGGA TTTTCTGTT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG 240
 CGGTTCGTGA TGGACTACTA TGTGCGGCGT TCAGACTGGA AGTTTGGGGA CATCCCTTGC 300
 CGGCTGGTGC TCTTCATGTT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG 360
 GTGGCGGTAG ACAGGTATTT CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC 420
 AATTGGACAG CAGCCATCAT CTCTTGCCCT CTGTGGGGCA TCACTGTGCG CCTAACAGTC 480
 CACCTCCTGA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC 540
 AGCATCTGCC ATACCTCCG GTGGCAGGAA GCTATGTTC TCCTGGAGTT CCTCTGCCC 600
 CTGGGCATCA TCTGTCTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG 660
 GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT 720
 GTCATCTGCT TCTTCCCGAG CGTGGTGTG CGGATCGCA TCTTCTGGCT CTGCGCACT 780
 TCGGGCAGC AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTTCTT TATCACTCTC 840
 AGCTTCACT CATGAACAG CATGCTGGAC CCGTGGTGT ACTACTTCTC CAGCCCATCC 900
 TTTCCCACT TCTTCCAC TTTGATCAAC CGCTGCCCTC AGAGGAAGAT GACAGGTGAG 960
 CCAGATAATA ACCGCAGCAC GAGCGTCGAG CTCACAGGGG ACCCCAACAA AACCAGAGGC 1020
 GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCCCTCTTA TCTGGGCCCA 1080
 ACCTCAATA ACATTCCAA GAAGGGACAT TGTCAACAG AACCAGCATC TCTGGAGAAA 1140
 CAGTTGGGAT GTTGATCGA G

Seq ID NO: 224 Protein sequence
 Protein Accession #: Eos sequence

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1 11 21 31 41 51
 MNRHHLQDHF LEIDKKNCV FRDDFIKVL PPVLGLEFIF GLLGNGLALW IFCFHLKSWK 60
 SSRIFLNLVA VADFLLIICL PFVMDYVRR SDWKFGDIPC RLVLFMFAMN RQGSIIPLTV 120
 VAVDRYFRV HPHALNKKIS NWTAAIISCL LWGITVGLTV HLLKKKLLIQ NGPANVCISF 180
 SICTFRWHE AMFLLEFLLP LGIILFCSAR IISLRQROM DRHAKIKRAI TFINVVAIVF 240
 VICFLPSVVV RIRIFWLLHT SGTQNCVYR SVDLAFFITL SFTYMNMLD PVVYFSSPS 300
 PFNFFSTLIN RCLQRKMTGE PDNNRSTSV LITGDPNKTG APEALMANS EPWSPSYLGP 360
 TSNHSHKKGH CHQEPASLEK QLGCCIE

Seq ID NO: 225 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1092

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1 11 21 31 41 51
 ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAAATAG ACAAGAAGAA CTGCTGTGTG 60
 TTCCGAGATG ACTTCATTGT CAAGGTGTG CGCCCGGTGT TGGGGCTGGA GTTTATCTTC 120
 GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCCCTGGAAA 180
 TCCAGCCGGA TTTTCTGTT CAACCTGGCA GTGGCTGACT TTCTACTGAT CATCTGCCTG 240
 CGCTTCTGA TGGCAACTA TGTGAGGCGT TGGGACTGGA AGTTTGGGGA CATCCCTTGC 300
 CGGCTGATGC TCTTCATGTT GGCTATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG 360
 GTGGCGGTAG ACAGGTATTT CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC 420
 AATGGACAG CAGCCATCAT CTCTTGCCCT CTGTGGGGCA TCACTATTGG CTTGACAGTC 480
 CACCTCCTGA AGAAGAAGAT GCGATCCAG AATGGCGGTG CAAATTGTG CAGCAGCTTC 540
 AGCATCTGCC ATACCTTCCA GTGGCAGGAA GCCATGTTC TCCTGGAGTT CTCTCTGCC 600
 CTGGGCATCA TCTGTCTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG 660
 GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT 720
 GTCATCTGCT TCTTCCCGAG CGTGGTGTG CGGATCGCA TCTTCTGGCT CTGCGCACT 780
 TCGGGCAGC AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTTCTT TATCACTCTC 840
 AGCTTCACT CATGAACAG CATGCTGGAC CCGTGGTGT ACTACTTCTC CAGCCCATCC 900
 TTTCCCACT TCTTCCAC TTTGATCAAC CGCTGCCCTC AGAGGAAGAT GACAGGTGAG 960
 CCAGATAATA ACCGCAGCAC GAGCGTCGAG CTCACAGGGG ACCCCAACAA AACCAGAGGC 1020
 GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCCCTCTTA TCTGGGCCCA 1080

Seq ID NO: 226 Protein sequence
 Protein Accession #: Eos sequence

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1 11 21 31 41 51
 MNRHHLQDHF LEIDKKNCV FRDDFIVKVL PPVLGLEFIF GLLGNGLALW IFCFHLKSWK 60
 SSRIFLNLVA VADFLLIICL PFLMDYVRR WDWKFGDIPC RLVLFMFAMN RQGSIIPLTV 120
 VAVDRYFRV HPHALNKKIS NWTAAIISCL LWGITVGLTV HLLKKKMPIQ NGGANLCSSF 180
 SICTFQWHE AMFLLEFLLP LGIILFCSAR IISLRQROM DRHAKIKRAI TFINVVAIVF 240
 VICFLPSVVV RIRIFWLLHT SGTQNCVYR SVDLAFFITL SFTYMNMLD PVVYFSSPS 300
 PFNFFSTLIN RCLQRKMTGE PDNNRSTSV LITGDPNKTG APEALMANS EPWSPSYLGP 360
 TSP

Seq ID NO: 227 DNA sequence
Nucleic Acid Accession #: NM_006018
Coding sequence: 61..1224

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5      1      11      21      31      41      51
CGCCACTTTG CTGGAGCATT CACTAGGCGA GGGCTCCAT CGGACTCACT AGCCGCACTC 60
ATGAATGGGC ACCATCTGCA GGATCACTTT CTGGAAATAG ACAAGAAGAA CTGCTGTGTG 120
TTCCGAGATG ACTTCATTGC CAAGGTGTTG CCGCGGTGTG TGGGGCTGGA GTTTATCTTT 180
10 GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCTCTGAAA 240
TCCAGCCGGA TTTTCTGTGT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG 300
CGTTCTGTGA TGGACTACTA TGTGGGGCGT TCAGACTGGA ACTTTGGGGA CATCCCTTGC 360
GGGCTGTGTC TCTTCATGTT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCAGGGTG 420
GTGGCGGTAG ACAGGTATTT CCGGTGTGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC 480
15 AATTGGACAG CAGCCATCAT CTCTTGCCTT CTGTGGGGCA TCACTGTTGG CCTAACAGTC 540
CACCTTCCTG AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC 600
AGCATCTGCG ATACCTTCCG GTGGCAACGA GCTATGTTCC TCCTGGAGTT CCTCCTGCCC 660
CTGGGCACTA TCTGTCTCTG CTCAGCCAGA ATTATCTGGA GCCTGGCGCA GAGACAAATG 720
GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGTGTGG CATCGTCTTT 780
20 GTACATCTGT TCCCTCCGAG CGTGGTTGTG CGGATCCGCA TCTTCTGGCT CCTGCACACT 840
TCGGGCAACG AGAATTGTGA AGTGTACCAG TCGGTGGACC TGGCGTCTCT TATCACTCTC 900
AGCTTCACCT CATGCTGGAC CCGTGTGTGT ACTACTCTCT CAGCCCATCC 960
TTTCCCAACT TCTTCTCCAC TTGTATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG 1020
25 CCAGATAATA ACCGCGACAC GAGCGTCGAG CTCACAGGGG ACCCCAACAA AACCAAGGCG 1080
GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCCCTCTTTA TCTGGGCCCC 1140
ACCTCAATAA ACCATTCCAA GAAGGACATC TGTACCAAG AACCCAGATC TCTGGAGAAA 1200
CAGTTGGGCT GTTGCAGCGA GTAAATGTAC TGGACTCGGC CTAAGGTTTC TGGAACTTTC 1260
CAGATTCAAG GAATCTGATT TAGGGAAACT GTGGCAGATG AGTGGGAGAC TGGTTGCAAG 1320
30 GTGTGACCAC AGGAATCTCT GAGGAACAGA GAGTAAAGCT TCTAGGCATC TGAAACTTGC 1380
TTCACTCTCT AGCTTCGACG GACTGAAGAT GGGCAAATTC TAGGCGTTTC TGCTGAGCAG 1440
AGTTGGAGCC AGAGATCTAC TTGTGACTTG TTGGCCTTCT TCCACATCTC GCCTCAGACT 1500
GGGGGGGGCT CAGCTCCTCG GGTGATATCT AGCCTGCTTG TGAGCTCTAG CAGGGATAAG 1560
GAGAGCTGAG ATTGGAGGGA ATTGTGTTGC TCCTGGAGGA AGCCCAAGCA TCATTAAACA 1620
35 AGCCAGTAGG TCACCTGGCT TCCGTGGACC AATTCACTTT TCAGACAAGC TTTAGAGAAA 1680
TGGACTCAGG GAAGAGACTC ACATGCTTTG GTTAGTATCT GTGTTCCGGT TGGGTGTAAT 1740
AGGGGATTAG CCCCAGAAGG GACTGAGCTA AACAGTGTTA TTATGGGAAA GGAATGGCA 1800
TTGCTGGCTT CAACCAAGCA CTAATGCAAT CCATTCTCTC CTGTTTATA GTAACTTAAG 1860
GGTTGAGCAG TTAATAACGG TTCAGGATAG AAAGCTGTTT CCCACCTGTT TCGTTTATCC 1920
40 ATTAAGAGGG AAACGTGCCT CTGCCCCACG GGTAGAGGGG GTGCACGTTT CTCTCTGGTC 1980
CTTCGCTTGT GTTCTGTATC TTACCAAAAA TCTACCACCT CAATAAATTT TGATAGGAGA 2040
CAAAAAAAA A

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Seq ID NO: 228 Protein sequence
Protein Accession #: NP_006009.1

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45      1      11      21      31      41      51
MNRHHLQDHF LEIDKKNCCV PRDDPIAKVL PFVLGLEFIF GLLQGLALW IFCFHLKSWK 60
SSRIPLFNLA VADFLLIICL PFVMDYYVRR SDWNPGDIPC RLVLPMFAMN RQGSIIPLTV 120
50 VAVDRYFRVY HPFHAIKNIK NWTAAIISCL LWGITVGLTV HLLKKKLLIQ NGPANVCISF 180
SICHTFRWHE AMPLLEFLFL LGIILFCSAR IIWSLRQRQM DRHAKIKRAI TFIMVVAIVP 240
VICFLESVVV RIRIFWLLHT SGTQNCVYR SVDLAFPIFL SFTYMSMLD PVVYFSPSPS 300
FPNFFSTLIN RCLQRMTGSE PDNNRSTSVS LTGDPNKTRG APEALMANSO EPWSPSYLGP 360
55 TSNNHKKKGH CHQEPASLEK QLGCCIE

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Seq ID NO: 229 DNA sequence
Nucleic Acid Accession #: NM_014398.1
Coding sequence: 64..1314

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60      1      11      21      31      41      51
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ACCATGCCCC GGCAGCTCAG CGCGGCGGCC CGCTCTTTCG CGTCCCTGGC CGTAATTTTG 120
65 CAGATGGCA GTCAAAATGAG AGCAAAAGCA TTTCCAGAAA CCAGAGATTA TTCTCAACCT 180
ACTGCAGCAG CAACAGTACA GGACATAAAA AAACCTGTCC AGCAACCAGC TAAGCAAGCA 240
CCTCAACAAA CTTTAGCAGC AAGATTATG GATGGTCATA TCACCTTTCA AACAGCGGCC 300
ACAGTAAAAA TTCCAACAAC TACCCAGCA ACTACAAAAA ACACGTCAAC CACCAGCCCA 360
ATTACCTACA CCCTGGTCAC AACCCAGGCC ACACCAACA ACTCACAC AGCTCCTCCA 420
GTTACTGAAG TTACAGTCGG CCTAGCTTA GCCCTTATT CACTGCCACC CACCATCACC 480
70 CCACAGCTC ATACAGCTGG AACCAATTCA TCAACCGTCA GCCACAAC TGGGAACACC 540
ACTCAACCCA GTAACAGAC CACCTTCCA GCAACTTTAT CGATAGCACT GCACAAAAGC 600
ACAAACGGTC AGAAGCCTGA TCAACCAACC CATGCCAG GAACAAAGCG AGCTGCCACC 660
AATACCAACC GCACAGCTGC ACCTGCCCTC ACGTTCTCTG GGCACACCTT TGCACTCAG 720
CCATGTCAGG TCAAGACTGG AATTATCAG GTTCTAAAG GAAGCAGACT CTGTATAAAA 780
75 GCAGAGATGG GGATACAGCT GATTGTTCAA GACAAGGAGT CGGTTTTC ACCTCGGAGA 840
TACTTCAACA TCGACCCCAA CGCAACGCAA GCTCTGGGA ACTGTGGCAC CGGAAAAATCC 900
AACCTTCTGT TGAATTTTCA GGGCGGATTT GTGAATCTCA CATTTACCAA GGATGAAGAA 960
TCATAATTATA TCAGTGAAGT GGGAGCCTAT TTGACGCTCT CAGATCCAGA GACAGTTTAC 1020
CAAGGAATCA AACATCGGGT GGTGATGTTT CAGACAGCAG TGGGCATTC CTTCAAGTGC 1080
80 GTGAGTGAAC AGAGCCTCCA GTTGTACGCC CACCTGCAGG TGAAAAACAC CGATGTCCAA 1140
CTTCAAGCCT TTGATTTTGA AGATGACCAC TTGGAAGATG TGGATGAGTG CTGCTCTGAC 1200
TACCAATTG TGCTTCTGTG GATTGGGCC ATCGTGGTTG GTCTCTGCCT TATGGGTATG 1260
GGTGTCTATA AAATCCGCTT AAGGTGTCAA TCATCTGGAT ACCAGAGAAT CTAATTGTTG 1320
CCCGGGGGGA ATGAAATAAT TGAATTTAG AGAAGCTCTT CATCCCTTCC AGGATGGATG 1380

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5 TTGGGAAATT CCCTCAGAGT GTGGGTCCTT CAAACAATGT AAACCACCAT CTCTATTCA 1440
 AATGAAGTGA GTCACTGTGTG ATTTAAGTTC AGGCAGCACA TCAATTTCTA AATACTTTTT 1500
 GTTTATTTTA TGAAGATAT AGTGAGCTGT TATTTTCTA GTTCTCTTA GAATATTTTA 1560
 GCCACTCAA GTCAACATT GAGATATGTT GAATTAACAT AATATATGTA AAGTAGAATA 1620
 10 AGCCITCAA TTATAAACA AGGTCATTT GTAACATA CTACTGTGTG TGCAATTGAG 1680
 ATTTTATTT ACCCTTGATC TTAACAAAGC CTTTGTCTTG TTATCAAATG GACTTTCAGT 1740
 GCTTTTACTA TCTGTGTTT ATGGTTTCAT GTAACATACA TATTCCTGGT GTAGCACTTA 1800
 ACTCCTTTTC CACTTTAAAT TTGTTTTTGT TTTTGTAGAC GGAGTTTCAC TCTTGTCAAC 1860
 CAGGCTGGAG TACAGTGGCA CGATCTCGGC TTATGGCAAC CTCGCTCC CGGTTCAAG 1920
 15 TGATTCCTCT GCTTCAGCTT CCGAGTAGC TGGGATTACA GGCACACACT ACCACGCTG 1980
 GCTAATTTT GTATTTTAT TATAGACGGG TTTCAACATG TTGGCCAGAC TGGTCTTGAA 2040
 CTCTTGACCT CAGGTGATCC ACCCACTCA GCCTTCCCAA GTGCTGGGAT TACAGGCATG 2100
 AGCCATTGCG CCGGCTTAA AATGTTTTT TTAATCATCA AAAAGAACAA CATATCTCAG 2160
 GTTGTCTAAG TGTTTTTATG TAAACCAAC AAAAGAACAA AATCAGCTTA TATTTTITAT 2220
 20 CTGTGACT CCGTCTCCAG AATTGCTAGA CTAAGAATTA GGTGGCTACA GATGGTAGAA 2280
 CTAAACAATA AGCAAGAGAC AATAATAATG GCCCTTAAT ATTAACAAG TGCCAGAGTC 2340
 TAGGCTAAGC ACTTTATCTA TATCTCATTT CATCTCACA ACTTATAAGT GAATGAGTAA 2400
 ACTGAGACTT AAGGGAACCT AATCACTTAA ATGTCACTG GCTAACTGAT GGCAGAGCCA 2460
 25 GAGCTTGAA TCACTGTTGT CTGACATCAA GGTCTTTGGT CTTCTCCCTA CACCAAGTTA 2520
 CCTACAAGAA CAATGACACC ACACCTGCCC TGAAGGCTCA CACCTCATAC CAGCATACGC 2580
 TCACCTTACA GGAATATGGG TTTATCCAGG ATCATGAGAC ATTAGGGTAG ATGAAAGGAG 2640
 AGCTTTGAG ATAACAAAT AGCCTATCCT TAATAAATCC TCCACTCTCT GGAAGGAGAC 2700
 TGAGGGGCTT TGTAAACAT TAGTCAGTTG CTCATTTTTA TGGGATTGCT TAGCTGGGCT 2760
 30 GTAAAGATGA AGGCATCAA TAACTCAA GTATTTTAA ATTTTGTGA TAATAGAGAA 2820
 ACTTCGCTAA CCAACTGTTT TTTCTTGA GTATAGCCCC ATCTGTGGT AACCTGCTGC 2880
 TTTGCACTT CATATCATATA TTTCTATTG TTCACCTTAT TCTGTAGAGC AGCCTGCCAA 2940
 GAATTTTAT TCTGCTGTT TTTTGTGTC TAAAGAAAG AACTAAGTCA GGATGTTAAC 3000
 AGAAAGTCC ACATAACCTT AGAATCTTA GTCAAGGAAT AATCAAGTC AGCCTAGAGA 3060
 35 CCATGTTGAC TTTCTCATG TGTTCCTTA TGACTCAGTA AGTTGGCAAG GTCCTGACTT 3120
 TAGTCTTAAT AAAACATTGA ATTGTAGTAA AGGTTTTGC AATAAAAACT TACTTTGG

Seq ID NO: 230 Protein sequence

Protein Accession #: NP_055213.1

35 1 11 21 31 41 51
 MPRQLSAAAA LFASLAVILH DGSQMRKAP PETRDYSQPT AAATVQDIKK FVQPAKQAP 60
 HQTLAARFMD GHITFQTAAT VKIPTTTPAT TRNTATTSPI TYTLVTQTAT PNNSTAPFV 120
 40 TEVTVGPSLA PYSLPPTITP PAHTAGTSSS TVSHITGNTT QPSNQTTLPA TLSLALHKST 180
 TGQKPDQPTH APGTTAAAHN TTRTAAPAST VPGETLAPQP SSVKTIQYQV LNSRLCIKA 240
 EMGIQLIVQD KESVFSPPRY FNIDPNATQA SGNCGTRKSN LLLNFQGGFV NLTFKDEES 300
 YYISEVGAYL TVSDPBTYQY GIKHAVVMFQ TAVGHSFKCV SEQSLQLSAH LQVKTDDVQL 360
 QAFDPEDDFH GNVDECSSDY TIVLPVIGAI VVGLCLMGMG VYKIRLRCSQ SGYQRI

Seq ID NO: 231 DNA sequence

Nucleic Acid Accession #: NM_005409.3

Coding sequence: 94..378

50 1 11 21 31 41 51
 TTCCTTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60
 CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120
 TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
 55 TGTCTTTGCA TAAGCCCTGG GGTAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
 ATAATGTACC CAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAT 300
 AAAGGACAAC GATGCTTAAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAGTT 360
 GAAAGAAAGA ATTTTAAAA ATATCAAAAC ATATGAAATC CTGGAAGAGG GCATCTGAAA 420
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAACTG 480
 60 AGACTTTTCT ATGGTTTGT GACTTTCAAC TTTTGTACAG TTATGTGAAG GATGAAAGGT 540
 GGGTGAAGAG ACCAAAAACA GAAATACAGT CTTCTGTAAT GAATGACAAT CAGAATTCCA 600
 CTGCCCAAAG GAGTCCAGCA ATTAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
 GGTACCATC GGAGTTTACA AAGTGCTTTC ACGTTCTTAC TTGTGTATT ATACATTCTAT 720
 GCATTICTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
 65 GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
 CTGTGGTTAC AGTGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
 CATCTATGTG TCGTAAAGCA TTCTCAAAAC ATTTTTCAT GCAAAATCAC ACTTCTTCC 960
 CCAAAATATCA TGTAGCACAT CAATATGTAG GGAACATTC TTATGCATCA TTTGGTTTGT 1020
 TTTATAACCA ATTCAATAAA TGTAAATTCAT AAAATGTACT ATGAAAAAAA TTATAGCTTA 1080
 70 TGGGATAGTG GCAACAGTGC ACATATTTC TAACCAAAAT AGCAGCACCG GTCTTAATTT 1140
 GATGTTTTTC AACTTTTAT CATGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
 TGTACTTTTT GTTTTGTATC GTTTGTATAA ATGATAGCAA TATCTGGAC ACATTGAAA 1260
 TACAAAATGT TTTTGTCTAC CAAAGAAAAA TGTGAAAAA TAAGCAAATG TATACCTAGC 1320
 75 AATCACTTTT ACTTTTGTGA ATCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380
 TTGTTCATGC CTATATACTG TAAAAATTAG GTATACTCAA GACTAGTTTA AAGAAATCAA 1440
 GTCATTTTTT TCTCTAATAA ACTACCACAA CCTTCTTTT TTAATAAAAA AAA

Seq ID NO: 232 Protein sequence

Protein Accession #: NP_005400.1

80 1 11 21 31 41 51
 MSVKGMAIAL AVILCATVVQ GPPMFKRGRC LCIGPGVKAV KVADIEKASI MYPSENCDKI 60
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF

Seq ID NO: 233 DNA sequence

Nucleic Acid Accession #: NM_000577.1

Coding sequence: 41..520

5 1 11 21 31 41 51
GGCAAGAGGG GAAGACCTCC TGTCTATCA GGCCCTCCCC ATGGCTTTAG AGACGATCTG 60
CCGACCTCTT GGGAGAAAAT CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAAACCA 120
GAAGACCTTC TATCTGAGGA ACAACCAACT AGTTGCCGGA TACTTGCAAG GACCAAATGT 180
10 CAATTTAGAA GAAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT 240
CCATGGAGGG AAGATGTGCC TGTCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT 300
GGAGGCGTGT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTGGCCTT 360
CATCCGCTCA GACAGTGGCC CCAACAACAG TTTTGAGTCT GCGCCTGCC CCGTTGGTT 420
CCTCTGCACA GCGATGGAAG CTGACCAGCC CGTCAGCCTC ACCAATATGC CTGACGAAAG 480
15 CGTCATGGTC ACCAAATTCT ACTTCCAGGA GGACGAGTAG TACTGCCAG GCCTGCCTGT 540
TCCCATTTCT GCATGGCAAG GACTGCAGGG ACTGCCAGTC CCGCTGCCCC AGGGCTCCCG 600
GCTATGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GCTCAACAAC 660
CCTGGTCA CA GACTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCCAGAAATG 720
GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCTTCA CAAAGCCCTT CCATGTGCTC 780
20 TCTGCATTCA GGATCAAAAC CCGACCACTT GCCAACCTG CTCTCTCTT GCCACTGCCT 840
CTTCTCCCTT CATTCACCTT TCCCATGCC TGGATCCATC AGGCCACTTG ATGACCCCCA 900
ACCAAGTGGC TCCACACACC TGTTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGGAGGTT 960
TTTAAGGTT TGTGGAAAT GAAATTAGG ATTTATGAT TTTTTTTTTT CAGTCCCGT 1020
GAAGGAGAGC CCTTCATTG GAGATTATGT TCTTTCGGG AGAGGCTGAG GACTTAAAT 1080
25 ATTCCTCAT TGTGAAATG ATGGTGAAG TAAATGATG CTTTCCCTT CTTTTCTTC 1140
TTTTTTTGT ATGTCCCAAC TTGTAATAAT TAAAGTTAT GGTACTATGT TAGCCCCATA 1200
ATTTTTTTT TCCTTTAAA ACACCTCCAT AATCTGGACT CCTCTGTCCA GGCACTGCTG 1260
CCGACCTCC AAGCTCCATC TCCACTCCAG ATTTTTTACA GCTGCTGCA GTACTTTACC 1320
TOCTATCAGA AGTTTCTCAG CTCCCAAGGC TCTGAGCAAA TGTGGCTCCT GGGGTTCTT 1380
30 TCTTCTCTG TGAAGGAAT AAATTGCTCC TTGACATTGT AGAGCTTCTG GCACCTGGAG 1440
ACTGTATGA AAGATGGCTG TGCCTCTGCC TGTCTCCCC ACCAGGCTGG GAGCTCTGCA 1500
GAGCAGGAAA CATGACTCGT ATATGTCTCA GGTCCCTGCA GGGCCAAGCA CCTAGCCTCG 1560
CTCTTGGCAG GTACTCAGCG AATGAATGCT GTATATGTTG GGTGCAAGT TCCTACTTTC 1620
35 CTGTGACTTC AGCTCTGTTT TACAATAAAA TCTTGAATAA GCCTAAAAAA AAAAAAAA 1680
AAAAAAA AAAA AAAA AAAA

Seq ID NO: 234 Protein sequence

Protein Accession #: NP_000568.1

40 1 11 21 31 41 51
MALETICRPS GRKSSMQAP RIWDVNQKTF YLRNNQLVAG YLQGNVNLB EKIDVVPFEP 60
HALPLGIHGG KMCLSCVRKG DETRLQLEAV NITDLSENK QDKRFAPIRS DSGPTTSFES 120
45 AACPGWFLCT AMEADQPVSL TNMFDEGVMV TKFYFQEDE

Seq ID NO: 235 DNA sequence

Nucleic Acid Accession #: NM_001840.1

Coding sequence: 149..1567

50 1 11 21 31 41 51
GGGGAATAGG GAGAGCTCTG CAGGAGAGCG AGGCCCCCGC CCGGGCCAA GAGGCTTCTG 60
TCCCGAGGAC CAGGGGATGC GAAGGGATTG CCCCTGTGG GTCACTTTCT CAGTCATTTT 120
GAGCTCAGCC TAATCAAAGA CTGAGGTAT GAAGTCGATC CTAGATGGCC TTGCAGATAC 180
55 CACCTTCGCG ACCATCACCA CTGACCTCCT GTACGTGGGC TCAAAATGACA TTCAATACGA 240
AGACATCAA GGTGACATGG CATCCAAAT AGGGTACTTC CCACAGAAAT TCCCTTTAAC 300
TTCTTTTAGG GGAAGTCCCT TCCAGAGAA GATGACTGCG GGAGACAACC CCCAGCTAGT 360
CCCAGCAGAC CAGGTGAACA TTACAGAAAT TTACAACAAG TCTCTCTGCT CTTCAAGGA 420
60 GAATGAGGAG AACATCCAGT GTGGGGAGAA CTTCATGAG ATAGAGTTT TCATGGTCTT 480
GAACCCAGC CAGCAGCTGG CCATTGCACT CCTGTCCCTC ACGCTGGGCA CCTTCACGGT 540
CCTGGAGAAC CTCTGTGTGC TGTGCGTCAT CCTCCACTCC CGCAGCCTCC GCTGCAGGCC 600
TTCTTACCAC TTCAATCGCA GCTTGGCGGT GGCAGACCTC CTGGGAGTG TCATTTTGT 660
CTACAGCTTC ATTGACTTCC ACGTGTCCA CCGCAAGAT AGCCGCAAGC TGTTCCTGTT 720
65 CAAACTGGGT GGGGTCAAGG CCTCTTCAC TGCCCTCGTG GGCAGCCTGT TCCTCAGAG 780
CATCGACAGG TACATATCCA TTCACAGGCC CCTGGCCTAT AAGAGGATTG TCACCAAGCC 840
CAAGGCCGTG GTGGGTTTT GCCTGATGTG GACCATAGCC ATTGTGATCG CCGTGTCTGC 900
TCTCTGGGC TGGAACTGCG AGAAACTGCA ATCTGTTTGC TCAGACATTT TCCACACAT 960
TGATGAAACC TACCTGATGT TCTGGATCGG GGTCAACAGC GTACTGCTTC TGTTCATGCT 1020
70 GTATGGGTAC ATGTATATTC TCTGGAAGGC TCACAGCCAC GCGTCCGCA TGATTACAGG 1080
TGGCACCAG AAGACATCA TCATCCACAC GTCTGAGGAT GGGAGGTAC AGGTGACCG 1140
GCCAGACCA GCCCGCATGG ACATTAGGTT AGCCAAAGAC CTGGTCTGTA TCTGTGTGTT 1200
GTTTCCCTCT TGTGAAGGCA CTCTGCTTGC AATCATGGTG TATGATGCTT TTGGGAAGAT 1260
75 GAACAAGCTC ATTAAGACGG TGTGTGATT CTGCAATATG CTCTGCTGTC TGAATCCAC 1320
CGTGAACCCC ATCATCTATG CTCTGAGGAG TAAGGACCTG CGACAAGCTT TCCGAGCAT 1380
GTTTCCCTCT TGTGAAGGCA CTCTGAGGAG TAAGGACCTG CGACAAGCTT TCCGAGCAT 1440
CCTGCACAA CACGCAACCA ATGCAGCCAG TGTTCACAG GCGCAGAAA GCTGCATCAA 1500
GAGCAGGCTC AAGATTGCCA AGGTAACCAT GTCTGTGTTC ACAGACAAGT CTGCGAGGC 1560
TCTGTGAGCC TGTGCTCTCC CTGGCAGCAC AGGAAAAGAA TTTTTTTTTT TAAGCTCAA 1620
80 ATCTAGAAGA GTCTATTGTC TCCTTGGTTA TATTTTTTTA ACTTTACCAT GCTCAATGAA 1680
AAGGTGATTG CCACATGTCA CTTATTGCT TAGTTTCGTT TTGGGCTAAT CTTCGGGGT 1740
TCGTAGGAAA CCTTT

Seq ID NO: 236 Protein sequence

Protein Accession #: NP_001831.1

1	11	21	31	41	51	
5	MKSILDLGLAD	TTFRITITDL	LYVGSNDIQY	EDIKGDMSK	LGYPFPQKFLP	TSFRGSPFQBE
	KMTAGDNPOL	VPADQVNITE	PYNKSLSSF	ENEENIQCGE	NFMDIECFMV	LNPQQQLAIA
	VLSILTLGFT	VLENLLVLCV	ILHSRSLRCR	PSYHFIGSLA	VADLLGSPVF	VYSPIDFEVF
	HRKDSRNVFL	PKLGGVTASF	TASVGSFLT	AIDRYISIHR	PLAYKRIVTR	PKAVVAFCLM
	WTIAIVIAVL	PLLGWNCEKL	QSVCSDFPH	IDETILMFWI	GUTSVLLLF	VYAYMYLWK
10	AHSHAVRMQ	RGTKSIIH	TSEDQKVQT	RPDQARMDIR	LAKTLVLILV	VLIICWGPLL
	AIMVYDFGK	MNKLKTVFA	PCSMCLLNS	TVPILYALR	SKDLRHAFRS	MFPSCBGTQA
	PLDNMSGDSD	CLHGHANNAA	SVHRAAESCI	KSTVKIAKVT	MSVSTDTSAE	AL
	Seq ID NO: 237 DNA sequence					
	Nucleic Acid Accession #: NM_016083.2					
15	Coding sequence: 64..1482					
	1	11	21	31	41	51
20	GATTGCCCCC	TGTGGGTAC	TTTCTCAGTC	ATTTTGAGCT	CAGCCTAATC	AAAGACTGAG
	GTTATGAAGT	CGATCCTAGA	TGGCCTTGCA	GATACCACT	TCCGCACCAT	CACCACTGAC
	CTCCTGTACG	TGGGCTCAA	TGACATTCAG	TACGAAGACA	TCAAAGGTGA	CATGGCATCC
	AAATTAGGGT	ACTTCCCA	GAAATTCCT	TTAACTTCT	TTAGGGGAAG	TCCCTTCAA
	GAGAAGATGA	CTGCGGGAGA	CAACCCCAAG	CTAGTCCAG	CAGACCAAGT	GAACATTACA
25	GAATTTTACA	ACAAGTCTCT	CTCGTCTCT	AAGGAGAATG	AGGAGAACAT	CCAGTGTGGG
	GAGAACTTCA	TGGACATAGA	GTGTTTCATG	GTCTGGAACC	CCAGCCAGCA	GCTGGCCATT
	GCAGTCTGCT	CCCTCAGCT	GGGCACCTTC	ACGGTCTGGG	AGAACCTCCT	GGTGTCTGTC
	GTCATCTCTC	ACTCCCGCAG	CTCCGCTG	AGGCTTCT	ACCACTTCAT	CGGCAGCCTG
	GCGGTGGCAG	ACCTCCTGGG	GAGTGTCTAT	TTTGTCTACA	GCTTCTATGA	CTTCCACGTG
	TTCCACCCCA	AAGATAGCCG	CAACGTGTTT	CTGTTCAAAC	TGGGTGGGGT	CACGGCCTCC
30	CTCATGCTCT	CCGTGGGCG	CTGTTCCTC	ACAGCCATCG	ACAGGTACGT	ATCCATTAC
	AGGCCCTGG	CCATTAAGAG	GATTGTCAAC	AGGCCCAAGG	CCGTGTGGG	GTTTGTGCTG
	ATGTGACCA	TAGCCATTGC	GATCGCGTG	CTGCTCTCC	TGGCTGGAA	CTGCGAGAAA
	CTGCAATCTG	TTTGCTCAGA	CATTTTCCA	CACATGATG	AAACCTACCT	GATGTCTG
	ATCGGGGTCA	CCAGCGTACT	GCTTCTGTT	ATCGTGTATG	CGTACATGA	TATCTCTG
35	AAGGCTCACA	CCACGCGCT	CCGATGATT	CAGCGTGGA	CCAGAGAG	CATCATCATC
	CACACGTCTG	AGGATGGGAA	GGTACAGGTG	ACCCGCGCAG	ACCAAGCCCG	CATGGACATT
	AGGTTAGCCA	AGACCCCTGT	CCTGATCTG	GTGGTGTGA	TCACTGCTG	GGGCCCTTGG
	CTTGCAATCA	TGGTGTATGA	TGTCTTTGGG	AAGATGAACA	AGCTCATTA	GACGGTGT
	GCATTCTGCA	GTATGCTCTG	CCTGCTGAAC	TCCACCGTGA	ACCCCATCAT	CTATGCTCTG
40	AGGAGTAAGG	ACCTGCGACA	CGCTTCCGG	AGCATGTTTC	CCTCTGTGTA	AGGCAGTGGG
	CAGCCTCTGG	ATAACAGCAT	GGGGGACTCG	GACTGCCTGC	ACAAACACGC	AAACAATGCA
	GCCAGTGTCT	CACGGGCGCG	AGAAAGCTGC	ATCAAGAGCA	CGGTCAAGAT	TGCCAAGGTA
	ACCATGTCTG	TGTCCACAGA	CACGTCTGCC	GAGGCTCTGT	GAGCCTGATG	CCTCCCTGGC
	AGCACAGGAA	AAGAATTTTT	TTTTTTAAGC	TCAAAATCTA	GAAGAGTCTA	TTGTCTCCTT
45	GGTATATATT	TTTTAACTTT	ACCATGCTCA	ATGAAAAGGT	GATTGTCAAC	ATGATCACTT
	ATCAGTTTGC	TAAATGTTCC	ATAGTTTAGG	TACTCAAAT	CCATCTCTCA	GGGGTTTACA
	GTGAAGAAAG	AGCTGTGTTT	AAGTGACTGA	ACGATCCTTC	AAAGTCTCAA	TGAATATGGA
	GGGAAACCTT	TGGCTACACA	ATTGGAAGTC	TAAGAACCAC	TGGAATAATG	CCATCAAATG
	AATAATGCCT	TTGTAACACC	AACCTTCACT	ATAATGTGAA	ATGTAAGTGT	CCGTAGTATC
50	AGAGATGTCC	ATTTTACAA	GTTATAGTAC	TAGAGATATT	TTGTAAATAT	TATTATGTCC
	TGTGAGATGT	GTATCAGTGT	TTATGTGCTA	TTAATATTGG	TTTAGTTCAG	CAAAACTGAA
	AGGTAGACTT	TTATGAGAAC	AATGACAAAG	CAGTGGATAC	GTGTCAATGT	GTGCATTTT
	TTTCTATATT	ATTGCCCATG	ATATAACTTT	AGAAATAAAC	CTTAATATTT	CTTCAATAT
	CTCTATTATA	TTTTGACACT	GAAATAACCG	TAAAGGTTTA	TTTTTCTGTT	ACCTCAACAA
55	GAAGAGATTG	AAGACTTCAA	AATATTGAGC	AGAATTCATT	CATCTCTAAA	AATTTATTAG
	CCCTGCATTT	TCATAGGAAG	ACACATTATC	TTCTGGACTA	TAGCTGTGCT	AATGGATTAT
	AATCAAGATG	GAAGAGAGAA	AGCATATTGA	CTTTTCTTGA	GCGACATCTC	TGACTTTCTT
	TAGTCTTTAG	CTATTACTGG	ATCTCTTAAG	ACAGCATGTG	TTAATCTTAA	TGTATATCGT
	TATCACTGTG	CAGTGTGCTG	TTACTTGAAT	AGTATTGTGT	TCCTATATTC	CAGGTTTAA
60	TAGATTTCAT	GCCTGGGTGG	CCAAACAACA	GTCTTCATTT	TTTTTAATTG	AAAAGAAGTA
	GTGCTGGAT	CAGTAAATTT	ATACTGTGTG	TGAGTGTGAA	TATAAATGTG	TGTATGTGTG
	TTTCTGTCCG	TAACTGTTAC	AGTAATGTCA	TAAAGTGAGA	AAACTGTGAC	CAAGTATAAA
	CTTTTACCAC	TTGCTGCAC	CTTGACATG	GATTCACTTT	CTAAATTTGA	GTTCTTCTCG
	TAACTCTGTT	GATAAAAATA	CTGACTCCAA	CCATTCAAAA	ATTTCACCCC	ATCCCTCCTT
65	AAGAGATTGG	ATCAAGTATT	ACTAAATTGA	CCTTTAGGTA	TTACACAAGA	CCAGTGTCTA
	GCAAAAAATA	ATGACAGGCA	TCCAAGGAAG	GGATGTATT	GTAGTGTAT	TGCCAGGAAA
	GGAGAGTACT	TTGGTTTCTG	AGCACCGAAT	ATTGAGCAAT	ATGTCAGTCA	CTAAAAGGAA
	GACAGTCTA	CAGAAAAACA	AATGGAATA	TTTTTCAATA	GCGTGTGTAG	ATAGTATGCA
	CTATATACAT	CAGTTTAAAG	TAGGACTATC	ACACCCAGCC	CATGTGGCTA	AAAAAGCTGA
70	ATCAGACAGT	GGATGAGACA	CACAACGCA	GTGAAGAACC	GATACACTTG	GCATTGACGT
	CTAGCTATGC	TGTATCTGTG	CTTTGCCAC	ATGCCCTTGG	TGACAGCTGA	GCACCCAGCT
	CTGTCTGTGT	AGGTTTGGG	TAAGGAACAA	ATCTCTCCTT	TGCTGTGTGT	TAGCAAGATA
	CACCTAAGCA	TGAAGATAAA	CACAGCTGCT	TTCTTCTTAC	ACCCCGGTCT	CATGCTCCTT
	AATGGGCCCA	TGGGTGCTTG	TTGGGCTT	TTCCAGTAAG	GAATGATATT	GCTGAAGAAT
75	CTACTTAACC	CTGACAAAT	TTAATTATA	TCTCTTCTTA	TACAGATAAA	ACATGACTCC
	TACAGGGCCC	CAAGGTTTAC	ATAGTCTGAA	GTGAAGTACA	GAGCTGGCAT	CTATCTGGTG
	ATTCTTAGCT	CTGAGATAC	CCAAGCAGCC	TGATGGGGCA	GTTCCCTCTT	TTACGGTTCA
	CGCTCTAAGG	CAGGATGTGG	CTTATGAGAT	ACTTTGCATT	GTCGTCTGCT	ACACCTTGAA
	TCTGCTGCT	GGCTCCCTTA	CTTTACCTCT	CTGTCTATGT	CAGATGAAGG	CTCAGGGTGC
80	TAGAGGATTA	GTAAGATCTC	TTTCTAAAGA	CAGGAGAGAT	TATTTACAA	AAGAAGTCA
	CAGGGTTTAC	TTTGCAATTA	AGAATTGCCA	GTCTTTTGTG	CTGCATCATC	TTGAACATTA
	ATCCAGATGT	TTACAGGCTC	ACCAGGCAGT	ACCAATGCTC	TTTTCAAGC	TATGAAGAGC
	TAGAGAAATT	CTGTATATGG	TAGAAAAATT	TCACGGTTCA	TTTTTGAAC	TGCATTGTG
	CGTATGCAGT	GTAGATTTTA	TAGTGTGTG	TGCTTTCAAG	ATCTAAATCA	TATATAATA

5 ATTAAGGGAC AATGGGGCTG ACAGCACTAA ACTTGGTGCT TATTGATATT CTAAGAAATA 4020
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 10 AATGAATATA CTCATTAGAA TTACCATTTG TTAATATCAC TCATTAATTA ACCCATAAT 4200
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 15 CTTACACTGT AGATGATTTT CAAGCCTCTC TGGCACTTTG AGTTAAGTCT ATCTGGTATT 4560
 AAATGCCAAG GACCTTTTGC TGCTTAAATC CACTCTGAG GAAATAGGCC CAACCCACAG 4620
 ATGAGAATTA GGCCCTGGAT GAGTAGCGCT ATAGTTACTG TCCTGTTGAT TAATTTCTGC 4680
 CATTTCATGT CCATAAAAGA GACCACCCAT ATCATGCACA CAATTAGATT TCTCACACTC 4740
 TAACGTATA TTGTATGAT ATTTTAAAT CTCTTAAATG CTGGGCAATG GCTATTAACA 4800
 20 ATTAATTGTC TTGCACTGGC CTTCTGATGA AATGTTAACA ATGCTATTG TAATATAGAA 4860
 AAAAACAATC TATCTACTGA TTTGGGCTGA ATGTATGTAA ATAGGTTTCT AAAAAGTCAG 4920
 ATGTTTAGC AGTGGCCTAA AATCAGTAA TTTTCGGGTG GGAGAGTTTC TTTACATTGC 4980
 CGTGGCATCT TAAAAGCTAT CTTTATGTAA ATTGACTGTA CTAGGCCTAC TGGGGATCAG 5040
 AGTTCCCAAG AAAGGAAACC TTTTCTTGTA TCTGGATTCA AATTTATTTT CAATGTTTCA 5100
 25 AGCGGAAAC ATGACTCTTT ATTGTCTGTA AATCTAACAT TATTACTTTT CCTCTTAGAA 5160
 GAATATTGTA TTGTTAGATG TTTGTTGAGC TGGTAACATC GTTGCAACCA CTGCAATATC 5220
 TCGTTAGAG ATCTGTATAC TACTTTGAT ACAAGTACTG GTAAGATTGT TATTAAATGT 5280
 AGCTTCAGTC ATTAATATAC TATAGCAAG TAGTACTTCT TCTGTAATAT TTACAATGTA 5340
 TTAAGCCAC AGTATATTTT ATTTCAATGT AATTAACACT TTAATTATT CAAAGAGAAA 5400
 30 ACATCTCATC ATGTCTATTG TCCAAAGTTA CTTGGAATCA AATAAAATTT CTAGATTACC 5460
 ATGAAGAACA TA

Seq ID NO: 238 Protein sequence
 Protein Accession #: NP_057167.1

30 1 11 21 31 41 51
 | | | | |
 MKSILDGLAD TTFRTITTDL LYVGSNDIQY EDIKGDMASK LGYFPQKPEL TSFRGSPFOE 60
 KMTAGDNPLQ VPADQVNITE FYNKSLSSPK ENEENIQCGE NFMDECFMV LNPSQQLAIA 120
 35 VLSLTGLTFT VLENLLVLCV ILHSRSLRCR PSYHFIGSLA VADLLGSVIF VYSPIDPHVF 180
 HRKDSRNVFL KLGGVTSASL TASVGSFLFT AIDRYVSIHR PLAYKRIVTR PKAVVAFCLM 240
 WTTAIAIIVL PLLGNCEKQL QSVCSDFPH IDETYLMFWI GVTSVLLLFV YAYMYILWK 300
 AHSHAVRMIQ RGTQKSIIH TSEDGKVQVT RPDQARMDIR LAKTLVLILV VLIICWGPILL 360
 40 AIMVYDVFGK MNLIKTVFAP PCSMLCLLNS TVNPIIYALR SKDLRHAFRS MPFSCBGTAG 420
 PLDMSGDSDC LHKHANNAAS SVHRAESCTI KSTVKIAKVT MSVSTDTSAE AL

Seq ID NO: 239 DNA sequence
 Nucleic Acid Accession #: NM_033181.1
 Coding sequence: 17..1252

45 1 11 21 31 41 51
 | | | | |
 ATGAAGTCGA TCCTAGATGG CCTTGCAGAT ACCACCTTCC GCACCATCAC CACTGACCTC 60
 CTGTACGTGG GCTCAAAATGA CATTGAGTAC GAAGACATCA AAGGAGAATG AGGAGAACAT 120
 50 CCAGTGTGGG GAGAACTTCA TGGACATAGA GTGTTTCATG GTCCTGAACC CCAGCCAGCA 180
 GCTGGCCATT GCAGTCCCTGT CCTCACGCT GGGCACCTTC ACGTCTCTGG AGAACCTCCT 240
 GGTGCTGTGC GTACCTCTCC ACTCCCGCAG CTTCCGCTGC AGGCCTTCTC ACCACTTCAT 300
 CGGCAGCCTG GCGGTGGCAG ACCCTCTGGG GAGTGTCTAT TTTGTCTACA GCTTCATTGA 360
 55 CTTCCACGTG TTCCACCCCA AAGATAGCCG CAACGTTGTT CTGTTCAAAC TGGGTGGGGT 420
 CACGGCCTCC TTCACCTGCT CCGTGGGCAG CCGTTCTCTC ACAGCCATCG ACAGGTACAT 480
 ATCCATTCAC AGGCCCTCTG CCTATAAGAG GATTGTCAAC AGGCCCAAGG CCGTGGTGGC 540
 GTTTTGCTCG ATGTGGACCA TAGCCATTGT GATGCGCGTG CTGCTCTCC TGGGCTGGAA 600
 CTGCGAGAAA CTGCAATCTG TTTGCTCAGA CATTTTCCCA CACATTGATG AAACCTACCT 660
 60 GATGTTCTGG ATCGGGGTCA CCAGCGTACT GCTTCTGTTC ATCGTGTATG CGTACATGTA 720
 TATTCTCTGG AAGGCTCACA GCCACGCCGT COGCATGATT CAGCGTGGCA CCCAGAAGAG 780
 CATCATCATC CACAGCTCTG AGGATGGGAA GGTACAGGTT ACCCGGCCAG ACCAAGCCCG 840
 CATGGACATT AGGTAGGCA AGACCTGTGT CTTGATCTGT GTGGTGTGTA TCATCTGCTG 900
 GGGCCCTCTG CTTGCAATCA TGGTGTATGA TGTCTTTGGG AAGATGAACA AGCTCATTAA 960
 65 GACGCTGTTT GCATTCTGCA GTATGCTCTG CCGTCTGAAC TCCACCGTGA ACCCATCAT 1020
 CTATGCTCTG AGGAGTAAGG ACCTGGGACA CGCTTTCCGG AGCATGTTTC CCTCTTGTA 1080
 AGGCACTGCG CAGCCTCTGG ATAACAGCAT GGGGACTCG GACTGCTGCG ACAACACGCG 1140
 AAACATGCA GCCAGTGTTC ACAGGCGCGC AGAAAGCTGC ATCAAGAGCA CGGTCAAGAT 1200
 TGCCAAGGTA ACCATGCTG TGTCCACAGA CAGTCTGCC GAGGCTCTGT GA

Seq ID NO: 240 Protein sequence
 Protein Accession #: NP_149421.1

70 1 11 21 31 41 51
 | | | | |
 MALQIPPSAP SPLTSCWMAQ MTFSTKTSKE NEENIQCGEN PMDECFMVL NPSQQLAIAV 60
 75 LSLTGLTPTV LENLLVLCVI LHSRSLRCR SYHFIGSLAV ADLLGSVIFV YSPIDPHVF 120
 RKDSRNVFLP KLGGVTSASL ASVGSFLFTA IDRYISIHPR LAYKRIVTRP KAVVAFCLMW 180
 TTAIVIAIVL PLLGNCEKQL QSVCSDFPHI DETYLMFWIG VTSVLLLFV YAYMYILWKA 240
 80 HSHAVRMQR GTQKSIIHT SEDGKVQVTR PDQARMDIR AKTLVLILV LIIICWGPILLA 300
 IMVYDVFGKM NKLIKTVFAP CSMLCLLNST VNPPIIYALRS KDLRHAFRS MPFSCBGTAGP 360
 LDMSGDSDC LHKHANNAAS VERAESCTI STVKIAKVT SVSTDTSAE L

Seq ID NO: 241 DNA sequence
 Nucleic Acid Accession #: NM_003596.1

Coding sequence: 82..1194

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1      11      21      31      41      51
5      |      |      |      |      |
      GTAGACTGTC CATGGCCTGA ACATTTTCCG AAAATCATT TGAGCAAAT ATCTGTTTAA 60
      TAACAAGATA ACCACATCAA GATGGTTGGA AAGCTGAAGC AGAAGTTACT ATTGGCATGT 120
      CTGGTGATTA GTTCTGTGAC TGTGTTTAC CTGGGCCAGC ATGCCATGGA ATGCCATCAC 180
      CGGATAGAGG AACGTAGCCA GCCAGTCAAA TTGGAGAGCA CAAGGACCAC TGTGAGAACT 240
      GGCCCTGGACC TCAAGGCCAA CAAACCTTT GCCTATCACA AAGATATGCC TTAAATATTT 300
10     ATTGGRGGTG TGCCCTCGAG TGAACACACA CTCATGAGGG CCATGCTGGA CGCACATCCT 360
      GACATTGCGT GTGGAGAGGA AACCAGGGTC ATTCCCGGAA TCCTGGCCCT GAAGCAGATG 420
      TGGTCACGGT CAAGTAAAGA GAAGATCCGC CTGGATGAGG CTGGTGTAC TGATGAAGTG 480
      CTGGATTCTG CCATGCAAGC CTCTTACTA GAAATTATCG TTAAGCATGG GGAGCCAGCC 540
      CCTTATTAT GTAAATAAGA TCCTTTTGCC CTGAAATCTT TAAGTTACCT TTCTAGGTTA 600
15     TTCCCAATG CCAATTTCT CCTGATGGTC CGAGATGGCC GGGCATCAGT ACATTCAATG 660
      ATTTCTCGAA AAGTTACTAT AGCTGGATT GATCTGAACA GCTATAGGGA CTGTTTGACA 720
      AAGTGAATC GTGCTATGA GACCATGTAT AACCATGTA TGGAGGTTG TTATAAAAG 780
      TGCAATGTGG TTCATATGA ACAACTTGT TACATCCGT AACGGTGGAT GAGAACATC 840
      TTAAAGTTCC TCAGATTTCC ATGGAACCA TCAGTATTGC ACCATGAAGA GATGATTGGG 900
20     AAAGCTGGGG GAGTGTCTCT GTCAAAAGT GAGAGATCTA CAGACCAAGT AATCAAGCCA 960
      GTCAATGTAG GAGCTCTATC AAAATGGGTT GGAAGATAC CGCCAGATGT TTTACAAGAC 1020
      ATGGCAGTGA TTGCTCCTAT GCTTGCCAAG CTGGATATG ACCCATATGC CAACCCACCT 1080
      AACTACGGAA AACCTGATCC CAAATTTATT GAAACACTC GAAGGCTCTA TAAGGGAGAA 1140
      TTCCAACTAC CTGACTTTCT TAAAGAAAA CCACAGACTG AGCAAGTGA GTAGCAGAAC 1200
25     CAGGAGCCTC TTCCATACAT GAGGAAAGAT TGCTGCTTT TCAGCAGAA GGAATTOCT 1260
      AGGATTGGCT GTCCCTGCC AAGCTTGGTG GAGGCTTGC ACCTTGGCTG CGCCGCTGT 1320
      GCATTTGCCA GTTTCCTGCC ACTGAGAGGA TGGAGGTGT CGCACAGCTT TGGGCTCGT 1380
      GAGGGATCTG CCTCTGAGC AAGAGCTCT TGATCCCGAT TTCATGCACA GCCCTGCACT 1440
      AAGGAGCCCA GAAGGAACAT GTGTTTCTG TTAAGTCTC TCTTGTCTC TTTTCTTACA 1500
30     TTATGAGGTT TGTCTTCAAG GAGAGGTTT AAAATGGGA TCCTGTAAAG AGACTTGGGC 1560
      AGTCTCCTTT TGAATAGGT TGTCTGACA TGTCTAATG TTTTGTAGAA CAGCTGTGCC 1620
      TGTTTAAGTG TATTGATGTG AATAATATTA AATATCTTAA TTATTTAATT CATTTGATG 1680
      TTTCTGAGAA GTTGGGAAAT TACCATTATA CATTTACAAC CTAATGACTT TTGTATTTA 1740
35     TTTTCAAAA TAAAGCTTT CAATGTGA

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Seq ID NO: 242 Protein sequence
Protein Accession #: NP_003587.1

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1      11      21      31      41      51
40     |      |      |      |      |
      MVGKLRQNL LACLVISSVT VFYLGQHAME CHHRIERSQ PVKLESTRIT VRTGLDLKAN 60
      KTFAYHRDMP LIFFGVPRPS GTTLMRAMLD AHPDIROGEE TRVLPRIAL QMWSRSSKE 120
      KIRLDEAGVT DEVLDSAMQA FLLEIIVKHG EPAPYLCKND PFALKSLTYL SRLFPNAKFL 180
45     LMVRDGRASV HSMISRKVTI AGFDLNSYRD CLTKWNAIE TMYNQCMFVG YKKCMLVHYE 240
      QLVLHPERWM RTLKPLQIP WNHSLHHEE MIGKAGGVSL SKVERSTDQV IKPVNVGALS 300
      KWKGIKPPDV LQDMAVIAPM LAKLGYDPYA NPPHYGKFPD KIIENRERVY KGEFQLPDFL 360
      KEKPQTEQVE

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Seq ID NO: 243 DNA sequence
Nucleic Acid Accession #: NM_001492.3
Coding sequence: 1395..2513

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1      11      21      31      41      51
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      CGAGCGGGCG GTATGGCGGC GCGGGGGCCC GCGCGGGGCG CGAGCGGGCC CGAGCCCATG 120
      CGAGCTACG CGCAGCTAGT GCAGCGCGGC TGGGGCAGCG CGCTGGCGGC GGCGCGGGCG 180
      TGCACGGAAT CGGCGTGGGG GCTGGCGGCT CGCGGCTTGG CTGAGCAGCG GCACCTGGCG 240
      CGCCCGAGC TGCTGCTGCT GCGCTCGGC GCGCTGGGCT GGACCGGCGT GCGCTCGCG 300
60     GCGCTGGGCT GCGCTTTCG GCGCTGGGG AAGCGGTGCT GCCTCCAGCC CAGAGATGCC 360
      GCCACTGGCG GCCTCTTTCG GCGCTGGGG AAGCGGTGCT GCCTCCAGCC CAGAGATGCC 420
      GCCAAGATGC CGGAGAGCGC TTGGAAGTTT CTCTTCTACC TGGGCGAGCT GAGCTACAGT 480
      GCCTACCTGC TGTTTGGCAC CGACTACCCC TTCTTCCATG ACCCACCATC TGTCTTCTAC 540
      GACTGGAGCG CGGGCATGCG AGTGCCACGG GACATTGCAG CGGCTACCT GCTCCAGGGA 600
      AGCTTCTATG GCCACTGCCA CTACGCTACG CTATACATGG ACACCTGGCG CAAGGACTCG 660
65     GTGGTCATGC TGCTCCACCA CGTGGTCACT CTCATCTTCA TCGTCTCTCT CTACGCTTTC 660
      CGGTACCACA ATGTGGGCAT CCTTGTGCTC TTCTGCAAG ATATCAGTGA CGTGCACTT 720
      GAGTTACCA AGCTCAACAT TTACTTCAAG TCCCGCGGCG GCTCTTACCA TCGGCTGCAT 780
      GCCTTGGCAG CAGACTTGGG CTGCTCAGC TTGCGCTTCA GCTGTTCTG GTTCCGCTC 840
70     TACTGTTTCC GCTCAAGGT CTTGATGCC ACCAGTCACT GCAGTCTGCG CAGGCTGCT 900
      GACATCCCTT TCTACTTCTT CTTCATGCG CTCTGCTGCT TGCTCACCTT TATGAACCTC 960
      TACTGTTTCC TGTACTCTGT GCGTGTGCA GCCAAGGTGT TGACAGGCCA GGTGCACGAG 1020
      CTGAAGGACC TGGGGGAGTA TGACACAGCC GAGGCGGAGA GCCTGAAGCC CAGCAAGGCC 1080
      GAGAAGCCAC TGAGGAACGG CCTGCTGAAG GACAAGCGCT TCTGAACCCC TCGGCCCCGC 1140
      CCCCTGGAC CCGGCCCCAC CCGAATACC CCGGCGGCG TCCCGTCTCT TGGCGGCCCC 1200
75     TCCACCCCTT CCAACTCTGC TCCTCTAGGG CCGCGGCCAC CTCCCTTGGG ACCCGCCCC 1260
      CTCACTCTGC CTCAATTTCC CGGCAAGCC CCGGCGGACC CTGCCCCCTC CGGGGACACC 1320
      GGCCCGGCC CTAGCCCACT GGTCCCGGCG CGCGCGGAC CTGCGCACT CTCTGTGCTAT 1380
      CGCTGGGAG GAAGATGCCA CCGCGGCGAG AAGGTCCCTG CCGGCCACAC CTCTCTCTCC 1440
80     TCTGCTGCTT GCTGCTGCTT TCGCTGCTT TGACCGGCG CCGGCTGCTT CAGGCGGCT 1500
      CCGCGGCTT GCTCCAGGCT CTAGGACTGC GCGATGAGCC CCAGGCTGCG CCCAGGCTCC 1560
      GCGCGGTTCC CCGGCTCATG TGGCGCTGT TTGAGCGCG GAGCCCCCAG GAGACAGGT 1620
      CTGCTCGCG CGGAGGCTCC CAGGCGTCA CCTTCAACC GTGCCACGTC GAGGAGCTGG 1680
      GGGTCGCGCG AAACATGCTG CGCCACATCC CGGACCGGCG TGCGCCCCAC CGGCGCTCGG 1740
      AGCCTGTCTC GCGCGGGGG CATTCCTCTG AGTGGACAGT CGTCTTCGAC CTGTGCGCTG 1800

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5 TGGAACCCCG TGAGCGCCCG AGCCGGGCCC GCCTGGAGCT GCGTTTCGCG GCGGCGGCGG 1860
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 CGGACCCCGG GCGGTGCTG CTCCGCCAGT TGGTGCCCGC CTGCGGGCGG CCAAGTGGCGG 1980
 CGGAGCTGCT GGGCGCCGCT TGGCTCGCA AGCCTCATG GCGCGCAGC CTCGCGCTGG 2040
 CGCTGGCGCT AGCGCCCGCG GCGCTGCGG CCTGCGCGG CCGGCGCGG GCGCTCGCTG 2100
 TGCTGGTGAC CCTCGACCGG CGCCTGTGCC ACCCCTGGC CCGGCGCGG GCGAGCGCGG 2160
 AACCCGTGTT GGGCGCGCGC CCGGGGGCGG CTTGTGCGGC GCGCGCGCTG TACGTGAGCT 2220
 TCCGCGAGGT GGGCTGGCAC CGCTGGGTCA TCGCGCGCG CCGCTTCCTG GCCAACTACT 2280
 10 GCCAGGTGTA GTGCGCGCTG CCGCTCGCGC TGTGCGGGTC GCGGGGGCGG CCGGCGCTCA 2340
 ACCAGCTGCT GCTGCGCGCG CTCATGCACG CGGCGCGCCC GGGAGCGCGC GACCTGCCCT 2400
 GCTGCGTGCC CGCGCGCGCT TCGCCCATCT CGGTGCTCTT CTTTGACAAC AGCGACAACG 2460
 TGGTGTGCGG GCGATATGAG GACATGGTGG TGGACGAGTG CCGCTGCGCG TAACCCGGGG 2520
 CCGGCGGGGA CCGGGGCCCA ACAATAAATG CCGCTGGTTC TGCTC

15 Seq ID NO: 244 Protein sequence
 Protein Accession #: NP_001483.2

20 1 11 21 31 41 51
 MPPFPQGGPCG HLLLLLLLALL LPSLPLTRAP VPPGPAAALL QALGLRDEPQ GAPRLRPVPP 60
 VMWRLFRRRD PQETRSRGR TSPGVTLQPC HVEELGVAGN IVRHIFDRGA PTRASEPVSA 120
 AGHCPEWTVV FDLSAVEPAE RPSRRLLELR FAAAAAARPE GGNELSVQA QGGAGADPGP 180
 VLLRLQVLPAL GPPVRAELLG AANARNASWP RSLRLALALR PRAPAACARL AEASLLLVTL 240
 DPLRLCHPLAR PRDAEPVLG GPGGACRAR RLYVSPREVQ WNRNVIAPRG FLANYCQGGC 300
 25 ALFVALSGSG GPPALNHAVL RALMHAAAPG AADLPCCVPA RLSPISVLPF DNSDNVVLRLQ 360
 YEDMVVDECG CR

30 Seq ID NO: 245 DNA sequence
 Nucleic Acid Accession #: NM_021267.1
 Coding sequence: 17..1125

35 1 11 21 31 41 51
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 CCGCCCGAGC TGCTGTGCTG GCGCTCGCG CCGCTGGGCT GGACCGCGCT GCGCTCGCGG 300
 40 GCCACTGCGC GCCTCTTTGG GCCCCTGGCG AAGCGGTGCT GCCTCCAGCC CAGAGATGCC 360
 GCCAAGATGC CCCAGAGCGC TTGGAAGTTT CTCTTCTACC TGGGCGAGCT GAGCTACAGT 420
 GCCTACCTGC TGTTTGGCAC GCACTACCCC TTCTTCCATG ACCCAACATC TGTCTTCTAC 480
 GACTTGGACG CGGCTTGGCG AGTGCCACCG GACATTGCAG CCGCCTACCT GCTCCAGGGA 540
 AGCTTCTATG GCCACTCCAT CTAGGCTACG CTATACATG ACACCTGGCG CAAGGACTCG 600
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 45 CGGTACACCA ATGTGGGCGT CCTTGTGCTC TTCTTCAAG ATATCAGTGA CGTGACAGTT 720
 GAGTTACACA AGCTCAACAT TTACTTCAAG TCCCGCGGCG GCTCCTACCA TCGGCTGCAT 780
 GCCTTGGCAG CAGATTTGGG CTGCTCAGC TTGGCTTCA GCTGGTTCTG GTTCCGCTTC 840
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 50 TACTGGTTCC TGTACATCGT GCGGTTTGCA GCCAAGGTGT TGACAGGCGA GGTGCACGAG 1020
 CTGAGGACCG TGCGGGAGTA TGACACAGCC GAGGCGCCAGA GCGTGAAGCC CAGCAAAGCC 1080
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 CCCGCTGGAC CCGGCCCCAC CCGGAATACC CCGGCCACGC TCCCGTCTCT TGGCGGCCCC 1200
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 55 CTCATCTGCG CTCATTCTCC CGGCCACGCC CCGGCGGACC CCGTGGCTCG CCGGCGGACC 1320
 GCGCGGCCCC TCAGCCCACT GGTCCCGGGC CGCGCGGACG CCGTGGCACT CTCTGCTCAT 1380
 CGCTTGGGAG GAGATGGCCA CCGCGCAGC AAGTCCCTG CGGCCACAC CTCTCTCTCC 1440
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 65 TGGAACCCCG TGAGCGCCCG AGCCGGGCCC GCCTGGAGCT GCGTTTCGCG GCGGCGGCGG 1860
 CGGCAGCCCC GGAGGGCGGC TGGGAGCTGA GCGTGGCGCA AGCGGGCCAG GCGCGGGCGG 1920
 CGGACCCCGG GCGGTGCTG CTCCGCCAGT TGGTGCCCGC CTGCGGGCGG CCAAGTGGCGG 1980
 CGGAGCTGCT GGGCGCGCGT TGGGCTCGCA AGCCTCATG GCGCGCAGC CTCGCGCTGG 2040
 CGCTGGCGCT AGCGCCCGCG GCGCCTGCGG CCGCGCGCGG CCGGCGGAG GCCTCGCTGC 2100
 70 TGCTGGTGAC CCTCGACCGG CGCCTGTGCC ACCCCTGGC CCGGCGCGCG CCGGACGCGG 2160
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 TCCGCGAGGT GGGCTGGCAC CGCTGGGTCA TCGCGCGCGG GCGCTTCTG GCCAACTACT 2280
 GCCAGGTGTA GTGCGCGCTG CCGTTCGCGC TGTGGGGTTC GCGGGGGCGG CCGGCGCTCA 2340
 ACCAGCTGCT GCTGCGCGCG CTCATGCACG CGGCGCGCCC GGGAGCGCGC GACCTGCCCT 2400
 75 GCTGCGTGCC CGCGCGCGCT TCGCCCATCT CGGTGCTCTT CTTTGACAAC AGCGACAACG 2460
 TGGTGTGCGG GCGATATGAG GACATGGTGG TGGACGAGTG CCGCTGCGCG TAACCCGGGG

80 Seq ID NO: 246 Protein sequence
 Protein Accession #: NP_067090.1

1 11 21 31 41 51
 MAAAGPAAGP TGPEPMPFSA QLVORGWGSA LAAARGCTDC GWGLARRGLA EHAHLAPPEL 60
 LLLALGALGW TALRSAATAR LPRFLAKRCC LQPRDAAKMP ESANKFLFYL GWSYSAYLL 120
 FGTDPYFFHD PPSVFYDWTG GMAVPRDIAA AYLLQGSFYG HSIYATLYMD TWRRDSVVML 180

LHHVVTLLILI VSSYAFRYHN VGILVLFHLD ISDVQLEPTK LNIYFKSRGG SYHRLHALAA 240
 DLGCLSFQFS WFWRLYWF LKVLATSHC SLRTVPDIPF YFFFNALLLL LTLMLNYWFL 300
 YIVAPAAKVL TQVHELKDL REYDTAEAS LKPSKAERPL RNLVKDKRF

5

Seq ID NO: 247 DNA sequence
 Nucleic Acid Accession #: NM_002081.1
 Coding sequence: 222..1898

10 1 11 21 31 41 51
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 CGGACCTTG GCTCTGCCCT TCGCGGCGCG GAACTGCGCA GGACCGCGCC AGGATCGAG 180
 AGAGGCGCGG CGCGGTGCGC GGGGCGCGCG CGCGCGCGCG CATGGAGCTC CGGGCCGAG 240
 15 GCTGGTGGCT GCTATGTGCG GCGCGAGCGC AGAGTCTACG AGCCAAGGCG TTCAGCTGA 300
 GCAAGAGCGG GAGCTGCGCG GAGGTCCGCC AGAGTCTACG AGCCAAGGCG TTCAGCTGA 360
 GCGAGCTGCC CAGGCGGAG ATCTCGGCTG AGCACTGCGG GATCTGTCCC CAGGCTTACA 420
 CTTGCTGCAC CAGCGAGATG GAGGAGAACC TGGCCAACCG CAGCCATGCC GAGCTGGAGA 480
 CCGCGCTCCG GGACAGCAGC CGGTCTCTGC AGGCAATGCT TGCCACCCAG CTGCGCAGCT 540
 20 TCGATGACCA CTTCAGCAGC CTGCTGAACG ACTCGGAGCG GACGCTGCAG GCCACCTTCC 600
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 AGCTGCGCTT GTACTACCGC GGTGCCAAC TGCACCTGGA GGAGAGCTG CGCGAGTTCT 720
 GGGCGCGCTT GCTGAGGCG CTCTCAAGC AGCTGCAACC CCAGCTGCTG CTGCTGATG 780
 ACTACCTGGA CTGCTGGGCG AAGCAGGCGG AGGCGCTGCG GCCCTTCCGG GAGGCCCGGA 840
 25 GAGAGCTGCG CCTCGGCGCG ACCCGTGCCT TCGTGGCTGC TCGCTCCTTT GTGCAAGGCC 900
 TGGCGGTGCG CAGCGAGCTG GTCCGGAAG TGGCTCAGGT CCCCTGCGCG CGGAGTGTCT 960
 CGAGAGCTGT CATGAAGCTG GTCTACTGTG CTCACTGCTT TGGCAACCGG GCCATCAACG 1020
 CTTGCCCTGA CTATTGCGA AATGTGCTCA AGGGCTGCTT TGGCAACCGG GCCATCAACG 1080
 ACGCGAGTGT GAGGAACCTC CTGACTTCCA TGGTGTCTAT CACCGACAAG TTCTGGGGTA 1140
 30 CATCGGCTGT GGAGAGTGTG ATCGGCGAGG TGCACAGTGT GCTGGCGGAG GCCATCAACG 1200
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 35 TGAGCACTGC CAGTGTGAGC CGCTGCTGGA ACGGGATGGC CAGAGGCGCG TACCTCCCGG 1500
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 40 GCTCCAGCTC CCGGAGCGCC TTGACCCATG CCTCCGAGG CCGTCTCAGG CAGGAAGGAC 1800
 AGAAGACCTC GGTCTGCCAG TGGCCCGAGC CCCCGACCTT CTCTCTGCCC CTCTCTCTCT 1860
 TCCTGGCCCT TACAGTAGCC AGGCCCCGCT GGGCGTAACT GCGCCAGGCG CCCAGGACA 1920
 GAGGCCAAGG ACTGACTTTG CCAAAAATAC AACACAGAG ATATTTTAAT CACTCAGCC 1980
 TGAAGAGGCC TGGGCTGGGA CAGGGAGGCG CGGCGGCTCT GAGCAGGGCG AGGCGCAGAG 2040
 45 GTCCAGCCCC CAGGCTGCGC CTGCGCTGCC TTTCTGCTT TTAATTTTGT ATGAGTCTCT 2100
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 TCGGCTGCC TAGCCCTCCC CCCAGCTCCC TGCAACCGCG CAGAAGCAGC CCTCGAGGC 2220
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 CGCTCTCTCC CACTGGGACT CCCAGCAGAG CCCACAGCC AGCCCTGGCC CACCCCCAG 2340
 50 CCTCCAGAGA AGCCCCGAC GGTCTGCTG GGTCTGCGC ATCCAGGCTC TGGCAGAGCC 2400
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 CTGCGCCCTT GAGGGGCCCC AGCGTCTGCA GGGTGACGCG TGAGACAGCA CCCTGCTGA 2520
 GGAATCTGAG GACTGTCTCT CCACAGACCC TGCAAGTGGG GGCCTTCCAT CCGCAGATGA 2580
 GGGGCCACTG ACCCACTGCG GCTTCTGCTG GAGGAGGGGA AGCTGGGCCC AAAGGCCAG 2640
 55 GGAGGCGAGG TGGGCTCTGC CAATGTGGGC TGCCCTCGC ACACAGGCTC CACAGGGCAG 2700
 GCCTTGTCTG GGTCCAGGGC TGTGTGAGGA CCGCGAGGCG TGAGGAGCAG CCAGGACCGC 2760
 CCTGTCTCCA TCCTCACCCA GATCAGGAAC CAGGGCTCTC CTGTTCACGG TGACACAGGT 2820
 CAGGGCTCAG AGTGACCCCT GGTGTCTGAG TGCTCACAGG GATGCTGGTG GCTGGTGAGA 2880
 CCGCGCACTG CACAGCGGAA TGCTAGGCTC CCTTCCGAG CAGGCGAGCT GCATGCAAG 2940
 60 GCACGGGGAC CTGGATAGTT AAGGGCTTTT CCAACATGC ATCCATTATC TGACACTTCC 3000
 TGTCTTGTGT CATGGAGAGC TGTTCGCTCC TCCAGATGG CTTCGAGGC CGCAGGGCC 3060
 CACCTTGGAC CCTGTGACCT TCCTGTCACT CACTGAGGCC ATCAGGGGCC TGCCCGAGGC 3120
 CTGGAOGGGC CCTCCTTCCC TCCTGTGCCC CAGCTGCCAG GTGGCCCTGG GAGGGGTGG 3180
 TGTGTGTGTT GGAAGGGGTC CTGAGGGGG AGGAGGACTT GGAGGGTCTG GGGGCGAGCT 3240
 65 TCCTGAACCG ACTGACCTG AGGAGGCGCG TTAGTGCTGC TTTGCTTTTC ATCACCGTCC 3300
 CGCACAGTGG ACGGAGGTCC CCGGTGCTG GTCAAGTCCC CATGGCTTGT TCTCTGGAAC 3360
 CTGACTTTAG ATGTTTGGG ATCAGGAGCC CCCAACACAG GCAAGTCCAC CCCATAATA 3420
 CCTGCCAGT GCCAGGGTGG GCTGGGACT CTGGCACAGT GATGCGGGCG GCCAGGACAG 3480
 CAGCACTCCC GCTGCACACA GACGGCTAG GGTGGCGCT CAGACCCAC CTAAGCTCA 3540
 70 TCTCTGGAAG GGCAGCCCT GAGTGGTCA TGGTCAGGGC AGTGGCCAG CCGTCTGTGT 3600
 CCTTCTCCA CAGGTCCCC CCACCGCTCA GTGTCAAGCG GTGACGTGTG TTCTTTTGA 3660
 TCCTGTATG AATAAAGGC TGAACCTA AA

75

Seq ID NO: 248 Protein sequence
 Protein Accession #: NP_002072.1

80

1 11 21 31 41 51
 MELRARGMWL LCAAAALVAC ARGDPASKSR SCGEVRQIYG AKGFSLSQVP QARISGEHLR 60
 ICQGYTTCCT SEMENLANR SHAELETALR DSSRVLAQL ATQLRSFDDH PQHLNDSER 120
 TLQATFPQAF GELYTONARA FRDLYSELRL YYRGANLHLE ETLAEFWARL LERLPQLQHP 180
 QLLLPDDYLD CLGKQAEALR PFGBAPRELR LRATRAFVA RSVQGLGVA SDVVRKVAQV 240
 PLGFECSRAV MKLVYCAHCL GVPGARPCPD YCRNVKGLCL ANQADLDAEW RNLLDSMVL 300
 TDKFWGTSGV ESVGSVHTM LABAINALQD NRDTLTAKVI QGCGNPKVNP QGPPEEKRR 360

RGKLAPRRP PSGLLEKLV EAKAQLRDVQ DFWISLPGTL CSEKMLSTA SDDRCWNGMA 420
RGRYLPEVMG DGLANQINNP EVEVDITKPD MTRQQIMQL KIMTNRLRSA YNGNDVDFQD 480
ASDDGSGSGS

5

Seq ID NO: 249 DNA sequence
Nucleic Acid Accession #: NM_001492.3
Coding sequence: 8..1864

10 1 11 21 31 41 51
GAAGGCCATG GTCTCCCCAC GGATGTCCGG GCTCCTCTCC CAGACTGTGA TCCTAGCGCT 60
CAITTTCTCT CCCAGACAC GGCCCGCTGG CGTCTTCGAG CTGCAGATCC ACTCTTTCGG 120
GCCGGGTCCA GGCCCTGGGG CCCCGCGGTC CCCCTGCAGC GCCCGGCTCC CTGCGCGCT 180
CTTCTTCAGA GTCTGCCTGA AGCCTGGGCT CTCAGAGGAG GCCCGGAGT CCGGTGCGC 240
15 CCGGGGGGCG GCGCTGAGTG CGCGGAGACC GGTCTACACC GAGCAGCCCG GAGCGCCCGC 300
GCCTGATCTC CCACTGCCCC AGCGGCTCTT GCAGGTGCCC TTCGGGGAGC CTGCGCTGG 360
CACCTTCTCT TCTCATCTG AAACCTGGAG AGAGGAGTTA GAGAGCCAGA TTGAGGGGCC 420
CGCTTGAGC CTGCTGGCGC GCGTGGCTGG CAGCGCGGCG TTGGCAGCG GAGGCGCGTG 480
GGCCCGGAGC ATTGAGCGCG CAGCGGCTCG GGAGCTGCGC TTCTCGTACC GCGCGCGCTG 540
20 CGAGCCGCTC GCGCTGCGGA CCGCTGCGAC GCGCCTCTGC CGTCCGCGCA GCGCCCCCTC 600
GCGGTGCGGT CCGGAGCTGC GCCCTGCGC ACCGCTCGAG GAGCAATGTG AGGCGCGCT 660
GGTGTGCGGA CAGGCTGCA GCCCTGAGCA TGGCTTCTGT GAACAGCCCG TTGGAATGCG 720
ATGCTTAGAG GGCTGAGCTG GACCCCTCTG CACGGTCCCT GTCTCCACCA GCAGCTGCGT 780
25 CAGCCCCAGG GGCCCGCTCT CTGCTACCA CCGATGCCCT GTCCCTGGGC CTGGGCGCTG 840
TGACGGGAAC CGGTGTGCCA ATGGAGGCAG CTGTAGTGAG ACACCCAGGT CCTTTGAATG 900
CACCTGCGCG CGTGGGTCTC ACGGGCTGCG GTGTGAGGTG AGCGGGGTGA CATGTGCGAG 960
TGGACCTCTC TTCAAACGCG GCTTGTGTGT CGGGGGTGCA GACCCCTGACT CTGCTTACAT 1020
CTGCCACTGC CCACTGCTGT TCCAAGGCTC CACTGTGAG AAGAGGGTGG ACCGGTGCA 1080
30 CCTGCAGCCA TGCCGCAATG CGGACTCTG CCTGACCTG GCGCAACGCC TGCGCTGCG 1140
CTGCCGCGCG GGCTTGGCGG GTCTTGGCTG CGAGCAGGAC CTGGAGGACT GCGCGGGCG 1200
CGCCTGCGCT AACCGCGGCA CGTGTGTGGA GGGCGCGGCG GCGCACCGCT GCTCCTGCGC 1260
GCTGGGCTCT GCGCGCGCGC ACTGCGCGCA GCGCGCGGAC CGGTGCGCGC GCGCGCGCTG 1320
TGCTCAGCGC GGCGCTGCTC ACGCCCACTT CTCCGGCTCT GTCTGCGCTT GCGCTCCCGG 1380
35 CTACATGGGA GCGCGGTGTG AGTTCCCACT GCACCCGAGC GCGCGCAAGC CCTTGGCCCG 1440
GGCCCGCGCG GGCTTCAAGC CCGGGGACCC TCAGCGCTAC CTTTGGCTCT CCGCTCTGGG 1500
ACTGCTCGTG GCGCGCGGCG TGGCGCGGCG TGCGCTCTTG CTGGTCCAGC TGCGCGCGCG 1560
TGGCCACTCC CAGGATGCTG GGTCTCGCTT GCTGGCTGGG ACCCGGAGC GGTCACTCCA 1620
CGCACTCCCG GATGCACTCA ACAACCTAAG GAGCAGGAG GGTTCGGGG ATGCTCCGAG 1680
40 CTCGTCGGTA GATTGGAATC GCCCTGAAGA TGTAGACCTT CAAGGGATT ATGTCAATC 1740
TGCTCCTTCC TGTACGCTC GGGAGGTAGC GAGCGCCCTT TTCCCCCGCG TACACACTGG 1800
GCGCGCTGGG CAGAGGCGAG ACCTGCTTTT TCCTTACCCT TCCTCGATTG TGTCCGTGAA 1860
ATGAATTGGG TAGAGTCTCT GGAAGGTTTT AAGCCCAATT TCAGTTCTAA CTTACTTTCA

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Seq ID NO: 250 Protein sequence
Protein Accession #: NP_058637.1

1 11 21 31 41 51
MVSPPRSGLL SQTIVILALIP LPQTRPAGVF ELQIHSFGPG PGPGAPRSPC SARLPCLRFP 60
15 RVCLKPGLSE EAAESPCALG AALSARGPVY TEQPGAPAPD LPLPDGLLQV PFRDAMPGTF 120
SFIIETWREB LGDQIGGPAM SLLARVAGRR RLAAAGFPAR DIQRAGAWEL RFSYRARCPE 180
PAVGTACTRL CRPRSAFPRC GPGLRPCAPL EDECEAPLVC RAGCSPEHGF CEQPGECRCL 240
EGWTGPLCTV PVSTSSCLSP RGPSSATTGC LVPGGPGCDG NPCANGSGSC ETPRSFECTC 300
20 PRGFYGLRCE VSGVTCADGP CFNGGLCVGG ADPDSAYICH CPPPGQGSNC EKRVDRCSLQ 360
PCRNGLCLD LGHALRCRCR AGPAGPRCEH DLDDCAGRAC ANGGTCVEGG GAHRCSCALG 420
FGGRDCRERA DPCAARPCAH GGRCYAHFSG LVCAACAPGM GARCEFPVHP DGASALPAAP 480
PGLRPGDPQR YLLPPALGLL VAAGVAGAAL LLVHVRRRGH SQDAGSRLLA GTFEPSVHAL 540
PDALNNLRQT EGSGDGPSSS VDWNRPEVDV PQGIYVISAP SIYAREVATP LFPPLHTGRA 600
60 GQRQHLFPY PSSILSVK

60

Seq ID NO: 251 DNA sequence
Nucleic Acid Accession #: CAT cluster

65 1 11 21 31 41 51
GAAATATAAC CATTGCAATT AGAAAAATAT CAAAATAGCC TGTATCTTC CAOGTGGCCT 60
AGATTATTGA CAATCCCAAA TATACAATTT TTCTTTAAAA GTAGTACAAT TTCCTTTGTA 120
GCTTCAATTC CTTATATGAC TTCAGACTGG AGAAGCCTGT TAAACCACTG TTAGTTTCAG 180
70 TTAGAAAGTC TGAGAGACTT TATACATAAA TTCTCAATTT GGCTGCTGTA CACGTGCCAG 240
AGTTTACTA CTGTAGTGAC CGTTGAGAAG ACCCTTGTGT ATTTACATTT GAAGCACTGT 300
TTGTGCAAAC AACCTTTCAT TGTAAAGTGC CTGTATTCCT TTCATTACT TCATGTCCAG 360
GGGTGCTATT TACCTAGAAC CATGTCTAC TACAATTAAC ATTTACATTA CAAAGTGTGT 420
GGTTTTCTTT TTCAAGGAGG TTCAATTAAG GCAATAAGAT GTTTGCTGGA GAAACCTATT 480
75 GTTTACTGAA AGCACTCAAT GAAGTCAAAT TACTGAAGCT TTTGCTACA TCTTGGTCTT 540
TTATGTAAT ATGTAAATA TAACATCTAA GGAAATAA CAATATTATA ATTATGTGTT 600
TGCCATTGTC ATATCAAACT TGCTTTGTAT CATACTAATG TTACATAACT TATCGATCAA 660
TAAAAATACA TTTCATGTGT AAAAAA AAAAAA

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Seq ID NO: 252 DNA sequence
Nucleic Acid Accession #: Bos sequence

1 11 21 31 41 51
AGGTACTGCC AGAAAGGATC AGGACCTGGA GTCTGGCAAG AGGAAAGAC AGGCGCTGTG 60

5 GGGAAGCGAG TTGTTATCTT TGGTTATCTA GCTGTATGAG TGTATTGGTC TTCATAAAGC 120
 TAGATAACCC AAAGTAAAAA CTTCTTCAAG ATCGCCGGGG AGCGTGTGAG AATGAAAGAC 180
 TACAGCCGAG AGACAGTAAA AACCAGAAAG GTCAGGAATA CTTATTGAAT CTAACCTTGT 240
 TTTTGTTTTG TTTTTCCTCT TATGATTAAA GGTGGGATGA GAGAAAAATTA AATGACACAC 300
 ACATGCTAAA ATATCAAGGT TCCAGATATG TCTTGAGAGG GGTGTGTGCA GCTGCAAAAG 360
 AGAAGTGTAT AGTGATAATG AGTAAAGATG CATGTGCAGT TTGTCTTATT TTAAGGCAAA 420
 AGTTATATCA GGGATTTTTT TCTTAGAAAG GTGTTGCAGA GATGTCGGT ACCTAGTTTA 480
 AAAATGATTC CATATATGT AGACTTGGGC AGTTCCTTTG GGAGGCACCT CCCTCTCAAA 540
 ATTTGAAGAT TGTGCTTGGG AATTACTTTA CATGTATTGT GGCTGTATGT CAATTTGTAC 600
 GAAATTAGAG TTTAGAAAAA GTTTATACTG GAAGGTTAAT AATTGTATAT TACTGAGGAC 660
 TTAGAGCTAG CAGGCAAAAT GAAAAAARG CAAGGGCTGA TTTTATTCTT 720
 TCTATTCAA ATACAAGGAC AGATGCTTCT CTGTCCAAG AGGTTTCCT TGAGGAAGCT 780
 ACTGAAGCAG AAAGACATGA TGGAGACGAG ATCGCCTCCC CTCTGTGCAA AGTGTAAAAA 840
 AAATGTTCTG TCTTACTCTG CGCCTAGCAT TGGAAATGAA AGTGACATT ACGCCACAAC 900
 CCACGTAGTC TCTTCTCTCT TTTTGTGTTA AGGATGATCA GGTCTATCCA GGAAACAGCT 960
 CTGGCATCCC AAACGTAAAT AATTAGGACG TATATAGACC TGACAAAAAT GGAAGGGGGG 1020
 TGGGGAATCT GAGGTCCTGT CTGCTCAAT TGATTCCGCT AAACGGAATG CAGGAGATGT 1080
 GAACGGCAGG ACCTCCGAT TCCCACGCTC GGGGGCAAGT GATAAAGCGG GGCGGGCAG 1140
 CCTATGACAG ACAGCCCTGT TGGGGGGTGG GGGTATGAAA AAAACATCAA GTGCACACAC 1200
 CATATCATC TTTCTGCTCT AAGAAAGTAA AGGCATTTC CACCCACAGC CATCTGCAGC 1260
 TTCCCAATG GCAGACCAA CTGGTCTGTA GCTGCTACAT AGTCTGCTTC TGTAAATTTT 1320
 TTAACCACTG TTTAATCTGG CCATAATTAA GTTTGGCTTT CTTCGTTGTT TGAGATTTC 1380
 AGAATTCAGG GCAAGCTAGT AGAAAGCAAT TCCAGAAAG TCCCATGACT GCCTGCCCT 1440
 AATGTCAAAA TCTCAGTCCA TGAGATTATG GCCTTGTGAC CACATTTTG CTITTTGTTT 1500
 GGGTGGGCAA ATGTGTATAG AGATAAAATA CATATCTCTA TATAACAGTC GTTATTATAA 1560
 TTTCTAGAGG CTTTTACCT CTTAACATGA TACATCTAGG AACTTGGTCT AATGTGCTA 1620
 GTAGATATAC ACTAGAAGTA AAACATATAA GTCATTAGCC TGTAGAAAGT TGATTATGAT 1680
 AACCAATATG TAAAAAGTTT GTTTTGAAT AGTCTCAGCT AGATGGGTCT AAATAGCCAT 1740
 TTTAATGTAA TCTAAAAATA ACATATGCC TAGCAGAAAC TTTGGCGCTT TGGAGGTCCC 1800
 CATGTGCGCT TTTCTATAA AGTCCCTAAG TTTTCCATAT GTCACCAAGC AAACATTGTT 1860
 ATAGGCATT ACACAGAAAT ATAACCATG CAATTAGAAA ATATCCAAA TAGCCTGTTA 1920
 TCTTCCAGT GGCCTAGATT ATTGACAAT CCAATATAC AATTTTCTT TAAAAAGTAG 1980
 ACAATTTCT TGTAGCTTC AATTCCTTAT ATGACTTCAG ACTGGAGAAG CCTGTTAAAC 2040
 CACTGTAGT TTCAGTTAGA AAGTCTGAGA GACTTTATAC ATAAATCTC AATTTGGCTG 2100
 CTGTACAGT GCGAGAGTT TACTACTGTA GTGACCGTTG AGAAGACCTT TGTATTATTA 2160
 CATTTGAGC ACTGTTTGTG CAAACAACCT TTTCTGTTA AGTGCCTGTA TTCTTTTCAT 2220
 TTACTTCATG TCCAGGGGTG CTATTACCT AGAACCATG TCTACTACAA TTAACATTTA 2280
 CATTACAAAG TGTGTGTTT TCTTTTCAA GGAGGTTCAA TTAAGGCAAT AAGATGTTG 2340
 CTGAGAAAC CTATTGTTTA CTGAAAGCAC TCAATGAAGT CAAATTACTG AAGCTTTTGC 2400
 CATCTCTG GTCTTTTATG TAAATATGTT AAATATAACA TCTAAGGAAA ATAAACAATA 2460
 TTATAATTAT GTGTTGCCA TTGTCATATC AAACCTGCTT TGTATCATAC TAATGTTACA 2520
 TAACCTATCG ATCAATAAAA ATACATTTCA ATGTT

Seq ID NO: 253 DNA sequence
 Nucleic Acid Accession #: NM_001650.2
 Coding sequence: 40..1011

50 1 11 21 31 41 51
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 AGGCGGTGGG GTAAGTGTGG ACCTTTGTGT ACCAGAGAGA ACATCATGCT GGCCTTCAAA 120
 GGGGTCTGGA CTCAGCTTT CTGAAAAGCA GTCACAGCGG AATTCTGGC CATGCTTATT 180
 TTGTTCTCC TCAGCCTGGG ATCCACCATC AACTGGGGTG GAACAGAAAA GCCTTTACCG 240
 TGCGACATGG TCTCATCTC CTTTGTCTT GGAATCAGCA TTGCAACCAT GGTGCACTGC 300
 TTTGGCCATA TCAGCGGGTG CCACATCAAC CCGTCACTGA CTGTGGCCAT GGTGTGCACC 360
 AGGAAGATCA GCATGCCCAA GTCTGTCTC TACATGSCAG CCCAGTGCCT GGGGGCCATC 420
 ATTGGAGCAG GAATCCTCTA TCTGGTCACA CTTCCAGTGT TGGTGGAGG CTTGGGAGTC 480
 ACCATGGTTC ATGGAATCT TACCGCTGCT CATGGTCTCC TGGTGTGATT GATAATCACA 540
 TTCAATTGG TGTTTACTAT CTTTGCAGC TGTGATTCCA AACGAGCTGA TGTCACTGGC 600
 TCAATAGCTT TAGCAATTGG ATTTCTGTT GCAATTGGAC ATTATTGTC AATCAATTAT 660
 ACTGGTGCCA GCATGAATCC GCCTGATCC TTTGGACCTG CAGTTATCAT GGGAAATTGG 720
 GAAAACCATG GSATATATTG GGTGGGCC ATCATAGGAG CTGTCTCTGC TGGTGGCCTT 780
 TATGAGTATG TCTTCTGTCC AGATGTTGAA TTCAAAGCTC GTTTTAAAGA AGCCTTCAGC 840
 AAAGCTGCCC AGCAAAACAA AGGAAGCTAC ATGAGGTTGG AGGACAACAG GAGTCAGGTA 900
 GAGACGGATG ACCTGATTCT AAAACCTGGA GTGGTGATG TGATTGACGT TGACCGGGA 960
 GAGGAGAAAG AGGGGAAAGA CCAATCTGGA GAGGTATTGT CTTCAGTATG ACTAGAAGAT 1020
 GGCATGAAA GCAGACAGA CTCCTTAGAA CTGTCTCTAG ATTTCTCTCC ACCCATTAAG 1080
 GAAACAGATT TGTATATAAT TAGAAATGTG CAGGTTTGT GTTTCTATGC ATATTACTCA 1140
 GTCTAAACAA TAAATATTTT ATAATTACA AAGGAGGAAC GGAAGAAACC TATTGTGAAT 1200
 TCCAAATCTA AAAAAAGAAA TATTTTAAAG ATGTTCTTAA GCATATATAT ACCTATTTTA 1260
 TCTAGTTACC TTTCAATTAAC AACCAATTTT AACCGTGTGT CAAGATTGTT TTAAGTCTTG 1320
 CCGACAGAAA CTCAAAGACA GGTCTATCAG CTTATTCCTT CTCTACTGGA ATATTGGTAT 1380
 AGTCAATTCT TATTTGAATA TTTATCTAT TAACTGAGT TTAACAAATG C

Seq ID NO: 254 Protein sequence
 Protein Accession #: NP_001641.1

80 1 11 21 31 41 51
 MSDRPTARRR GKCGPLCTRE NIMVAPKGVW TQAFWKAVTA EFLAMLIFVL LSLGSTINWG 60
 GTEKPLPVDV VLISLCFGLS IATMVQCFGH ISGGHINPAV TVAMVCTEKI SIAKSVFYIA 120
 AQCLGAIIGA GILYLVTPPS VVGLGVMTMV HGNLTAGHGL LVELIITFQL VPTIFASCDS 180
 KRITDVTGSIA LAIGSVVAIG HLFAINVTGA SMNPARSFPG AVIMGNWENH WIYVWGPRIIG 240
 AVLAGGLYEV VFCPDVEFKR RFKEAFSKAA QQTGKSYMEV EDNRSQVEDL DLILKPGVVH 300

VIDVDRGEEK KGKQSGEVL SSV

Seq ID NO: 255 DNA sequence

Nucleic Acid Accession #: U26742.1

Coding sequence: 325..1449

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CAGGAAACCC	TGGTACTGGC	AGCAGCCAGC	CTCTGCTGTG	CCCACATGAC	CCACAACCTCT	60
GGCAGCGGAC	CGGCACTTC	CAACATTATT	AAATAATAAG	AAAGCGGCTC	CTACTCCAGG	120
CTCAAAACCTC	CCTGCAGACC	AATGGACACC	TTCTAAGAGT	TTGGCGAGTC	AGTGACTGAA	180
GGSCCCGTCC	ATTCCAAGAT	AAATAGGATT	TACCAATCCT	TGGATGAAGT	GCTTGGGAAG	240
TCITTAAGTG	CCATAATCAA	CTGCCATTTC	AAAGAATATA	GATGGTTTGT	AAAAGTTCAT	300
GCTGTCCCTT	CATTGAATTT	TAGAATGATT	GAAGATAGTG	GGAAAAGAGG	AAATACCATG	360
GCAGAAAGAA	GACAGCTGTT	TGCAGAGATG	AGGGCTCAAG	ATCTGGATCG	CATCCGACTC	420
TCCACCTACA	GAACAGCATG	CAAGCTTAGG	TTTGTTCAGA	AGAAATGCAA	TTTGACCTCG	480
GTGGACATAT	GAATATGTAT	AGAAGCATTG	CGGGAATAATG	CTCTGAACAA	CCTGGACCCA	540
AACACTGAAC	TCAAAGTGTG	COGCTTAGAG	GCTGTGCTCT	CCACTATTIT	TTACCACTCT	600
AACAAACCGA	TGCCAACACC	TCACCAAAATC	CATGTGGAGC	AGTCCATCAG	CCTCTCTCCT	660
AACITTCCTGC	TTGCAGCGTT	TGATCCGGAA	GGCCATGGTA	AAATTTTCAGT	ATTGTCTGTC	720
AAAAATGGCTT	TAGCCACATT	GTGTGGAGGG	AAGATCATGG	ACAAATTAAG	ATATATTTC	780
TCATATGATT	TGGATCCAG	TGGGGTGATG	GTITATGGAC	GATATGACCA	ATTCTCTCGG	840
GAAGTTCCTCA	AACCTACCCAC	GGCAGTTTTT	GAAGGTCCTT	CATTGTGTTA	CACAGAACAG	900
TCAGCCAGAT	CCTGTTTCTC	CCACAGAAA	AAAGTCACGT	TAAATGGTTT	CTTGGACACG	960
CTATGTCTAG	ATCCTCCCCC	GCAGTGTCTG	GTCTGGTTGC	CTCTTCTGCA	TGACTAGTCA	1020
AATGTGGAAA	ATGTCTTCCA	TCCGTTTGG	TGTTCTCTACT	GCCACAGTGA	GAGTATGATG	1080
GAATTTCCCT	ACCGATGCCA	ACAGTGTCTC	AAATACCAAGC	TCTGTCAAGG	CTGCTTCTGG	1140
AGGGGACATG	CCGGTGGTTC	TCATAGCAAC	CAGCACCAAA	TGAAAGAGTA	CAOGTCATGG	1200
AAATCACCTG	CTAAGAAGCT	GACTAATGCA	TTAAGCAAGT	CCCTGAGCTG	TGCTTCCAGC	1260
OGTGAACCTT	TGCACCCCAT	GTTCOCAGAT	CAGCCTGAGA	AGCCACTCAA	CTTGGCTCAC	1320
ATCGTTGATA	CTTGGCCTCC	CAGACCTGTA	ACCAGCATGA	ACGACACCTT	GTCTTCCACC	1380
TCGTCTCCCT	CCTCAGGAAG	TCCTTTTATT	ACCAGGAGCT	OGGACGGTGC	TTTGGTGGA	1440
TGCGTCTAGA	TGATATACAT	GACTTCTTCT	ACCTTAAAT	ATTCTATATA	TACTTTGAGC	1500
TGTTCTGTTT	CCTCCAGGGT	GCATGGTACC	CATTAAACCA	AAATATGATT	ATTTCCTTTT	1560
TTTCCCATTT	TCAGTCATTT	TGGAATGTTT	TCTGTGAACC	ACAGTTGGGT	TGTTTAAAGC	1620
TCACATTTCT	TTCTGTCAAC	ACAGAGATTG	GCCTACGGTT	TCTGTTTGA	GGGTGCTGTT	1680
CAATAAAGCT	GTGTACACTA	AATGTCC				

Seq ID NO: 256 Protein sequence

Protein Accession #: AAC50424.1

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1	11	21	31	41	51	
MIEDSGKRGK	TMAERRQLFA	EMRAQDLDR	RLSTYRTACK	LRFVQKKCNL	HLVDIWNVIE	60
ALRENALNNL	DPNTEINVS	LEAVLSTIFY	QLNKRMPPTH	QIHVEQSISL	LINFLAAFPD	120
PEGHGKISVF	AVKMLATL	GGKIMDKLRY	IFSMISDSSG	VMVYGRYDQF	LREVLKLP	180
VFBGPGFTY	EQSARSCFQ	QKKVTLNGFL	DTLMSDPPQ	CLVNLPLLHR	LANVENVFHP	240
VECSYCHSES	NMGFRYRCQ	CHNYQLQDC	FWRGHAGGSH	SNQHQMKRYT	SWKSPAKKLT	300
NALSKLSLCA	SSREPLHPMF	PDQPEKPLNL	AHIVDTWFFR	PVTSMNDTLF	SHSVPSSGSP	360
FITRSSDGA	GGCV					

Seq ID NO: 257 DNA sequence

Nucleic Acid Accession #: NM_004172.1

Coding sequence: 179..1807

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1	11	21	31	41	51	
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CACCCCTTAC	AAAATCAGAA	AAGTTGTGTT	TTCTAATACC	AAAGAGGAGG	TTTGGCTTTC	120
TGTGGGTGAT	TCCAGACAC	TGAAGTGCAA	AGAAGAGACC	CTCCTAGAAA	AGTAAAATAT	180
GACTAAAGAC	AATGAGAAAG	AGCCCAAGAT	GGGGGGCAGG	ATGGAGAGAT	TCCAGCAGGG	240
AGTCCGTAAG	GCACACTTT	TGGCCAAGAA	GAAAGTGCA	AACATTACAA	AGGAGGATGT	300
TAAAAGTTAC	CTGTTTCCGA	ATGCTTTTGT	GCTGCTCACA	GTCAOCCGCTG	TCAATGTGGG	360
TACAATCCTT	GGATTTACCC	TCCGACCATA	CAGAATGAGC	TACCGGGAGG	TCAAGTACTT	420
CTCCTTTCTT	GGGGAACTTC	TGATGAGGAT	GTACAGATG	CTGGTCTTAC	CACCTATCAT	480
CTCAGTCTT	GTCAAGGAA	TGGCGGCGCT	AGATAGTAAG	GCATCAGGGA	AGATGGGAAT	540
GCGAGCTGTA	GTCTATTATA	TGACTACCAC	CATCATTTGCT	GTGGTGATTG	GCATAATCAT	600
TGTCATCATC	ATCCATCCTG	GGAAGGSCAC	AAAGGAAAC	ATGCACAGAG	AAGGCAAAAT	660
TGTACGAGTG	ACAGCTGCAG	ATGCCCTTCT	GGACTTGATC	AGGAACATGT	TCCCTCCAAA	720
TCTGGTAGAA	GCCTGCTTTA	AACAGTTTAA	AACCAACTAT	GAGAAGAGAA	GCTTTAAAGT	780
GCCCATCCAG	GCCACGAAA	CGCTTGTGGG	TGCTGTGATA	AACAAATGTT	CTGAGGCCAT	840
GGAGACTCTT	ACCGAATFCA	CAGAGGAGCT	GGTCCAGTT	CCAGGATCTG	TGAATGGAGT	900
CAATGCCCTG	GGTCTAGTTG	TCTTCTCCAT	GTGCTTCGGT	TTTGTGATTG	GAAACATGAA	960
GGAACAGGGG	CAGGCCCTGA	GAGAGTTCTT	TGATTCCTCT	AACGAAGCCA	TCATGAGACT	1020
GGTAGCAGTA	ATAATGTGGT	ATGCCCCCGT	GGGTATTCTC	TTCTGTGATTG	CTGGGAAGAT	1080
TGTGGAGATG	GAAGACATGG	GTGTGATTGG	GGGGCAGCTT	GCCATGTACA	CCGTGACTGT	1140
CATTGTGGC	TACTTATTTC	ACGCAGTCAT	CGTCTTGCCA	CTCCTCTACT	TCTTGGTAAC	1200
ACGGAAGAAC	CCTTGGGTTT	TTATTGGAGG	GTGCTGCACA	GCACTCATCA	COGCTCTGGG	1260
GACCTCTTCA	AGTTCGTCCA	CCCTACCCAT	CACCTTCAAG	TGCGTGGAGG	AGAACAATGG	1320
CGTGACAGAG	CGCGTCAOCA	GATTGCTGCT	CCCGTAGGAA	GCCACCATTA	ACATGGATGG	1380
GACTGCCCTC	TATGAGGCTT	TGGCTGCCAT	TTTCATTGCT	CAAGTTAACA	ACTTTGAAC	1440
GAACTTCCGA	CAAAATTATA	CAATCAGCAT	CACAGCCACA	GCTGCCAGTA	TTGGGGCAGC	1500
TGGAATTCCT	CAGGCGGGCC	TGGTCACTAT	GGTCATTGTG	CTGACATCTG	TCCGCTGCC	1560
CACTGACGAC	ATCAGCTCA	TCATCGCGGT	GGACTGGTTC	CTGATCGCC	TCCGACCCAC	1620

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CACCAACGTA CTGGGAGACT CCTGGGAGC TGGGATTGTG GAGCACTTGT CACGACATGA 1680
ACTGAAGAAC AGAGATGTTG AAATGGGTAA CTCAGTGATT GAAGAGAATG AAATGAAGAA 1740
ACCATATCAA CTGATTGCAC AGGACAATGA AACTGAGAAA CCCATCGACA GTGAACCAA 1800
GATGTAGACT AACATAAGA AACACTTTCT TGAGCACCAG GTGTAAATAA CCATTATAAA 1860
ATCTTTCCAT CTCATTACAG CTCATTCCGT CCAGCAAGCC CGTCATCTTC CCTTTCCTCC 1920
CTTCTGATAA GACTGGAAAA TAGTCCTCCA AAACACAAGG GAGGATTTTG GGTGGCCAAA 1980
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Seq ID NO: 258 Protein sequence
Protein Accession #: NP_004163.1

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5	CACCTCTCCA	GGCGCCAGCA	AGGGCAGTCC	TGCAGCCTGG	TGCATCAGCA	CTTCTGATG	1620
	GAGAGTCAGA	AGCTTCCAGG	CCTCCAAGGG	TCCATGGACC	ACCTACTGAG	ACTCTGCCCA	1680
	CTCCCAGGGA	GAGGAACCTA	GCATCCCCAT	CACCTTCCAC	TCTGGTTGAG	GCAAGAGAGG	1740
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	CCGCATCAGG	TGACTGTGTC	CCCAGCCCCCT	GCCACAAATG	TGGGACATGC	TTGGAGGAGG	2040
	AGGAAGGGGT	CCGCTGCCTA	TGTCTGCCTG	GCTATGGGGG	GGACCTGTGC	GATGTTGGCC	2100
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	TGGGACTCAA	CGACAGGACC	ATCGAAGGCG	ACTTCTTGTT	GTCCGATGGC	GTCCCCCTGC	2340
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Seq ID NO: 260 Protein sequence
Protein Accession #: NP_068767.1

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	SLALSELRPN	DSGIYRCFVQ	HGIDDSDAV	EVKVKGVVFL	YREGSARYAF	SFSGAQEACA	180
35	RIGAHATPE	QLYAAYLGGY	EQCDAGWLS	QTVRYPIQTP	REACYGDMGD	FPGVRYNGVV	240
	DPDDLVDVYC	YAEDNLGELF	LGDPPFKITL	BEARAYCQER	GABLIATGQL	YAAWDGGLDH	300
	CSPGWLADGS	VRYPIVTPSQ	RCGGGLPGVK	TLFLFPNQTG	FPNKHRSFNV	YCFRDSAQPS	360
	AIPEASNPA	NPASDGLLEAI	VTVTETLEEL	QLPQBEATESE	SRGAIYSIPI	MEDGGGSGST	420
	PEDPAPAPT	LLEFETQSMV	PPTGFSEBEG	KALEEERKEYE	DEEKEEEREE	EVEEDREALN	480
40	AMPSELSSPG	PEASLPTPEA	AQEESLSQAP	ARAVLPQAS	PLPDGESEAS	RPPRVHGPPT	540
	ETLPTPRERN	LASPSPTSLV	EAREVGEATG	GPGLSGVPRG	ESEETGSSEG	APSLLPATRA	600
	PBGTRELEAP	SEDNSTRTAP	AGTSVQAQPV	LPTDSASRGG	VAVVPASGDC	VPSPCHNGGT	660
	CLEEEBGRVC	LCLPGYGGDL	CDVGLRFCNP	GWDAPQGACY	KHFSTRRSWE	EASTQCRMVY	720
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	GENCVVMVNH	DQGGNSDVPC	NYHLSYTCMK	GLVSCGPPPE	LPLAQVFGRP	RLRYEVDTVL	840
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Seq ID NO: 261 DNA sequence
Nucleic Acid Accession #: NM_004386.1
Coding sequence: 2..3967

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	CTTTACCCTG	CAGCCACGGC	CAAGCGCAGC	CCGAGATGCC	CCTCGGATAA	AGTGGACCAA	240
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60	CGTGAGGGTG	GCCAAAAGCT	GGCAGGGACG	AGTGTCACTG	CCTTCCTACC	CCCGGCGCCG	360
	AGCCAACGCC	ACGCTACTTC	TGGGGCCACT	GAGGGCCAGT	GACTCTGGGC	TGTACCGCTG	420
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	CCCCACGTCA	CAACATGGAG	ACCTAGAGAC	CCCATCTCTT	GGGGATGAGG	GGGAGATTCT	1140
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Seq ID NO: 262 Protein sequence

Protein Accession #: NP_004377.1

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Seq ID NO: 263 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 7..2085

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Seq ID NO: 264 Protein sequence
Protein Accession #: Eos sequence

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Seq ID NO: 265 DNA sequence
Nucleic Acid Accession #: AB020684.1
Coding sequence: 1..1744

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Seq ID NO: 266 Protein sequence

Protein Accession #: BAA74900.1

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Seq ID NO: 268 Protein sequence

Protein Accession #: AAC50426.1

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40 GCCTCAGTCT CCCTCCCTTG GGGCCTATGC AGAGGTCCAC AACACACAGA TTGAGCTCA 1440
GCCTCGTGG GCGAGAGGT AGGGATGGGG CTGTGGGAT AGTGAGGCAT CGCAATGTAA 1500
GACTCGGGAT TAGTACACAC TTGTGATGA TTAATGGAAA TGTTTACAGA TCCCAAGCC 1560
TGGCAAGGGA ATTTCCTCAA CTCCTGCCCC CTTATCAAAG GACACCATTT 1620
45 TGGCAAGCTC TATCACCAG GAGCCAAACA TCCTACAAGA CACAGTGACC ATACTAATTA 1680
TACCCCTGTC AAAGCCAGCT TGAACCTTC ACTTAGGAAC GTAATCGTGT CCCCTATCCT 1740
ACTTCCCTTT CCTAATTCAC CAGCTGCTCA ATAAAGTACA AGAGTTTAA AGTGTGTGG 1800
CGCTTTGCTT TGGTCTATCT TTGAGCGCCC ACTAGACCCA CTGAGCTCAC CTCGCCATC 1860
TCTTCTGGGT TCCTTCTCT GAGCCTTGGG ACCCCTGAGC TTGCAGAGAT GAAGGCCGCC 1920
ATGTT

Seq ID NO: 270 Protein sequence
Protein Accession #: NP_001267.1

55 1 11 21 31 41 51
MGVKASQTGF VVLVLLQCCS AYKLVCIYTS WSQYREGDGS CFPDALDRFL CTHIISFAN 60
ISNDHIDTWE WNDVLYGLM NTLKRNPNL KTLLSVGGWN FGSQRFSKIA SNTQSRRTPI 120
KSVPPFLRTH GFDGLDLAWL YPGRDKQHF TTLIKEMKAE FIKERQPKKK QLLLSAALSA 180
60 GKVTIDSSYD IAKISQHLDF ISIMTYDFHG AWRGTTGHS PLFRGQEDAS PDRFSNTDYA 240
VGMYLRLGAP ASKLVMGIFT FGRSFTLASS ETGVGAPISG PGIPGRPTKE AGTLAYVEIC 300
DFLRGATVHR TIGQQVPYAT KGNQWVGYYD QESVSKVQY LKDRQLAGAM VWALDLDDFQ 360
GSFCGQDLRF PLTNAIKDAL AAT

Seq ID NO: 271 DNA sequence
Nucleic Acid Accession #: NM_006474.1
Coding sequence: 181..669

70 1 11 21 31 41 51
GCTGCCTAGG GTCTGGAAG CTGGGACACC CTCCTCTCC GGGGCTCCTG CTCCCACCCC 60
TCGGSCCCCC CCACCGTGC GCTCCTCCAG GCTGGGCTGT TGGCCGCGST GCTTTTAATT 120
TTCCCCCAGC TCAGAATCTT GCTGCTCGGC CCCCAGGAGA GCAACAATC AACGGGAACG 180
ATGTGGAAAG GTGCACTCT GCTCTCTGTT TTGGGAAGCG CGTGGCTCTG GGTCTGTGCA 240
GAAGGAGCCA GCACAGGCCA GCCAGAGAT GACACTGAGA CTACAGGTTT GGAAGGCGGC 300
75 GTTGCCATGC CAGGTGCCGA AGATGATGTG GTGACTCCAG GAACCAAGCA AGACCGCTAT 360
AAGTCTGGCT TGACAATCT GGTGGCAACA AGTGTCAACA GTGTAAACAG CATTOGCATC 420
GAGGATCTGC CAACTTCAGA AAGCACATC CACGCGCAAG AACAAAGTCC AAGGCCACA 480
GCCTCAACG TGGCCACCG TCACTCCAG GAGAAAGTGG ATGGAGACAC ACAGACAACA 540
GTTGAGAAAG ATGTTTGTG AACAGTGACC CTGGTTGGAA TCATAGTTG GGTCTTACTA 600
80 GCCATCGGTT TCATTGTGG AATCATCGTT GTGGTTATGC GAAAATGTC GGAAGGTAC 660
TGCCCTTAA GAGCTGAAG GTTACGCCCT GCTTGCCAAC GTGCTTTAA AAAAGACCTT 720
TTCTGACTCT GTGGCCCTGT CCCTGAGCTC GTGGGGAGAA GATGACCCTG GSAACATTG 780
CGGGCCCATC CAGATTCCAC GGTGACTTTC CGTTTGCCAA ATTAACCGAG GAAAGACCTT 840

TCACCAGATT TGATTCTTAA ACTTT

Seq ID NO: 272 Protein sequence
 Protein Accession #: NP_006465.1

5

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1      11      21      31      41      51
|      |      |      |      |      |
MKVKSALLFV LGSASLWVLA EGASTGQPED DTFTTGLEGG VAMPGAEDDV VTPGTSBDRY 60
KSLGLTTLVAT SVNSVTGIRI EDLPTSESTV HAQDQSPSAT ASNVATSHST EKVDGDTQTT 120
VERDGLSTVT LVGIIVGVLL AIGFIGGIIV VVMRIKMSGRY SP

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10

Seq ID NO: 273 DNA sequence
 Nucleic Acid Accession #: CAT cluster

15

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1      11      21      31      41      51
|      |      |      |      |      |
GCGGCGGCCA GCTTGCAAAG CCGAAGTCTG GCGGCGCTCT TCGACTCGCT GCGCCACGTC 60
CCCCGGGGTG CCGAGCCGGC GGGGGGTGAG GTGGCTGCGC CGGCGGCCGG GCTAGGAGGT 120
GCGGGCACTG GGGCGCGGGG AGGGGACGTG GCAGGCCCGG CGGGGGCCAC GCGATCCCA 180
GGGGCCAGGA AGGTCCCGCT GCGGGCACGC AATCTGCCTC GTCTCTTCTT CACGGAGCCG 240
TCCCGGCAGG GCGGCGCGGG GTGTGGCCCG TCGGGGCGGG ACGTGAGCTT GGGCGACCTG 300
GAGAAGGGCG CGGAGGCCGT GGAGTTCTTT GAGCTGCTGG GCGCCGACTA CGGCGCCGGC 360
ACGGAGGCGG CAGTCTTGCT TGCCGCGGAG CCTCTCGAAG TGTTCGCCGC CGGAGCCTCC 420
GTACTGCGGG GACCCCGGGA GCTGGAGCCC GGCTCTTTTG AGCCGCCGCC GGCAGTGGTG 480
GGAAACCTAC TGTACCCCGA GCCCTGGAGC GTCCCGGGCT GCTCCCGGAC CAAAAAGAGC 540
CCCTGACTG CCCTCCCGGG CGGGTTGACC TTGAACGAGC CCTTGAGCCC CTGTACCCC 600
GCGCTGCGA ATTTCTCCCG GCGGGGAGGA CGGGCGGGC CATTTGGCTT CTTTCGCCCC 660
CTTCTTCCA GACTGCGCTT TGC

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30

Seq ID NO: 274 DNA sequence
 Nucleic Acid Accession #: Bos sequence

35

```

1      11      21      31      41      51
|      |      |      |      |      |
CAAAGAGGCC GGGCTCCAGC TCCGGGGGTC CCCGCACTAC GGAGGCTCCG GCGGGGAACA 60
CGTCGAGAGG CTGCGCGGCA AGCAAGACTG CCGCCTCCGT GCGCGGCGCG TAGTCGCGGC 120
CCAGCAGCTC AAAGAACTCC ACGGCTCCCG CGCCTTCTC CAGGTGCGCC AAGCTCAGGT 180
CGGGCCCGGA CGGGCCACAC CCGCCGCGCG CTGCCCGGGA CGGCTCCGTG AAGAAGGAGC 240
GAGGCAGATT GCGTCCCGCG AGCGGACCTT TCCTGGCCCC TGCGATGCGC GTGGCCCCCG 300
CGGGGCTGCG CACGTCCCGT CCGCGCCCCC CAGTGCCTGC ACCTCCTAGC CGGCGCGCGC 360
GGCAGCCAC CTCACCCCCC GCGGCTCCG CACCCCGGGG GAGTGGCGC AGCGAGTCCA 420
AGAGCGCGGC CAGACTTCGG CTCTGCAAGC TGGCGCCCGC

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45

Seq ID NO: 275 DNA sequence
 Nucleic Acid Accession #: NM_001118.1
 Coding sequence: 74..1651

50

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1      11      21      31      41      51
|      |      |      |      |      |
AGCCAGAGA CACATGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG 60
GCCAAGAAGT GTCATGGCTG GTGTCTGTCA CGTTTCCCTG GCTGCTCACT GCGGGGCGTG 120
TCGGTGGGGC CGGGGAGAC TCCGCAAAAG ACGGCGAGCC TGCAAGTCCG CGGCCAGAG 180
ACACATTGGG GCTGACCTGC CGCTGCTGTC AGTGGGAGGC CAGTGGTGCT GGCCCAAGAG 240
TGTCTAGGCT GGTGTCTGTC ACGTTTCCCT GGCTGCTCTC CTCTGCTGTC CTATGGCCCC 300
TGCCATGCAT TCTGACTGCA TCTTCAAGAA GGAGCAAGCC ATGTGCTCTG AGAAGATCCA 360
GAGGGCCAAT GAGCTGATGG GCTTCAATGA TTCTCTCCA GGCTGTCTTG GGATGTGGGA 420
CAACATCAGC TGTGGAAGC CCGCCCATGT GGGTGAGATG GTCCTGGTCA GCTGCCCTGA 480
GCTCTTCCGA ATCTTCAACC CAGACCAAGT CTGGGAGACC GAAACCATTG GAGAGTCTGA 540
TTTGTGTGAC AGTAACTCCT TAGATCTCTC AGACATGGGA GTGGTGAGCC GGAAGTGCAC 600
GGAGGATGGC TGGTCGGAAC CCTTCCCTCA TTAATTGAT GCCTGTGGGT TTGATGAATA 660
TGAATCTGAG ACTGGGGAAC AGGATTATTA CTACTGTGTA GTGAAGGCCCT TCTACACGGT 720
TGGCTACAGC ACATCCCTCG TCACCTCAC CACTGCCATG GTCATCCTTT GTGCTTCG 780
GAAGCTGCAC TGCAACGCA ACTTCATCCA CATGAACCTG TTTGTGTGCT TCATGCTGAG 840
GGCGATCTCC GTCTTCATCA AAGACTGGAT TCTGTATGCG GAGCAGGACA GCAACCACTG 900
CTTCATCTCC ACTGTGGAAT GTAAGGCCGT CATGGTTTTC TTCCACTACT GTGTTGTGTC 960
CACTACTTTC TGGCTGTTC TCGAGGGCCT GTACCTCTTC ACTCTGCTGG TGGAGACCTT 1020
CTTCCCTGAA AGGAGATACT TCTACTGGTA CACCATCATI GGCTGGGGA CCCCACCTGT 1080
GTGTGTGACA GTGTGGGCTA CGCTGAGACT CTACTTTGAT GACACAGGCT GCTGGGATAT 1140
GAATGACAGC ACAGCTCTGT GGTGGGTGAT CAAAGGCCCT GTGGTTGGCT CTATCATGGT 1200
TAACCTTTGT CTTTATATG GCATATCGT CATCCTTGTG CAGAAACTTC AGTCTCCAGA 1260
CATGGGAGGC AATGAGTCCA GCATCTACTT GCGACTGGCC CGGTCCACCC TGCTGCTCAT 1320
CCCACTATTG GGAATCCACT ACACAGTATT TGCCTTCTCC CCAGAGAATG TCAGCAAAAG 1380
GGAAAGACTC GTGTTTGAGC TGGGGCTGGG CTCCTTCCAG GGCTTTGTGG TGGCTGTTCT 1440
CTACTGTTTT CTGAATGGTG AGGTACAAGC GGAGATCAAG CGAAAATGGC GAAGCTGGAA 1500
GGTGAACCGT TACTTCGCTG TGGACTTCAA GCACGACAC CCGTCTCTGG CCAGCAGTGG 1560
GGTGAATGGG GGCACCCAGC TCTCCATCCT GAGCAAGAGC AGCTCCCAA TCCGATGTTC 1620
TGGCTCCCT GCTGACAATC TGGCCACCTG AGCCATGCTC CCTT

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80

Seq ID NO: 276 Protein sequence
 Protein Accession #: NP_001109.1

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1      11      21      31      41      51
|      |      |      |      |      |
MAGVVHVSLSA AHGACAPNGR GRLRKGRAAC KSAAQRHIGA DLPLLSVGGQ WCNPRSVMAG 60

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5 VVHVSIAALL LLPMAPAMHS DCIFKKEQAM CLEKIQRANE IMGFNDSPPG CPGMMDNITC 120
 WKPAHVGEV LVSCPELRFRI FNPQVWETE TIGESDFGDS NSLDLSDMGV VSRNCTEDGW 180
 SEPFPHYFDA CGFDEYSEST GDQDYIYLSV KALYTVGYST SLVTLTAMV ILCRFKLHC 240
 TRNFHIMNLF VSFMLRAISV FIKDWILYAE QDSNHCPIST VECKAVMVFP HYCVVSNYFW 300
 LPFIEGLYLF LLVETFFPER RYFYWTIIG WGTPTVCIV WATLRLYFDD TGCWDMNDST 360
 ALMWIKGPV VGSIMVNFVL FIGIIVILVQ KLQSPDMGWN ESSIYLRILAR STLLLIPLFG 420
 IHYTVFAPSP ENVSKRERLV FELGLGSFQG FVAVLYCFL NGEVQAEIKR KWRSWKVNYR 480
 FAVDFKRRHP SLASSGVNGG TQLSILSKSS SQIRMSGLPA DNLAT

10 Seq ID NO: 277 DNA sequence
 Nucleic Acid Accession #: NM_004000.1
 Coding sequence: 36..1193

15 1 11 21 31 41 51
 AGAAGAAGCT GGCCAAGGAT ATGGGAGCAA CCACCATGGA CCAGAAGTCT CTCTGGGCAG 60
 GTGTAGTGGT CTGTCTGCTT CTCCAGGAG GATCTGCCTA CAAACTGGTT TGCTACTTTA 120
 CCAACTGGTC CCAGGACCGG CAGGAACCGA GAAATTCAC CCCTGAGAAT ATTGACCCCT 180
 TCCTATGCTC TCATCTCATC TATTTCATCG CCAGCATCGA AAACAACAAG GTTATCATCA 240
 20 AGGACAAGAG TGAAGTGATG CTCTACCAGA CCATCAACAG TCTCAAAACC AAGAATCCCA 300
 AACTGAAAT TCTCTGTGCC ATTGGAGGGT ACCTGTTTGG TTCCAAAGGG TTCCACCCCTA 360
 TGGTGGATTC TTCTACATCA CGCTTGAAT TCATTAATC CATAATCCTG TTCTGAGGA 420
 ACCATAACTT TGATGGACTG GATGTAAGCT GGATCTACCC AGATCAGAAA GAAACACTC 480
 ATTTCACTGT GCTGATTCAT GAGTTAGCAG AAGCCTTTCA GAAGGACTTC ACAAAATCCA 540
 25 CCAAGGAAAG GCTTCTCTTG ACTGCGGGCG TATCTGCAGG GAGGCAATG ATTGATAACA 600
 GCTATCAAGT TGAGAAACCT GCAAAAGATC TGGATTTCAT CAACCTCTGT TCCTTTGACT 660
 TCCATGGGTC TTGGGAAAGC CCCCTTATCA CTGGCCACA CAGCCCTCTG AGCAAGGGGT 720
 GGCAGGACAG AGGGCAAGC TCCTACTACA ATGTGGAATA TGCTGTGGGG TACTGGATAC 780
 ATAAGGAAAT GCCATCAGAG AAGGTGGTCA TGGGCATCCC CACATATGGG CACTCCTTCA 840
 30 CACTGGCCTC TGCAGAAACC ACCGTGGGGG CCCCTGCCTC TGGCCCTGGA GCTGTGGGAC 900
 CCATCAGACA GTCTTCAGGC TTCTTGGCCT ATTATGAGAT CTGCCAGTTC CTGAAAGGAG 960
 CCAAGATCAC GGCCTCCAG GATCAGCAGG TTCCCTACGC AGTCAAGGGG AACCAAGTGG 1020
 TGGGCTATGA TGATGTGAAG AGTATGAGA CCAAGGTTCA GTTCTTAAAG AATTTAAACC 1080
 TGGGAGGAGC CATGATCTGG TCTATTGACA TSGATGACTT CACTGGCAAA TCCTGCAACC 1140
 35 AGGGCCCTTA CCTCTTGTG CAAGCAGTCA AGAGAAGCCT TGGCTCCTTG TGAAGGATTA 1200
 ACTTACAGAG AAGCAGGCAA GATGACCTTG CTGCGTGGGG CCGTCTCTCT CCCAGGAATT 1260
 CTCATGTGGG ATTCCTCTG CCAGGCTGGC CTTTGGATCT CTCTTCCAAG CCTTCTCTGA 1320
 CTTCTCTTGA GATCATAGAT TGGACCTGGT TTGTGTTTCC TGCAGCTGTT GACTTGTGTC 1380
 CCTGAAGTAC AATAAAAAAA ATTCATTTTG CTCACGTA

Seq ID NO: 278 Protein sequence
 Protein Accession #: NP_003991.1

45 1 11 21 31 41 51
 MDQKSLWAGV VVLLLLQGGG AYKLVCFYTN WSQDRQEPGK FTPENIDPFL CSHLIYSFAS 60
 IENNKVLIKD KSEVMLYQTI NSLKTNPFL KILLSIGGYL PGSKGFHPMV DSSTSRLEFI 120
 NSIILFLRNH NFDGLDWSVI YPDQKENTHF TVLIHELAEA FQKDFTKSTK ERLLLTAGVS 180
 50 AGROMIDNSY QVEKLAKDLF FINLLSDFDH GSWEKPLITG HNSPLSKGWQ DRGPSSTYINV 240
 EYAVGYNIHK GMPSEKVVVG IPTYGHSPFL ASAEVTVGAP ASGPGAAGPI TESSGFLAYY 300
 EICQFLGAK ITRLDQGVV YAVKGNQWVG YDDVKSMETK VQFLKLNILG GAMINSIDMD 360
 DFTGKSCNQG PYPVQAVKR SLGSL

55 Seq ID NO: 279 DNA sequence
 Nucleic Acid Accession #: NM_015166.1
 Coding sequence: 116..1249

60 1 11 21 31 41 51
 TGCTGGAAGT CCTCACCCA GAGACCAGTG CTCCCAACGG CAGAGCAGCG GGGGAGATAA 60
 AGAACTGGTG ACACGTGGCT GTACATTCAG CACAGCTGTG GTGTCCCAAA GTGCCATGAC 120
 CCAGGAGCCA TTCAGAGAGG AGCTGGCCTA TGACCGGATG CCCACGCTGG AGCGGGGCCG 180
 GCAAGACCCC GCCAGCATATG CCCAGACGCG GAAGCCGAGC GACCTGCAGC TGTGGAAGAG 240
 65 ACTGCCCCCG TGCTTCAGCC ACAAGAAGTG GGTCTTCTCT GTGCTGATGG GGAGCTGCTT 300
 CCTGGTGACC TCGGGGTTTT CGCTGTACCT GGGGAACGTG TTCCCGCTG AGATGGATTA 360
 CTTGCGCTGT GCTGCAGGCT CTTGCATCCC CTGCGCAATT GTGAGCTTCA CGCTCTCCAG 420
 GAGGAACGCC AATGTGATTC CCAACTTTCA GATATTGTTT GTTCCACGT TTGCTGTGAC 480
 CACTACGTGT TTAATTGGT TTGGATGCAA ACTAGTCTCT AACCCATCAG CAATAAACAT 540
 CAACTTCAAC CTAATCTGCG TGCTCTGCTG GGAGCTGCTC ATGGCGGCCA CGTGATCAT 600
 70 CGCTGCACGG TCCAGCGAGG AGGACTGCAA GAAAAGAAAG GGCTCCATGT CTGACAGCGC 660
 CAACATTTCT GACGAAGTGC CATTTCTGCT TCGGGTCTCT AAATCTTACT CAGTCTGCGA 720
 GGTAATCGCA GGCATCTCTG CGGTCTCTGG GGGATCAATT GCCCTGAAAG TGGATGACTC 780
 AGTTTCAGCG CCACACTCTC CAGTGACGTT CTTTGGATTC CTAGTGGCCT GCTTCTCAAG 840
 TGGCATTGCC AGTCATGTGG CAGCAGAGTG TCCAGCAAG TGCTGTGGTG AGGTCTGTAT 900
 75 TGGCATAAGC AGCCTCACGT CTCGCTGCT GTTCAAGCC TCTGATATC TGTCTTCAG 960
 CATCATGAGA ATCGTGAGA TGTTTAAGGA TTACCCGCCA GCCATAAAAC CATCTACGA 1020
 TGTGCTGCTG CTGCTGCTGC TGCTAGTGCT CCGTCTGAGC GCCGGCTTCA ACACGGGCAC 1080
 CGCCATCCAG TCGGTGCGCT TCAAGGTCAG TGCAAGGCTG CAGGCTGCAT CCTGGGACAC 1140
 80 CCAGAACGCG CCGCAGAGC GCCTGCTGCG GAGAGTGGCC AGGAGCCCCC TGAAGGAGTT 1200
 CGACAAGGAG AAAGCCTGGA GAGCCGTCTG GGTGCAATG GCCAGTGAC CCCAGAGCGC 1260
 GGAACACGGG TGGCAGCGCC CAGCCTGGCC CCAAGCATGG AAACGCACAA CCCCTAATCG 1320
 CCTGAGCTA CTGCTCTTAA CACTCTTTT CCCTGTGTG AGGGCAAAAC AGGCTGCAGG 1380
 TGGGGTTTTC ACTTCTTAGG GTAGTTTAAAT TTTAAATAG GCCAATGTGT GCTAGTCTGT 1440
 GCCTCAGTGA GATCAGTCAG CTCGAGTGG CTCGCTGTC GTAACAGCAG GAGCATGCC 1500

5 GCAACTTCCC AGGCGAGGGA AGGGCCCCCG GCTGGGCTTC TTGAGAGCCC CACCCCTGAA 1560
 CTGGCCCCAG TCCTCTCTTC TGCTCTCTTC ATGGCTTGGG CTGGAGTGGG CTCTCTGGAC 1620
 CTGACCCAGC TGTGGGTCCC TGCGTCTCTC GCCACTCTTG ACCGGGCTTC CTCCCTCCAC 1680
 GCTTAGGGGT TGTCCCGGT ACTCAGTCAG CCCAGTGGGA TCTTACCAC TTCCCTGCAA 1740
 GGTGCACCTG CCCCAGGCTC AGGCTGCCCA GCGGCTCTTC CTGACAGTG AGAGCAGGGC 1800
 TTGGGCTCTC TGTCTGGCC CGGGAGCCGC AGGGGCCCCC CTCCAGAGC CTGGGCGCAA 1860
 GCGACACAGG CTGCGCTGTC TCTCCAGGT GAAATCCACA CCAGTCCACG CCGGCTCGCC 1920
 TGCCCTGTCT CCTACTTTC ACCCAGTCAT TCTAGAGGGA TCCACGCCCA CACTGGCGGG 1980
 CCCAGTCTCT GGGTCTGTGC ATGCCAGCT TGGAGTGCCA CGTGGCGCT GCCCAGTCC 2040
 10 CCGGCACTGT CATGCCCAGC TTGGAGTGCC ACATGGCCGC TGCCACGTC CCGGCACTGT 2100
 TCATGCCAGC CTGGAGTGC CAGTGGCCG CTGCTGTGAC AGGCAGTGT CTGGGGGTG 2160
 GGGCTGCATC CAAGGCTTTG TAAACCGCT GAGCCAGTC TCCTGGCCC CAGTGACCG 2220
 GGGAGCTGA GCCCTCCCT OCTGTGTTG CTCCATTAC TCAAAATGCA GACAGATCA 2280
 GGTGAGAGCC CAGGAATTCT CACAGTTCA CCCAGCGCCC TCTACTCTCT AGCAAGTACT 2340
 15 TTGTCTGAT CCTACTGAG AAGGCCCCAG GGCAGGGTC TTCTCCATCT CGCTGTTTT 2400
 GGGGTCTTAG GGTACAGCCC AGGCGGTAC TGCCCACTG CCAGGCTGCA GGGAGGTG 2460
 GGTGTGAGAA TAACTACTGC TTTGGGTAG GCCATGGCCA GAGTGGGT TTCTGCTC 2520
 TTCTGTCCC GAGGGCGCT GGTCTCTCC AGCTGACGG AGTAAATCCA CAGTGTGTTG 2580
 GGGGACTGT GAACTGGA TGCTGTACT TTGATAATTA CTTCACGCA GGTGTTTTCC 2640
 20 TTCACAATG TTTGTGTTCT TTCTTCTGA TCTGAGAAGA CATGAACGT TTCTCTTCAC 2700
 CGCGTGGGG TGTATTGACT GGTCCCCAT GGGCTGTGAG AAGGCGCCG AGATGCACT 2760
 GTGGCTGGG GCCATCAAGA TCAAGAACC AGGAGGCTG GAGATGCAG CTGGATGGG 2820
 CGGCTGCAG ACCCTGCCAG GGGGTGAG GACCTCCCA GGTTCCTCC TGCGAACAG 2880
 GAGTGACTT GGCTGCCAG ATACCTTCAT GGTGTTTAT ACAAGTGA TCAATTATTT 2940
 25 CAACATTGA AGGGGATGC AGGCAAGACA CCTTCCAGC TGCTCTAGA GGGGACAAGC 3000
 CAGGCCCTCT CTGAGTCTC CGGCACTCC GGAAGGACAC AGTCAGGGC CGGGCAACA 3060
 CTTTGGCCAC AGCCCCAACC AAGCGCCACC GTGGGAGAG AGAGGCTGCT GTCACTGGA 3120
 CGGATGCAG ACCCACTCT GTCTGCAGG CACCCCACT TCCTGTCAGC TTTGAGGCTG 3180
 CGGGGTCTG CTCTGGGAA TGGGTGGGA GCCACAGGA CGACCGGGG CCGGCTGATG 3240
 30 TCTTCTGGG GGCAGACAG AGAGCTCAAG TTTGAGATC AGAATTAGGC ACTTGAAGC 3300
 TTTTGTCTG CTTCAGCTT CTTATTTCT TATTTTAGAG CGCTTAAAA ATCCGGAAGA 3360
 ATGGGGTTA AAGAAGCTG CTCTTCAGT CTACATTTT GTTTAATACG CTTGAGCAAT 3420
 AAAGCTGAC TTGACAGCT G

Seq ID NO: 280 Protein sequence
 Protein Accession #: NP_055981.1

40 1 11 21 31 41 51
 MTQEPFREEL AYDRMPTLER GRQDPASYAP DAKPSDLQLS KRLPPCFSHK TWVFSVLMGS 60
 CLLVTSGLSL YLGNVFPDEM DYLRCAAGSC IPSAIVSFTV SRNANVIPN PQILFVSTFA 120
 VTTTCLWIFG KLVLPNSAI NINFNLLILL LLELLMAATV IIAARSSEED CKKKKGSMSD 180
 SANILDEVFP PARVLKSYV VEVIAGISAV LGGIILMVD DSVSGPHLSV TFPWILVACP 240
 45 PSAIAHVAA ECPSKCLVEV LIAISSLTSP LLFTASGYLS PSIMRIVEMF KDYPFAIKPS 300
 YDVLILLILL VLLLQAGLNT GTAIQCVRFK VSARIQASW DTQNGPQERL AGEVARSPLK 360
 EFDKEAWRA VVQMAQ

Seq ID NO: 281 DNA sequence
 Nucleic Acid Accession #: NM_004518.1
 Coding sequence: 43..2577

55 1 11 21 31 41 51
 GCTGAGCCTG AGCCCGACCC GGGGCGCTC CGCCAGGCA CCATGGTGCA GAAGTGGGC 60
 AACGGCGCGG TATACCCCGG CCGAGCGCG GAGAAGAAGC TGAAGTGGG CTTCGTGGG 120
 CTGACCCCGG GCGCGCCCGA CTCCACCCCG GACGGGGCGC TGCTGATGCG CGGCTCGAG 180
 GCCCCCAAGC GCGGACGAT CCTCAGCAA CCTCGCGCG GCGGCGCGG CGCGGGGAA 240
 CCCCCAAGC GCAACGCTT CTACCGCAAG CTGACGAAT TCTCTACAA CGTGTGAG 300
 60 CCGCGCGCGG GCTGGCGTT CATCTACCAC GCCTACGTT TCTCTGCTG TTTCTCTGC 360
 CTGTGCTGT CTGTGTTTC CACCATCAAG GAGTATGAGA AGAGCTCGGA GGGGCGCTC 420
 TACATCTGAG AAATCGTGAC TATCGTGTG TTTGGCGTG AGTACTCTG GCGATCTGG 480
 GCGCAGGCT GCTGCTGCG GTACCGTGGC TGGAGGGGGC GGCTCAAGTT TGCCCGGAA 540
 CGGTCTGTG TGAATGACAT CATGGTGCTC ATCGCTCCA TTGGGTGCT GGCOCGCGG 600
 65 TCCAGGGCA ACCTCTTTGC CACATCTGCG CTCGGAGCC TGCGTTCTCT GCAGATTCTG 660
 CGATGATCC GCATGACCG GCGGGAGGC ACCTGGAAGC TGCTGGGCTC TGTGTCTAT 720
 GCCCAGACA AGGAGCTGGT CACTGCTGG TACATCGGT TCTTTGTTCT CATCTGGCC 780
 TGTTCCTGG TGTACTTGGC AGAGAAGGGG GAGAAGGACC ACTTTGACAC CTACGCGGAT 840
 GCACTCTGCT GGGGCTGAT CACGCTGACC ACCATTGGCT ACGGGGACAA GTACCCCGAG 900
 70 ACCTGGAAAG CGAGGCTCTT TGCGCAACC TTCACCTCA TCCTGTCTC CTCTCTCGG 960
 CTGCTGCAAG GCATCTTGGG GTCTGGGTTT GCGCTGAAG TTCAGGAGCA GCACAGGCG 1020
 AAGCACTTTG AGAAGAGGGG GAACCGGCA GCAGGCGTGA TCCAGTGGC CTGAGATTCT 1080
 TACGCCACCA ACCTCTCGCG CACAGACCTG CACTCCAGT GCAGTACTA AGAGCGAAG 1140
 GTCACCGTGC CCATGTACAG ACTTATCCCC CGCTGAACC AGCTGAGCT GCTGAGGAAC 1200
 CTCAGAGTA AATCTGGAAT OGCTTTCAGG AAGGACCCCC CGCGGAGCC GTCTCCAGC 1260
 75 CAGAAGTCC GTTTGAAGA TGTGTCTTC TCCAGCCCC GAGGCGTGGC TGCCAGGGG 1320
 AAGGGTCCC CGCAGGCCCA GACTGTGAGG CGGTCAACCA GCGCGGACCA GAGCCTGAG 1380
 GACAGACCA GCAAGGTGCC CAAGAGCTGG AGCTTGGGG ACCGAGCGG GGCAGCGGAG 1440
 GCTTTCGCA TCAAGGTGCG CGGCTCACGG CAGAATCAG AAGAAGCAAG CCTCCCCGA 1500
 80 GAGGACATTG TGGATGACAA GAGCTGCCCC TGCGAGTTTG TGACGAGGA CCTGACCCCG 1560
 GGCCTCAAAG GTTTCAGCAG AGCGGTGTGT GTCATGCGGT TCCTGTGTG CAGCGGAG 1620
 TTCAAGGAGA GCGTGGGCC CTACAGCGTG ATGGAAGTCA TCAGCAGTA CTCAGCGGCG 1680
 CACCTGACA TGCTGTCCCG AATTAGAGC CTGCACTCCA GAGTGGACCA GATCGTGGG 1740
 CGGGGCCAG CGATCACGGA CAAGAGCCGC ACCAAGGGC CGCGGAGCG GAGCTGCCC 1800
 GAGGACCCCA GCATGATGGG ACGGCTGGG AAGGTGAGA AGCAGGTCTT GTCCATGGAG 1860

	AAGAAGCTGG	ACTTCTCTGGT	GAATATCTAC	ATGCAGCGGA	TGGGCATCCC	CCGACAGAG	1920
	ACCGAGGCCT	ACTTTGGGGC	CAAAGAGCGG	GAGCCGCGCG	CGCCGTACCA	CAGCCCGGAA	1980
	GACAGCCGGG	AGCATGTGGA	CAGGCACGGC	TGCATTGTCA	AGATCGTGGG	CTCCAGCAGC	2040
5	TCCACGGGCC	AGAAGAAGTT	CTCGGCGCCC	CCGGCCGCGC	CCCTGTGCA	GTGTCCGCCC	2100
	TCCACCTCCT	GGCAGCCACA	GAGCCACCCG	CGCCAGGGCC	AOGGACCTC	CCCCGTGGGG	2160
	GACCACGGCT	CCCTGGTGGC	CATCCCGCGG	CGGCTGCCC	ACGAGCGGTC	GCTGTCCGCC	2220
	TACGGCGGGG	GCAACCGCGC	CAGCATGAG	TTCTGTGCGG	AGGAGGACAC	CCCGGGCTGC	2280
	AGGCCCCCCG	AGGGGACCCCT	GCGGACAGC	GACACGTCCA	TCTCCATCCC	GTCCGTGGAC	2340
10	CACGAGGAGC	TGGAGCGTTC	CTTCAGCGGC	TTACAGTCT	CCCACTCCAA	GGAGAACCTG	2400
	GATGCTCTCA	ACAGCTGTCTA	CGCGGCGGTG	GCGCTTGTG	CCAAAGTCAG	GCCCTACATT	2460
	GCGGAGGGAG	AGTCAGACAC	CGACTCCGAC	CTCTGTACCC	CGTGCGGGCC	CCCGCCACGC	2520
	TCGGCCACCG	GCGAGGGTCC	CTTTGGTGAC	GTGGGCTGGG	CCGGGCCACG	GAAGTGAGGC	2580
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Seq ID NO: 282 Protein sequence
Protein Accession #: NP_004509.1

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Seq ID NO: 2838 DNA sequence
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Seq ID NO: 284 Protein sequence
Protein Accession #: AAD43757.1

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75 Seq ID NO: 286 Protein sequence
 Protein Accession #: NP_001785.2

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Seq ID NO: 287 DNA sequence
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 ACGGAGAGTG GCTCCTTTGT GGCCAATTGT TTAAGAGACC TGGGGCTGGA GATAGGAGAA 180
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 AGGCAGACCG GGGATTGTGT GTTAAATGAG AAATGGACC GGGAGGAGCT GTGCGGCCCC 300
 ACAGAGCCCT GTGCTCTACC TTTCAGGTG TTAAGTAAA ATCCCTTGCA GTTTTTCAG 360
 GCGGAGCTAC GGATTAGGGA CGTAAATGAT CATTCCCCAG TTTTCTAGA CAAAGAAATA 420
 CTTTGAATA TTCCAGAAAG TATCACTCCT GGAAGTACTT TCTTAATAGA ACGTGCCAG 480
 GACTTGGATG TAGGAACCAA CAGTCTCCAA AATTACCAA TCAGTCCCAA TTTCCACTT 540
 CATCTTAATT TACAAGACAG TCTGATGGC ATAATATTAC CACAGCTGGT GCTGAACAGA 600
 GCGCTGGATC GCGAGGAGCA GCCTGAGATC AGGTAAACCC TCACAGCGCT AGATGGCGGG 660
 AGTCACCCCA GGTCGCGCAC GGCCCTGGTA CGGATTGAAG TTGTGGACAT CAATGACAAC 720
 GTCCAGAGT TTGCAAAAGT GCTCTATGAG GTGCAGATCC GCGAGGACAG CCGCGTTGGA 780
 TCCAGGTTG CCATCGTCTC TGCCAGGGAT TTAGACATTG GAACTAATGG AGAAATATCT 840
 TATGCAATTT OCCAAGCATC TGAAGACATT GCAAAAACGT TTCGATTAAG TGCAAAATCG 900
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 CCCTCGTGC TGATACCGCT GCAGAACGGC TCCGCGCCTC GCACCGAGCT GGTGCCCGG 1740
 GCGGCGGAGC CGGGCTACCT GGTGACCAAG GTGGTGGCGG TGGACGGCGA CTGGGCGCAG 1800
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 TGCTCTTCC TCTCTGGGT GTGGCGGTGC GCTGTGTCAG GAGGAGCAGG 2160
 GCGGCTCGG TGGGTGCGCT CTGGTGGCCC GAGGCGCCCT TTCCAGGGCA GATGGTGGAC 2220
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 GCAGAGAGGG TTAGCGAGGC AAATCCAGT TTCAGGAAGA GCTTTGAATT CACTTAA

Seq ID NO: 288 Protein sequence
 Protein Accession #: AAD43756.1

1 11 21 31 41 51
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 ABLRIRDVND HSPVFLDKAI LLKIPESITP GTTFLIERAQ DLDVGTNSLQ NYTISFNPFP 180
 HNLQDSLDG IILPQLVLNR ALDREEQPEI RLTLALDGG SPFRSGTALV RIEVVDINDN 240
 VPEFAKLLYE VQIPEDSPVG SQVAIVSARD LDIGTNGEIS YAFSQASEDI RKTFRLSAKS 300
 GELLRLKQLD PESIQTYTVN IQATDGGGLS GTCVFPVQVM DLNDNPPELT MSTLINQIPE 360
 NLQDTLIAVF SVSDPDSGDN GRMVCSIQDD LPFFLKPSVE NFYTLVISTA LDRETRSEYN 420
 ITITVTDFGT PRLKTEHNIT VLVSDVNDNA PAFTQTSYTL FVREMNSPAL HIGSVSATDR 480
 DSGTNAQVTV SLLPPQDPHL PLASLVNSINA DNGHLFALQS LDYEALQAFE FRVGAADRG 540
 PALSSEALVR VLVLDANDNS PFVLYPLQNG SAPCTELVPR AAEFGYLVTK VVAVDGDSQ 600
 NAWLSYQLLK ATEPGLFQGV AHNGEVRTAR LLRERDAKQ RLVLVLDKNG EPPRSATATL 660
 HVLLVDGFVF FYLLLPFAAP AQAQADLLTV YLVVALASVS SLFLPSVLLP VAVRLCRRSR 720
 AASVGRCSVP EGFPFGQMDV VSGTGTLSQS YQVEVCLTGG SGTNEPKFLK PIIPNFVAGG 780
 AERVSEAMP8 PRKSPEFT

Seq ID NO: 289 DNA sequence
 Nucleic Acid Accession #: NM_018674.1
 Coding sequence: 390..2009

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CGGAGCACAT GCTGAGCGGA GGGGCTGGGG CTGGCGGGCG TGGCGGAGCA GCGCTCGCTC 60
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GGCAGAGGCA GCACAGGGGC TGCGGAGCTG CTGGGAGTGG GAGTGACTCC CCCACCTCGG 240
GCCCCACGCC TGTCCCTGTC CTCTTCCCGC TTGCCCTGAG TTTAGAAGAG CAGCCGCTGC 300
CACCACTGCC ACTCGGGAGG GCACAGGGGC TGCTGGCTAG GGAGGGACAG GGCAGGGAGG 360
CTCTGGCCAG TCCAGCAGC CGGGGACAGA TGCCGATCGA GATTGTGTGC AAAATCAAAT 420
TTGCTGAGGA GGATGCGAAA CCCAAGGAGA AGGAGGCAGG GGATGAGCAG AGCCTCCTCG 480
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GCTTCCCGGC TGTACCCCTC TGCAATATCA ACCGCTTCCG GCATTGCGCA CTCAGCGATG 780
CCGACATCTT CCACCTGGCC AATCTGACAG GGTGCCCCC CAAAGACCGG GATGGGCACC 840
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ACCAGCTCGC CGACATGCTT AAGAGCTGCA ACTTCACTGG GCATCACTGC TCCGCCAGCA 960
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TTCCGGGTGA GTCCACAGC CAGGAGGAGC GCGCTACAT CCACAGCTG GGGTTGCGGG 1200
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GCCACTCGCG GATGGTGAC ATGCCAGGCA ATGAGACCAT CTGCCACCA AATATCTACA 1440
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GCCCCACCCC CTGCAACCTG ACACGCTATG GAAAGAGAT CTCCATGGTC AGGATCCCCA 1560
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AGAAGCTTCT GGTCTAGAT GTCTTCTTTG AGGCCCTGAC CTCTGAAGCC ATGAGCAGC 1680
GAGCAGCCTA TGGCTGTCA GCCCTGTGAG GAGACCTCG GGCACAGATG GGCCTGTTC 1740
TTGGGGCCAG CATCTCAGG TTGCTGGAGA TCCTCGACTA CATCTATGAG GTGTCCTGG 1800
ATCGACTGAA GGGGTATGG AGGCGTCCCA AGACCCCTCT GCGGACCTCC ACTGGGGGCA 1860
TCTCCACTTT GGGGCTTCAG AGCTGTAAGG AACAGAGTCC CTGCGCGAGC CTGGCCCGAG 1920
CGGAGGGTGG GGGGCTCAG AGTCTGTCC CCAATCAGCA CCAACCCAC GGTCCCCAG 1980
GAGGTCTCTT TGAAGATTTT GCTTGTCTAG ACGGTGCTGT GACTGAAAG ACCCAGGAGT 2040
CTGGGACCCC TCTGGGATC CCCAGCACAT TCTCTGTCTC CTGGGAGAGG CCTGGGGCG 2100
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GCTGCTTTGC ACAAAGGTCC TTCTGTGCTA CACCCCTTAT CCCCAGGCTG GTGCCCCGG 2220
AGGGCTGGAG ACCAGGCCAT GGGCCCTCAC GGAGAGGAAG GGAAGGAAGG AGAGGGAGGG 2280
GGAGGATAGA GCCATCCCA GCGGGGAGG GGGAGCCCTC TGTACATTTG TAAATATTTA 2340
GGGAAGCCG GGTGGGGGGA GGGGATACAG ATGTAGAGG TGGGTAGGGC TACAGGGGTG 2400
GGTGATTAG GACAGCCAG GGTCCAGCC CCAATGTGAG CAGGATAGGG AGAGCCCCAG 2460
GACTCAGGAG TGCTGGGCTG GTCTACTTTC CTGCCCCCTC CCAGGCCAGC CTCCCCCTT 2520
GGCAGGGGGA GAGGATGGCC CAGCAGGCTC GCGCCAGCTC CAGTTCGCC CTGCACAGC 2580
CCACCCCTTA GAGTCCCTTC TATAGGAGG GGGCAGGAGA CCTTCCAGAC TTCGCTGAG 2640
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TGCTGACGAG

Seq ID NO: 290 Protein sequence
Protein Accession #: NP_061144.1

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1 11 21 31 41 51
MPIEIVCKIK PAEEDAKPKE KEAGDEQSLI GAVAPGAAPR DLATFASTST LHGLGRACGP 60
GPHGLRRTLW ALALLTSLAA FLYQAAGLAR GYLTRPHLVA MDPAAPAPVA GPPAVTLNLI 120
NRFRLSALS ADIPLHLNLT GLPPKDRDGH RAAGLRYPEP DMVDILNRTO HQLADMLKSC 180
NFSGHEHCAS NFSVYVTRYG KCYTFNADPR SSLPSRAGGM GSGLEIMLDI QQBEYLPWR 240
ETNETSPFAG IRVQIHQEE PPYIHQLGFG VSPGFQTFVS CQEQLTYLF QPWGNCRAS 300
ELREPELQGY SAYSVSACRL RCEKEAVLQR CCRMVEMPG NETICPPNIY IECADHTLDS 360
LGGGPEGPGCF CPTPCNLTRY GKEISMVRIP NRGSARYLAR KYNRNETYIR ENFLVLVDFP 420
EALTSEAMEQ RAAVGLSALL GDLGGQMLF IGASILTLE ILDYIYEVSW DRLKRVNRRP 480
KTPLESTGG ISTLGLQELK EQSPCFSLGR ABGGVSSLL PNHRHPHPP GGLFEDFAC

Seq ID NO: 291 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 62..895

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1 11 21 31 41 51
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CAAGGATGGA ATTTTTCATA ACTCCATATG GCTTGAACGA GCAGCCGGTG TGTACCAAG 180
AGAAAGCAGG TCTGGCAAAT ACAAGCTCAC CTACGAGAA GCTAAGCGCG TGTGTGAATT 240
TGAAGCGCGC CATCTGCAA CTTACAAGCA GCTAGAGGCA GCCAGAAAAA TTGGATTTC 300
TGTCGTGTCT GCTGGATGGA TGGCTAAGGG CAGAGTTGGA TACCCCATG TGAAGCCAGG 360
GCCCACTGT GATTTTGGAA AAACCTGGCAT TATTGATTAT GGAATCCGTC TCAATAGGAG 420
TGAAGATGG GATCCCTATT GCTACAACCC ACACGCAAG GAGTGTGGTG GCGTCTTTAC 480
AGATCCAAAG CAAATTTTAA AATCTCCAGG CTTCCCAAT GAGTACGAG ATAACCAAT 540
CTGCTACGCG CACATTAGAC TCAAGTATGG TCAGCGTATT CACTCGATT TTTTAGATT 600
TGACCTTGA GATGACCCAG GTTGTCTGGC TGATTATGT GAAATATATG ACAGTTACGA 660
TGATGTCCAT GGTCTTGTGG GAAGATACTG TGGAGATGAG CTTCCAGATG ACATCATCAG 720
TACAGGAAAT GTCATGACCT TGAAGTTTCT AAGTGTATGT TCAGTGACAG CTGGAGGTTT 780
CCAAATCAAA TATGTTGCAA TGGATCTGT ATCCAAATCC AGCTGGAAGA TTAGCCACT TATAAAAAA 840
TACTACTTCT ACTGGAAATA AAAACTTTT AGCTGGAAGA TTAGCCACT TATAAAAAA 900
AAAAAAGGA TGATCAAAAC ACACAGTGT TATGTTGAA TCTTTTGGAA CTCCTTTGAT 960

5 CTCACGTGTA TTATTAACAT TTATTATTA TTTTCTAAA TGTGAAAGCA ATACATAATT 1020
 TAGGGAAAT TGGAAATAT AGGAAACTTT AAACGAGAAA ATGAAACCTC TCATAATCCC 1080
 ACTGCATAGA AATAACAAGC GTTAACATTT TCATATTTT TTCTTTCAGT CATTTTCTTA 1140
 TTTGTTGAT ATGTATATAT GTACCTATAT GTATTTCAT TGTAAATTTT GGAATCTCGC 1200
 TCTATGTACA GTTTGTATT ATACTTTTA AATCTTGAAC TTTATAAACA TTTTCTGAAA 1260
 TCATTGATTA TTCTACAAA ACATGATTTT AAACAGCTGT AAAATATTCT ATGATATGAA 1320
 TGTTTATGC ATTAATTTAAG CCTGTCTCTA TTGTGGGAAT TTCAGGTCAT TTTCAATAAT 1380
 ATTGTGCAA TAAATATCTT TGAACACACA AAAAAAAAAA AA

10 Seq ID NO: 292 Protein sequence
 Protein Accession #: Eos sequence

15 1 11 21 31 41 51
 MIILYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEP 60
 EGGLHATYKQ LEAARKIGPH VCAAGWMKAG RVGYPIVKPG PNCGPFGTKGI IDYGIRLNRS 120
 ERNDAYCYNP HAKECGGVFT DPKQIFKSPG FPNYEEDNQI CYWHIRLKYG QRIHLSPLDF 180
 DLEDDPGCLA DYVEIYDSYD DVEHGFVGRYC GDELFPDDIIS TGNVMTLKPL SDASVTAGGF 240
 QIKYVAMPDV SKSSQGRNTS TTSTGNKNFL AGRFSLH

20 Seq ID NO: 293 DNA sequence
 Nucleic Acid Accession #: NM_007115.1
 Coding sequence: 69..902

25 1 11 21 31 41 51
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 GGGGATTCAA GGTATGGAAT TTTTATAACT CCATATGGCT TGAACGAGCA GCCCGTGTGT 180
 ACCACAGAGA AGCACGGTCT GGCAAAATACA AGCTCACCTA CGCAGAAGCT AAGGCGGTGT 240
 GTGAATTGTA AGCGGCGCAT CTGCGCAACT ACAAGCAGCT AGAGGCGACC AGAAAAATTG 300
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 AGCCAGGGCC CACTGATGTA TTTGAAAAA CTGGCATTAT TGATTATGGA ATCCGTCTCA 420
 ATAGGAGTGA AAGATGGGAT GCCTATTGCT ACAACCCACA CGCAAGGAG TGTGGTGGCG 480
 TCCTTACAGA TCCAAAGCGA ATTTTAAAT CTCCAGGCTT CCCAAATGAG TACGAAGATA 540
 ACCAAATCTG CTACTGGCAC ATTAGACTCA AGTATGGTCA GCGTATTAC CTGAGTTTTT 600
 TAGATTTTGA CCTTGAAGAT GACCCAGGTT GCTTGGCTGA TTATGTTGAA ATATATGACA 660
 GTTACGATGA TTTCCATGGC TTTGTGGGAA GATACTGTGG AGATGAGCTT CCAGATGACA 720
 TCATCAGTAC AGGAAATGTC ATGACCTTGA AGTTTCTAAG TGATGCTTCA GTGACAGCTG 780
 GAGGTTTCCA AATCAAATAT GTTGCAATGG ATCCTGTATC CAAATCCAGT CAAGGAAAAA 840
 ATACAAGTAC TACTTCTACT GGAATAAATA ACTTTTATGC TGGAGATTT AGCCACTTAT 900
 AAAAAAATA AAGGATGATC AAAACACACA GTGTTTATGT TGGAACTTT TGGAACTCCT 960
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 TAATTTAGGG AAAATTGGAA AATATAGGAA ACTTTAAACG AGAAATGAA ACCTCTCATA 1080
 ATCCCATCTG ATGCAATAAT CAAGCGTTAA CATTTTCATA TTTTTCCT TCAGTCATT 1140
 TTGTATTGT GGTATATGTA TATATGTACC TATATGTATT TGCAATTGAA ATTTTGGAA 1200
 CCTGCTCTAT GTACAGTTTT GTATTATACT TTTTAAATCT TGAACCTTAT GAACATTTTC 1260
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50 Seq ID NO: 294 Protein sequence
 Protein Accession #: NP_009046.1

55 1 11 21 31 41 51
 MIILYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEP 60
 EGGLHATYKQ LEAARKIGPH VCAAGWMKAG RVGYPIVKPG PNKXFGTKGI IDYGIRLNRS 120
 ERNDAYCYNP HAKECGGVFT DPKRIFKSPG FPNYEEDNQI CYWHIRLKYG QRIHLSPLDF 180
 DLEDDPGCLA DYVEIYDSYD DVEHGFVGRYC GDELFPDDIIS TGNVMTLKPL SDASVTAGGF 240
 QIKYVAMPDV SKSSQGRNTS TTSTGNKNFL AGRFSLH

65 Seq ID NO: 295 DNA sequence
 Nucleic Acid Accession #: NM_001218.2
 Coding sequence: 116..1180

70 1 11 21 31 41 51
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 CAGCCCGCGC CCAGTGAACG GTTCCAAGTG GACTTATTTT GGTCTGATG GGGAGAAATG 240
 CTGGTCCAGG AAGTACCCGT CGTGTGGGGG CCTGCTGCGA TCCCCATAG ACCTGCACAG 300
 TGACATCTCT CAGTATGAGC CCAGCCTCAC GCCCTCGAG TTCCAAGGCT ACAATCTGTC 360
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 CCGGGGATTC AACATTGAAG AGCTGCTTCC GGAGAGGACC GCTGAATATT ACCGCTACCG 780
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5 GGACGACCCT TCCCCAGAG AAATGATCAA CAACTTCCGG CAGGTCCAGA AGTTGATGA 960
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 15 AGAAAAAGA AAACAGAGA TATACATTGT GATATATTAG GGACACTTTC ACAGTCTGCT 1800
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 TCTGGGAGAG TCTCACTTTG GAATCAGAAT TGGAAATACA TTCTGTTTAT CAAGCCATAA 1980
 20 TGTAAGGACA GAATAATACA ATATTAAGTC CAAATCCAAC CTCCTGTCTG TGGAGCAGTT 2040
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 25 CTGAAGATGT CAAATGCTGG TTTAGATCAA ATATATTTCA AGCTATAAAA GCAGGAGGTT 2340
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 30 GACAGCATGA AATGCTCTCT TGAAGCATAG CTTTTTAAAT ATCTTTTCC TTCTACTCTCT 2640
 CCCTCTGACT CTAAGAATTC TCTCTCTG AATCGCTTGA ACCCAGGAGG CGGAGGTTGC 2700
 AGTAAGCCAA GGTCAATGCA CTGCACTCTA GCCTGGGTGA CAGAGCGAGA CTCATCTCA 2760
 AAAAAA AAAA

Seq ID NO: 296 Protein sequence
 Protein Accession #: NP_001209.1

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 HWGNPNPDPHG SEHTVSGQHF AAEHLHVHYN SDLYPDASTA SNKSEGLAVL AVLIEMGSPFN 180
 PSYDKIFSHL QHVYKYGQBA FVPGFNIEEL LPERTAERYR YRGLSLTPPC NPTVLMTVFR 240
 NPVOISQEQGL LALETALYCT HMDDPSPREM INNFRQVQKF DERLVTSTFS QVQVCTAAGL 300
 SIGIILSLAL AGILGICIVV VVSIWLFRK SIRKGDNRKV IYKPKMT EABA

Seq ID NO: 297 DNA sequence
 Nucleic Acid Accession #: NM_006632.1
 Coding sequence: 377..1582

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 GACAAGAGA CCGCATCAT CCTGCGCCAC CTGTAGCTGG CCATTGCGAA CGGCGAGGAG 180
 55 CTTAACAAGC TGCTGGGCGA AGTCACCATC GCGCAGGGCG GTGTCTGTGC CAACATTTCAG 240
 GCGGTGCTTC TGCCCCAGAA GACCAAGAGC CACCACAGG CCAAGGGTGA AAACATTCA 300
 CTAGGAGAGG AGAAACACAA TGGCCACCAA GACAGAGTTG AGTCCACAG CAAGGGAGAG 360
 CAGAACGCA CAGATATGC AAGTGGATGA GACACTGATC CCCAGGAAAG GTCCAAGTTT 420
 60 ATGTTCTGCT CGCTATGAA TAGCCCTCGT CTTACATTTC TGCAATTTCA CAACGATAGC 480
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 CCAGCTCAAT GATTCCTCTG AGGTGCTGCC TGTGACTCA TTTGGTGGCC TAAGTAAAGC 600
 CCAAGAGAT CTTCCTGCAA AGTCTCAAT ACTTGGGGGT CAGTTTGCAA TTTGGGAAAA 660
 GTGGGGCCCT CCACAAGAAC GAAGCAGACT CTGCAGCATT GCTTTATCAG GAATGTTACT 720
 65 GGGATGCTTT ACTGCCATCC TCATAGGTGG CTTCAATAGT GAAACCCCTG GGTGGCCCTT 780
 TGTCTTCTAT ATCTTTGGAG GTGTTGGCTG TGTCTGCTGC CTTCTCTGGT TTTGTGTGAT 840
 TTATGATGAC CCTTTTCTCT ATCCATGGAT AAGCACTCA GAAAAAGAA ACATCATATC 900
 CTCTTGAA CAACAGGTGG GGTCTTCTAA GCAGCCTCTT CCATCAAG CTATGCTCAG 960
 ATCTCTACCC ATTTGGTCCA TATGTTTAGG CTGTTTCAGC CATCAATGGT TAGTTAGCAC 1020
 70 AATGGTTGTA TACATACCAA CTTACATCAG CTCTGTGATC CATGTTAACA TCAGAGACAA 1080
 TGGACTCTTA TCTGCCCTTC CTTTATTGT TGCCTGSGTC ATAGGCATGG TGGGAGGCTA 1140
 TCTGGCAGAT TTCTTCTAA CCAAAAGTT TAGACTCATC ACTGTGAGGA AATTGCCAC 1200
 AATTTTAGGA AGTCTCCCTT CTTGAGCACT CATGTGTCT CTGCTTACC TCAATCCGG 1260
 CTATATCACA GCAACTCGCT TGCTGACGCT CTCCTGCGGA TTAAGCAGT TGTGTCACT 1320
 75 AGGGATTAT ATCAATGTCT TAGATATGCT TCCAAGGAT TCCAGTTTC TCATGGGAGC 1380
 ATCAAGAGGA TTTTGGAGCA TAGCACCTGT CATGTACCC ACTGTGACCG GATTCTCTCT 1440
 TAGTCAGGAC CTTGAGTTTG GGTGGAGGAA TGTCTTCTC TTGCTGTTG CCGTTAACCT 1500
 GTTAGGACTA CTCTTCTACC TCATATTTGG AGAAGCAGAT GTCCAAGAA GGGCTAAGA 1560
 GAGAAACTC ACTCGTTTAT GAAGTTATCC CACCTTGGAT GGAAGAGTCA TTAGGCACCG 1620
 80 TATTGCATAA AATAGAAGGC TTCCGTGATG AAAATACCAG TGAAGAGATT TTTTCTCT 1680
 GTGGCTCTTT TCAATTATGA GATCAGTTCA TTATTTTATT CAGACTTTT TTTGAGGAA 1740
 ATGTAAGATG AATAAAAT CAAATAAAT GATAACTAAG AAAAAA AAAA

Seq ID NO: 298 Protein sequence
 Protein Accession #: NP_006623.1


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1      11      21      31      41      51
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      MQVDLTIPR  KGPSLCSARY  GIALVLHFCN  FTTIAQNVIM  NITMVMVNS  TSPOSQNLDS  60
      SEVLFPVDSFG  GLSKAPKSLP  AKSSILGGQF  AIWEKMGPPQ  ERSRLCSIAL  SGMILLGCPTA  120
      ILIGGFISET  LGWPFVIFYIF  GGVGCVCCLL  MFVVIYDDPF  SYFWISTSEK  EYIISSLKQQ  180
      VGSSKQPLPI  KAMLRSLPIW  SICLGCPSHQ  WLVTMVMVYI  PTYISSVYHV  NIRDNGLLSA  240
      LFFIVANVIG  MVGGYLADFL  LTKKFLRITV  RKIATILGSL  PSSALIVSLP  YLNSGYITAT  300
      ALLTLSCGLS  TLCQSGIYIN  VLDIAPRYSS  FLMGASRGFS  SIAPVIVPTV  SGFLLSQDPE  360
10     FQWRNVFFLL  FAVNLLGLLP  YLIFGEADVQ  EMAKERKLTR  L

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Seq ID NO: 299 DNA sequence

Nucleic Acid Accession #: NM_003058.1

Coding sequence: 145..1812

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      GGGTTTGTGC  TGAGCTGGCT  GCAGCCGCTC  TCAGCCTCGC  TCGGGCACG  TCGGGCAGCC  120
      TOGGGCGCTC  CTGCCCTGCG  GATCATGCC  ACCACCGTGG  ACGATGTCT  GGAGCATGGA  180
      GGGGAGTTTC  ACTTTTTCCA  GAAGCAAATG  TTTTCTCTCT  TGGCTCTGCT  CTGGCTACCC  240
      TTGCGGCCCA  TCTACGTGGG  CATCGTCTTC  CTGGGCTTCA  CCTCTGACCA  CCGCTGCGGG  300
      AGCCCGCGAG  TGGCGAGCT  GAGTCTGCGC  TGGGCTGGA  GTCTGCAGA  GGAACGTAAAC  360
      TACAGGTGCG  CGGGCCAGG  ACCTGCGGGC  GAAGCCTCCC  CAAGACAGTG  TAGGCGCTAC  420
      GAGGTGGACT  GGAACGAGG  CACCTTTGAC  TGGGTGGACC  CCTGGGCCAG  CCGTGGACCC  480
      AACAGGAGCC  GCGTCCACT  GGGCCCTGCG  CGGAGCGGCT  GGGTGTACGA  GAGCCTGGCC  540
      TCGTCCATCG  TCACGAGTGT  TAACCTGGTA  TGTGCCAACT  CCTGGATGTT  GGACCTATTG  600
      CAGTCATCAG  TGAATGTAGG  ATTCTTATT  GGCTCTATGA  GTATCGGCTA  CATAGCAGAC  660
      AGGTTTGGCC  GTAAGCTCTG  CCTCCTAACT  ACAGTCTCCA  TAAATGCTGC  AGCTGGAGTT  720
      CTCTAGGCCA  TTTCCCCAAC  CTATAGCTGG  ATGTTAATTT  TCGCTTAAT  CCAAGGACTG  780
      GTCAGCAAG  CAGGCTGGTT  AATAGGCTAC  ATCCTGATTA  CAGAATTTGT  TGGGCGGAGA  840
      TATCGAGAA  CAGTGGGGAT  TTTTACCAA  GTTGCCCTATA  CAGTTGGGCT  CCGTGTGCTA  900
      GCTGGGGTGG  CTTAGCCTCT  TCCTCACTGG  AGGTGGTGGC  AGTTCACAGT  TGCTCTGCCC  960
      AACTTCTTCT  TCTTGTCTTA  TTACTGGTGC  ATACCTGAGT  CTCCAGGTG  GCTGATCTCC  1020
      CAGAAATAAG  ATGCTGAAGC  CATGAGAATC  ATTAAGCACA  TCGCAAGAA  AAATGGAAAA  1080
      TCTCTACCCG  CCTCCCTTCA  GCGCCTGAGA  CTGGAAGAGG  AAAGTGGCAA  GAAATGGAAC  1140
      CCTTCATTTC  TTGACTTGGT  CAGAACTCCT  CAGATAAGGA  AACATACTAT  GATATTGATG  1200
      TACAACGGT  TCACGAGCTC  TGTGCTCTAC  CAGGGCCTCA  TCATGCACAT  GGGCCTTGCA  1260
      GGTGACAATA  TCTACTCGGA  TTTCTTCTAC  TCTGCCCTGG  TTGAATTCCT  AGCTGCTTCC  1320
      ATGATCATCC  TCACCATCGA  CCGCATCGGA  CGCGTTTACC  CTGGGCTGCG  ATCAAAATATG  1380
      GTTGAGGGG  CAGCCTGTCT  GGCCTCAGTT  TTTATACCTG  GTGATCTACA  ATGGCTAAAA  1440
      AATTATTATCT  CATGCTTGGG  AAGAAATGGG  ATCACAATGG  CCTATGAGAT  AGTCTGCTGG  1500
      GTCAATGCTG  AGCTGTACCC  CACATTCAAT  AGGAATCTTG  GCGTCCACAT  CTGTTCTCTA  1560
      ATGTGTGACA  TTGGTGGCAT  CATCAGCCCA  TTCTGTGTCT  ACCGGCTCAC  TAACATCTGG  1620
      CTTGAGCTCC  CGCTGATGGT  TTTGCGGCTA  CTGGGCTTGG  TTGCTGGAGG  TCTGGTGTCTG  1680
      TTGCTTCCAG  AAATCAAGAG  GAAAGCTTTG  CCTGAGACCA  TCGAGGAAGC  CGAAATATATG  1740
      CAAAGACCAA  GAAAAAATAA  AGAAAAAGATG  ATTTACCTCC  AAGTTCAGAA  ACTAGACATT  1800
      CCATTGAAC  AAGAAGAGAG  ACCGTTGCTG  CTGTCTATGAC  CTAGCTTTGA  TGGCAGCAAG  1860
      ACCAAAGATA  GAAATCCCTG  CACTCATCAC  AAAGCCCAT  CACTCAACC  AAATTAACCC  1920
      CTGAGCCCTA  TCACCTAGG  TCTACAGCCA  GTGGAGTCTA  TTGTACACTG  TGGAAAAATA  1980
      CCCATGGGAC  CAGATCCTGC  CAAATCTTTC  CAGCTCACTT  TATTCTCAGC  ATTCTTAGGA  2040
      CATGTGACAT  TGGTTTCTG  GAGGGTTTTT  TTTCTGATCT  TTGTATTTTT  TTAATTTTGA  2100
      TTCTTTTCTT  TGCATGTCTA  GCAACAGAA  TACATAGGGG  AACTGTGGGC  TAGGCAANA  2160
      AAATAGAAAA  AGTGTGAAAA  ACAGTAAAGT  TGGGAGAGGA  GCATCTATTT  TCTTAAAGAA  2220
      ATAAACACC  NAAAAACAAA  AAAAAA

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Seq ID NO: 300 Protein sequence

Protein Accession #: NP_003049.1

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60     1      11      21      31      41      51
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      LRCGWSPAEE  LNYTVPGPG  AGEASPRQR  RYEVWNQST  FDCVDPLASL  DTNRSRLPLG  120
      PCRDGWVYET  PGSSIVTEFN  LVCANSWMLD  LFQSSVNVGF  FIGSMSIGYI  ADRPGRKLCL  180
      LTTVLINAAA  GVLMAISPTY  TWMLIFRLIQ  GLVSKAGWLI  GYILITEFVG  RRYRRTVGIF  240
      YQVAYTVGLL  VLAGVAYALF  HWRNLQFTVA  LFNFPFLYY  WCIPESPRWL  ISQNKNAEAM  300
      RIHKHIAKKN  GKSLPASLQR  LRLEBETGKK  LNPSFLDLVR  TPQIRKHTMI  LMYNWFSSV  360
      LYQGLIMBMG  LAGDNIIYLF  FYSALVEFPA  AFMIILTIDR  IGRYPNAAS  NMVAGAACLA  420
      SVPIPGDLQW  LKIIISCLGR  MGIIMAYEIV  CLVNAELYPT  FIRNLGVHIC  SSMCDIGGII  480
      TPLVYRLTN  IMLELPLMVF  GVLGLVAGGL  VLLLPETKYG  ALPETIEEAE  NMQRPRKNKE  540
      RMIYLVQVKL  DIPLN

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Seq ID NO: 301 DNA sequence

Nucleic Acid Accession #: NM_012206.1

Coding sequence: 52..1131

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      CAAGTGGTCA  TCTTAAGCCT  CATCTACAT  CTGGCAGATT  CTGTAGCTGG  TTCTGTAAAG  120
      GTTGGTGGAG  AGGCAGGTCC  ATCTGTACCA  CTACCTGCCC  ACTACAGTGG  AGCTGTACCA  180
      TCAATGTGCT  GGAATAGAGG  CTCATGTCTT  CTAATCACAT  GCCAAAAATG  CATTGTCTGG  240
      ACCAATGGAA  CCCAGCTCAC  CTATCGGAAG  GACACACGCT  ATAAGCTATT  GGGGGACCTT  300
      TCAAGAAGGG  ATGTCTCTTT  GACCATAGAA  AATACAGCTG  TGTCTGACAG  TGGCGTATAT  360

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5 TGTGCGCGT TTGAGCACCG TGGGTGGTTC AATGACATGA AAATCACCGT ATCAITGGAG 420
 ATTGTGCCAC CCAAGGTCAC GACTACTCCA ATTGTACAA CTGTTCCAAC CGTCACGACT 480
 GTTCGAACGA GCACCACTGT TCCAACGACA ACGACTGTTT CCAAGACAAC TGTTCCACAA 540
 ACAATGAGCA TTCCAACGAC AAGACTGTT CCGACGACAA TGACTGTTTC AAGCACAACG 600
 AGCGTTCCAA CGACAACGAG CATTCACAACA ACAACAAGTG TTCCAGTGAC AACACAACGTC 660
 TCTACCTTTG TTCTCCAAT GCCTTTGCCC AGGCAGAAC ATGAACCGT AGCCACTTCA 720
 CCATCTTCAC CTCAGCCAGC AGAAACCCAC CCTACGACAC TGCAGGGAGC AATAAGGAGA 780
 GAACCCACCA GCTCACCAT GTACTCTTAC ACAACAGATG GGAATGACAC CGTGACAGAG 840
 10 TCTTCAGATG GCCTTTGGAA TAACAATCAA ACTCAACTGT TCCTAGAACA TAGTCTACTG 900
 ACGGCCAATA CCATCAAGG AATCTATGCT GGAGTCTGTA TTTCTGCTT GGTGCTTCT 960
 GCTCTTTTGG GTGTCATCAT TGCCAAAAG TATTTCTCA AAAAGGAGGT TCAACAACTA 1020
 AGTGTTCAT TTAGCAGCT TCAAAATAAA GCTTTGCAAA ATGCAGTTGA AAAGGAAGTC 1080
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 15 GTGCTCTTG AGAGTTTACG CCGATGACTG CAGAAGACTG AACAGGTATC AGCAGCATCAG 1200
 ATGTCTTTA GACTCCAAGA CAATTTTCT GTTTCAGTTT CATCTGGCAT TCCACATGT 1260
 CAGTGATACT GGTAGAGTA ACTCTCCAC TCCAAACTGT GTATAGTCAA CCTCATCAT 1320
 AATGTAGTCC TAAATTGTTT TGCTAAACT GCGTCAATCC TTCTGATCAT TGCAGAGTTT 1380
 TCTCTCAAC ATGAACACTT TGAATTGTA TGTTCTCTT AGACCCATA AATCTGTAT

20 Seq ID NO: 302 Protein sequence
 Protein Accession #: NP_036338.1

25 1 11 21 31 41 51
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 IVWNGTHVY YRKDTRYKLL GDLSRRDVS L TIENAVSDS GVYCCRVEHR GWFNDMKITV 120
 SLEIVPFKVT TPIVITVPT VTVRTSTTV PTTTVPVPT VPTTMSIPT TTVPTMTVS 180
 TTSVPTTTS IPTTSTVPT TTVSTFVPM PLPRQNHVP ATSPSPQPA ETHEPTLQGA 240
 30 IRRPTSSPL YSYTTDNDT VTSSDGLWN NNQTLFLEH SLTANTTKG IYAGVCISVL 300
 VLLALLGVII AKKYFPKKEV QQLSVSFSSL QIKALQNAVE KEVQARDNIY IENSLYATD

Seq ID NO: 303 DNA sequence
 Nucleic Acid Accession #: NM_001044.1
 Coding sequence: 129..1991

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 40 GTGTGCCCAT GAGTAAGAGC AATGCTCCG TGGACTCAT GTCTTCGGT GTGGCCCCGG 180
 CTAAGGAGCC CAATGCGGTG GCGCCGAAG AGGTGGAGCT CATCTTGTG AAGGAGCAGA 240
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 AGGATCGGGA GACCTGGGCG AAGAAGATCG ACTTCTCTCT GTCCGTCTT GGCCTTGCTG 360
 45 TGGACCTGGC CAACGCTGGG CGGTTCCCTT ACCTGTGCTA CAAAATGGT GCGGTGCTG 420
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 TCATCATGCG CTGGGGCGTG CACTATCTCT TCTCTCTCT CACCAGGAG CTCCCTGGA 660
 50 TCCAGTCAA CACTCCTCG AAGAGCCCCA ACTGCTCGGA TGCCCATCT GGTGACTTCA 720
 GTGAGTCAAG CTCGGGCTC AAGCAGACTT TTGGGACCA ACCTGCTGCC GAGTACTTTG 780
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 GCGAGCTCAC AGCTCGCTGT GTGCTGGTCA TCGTGTGCT CTACTTCAGC CTCTGGAAGG 900
 GCGTGAAGAC CTCAGGAAG GTGATATGGA TCACAGCCAC CATGCCATAC GTGGTCTCA 960
 55 CTGCGCTGCT CCGCGTGGG GTACCCCTCC CTGAGCCAT AGACGCGATC AGACATACC 1020
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 60 CCATCGGGGA CGTGCCCAAG GACGGGCCAG GGTGATCTT CATCATCTAC CCGGAAGCCA 1320
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 65 TCTGTCTCT GTTCTGCTG TCACACGCTG GCATCTACGT CTTCACTGCT CTGACCAT 1560
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 70 ACGCGCTGGG CTGGGTCATC GCCACATCTT CCATGGCCAT GGTGCCATC TATGCGGCT 1860
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 75 TCOGTGCGG GAGCGCACT GCGCGTGTCT TGTGTTGCTG TAATAACGAC GTAGTCTGT 2220
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5 AGGAGCATGT CCTATCCCTG GACGCATGCA GGGCCCCCAC AGGAGCGTGT ACTACCCAG 2880
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 15 GCGTGTGAAC TGCCAGGCAG CTGCAGTTAG CACAGAGGAT GGCTTCCCA TTGCTTCTG 3660
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 GTTGTGTTAG CACAGCAGCA GAGCGGCTTC CCCATCGCCT TCTGGGAGG GGCTCGGTG 3840
 AGCAACCCAG GTGTGTCTCG TGTCTGTGA CCAATCTCTA TTCAGCATCG TGTGGGTCCC 3900
 20 TAAGCAAT AAAAGACATC CACAATGGAA AAAAAAAG GAATTC

Seq ID NO: 304 Protein sequence
Protein Accession #: NP_001035.1

25 1 11 21 31 41 51
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 ETWGGKIDPL LSVIGFAVDL ANVWRFPYLC YKNGGGAFV PYLLFMVIAG MPLFYMELAL 120
 GGFNREGAAG VVKICPILKG VGFTVILISL YVGFYFNVII AMALHYLFSS FTTELPMIHC 180
 30 NNSWNPNCNS DAHPDSSGSD SSGINDTFGT TPAAEYFERG VLHLHQSHGI DDLPFRWQL 240
 TACLVLVLVL LYFSIWKGVK TSGKVVWITA TMPYVVLTA LRGVTLPGA IDGIRAYLSV 300
 DFLRLCEASV WIDAATQVCF SLGVGPGVLI AFSSYNKPTN NCRDAIVTT SINSLTSPSS 360
 GPFVPSFLGY MAQKHSVPIG DVAKDGPGLI FIYPEAIAT LPLSSAWAVV PFIMLLTLGI 420
 DSAMGGMSBV ITGLIDEFQL LHRHRELFIL FIVLATFLLS LFCVTNGGIY VFLLDHPFAA 480
 35 GTSILFGLVI BAIGVAFYFG VQGFSDDIQ MTQQRPSLYW RLCWKLVSFC PLLFVVVSVI 540
 VTFRPPHYGA YIFPDWANAL GWVIATSSMA MVPIYAAKPF CSLPGSFREK LAYAIAPKED 600
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Seq ID NO: 305 DNA sequence
Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

45 1 11 21 31 41 51
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 CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCAGAGGTG TGCCCCGGAT GCAGGAGGAT 180
 TCCCCCTGG GAGGAGGCTC TTCTGGGGAA GATGACCCAC TGGGCGAGGA GGATCTGCCC 240
 AGTGAAGAGG ATTCACCCAAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG 300
 GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAATCAGA AGAAGAGGGC 360
 50 TCCTCAAGT TAGAGGATCT ACCTACTGTT GAGGCTCTG GAGATCCTCA AGAACCCAG 420
 AATAATGCC ACAGGACCAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCGAC 480
 CGCGCTGGC TCGCGGTGTC CCCAGCTGC GCGGGCGGCT TCCAGTCCCC GGTTGATATC 540
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 55 CTTCTGGGC TAGAGATGGC TCTGGGTCCC GGGCGGGAGT ACCGGGCTCT CGAGCTGCAT 720
 CTGCACTGGG GGGCTGCGAG TCGTCCGGGC TCGGAGCACA CTGTGGAAGG CCACCGTTTC 780
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 60 CAGTCCCGAG GACTGGACAT ATCTGCATC CTGCCCTCTG ACTTCAGCGG CTACTTCCAA 1020
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 CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCTCT CTGACACCT GTGGGGACCT 1140
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 GAGGCTCTCT TCCTGCTGAG AGTGGACAGC AGTCTCTGG CTGCTGAGCC AGTCCAGCTG 1260
 65 AATTCTGTCC TGGCTGCTGG TGACATCCTA GCGCTGGTTT TTGGCTCCT TTTTGTCTG 1320
 ACCAGCGTGG CGTCTCTTGT GCAGATGAGA AGGCAGCACA GAAGGGGAAC CAAAGGGGGT 1380
 GTGAGCTACC GCCCAGCAGA GGTAGCGAG ACTGGAGCCT AGAGGCTGGA TCTTGAGAA 1440
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 70 ATGCCACTTC CTTTAACTG CCAAGAAATT TTTTAAATA AATATTATA AT

Seq ID NO: 306 Protein sequence
Protein Accession #: NP_001207.1

75 1 11 21 31 41 51
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 GEEDLPSEED SPREDPPGE EDLPGBEDLP GEEDLPVVKP KSEEEGSLKL EDLPTEAPG 120
 DPQEPQNAH RDKGGDQSH WRYGGDPWP RVSPACAGRF QSPVDIRPQL AAPCPALRFL 180
 80 ELLGFPQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT 240
 VEGHRFPAEI HVVHLSTAPA RVDEALGRPG GLAVLAAPLE EGPEENSAYE QLLSRLEBIA 300
 EGGSETQVPG LDISALLPSD PERYPQYEGS LTPFPACQV IWTVPNTVM LSAQLHTLS 360
 DTLMPGDGR LQLNFRATOP LNRGVIBASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF 420
 GLLFAVTSVA FLVQMRQRH RGTKGGVSYSR PAEVAETGA

Seq ID NO: 307 DNA sequence
Nucleic Acid Accession #: NM_003039.1
Coding sequence: 76..1581

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GTGCTTGCCC TGGCAACCCCT GATAGCTGCC TTTGGGTGCT CCTTCCAGTA TGGGTACAAC 180
GTGGCTGCTG TCAACTCCCC AGCACTGCTC ATGCAACAAT TTTACAATGA GACTTACTAT 240
GGTAGGACCG GTGAATTTCAT GGAAGACTTC CCCTTGACGT TGCTGTGGTC TGTAAACGCTG 300
TCCATGTTTC CATTGGGAGG GTTTATCGGA TCCCTCCTGG TCGGCCCTTT GGTGAATAAA 360
TTGGGCAGAA AAGGGGCTT GCTGTTCAAC AACATATTTT CTATCGTGCC TGCGATCTTA 420
ATGGGATGCA GCAGAGTCGC CACATCATTT GAGCTTATCA TTTATTTCCAG ACTTTTGGTG 480
15 GGAATATGTG CAGGTGTATC TTCCAACGTG GTCCCATGT ACTTAGGGA GCTGGCCCTT 540
AAAAACCTGC GGGGGGCTCT CGGGGTGGTG CCCAGCTCT TCATCACTGT TGGCATCCTT 600
GTGGCCAGAA TCCTTGGTCT TCGGAATCTC CTTCGAAACG TAGATGGCTG TGCGATCCTT 660
CTGGGGCTGA CCGGGGTCCC CGCGGCGCTG CAGCTCCTTC TGCTGCCCTT CTTCCCGAG 720
AGCCCCAGGT ACCTGCTGAT TCAGAAGAAA GACGAAGCGG CCGCCAGAA AGCCCTACAG 780
20 AGCTGCGCGG GCTGGGACTC TGTGACAGG GAGGTGGCGG AGATCCGGCA GGAGGATGAG 840
GCAGAGAAGG CCGGGGCTT CATCTCCGTG CTGAAGCTGT TCCGGATGCG CTCGCTGCGC 900
TGGCAGCTGC TGTCCATCAT CGTCTCATG GCGGCGCAGC AGCTGTGCGG CGTCAACGCT 960
ATCTACTACT ACGCGACCCA GATCTACCTG AGCGCCGGCG TGCCGGAGGA GCACGTGCAG 1020
TACGTACAGG CCGGCACCGG GGCCTGAAC GTGGTCAATG CCTTCTGCGC CGTGTTCGTG 1080
25 GTGAGCTCC TGGTTCGGAG GCTGCTGCTG CTGCTGGGCT TCTCCATCTG CCTCATAGCC 1140
TGCTGCGTGC TCACGTGACG TCTGGCACTG CAGGACACAG TGCTCTGGAT GCCATACATC 1200
AGCATCGTCT GTGTCTCTC CTACGTCATA GGACATGCCC TCGGGCCAG TCCCATACCC 1260
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30 GGCAGTGTGC ACTGGCTCTC CAATCTCACC GTGGGCTTGA TCTTCCGCTT CATCCAGGAG 1380
GGCCTCGGCC CGTACAGCTT CATTGTCTTC GCGGTGATCT GCCTCCTCAC CACCATCTAC 1440
ATCTTCTTGA TTGTCCCGGA GACCAAGGCC AAGAGCTTCA TAGAGATCAA CCAGATTTTC 1500
ACCAAGATGA ATAAGGTGTC TGAAGTGTAC CCGGAAAAGG AGGAACTGAA AGAGCTTCCA 1560
CCTGTCACTT CGGAACAGTG ACTCTGGAGA GGAAGCCAGT GGAGCTGGTC TGCCAGGGGC 1620
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40 GTAAAGTGGC TCCACCTTGA TGGGTCAACC TTGTGTGGC TCCTGGTAA CATAACACAA 1920
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GATCCTTTTC CAGAAATACC TGTCTAGGAA GGTGTGATGT CAGAAACAT GACATCCAGA 2100
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45 Seq ID NO: 308 Protein sequence
Protein Accession #: NP_003030.1

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1 11 21 31 41 51
| | | | |
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FMEDPFLTL LWSVTSMFPF GGFISGLLVG PLVNFGRKRG ALLFMNIFSI VPAILMGCSR 120
VATSFELIII SRLLVGICAG VSSNVVPMYL GELAPKRLRG ALGVVPQLFI TVGILVAQIF 180
GLRNLLANVD GWPILLGITG VPAALQLLLL PFFPESPRYL LIQKIDBAAA KXALQTLRGW 240
DSVDREVAEI RQDEAEAKAA GFISVLKLFMR MSLRWQLLS IIVLMGGQQL SGVNAIYYIA 300
55 DQIYLSAQVP EEHVQYVTAG TGAIVNVMTF CAVFVVELLG RRLILLGFS ICLIAACVLT 360
AALALQDTSV WMPYISIVCV ISYVIGHALG PSPIPALLIT EIFLQSSRFS AFMVGGSVHW 420
LSNFTVGLIF PFIQBLGPHY SPVIFAVICL LTIYIYFLIV PETKAKTPIR INQIFTRMK 480
VSEVYFEKEE LKELPPVTSE Q
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60 Seq ID NO: 309 DNA sequence
Nucleic Acid Accession #: NM_001252.1
Coding sequence: 138..719

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70 TGGTGTGCAT CCAGCGCTTC GCACAGGCTC AGCAGCAGCT GCGGCTGAG TCACTTGGGT 300
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GGCAGGGGGG CCCAGCACTG GGCCTCTCCT TCTGCTATGG ACCAGAGCTG GACCAAGGGC 420
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GCTCCTCCAC GACGCGCTCC AGGCACCAAC CCACCACCTT GGCCGTGGGA ATCTGCTCTC 540
75 CCGCTCTCCG TAGCATAGC CTGCTGCGTC TCAGCTTCCA CCAAGGTTGT ACCATTGCCT 600
CCCAGCGCTT GACGCGCTG GCGCGAGGGG ACACACTCTG CACCAACCTC ACTGGGACAC 660
TTTTGCCTTC CGAAACACT GATGAGACCT TCTTTGGAGT GCAGTGGGTG CGCCCTGAC 720
CACTGCTGCT GATTAGGGTT TTTTAAATTT TATTTTATTT TATTTAAGTT CAAGAGAAA 780
80 AGGTACACAG CAGGGGCCAC CCGGGGTGGG GGTGGGAGTG TGGTGGGGG TAGTGGTGGC 840
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Seq ID NO: 310 Protein sequence
Protein Accession #: NP_001243.1

1 11 21 31 41 51
 5 MPEBGSQCSV RRRPYGCVLR AALVPLVAGL VICLVVCIQR FAQAQQQLPL ESLGWDVAEL 60
 QLNHTGPOQD PRLYVQGGPA LGRSFLHGPE LDKQLRIHR DGIYVHIVQV TLAICSSTTA 120
 SRHHPTTLAV GICSPASRSI SLLRLSPHQG CTIASQLRTP LARGDTLCTN LTGTLPLPSRN 180
 TDETFFGVQW VRP

Seq ID NO: 311 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..3978

1 11 21 31 41 51
 15 ATGTGTGGTG AAGGACCCTA CCTTATCTCA GATCTGGACC AGCGAGGCCG GCGGAGATCC 60
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 AGCCCGGTGA TGGTGAAAGG CTACCGGCAA AGGCTGAOCG TAGACACCCG GCCCCATTG 240
 TCGACATATG ACTCATCTGA CACCAATGCC AAAAGATTTC GAGTCCTTTG GGATGAAGAG 300
 GTAGCAAGGG TGGTCTCTGA GAAGGCTCT CTGAGCCACG TGGTGTGAAA ATTCCAGAGG 360
 20 ACACGCGTGT TGATGGACAT CGTGGCCAAAC ATCTGTGCA TCATCATGGC AGCCATAGGG 420
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 GCCCTTGCCCT GGGCCATCAA CTACCGCAG GCCATCCGGT TGAAGGTGGC GCTCTCCACC 600
 25 TTGGTTTTTG AAAACCTAGT GTCTTCAAG ACATTGACCC ACATCTCTGT TGGGAGGTG 660
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 35 ATGGCTGAAG CGAATGTCTC TCTAAGGAGA ATGAAGAAAA TTCTCATAGA TAAAGGCCCC 1260
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 AGGCATTATC TGGCAAAACA GAGGTGAGAG GCATACAGTG AGAGGAGTCC ACCAGCCAAG 1440
 GGAGCCACTG GCCCAGAGGA GCAAGTGAC AGCCTCAAAT CGGTTCTGCA CAGCATAAAC 1500
 40 TTTGTGGTGA GAAAGTTATG TCGTTATCCC GAAGCCGAGC TCCTGGCTTG GAGGTGGCCA 1560
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 45 ACTTTGSCCT ACGTTTCA CAAGGCTAGG ATCTTTCATG GAAATGTGAG AGAAACATA 1860
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 50 TTTGAGGAGT GCATTAGAA GACGCTCAGG GGAAGACAG TCGTCTGTGT GACCCACCAG 2160
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 ACTGCAAGCA TGGTGTTCAT GCTGGTGTG GCGTCAOCA AAGGCTTGT CTTCACCAAG 2640
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 60 CCAATGAGTT TCTTTGACAC GACTCCCACT GGCAGGCTAA TGAACGGTT TTCCAAGGAT 2760
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 65 CAGGGCCTGG GCATCATTC ACGCTATGGC AAGAAGGAGA GCTGCATCAC CTATACTTCA 3060
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 TCGACCTGTG TTCTGAATG CACTCATCCC CTCAAAGTGG GGAACCTGTC CAAGGACTGG 3240
 CCCAGCTGTG GGGAGATCAC CTTGAGAGAC TATCAGATGA GATACAGAGA CAACACCCCC 3300
 70 CTTGTCTCTG ACAGCCTGAA CTTGAACATA CAAAGTGGGC AGACAGTCGG GATTGTTGGA 3360
 AGAACAGGTT CCGGAAAGTC ATCGTTAGGA ATGGCTTTGT TTCGTCTGTT GGAGCCAGCC 3420
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 ACCAAGCTCT CAGTAGGCTC ACAGGATCCT GTCTGTGTTG TAGGTACAGT AAGGTACAAC 3540
 75 TTGGATCCCT TTGAGAGTCA CACCGATGAG ATGCTCTGGC AGGTTCTGGA GAGAACATT 3600
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 GAAAACCTCT CAGTAGGGGA AGTCAAGCTG CTTTGTGTGG CCGAGCTCT TCTCCGTAAT 3720
 TCAAGATACA TTCTCCTTGA TGAAGCCACC GCCTCTATGG ACTCCAAGAC TGACACCCGT 3780
 GTTCAAGACA CCATCAAAGA TGCTTCAAG GGTGCACTG TGCTGACCAT CGCCACCGC 3840
 CTCACACAG TTCTCAACTG CGATCAGTCT CTGGTTATGG AAAATGGGAA GGTGATTGAG 3900
 80 TTTGACAAGC CTGAAGTCTT TGCAGAGAAG CCAGATTCTG CATTTGCGAT GTTACTAGCA 3960
 GCAGAAGTCA GATTGTAG

Seq ID NO: 312 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51
 5 MVGEGPYLIS DLQQRGRRS FAERYDPSLK TMIPVRPCAR LAPNPVDDAG LLSFATPSWL 60
 TPVMVKGVRQ RLTVDLPLPL STYDSSDTNA KRFRVLWDEE VARVGPEKAS LSHVVVKFQR 120
 TRVLMDIVAN ILCIIMAAIG PTVLIHQILQ QTERTSGKVM VGIGLCIALF ATEFTKVFFW 180
 ALAWAINYRT AIRLKVALST LVFENLVSEK TLTHISVGEV LNLSSDSYS LFEAALFCPL 240
 PATIPILMVF CAAYAFFILG PTALIGISVY VIFIPVQMFV AKLNSAFRRS AILVTDKRVQ 300
 TMNEFLTICR LIKMYAWEKS FTNTIQDIRR RERKLEKAG FVQSGNSALA PIVSTIAIVL 360
 10 TLSCHILLRR KLTAPVAFVS IAFNVVMKFS IAILPFSIKA MAEANVSLRR MKKILIDKSP 420
 PSYITQPEDE DTVLLLANAT LTWEHEASRK STPKKLQNK RHLCKQRSE AYSESPPAK 480
 GATGPEEQSD SLKSVLHSL FVVRKLCRYE EAQLLAWRF AVFVGRIIRG YRPHGFSAXD 540
 KDESRRLLTW PQEVDRTORA AKYLGKILGI CGNVGSGKSS LLAALLGQMQ LQKGVVAVNG 600
 TLAVVSQAW IFHGNVRENI LFGEKYDHQR YQHTVRVCG LQDLNLPGY DLTEIGERGL 660
 15 NLSGGQRQRI SLARAVYSR QLYLLDDPLS AVDAHVGHV FEBCIKKTLR GKTVVLVTHQ 720
 LQFLESCDEV ILLEDGEICE KGTHKELMEB RGRYAKLIEN LRGLQFKDPE HLYNAMVEA 780
 FKESPAEREE DAGIIGYLLS LFTVFLFLM IGSAAFSNMW LGLMLDKGSR MTCGPQGNRT 840
 MCEVGAVALD IGQHVYQWVY TASMVFLVF GVTGKGFVTK TITLMASSSLH DTVFDEKILKS 900
 PMSFDTTPT GRLMNRFSKD MDELDRVLPF HAENFLQOFF MVVFILVILA AVFPAVLIVV 960
 20 ASLAVGFPII LRIFHRGQVE LKKVENVSRS PWFTHITSSM QGLGIIHAYG KKEESCITYTS 1020
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 25 VQNTIKDAFK GCTVLTIAHR LNTVLNCDHV LVMENGVIE FDKPEVLARK PDSAFAMLLA 1320
 AEVRL

Seq ID NO: 313 DNA sequence
 Nucleic Acid Accession #: Z31560
 Coding sequence: 1-966

1 11 21 31 41 51
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 35 AGCCCGGACC GCGTCAAGCG GCCCATGAAT GCCTTCATGG TGTGTCCTCG CCGGACGCGG 180
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 40 AAGACGCTCA TGAAGAAGGA TAAGTACACG CTGCCCGGCG GGTGCTGTGC CCGCGGCGGC 420
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 CAGCTGGGCT ACCCGCAGCA CCGCGGCTCT AATGCGCAG GCGCAGCGCA GATGCAGGCC 600
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 45 ATGAACGCGT CGCCACCTA CAGCATGTCC TACTGCGAGC AGGCGACCCC TGGCATGGCT 720
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 50 ATGTGAGGGC CGGACAGCGA ACTGGAGGGG GGAGAAATTT TCAAGAAAAA ACCAGGGAAA 1020
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Seq ID NO: 314 Protein sequence
 Protein Accession #: CAA83435

1 11 21 31 41 51
 55 HSARMYNMME TELKPPGPQO TSGGGGGNST AAAAGGNQKN SPDRVKRPMN AFMVWSRQOR 60
 60 RMAQENPKM HNSEISKRLG AEWKLLSETE KRPFIDEAKR LRALHMKEPH DYKYRPRRKT 120
 KTIAMKDKYT LPPGLLAPGG NSMASGVGVG AGLGAGVNR MDSYAHMNGW SNGSYSNMQD 180
 QLGYPHQFGL NAHGAQMOP MERYDVSAIQ YNSMTSSQTY MNGSPTYSMS YSQQTGPM 240
 LGSMGSVVKS EASSPFPVVT SSSHSRAFQ AGDLRDMISM YLPGAARPEP AAPSRLEMSQ 300
 HYQSGPVEGT AINGTLPLSH M

Seq ID NO: 315 DNA sequence
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 Coding sequence: 29..541

1 11 21 31 41 51
 70 CGGACTTGGC TTGTTAGAAG GCTGAAAGAT GATGGCAGGA ATGAAAAATCC AGCTTGTATG 60
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 75 TCCCTCTTGG AAGATGACTC TGCTAAATGT TTGCACTCTT GTAAATAATT TGAACAGCCC 240
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 80 GCTGTATGAG AATAAACCCA GAAGACCTCA CATACTCAA AGAGATTCTT ACTTATCTG 540
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Seq ID NO: 316 Protein sequence
Protein Accession #: AAB50564

5 1 11 21 31 41 51
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LIQEDILDGT NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSTYY

10 Seq ID NO: 317 DNA sequence
Nucleic Acid Accession #: NM_006536.2
Coding sequence: 109..2940

15 1 11 21 31 41 51
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20 GAACCTCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC 240
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TCATATGAAA AGGCAATGT CATAGTGACT GACTGGTATG GGGCACATGG AGATGATCCA 480
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25 TCCTTACTGA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCGAGT GTTTGTCCAT 600
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30 AGTTTATCTT TCGTGGGTGA ATTTGTAAAT GCAAGTACCC ACAACCAAGA AGCACCAAAC 900
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35 ATTCTACTCT TCGTGGGCAT TGCCAGTTTC GACAGCAAA GAGAGATCAG AGCCACGCTA 1200
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40 CTGGGTCTAT CTGAGGCCCC AAATCTGGAG GAATTATCAC GTCTTACAGS AGGTTTAAAG 1500
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TCTGGAACCTG GAGACATTTT CCAGCAACAT ATTGAGCTTG AAAGTACAGS TGAATAATGTC 1620
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45 ATGTTTCTAG TTACGTGGCA GGCCAGTGGT CCTCTGAGA TTATATTATT TGATCCTGAT 1740
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50 TATGCCAATG TGAACAGGG ATTTTATCCC ATTCTTAATG CCACTGTGAC TGCCACAGTT 2040
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55 AGCTCAGGAG GCTCCTTTTC AGTGCTGGGA GTTCCAGCTG GCCCCACCC TGATGTGTTT 2400
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80 Seq ID NO: 318 Protein sequence
Protein Accession #: NP_006527.1

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	KPFYINGQMQ	IKVTRCSSDI	TGIFVCEKGP	CPQENCIISK	LFKEGCTFIY	NSTQNATASI	240
5	MFMQSLSSVV	EPCNASTHNQ	EAPNLQNMCM	SLRSANDVIT	DSADFHHSFP	MNGTELPPPP	300
	TFSLVQAGDK	VVCLVLDVSS	KMAEADRLQ	LQQAABFYLM	QIVEIHTFVG	IASFDSKGEI	360
	RAQLHQINSN	DDRKLIVSYL	PTTVSAKTDI	SICSGLKKGF	EVVEKLANGA	YGSVMILVTS	420
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	SRISSTGTDI	PQQHIQLEST	GENVKPHQL	KNTVTVDNTV	GNDTMFLVTW	QASGPPEIIL	540
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	AVFPATVEAF	VERDSLHPPH	PVMYIANVKQ	GFYFILNATV	TATVEPETGD	PVTLRLDDG	660
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	CAGGTCCACG	ATGTCTGTGT	CTGCCAGCAC	AACACTGCCG	GCCCAAAATT	TGAGCGCTGT	960
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	GCCATCTCTT	CCCTCAGGCG	AACTCTCCAG	GGCCTGCAGC	TGGATCTGCC	CCTGGAGGAG	2100
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 Protein Accession #: NP_000219.1

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Seq ID NO: 324 Protein sequence
 Protein Accession #: P39900

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80 Seq ID NO: 325 DNA sequence
 Nucleic Acid Accession #: NM_024423.1
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 Protein Accession #: NP_077741.1

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	GTGTGTCAGC	ACAAACAAGG	CATTCAATGG	AATTGTTGTA	TTCCCTCTGC	AGCCCTCCTT	4620
	CTGGGCACTA	AGAAGGTCTA	TGAATTAAT	GCCTATCTAA	AATCTGATTT	TATCTCTACA	4680
	TTTTCTGTTT	TCTAATTTGA	CCCTAAAAATC	TATGTGTTTT	AGACTTAGAC	TTTTTATGTC	4740
	CCCCCCCCCT	TTTTTTTTTT	AGACGAGATC	TGCTCTGAC	GCACAGGCTG	GAGTGCAGTG	4800
60	GCTCCGATCT	CTGCTCACTG	AAAGCTCCGC	CTCCCGGTTT	CATGCCATTC	TCTTGCCTCA	4860
	GCCTCCTGAG	TAGCTGGGAC	TACAGGCGCC	CACCACCAAG	CCCGGCTAAT	TTTTTGTATT	4920
	TTTAATAGAG	ACGGGGTTTC	ACTGTGTAG	CCAGGATGGT	CTCGATCTCC	TGACCTCGTG	4980
	ATCCGCTCTG	CTCGGCTCTC	CAAGTGCTG	GGATTACAGG	CATGACCCAC	CGCTCCCGGC	5040
	CTGTGTTTCC	GTTTAAAGTC	GTCTTCTTTT	AATGTAATCA	TTTTGAACAT	GTGTGAAAGT	5100
65	TGATCATACG	AATTGGATCA	ATCTTGAAT	ACTCAACCAA	AAGACAGTGG	AGAAAGCCAGG	5160
	GGGAGAAAGA	ACTCAGGGCA	CAAAATATTG	GTCTGAGAAAT	GGAAATCTCT	GTAAGCCTAG	5220
	TTGCTGAAT	TTCTGCTGT	AACCAGAGC	CAGTTTTATC	TACCGCTTAC	TGAACACCCC	5280
	ACTGTGTTTT	GCTCACTCCC	TCACCTACCG	ATCAAAACCT	GCTACCTCCC	CAAGACTTTA	5340
	CTAGTGCCGA	TAAACTTTCT	CAAGAGGCAA	CCAGTATCAC	TTCCCTGTTT	ATAAAACCTC	5400
70	TAAACATCTC	TTTGTCTCTT	GAACATGCTG	AAAACCACT	GGTCTGCATG	TATGCCCGAA	5460
	TTTGTAAATC	TTTTCTCTCA	AATGAAAAT	TAAATTTAGG	GATTCAATTC	TATATTTTCA	5520
	CATATGTAGT	ATTATTAAT	CCTTATATGT	GTAAGGTGAA	ATTTATGGTA	TTTGAAGTGT	5580
	CAAGAAAATA	TATTTTTTAA	GCTTTCAATT	TTCCCCAGT	GAATGATTIA	GAATTTTTTA	5640
	TGTAATATATA	CAGAAATGTT	TTTCTTACTT	TTATAAGGAA	GCAGCTGTCT	AAAATGCAGT	5700
75	GGGGTTTGGT	TTGCAATGTT	TTAAACAGAG	TTTTAGTATT	GCTATTAAAA	GAAGTTACTT	5760
	TGCTTTTAAA	GAAACTTGGC	TGCTTAAAT	AAGCAAAAAT	TGGATGCATA	AAGTAATATT	5820
	TACAGATGTG	GGGAGATGTA	ATAAAACAAT	ATTAACCTGG	TTTCTTGTTT	TTGCTGTATT	5880
	TAGAGATTAA	ATAATCTAA	GATGATCACT	TTGCAAAAAT	ATGCTTATGG	CTGGCATGGA	5940
80	AATAGAAATA	CTCAATTATG	TCTTTGTTGT	ATTAATGGGG	AATATTTTGG	ACAATGTTTC	6000
	ATTATCAAAAT	TGTCGACATC	ATTAATATAT	ATTGTAATGT	TGGGAAGAGA	TCATATTTT	6060
	GAAGCAGAGC	TTTACAGATG	AGTATCTATG	ATACATATGT	ATAATAAAT	TTGATCGGGT	6120
	ATTAAAGATA	TTAGAAGGTG	GTATAAATG	CAGAGTATTC	CATGAATAGT	ACACTGACAC	6180
	AGGGGTTTTA	CTTTGAGGAC	CAGTGTAGTC	AAGGGAAAAC	ATGAGTTAAA	AAGAAAAGCA	6240
	GGCAATATTG	CAGTCTTGAT	TCGGCACTT	ACAGGATAGA	TAATGCCTGA	ACTTTAATGA	6300
	CAAGATGATC	CAACCATAAA	GGTGCTCTGT	GCTTCACAGT	GAATCTTTTC	CCCATGCAGG	6360

5 AGTGTGCTCC CCTACAAACG TTAAGACTGA TCATTTCAAA AATCTATTAG CTATATCAAA 6420
 AGCCTTACAT TTTAATATAG GTTGAACCAA AATTTCAATT CCAGTAACTT CTATTGTAAAC 6480
 CATTATTTTT GTGTATGTCT TCAAGAATGT TCATTGGATT TTTGTTTGTA ATAGTAAAT 6540
 ACCGGATACA TTTCACTGTG CCTTCAGTAT TGATTGGTT GAATATTGGG TCATATGGT 6600
 TGAGAAGCAT GGACACTAGA GCCAGAAATG TGGATATGA ATCCTGGATC TGTCACCTAC 6660
 TTCTGTGTGA CCTTTGAAAG GCTACTTATT TCCCTCTCTA GCTTTCAT TAAATCAAT 6720
 GAACAATGCC AGCCTCATGG GGTGTGTGAA TGATTAAAT AGTTAATATA CCTAAAGTAC 6780
 ATAGAACACT GCCTGCACAT AGTAAAGAA TTATAAGTG GAGGTAGTTG GTAAATATAT 6840
 GTAGTTGGAT ATACTACCGA ACAATATCTA ATCTCTTTT AGGGAAATAA AGTTTGTGCA 6900
 TATATATAAT CCCGAAACAT G

Seq ID NO: 328 Protein sequence
 Protein Accession #: NP_001932.1

15 1 11 21 31 41 51
 MAAAGPRRSV RGAVCLHLL TLVIFSRDGE ACKKVILNVP SKLEADKIIG RVNLEECFRS 60
 ADLIRSSDFD FRVLNDGSDVY TARAVALSDD KRSFTIWLSD KRKQTQKEVT VLEHQKKVS 120
 KTRHRTETVL RRAKRWRAP PCSMQENSLG PFPLFLQVVE SDAQNYTVF YSISGRGVDK 180
 20 EPLNLFYIER DTGNLFCRTP VDREEDVDVD LIAYASTADG YSADLEPLPL IRVEDENDNH 240
 PVFTEAIYNF EVLESSRPGT TVGVVCATDR DEFDTMHTRL KYSILQOTPR SPGLFSVHPS 300
 TGVIITVSHY LDREVVKYIS LIMKVQDMDG QFFGLIGTST CIITVTDSND NAPTFRQNAV 360
 EAPVHENAEN VEILRIPIED KDLINTANWR VNFTILKGNE NGHFKISTDK ETNEGVLVSV 420
 KPLNYEENRQ VNLEIGVWNE APFARDIPRV TALNRALVTV HVRDLDEGPE CTPAAQYVRI 480
 25 KENLAVGSKI NGYKAYDPEN RNNGNLRVKK LHDPKGMITI DEISGSIITS KILDREVETP 540
 KNELNYITVL AIDKDDRSCT GTLAVNIEDV NDNPPETLQE YVVICPKMG YTDILAVDFD 600
 EPVHGAPFYF SLPTSPSPIS RLMSLTQVND TAARLSYQKN AGPQBYTIFI TVKDRAGQAA 660
 TKLLRVNLCB CTHPTQCRAT SRSTGVILGK WAILAILLGI ALLPSVLLTL VGVVFGATKG 720
 KRFPEDLAQ NLIIISNTEAP GDDRVCSANG FMTQTINNS QGFCGTMSGG MKNGGQETIE 780
 30 MMKGGNQTLE SCRGAGHHT LDSCRGGHTE VDNCRYTSE WHSPTQPLRG EKLHRCNQNE 840
 DRMPSDQYVL TYNVYBGRGSP AGSVGCCSEK QEEGDLDFIN NLEPKFITLA EACTKR

35 Seq ID NO: 329 DNA sequence
 Nucleic Acid Accession #: NM_016583.2
 Coding sequence: 72..842

40 1 11 21 31 41 51
 GGAGTGGGGG AGAGAGAGGA GACCAGGACA GCTGCTGAGA CCTCTAAGAA GTCCAGATAC 60
 TAAGAGCAAA GATGTTTCAA ACTGGGGGCC TCATTGTCTT CTACGGGCTG TTAGCCCAGA 120
 CCATGGCCCA GTTTGGAGGC CTGCCCCGTC CCTTGAGACA GACCCGCGCC TTGAATGTGA 180
 ATCCAGCCCT GCCCTTGAGT CCCACAGGTC TTGACGGAAG CTTGACAAAT GCCCTCAGCA 240
 45 ATGGCCCTGT GTCTGGGGGC CTGTGGGCA TTCTGGAAA CCTTCGCTC CTGGACATCC 300
 TGAAGCCTGG AGGAGGTACT TCTGGTGGCC TCCTGGGGG ACTGCTTGA AAAGTGACGT 360
 CAGTGATTCC TGGCTGAAC AACATCATTG ACATAAAGGT CACTGACCCC CAGCTGCTGG 420
 AACTGGCCT TGTGCAGAGC CCTGATGGCC ACGTCTCTTA TGTCAACATC CCTCTGGCA 480
 TAAAGCTCCA AGTGAATACG CCCCTGGTCG GTGCAAGTCT GTTGAGGCTG CTGTGGAAGC 540
 TGGACATCAC TGCAGAAATC TTAGCTGTGA GAGATAAGCA GGAGAGGATC CACCTGGTCC 600
 50 TTGCTGACTG CACCCATTCC CTGGACAGCC TCACAGGGAT CTGTAATAA GTCTCGCCTG 660
 CCCTCCCAT TCAAGGCTCT CTGGACAGCC TCACAGGGAT CTGTAATAA GTCTCGCCTG 720
 AGTTGGTCA GGGCAACGTG TGCCCTCTGG TCAATGAGGT TCTCAGAGGC TTGACATCA 780
 CCCTGGTCA TGACATGTT AACATGCTGA TCCACGACT ACAGTTTGT ATCAAGGTCT 840
 AAGCCTCCA GGAAGGGGCT GGCCTCTGCT GAGCTGCTC CAGTGTCTA CAGATGGCTG 900
 55 GGCATGTGC TGAAGATGA CACAGTTGCC TTCTCTCGA GGAACCTGCC CCCTCTCTT 960
 TCCACACAGG CGTGTGTAAC ATCCATGTG CCTCACCTAA TAAATGGCT CTTCTCTGCT 1020
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

60 Seq ID NO: 330 Protein sequence
 Protein Accession #: NP_057667.1

65 1 11 21 31 41 51
 MFQTGGLIVF YGLLAQTMAG FGLFVPLDQ TLEPLVNPAL PLSPTGLAGS LTNALSNGLL 60
 SGGILGILEN LPLLDILKPG GGTSGGLLGG LLGKVTSPV GLNNIIDIKV TDPQLLELGL 120
 VQSPDGHRLY VTPIGLIKLQ VNTPLVGASL LRLAVKLDIT ABILAVRDKQ ERIHLVLGDC 180
 THSPGSLQIS LLDGLGLPLI QGLLDSLTI LNKVLPVLVQ GNVCPLVNEV LRGLDITLVH 240
 DIVNMLIHGL QFVIK

70 Seq ID NO: 331 DNA sequence
 Nucleic Acid Accession #: NM_004363.1
 Coding sequence: 115..2223

75 1 11 21 31 41 51
 CTCAGGCGAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT 60
 TCTTGGAACT CAAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG 120
 TCTCCCTCGG CCCCTCCCCA CAGATGGTGC ATCCCTGGC AGAGGCTCTT GCTCACAGCC 180
 80 TCACTTCTAA CCTTCTGGAA CCCGCCACCC ACTGCCAAGC TCACTATTGA ATCCACGCCG 240
 TTCAATGTGC CAGAGGGGAA GGAGGTGCTT CTACTTGTCC ACAATCTGCC CCAGCATCTT 300
 TTTGGCTACA GCTGGTACAA AGGTGAAGA GTGGATGGCA ACGTCAAT TATAGGATAT 360
 GTAATAGGAA CTACACRAGC TACCCAGGG CCCGCATACA GTGGTCGAGA GATAATATAC 420
 CCCAATGCAT CCTGCTGAT CCAGAACATC ATCCAGAAAT ACACAGGAT CTACACCTA 480

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CACGTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCGG GGTATACCGG 540
GAGCTGCCCC AGCCCTCCAT CTCAGCAAC AACTCCAAAC CGTGGAGGA CAAGGATGCT 600
GTGGCCTTCA CCTGTGAACC TGAGACTCAG GAGCAACCT ACCTGTGGTG GGTAAACAAAT 660
CAGAGCCTCC CGGTGAGTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720
TTCATGTGCA CAAGAAATGA CACAGCAAGC TACAATGTG AAACCCAGAA CCCAGTGAGT 780
GCCAGGGGCA GTGATTCAGT CATCCTGAAT GTCTCTATG GCCCGGATGC CCCCAACATT 840
TCCCCTCTAA ACACATCTTA CAGATCAGGG GAAAATCTGA ACCTCTCCTG CCACGCAGCC 900
TCTAACCCAC CTGCACAGTA CTCTGGTGT GTCAATGGGA CTTTCCAGCA ATCCACCCAA 960
GAGCTCTTTA TCCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1020
AACTCAGACA CTGGCCTCAA TAGGACCACA GTCAAGCAGA TCACAGTCTA TGCAGAGCCA 1080
CCCAACCCCT TCATCACCAG CAACAACTCC AACCCCGTGG AGGATGAGGA TGCTGTAGCC 1140
TTAACCTGTG AACCTGAGAT TCAGAACACA ACCTAOCCTGT GGTGGGTAAA TAATCAGAGC 1200
TCCCGGTGCA GTCCAGGCTG GCAGCTGTCC AATGACAACA GGACCCCTAC TCTACTCAGT 1260
GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAATT AAGTGTGAC 1320
CACAGCGAGC CAGTCATCCT GAATGTCTC TATGGCCGAC ACGACCCAC CATTTCCCCC 1380
TCATACACCT ATTACCGTCC AGGGGTGAAC CTCAGCCTCT CCTGCCATGC AGCCTCTAAC 1440
CCACCTGCAC AGTATTCTTG GCTGATTGAT GGGAACTAC AGCAACACAC ACAAGAGCTC 1500
TTTATCTCCA ACATCACTGA GAAGAACAGC GGACTCTATA CCTGCCAGGC CAATAACTCA 1560
GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCACAG TCTCTGCGGA GCTGCCAAG 1620
CCCTCCACTC CTGAGCAACA CTCCAAACCC GTGGAGGACA AGGATGTGTG GGCCTTCACC 1680
TGTGAACCTG AGGCTCAGAA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1740
GTCAGTCCCA GGCTGCAGCT GTCCAAATGGC AACAGGACCC TCACTCTATT CAATGTGACA 1800
AGAAATGAGG CAAGAGCCTA TGTATGTGGA ATCCAGAAGT CAGTGAGTGC AAACCGCAGT 1860
GACCCAGTCA CCTGTGATGT CCTCTATGGG CGGACACCCC CCATCATTTT CCCCCAGAC 1920
TGCTCTTACC TTTCTGGGAGC GAACCTCAAC CTCTCCTGCC ACTCGGCCTC TAAACCATCC 1980
CCGAGTATT CTGTGGGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTTATC 2040
GGCAAAATCA CGCCAAATAA TAACGGGACC TATGCTCTTA TTGCTCTTAA CTGGGCTACT 2100
GGCCCGAATA ATTCCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCTGGT 2160
CTCTCAGCTG GGGCCACTGT CGGCATCATG ATTGGAGTGC TGGTGGGGT TGCTCTGATA 2220
TAGCAGCCCT GGTGTAGTTT CTTCAATTCA GGAAGACTGA CAGTTGTGTT GCTTCTCTCT 2280
TAAAGCATTT GCAACAGCTA CAGTCTAAAA TTGCTCTTT ACCAAGGATA TTTACAGAAA 2340
AGACTCTGAC CAGAGATCGA GACCATCCTA GCCAATCG TGAAACCCCA TCTCTACTAA 2400
AAATACAAAA ATGAGCTGGG CTGTGTGGCG CGCACCTGTA GTCCAGTTA CTGGGAGGC 2460
TGAGGCAGGA GAATGCTGTG AACCCGGGAG GTGGAGATTG CAGTGAGCCC AGATCGCACC 2520
ACTGCCTCC AGTCTGGCAA CAGAGCAAGA CTCCTCTCA AAAAGAAAAG AAAAGAAGAC 2580
TCTGACCTGT ACTCTGAAT ACAAGTTTCT GATACCACCTG CACTGTCTGA GAATTTCCAA 2640
AACTTTAATG AACTAAGTGA CAGCTTCATG AAAGTGTCCA CCAAGATCAA GCAGAGAAAA 2700
TAATTAATTT CATGGGACTA AATGAACATA TGAGGATTGC TGATTTCTTA AATGTCTTGT 2760
TTCCAGATT TCAGGAAACT TTTTCTCTT TAAGCTATCC ACTCTACAG CAATTTGATA 2820
AAATATACTT TGTGAACAAA AAATGAGAC ATTACATT TCTCCTATG TGTGCTCTCC 2880
AGACTTGGGA AACTATTCAT GAATATTAT ATTGTATGGT AATATAGTA TTGCACAAGT 2940
TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA

Seq ID NO: 332 Protein sequence
Protein Accession #: NP_004354.1

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1 11 21 31 41 51
MESPSAPPFR WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLVHNLQP 60
HLFGYSWYKG ERVDGNRQII GYVIGTQQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFE 120
TLHWIKLSDLV NEEATGQFRV YPELPKPSIS SNNSKPVEDK DAVAFTCEPE TQDATYLMWV 180
NNQSLFVSFR LQLSNGNRTL TLFNVTRNDT ASYKCTQNP VSARRSDSVI LNVLYGEDAP 240
TISPLNTSYR SGENLNLSCH AASNPPAQYS WFNVTGTPQS TQELFIPNIT VNNSGSYTOQ 300
AHNSDTGLNR TTVTTITVYA EPPKPFITSN NSNPVEDEDA VALTCBPBIQ NMTYLMWVNR 360
QSLFVSPRLQ LSNDRNLTL LSVTRNDVGP YECQIQNELS VDHSDPVLN VLYGPDPTI 420
SPSYTYRPG VNLISLSCHAA SNPPAQYSWL IDGNIQHTQ ELFISNITEK NSGLYTCQAN 480
NSASGHSRRT VKTITVSABL PKPSISSNNS KPVEDKDAVA FTCEPEAQT TYLWVWNGQS 540
LPVSPRLQLS NGNRTLTLFN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDPTIISP 600
PDSSYLSGAN LNLSCSASN PSPQYSWRIN GIPQHTQVL FIAKITFNIN GTYACFVSNL 660
ATGRNNSIVK SITVSAGTIS PGLSAGATVG IMIGVLVGA LI

Seq ID NO: 333 DNA sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11..793

65
70
75
80

1 11 21 31 41 51
AATCCGAGCA ATGGCGAAAG ACAACTCAAC TGTTCGTGTC TTCCAGGGCC TGCTGATTTT 60
TGGAAATGTG ATTATTGGTT GTTGGCGCAT TGCCCTGACT GGGAGTGA TCTTCTTGT 120
ATCTGACCAA CACAGCTCTT ACCCACTGCT TGAAGCCACC GACAAAGATG ACATCTATGG 180
GGCTGCCTGG ATCGGCATAT TTGTGGGCAT CTGCTCTTC TGCCGTGCTG TTTCTAGGAT 240
TGTAGGCATC ATGAAGTCCA GCAGGAAAAT TCTTCTGGCG TATTCAATC TGATGTTTAT 300
AGTATATGCC TTTGAAGTGG CATCTTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360
ACCCAACCTC TTCTCTGAAGC AGATGCTAGA GAGGTACCAA AACACAGCC CTCCAAACAA 420
TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480
CAATTGCTGT GGGGTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC 540
TGAGAATAAT GATGCTGACT ATCCCTGGCC TGTCTAATGC TGTGTTATGA ACAATCTTAA 600
AGAACCTCTC AACCTGGAGG CTGTGAACCT AGGCGTGCTT GGTTTTATC ACAATCAGGG 660
CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACAACCC TGGGGGGTTG CTTGTTTGG 720
ATTTGCCATT CTGTCTGGA CTTTTTGGGT TCTCCTGGGT ACCATGTCTT ACTGGAGCAG 780
AATTGAATAT TAAGAA

Seq ID NO: 334 Protein sequence
Protein Accession #: NP_008883.1

1 11 21 31 41 51
 5 MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW 60
 IGIPVIGICLP CLSVLGIIVGI MKSSRKILLA YFILMPIVYA FEVASCITAA TQRDFFTPNL 120
 FLKQMLERYQ NNSPPNDDQ WKNNGVTKTW DRMLQDNCC GVNGPSDWQK YTSAFRTENN 180
 DADYPWPRQC CVMNMLKEFL NLEACKLGVP GFYHNGQCYE LISGPMNRHA WGVANWFGPAI 240
 LCWTFWVLLG TMFYWSRIEY

10 Seq ID NO: 335 DNA sequence
 Nucleic Acid Accession #: NM_002638.1
 Coding sequence: 120..473

1 11 21 31 41 51
 15 CAATACAGCT AAGGAATTAT CCCTTGTAAT TACCACAGAC CGCCCTTGA GCCAGGCCAA 60
 GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
 TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCTCAT CGCTGGGAGC CTGTTCTTAG 180
 AGGCAGCTGT CACGGGAGTT CCTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTCTCAT 240
 20 TCAATGACA AGATCCCGTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG 300
 CGCAAGAGCC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCCTGCCCC ATTATCTTGA 360
 TCCGTGCGC CATGTTGAAT CCCCCTAACC GCTGCTTGA AGATACTGAC TGCCCAAGAA 420
 TCAAGAAGTG CTGTGAAGGC TCTTGCGGGA TGGCTGTITT CGTTCCTCAG TGAAGGGAGC 480
 25 CGGTCTTGC TGCACCTGTG CGTCCCCAG AGCTACAGGC CCCATCTGCT CTAAGTCCC 540
 TGCTGCCCTT CCCCTTCCA CACTGTCCAT TCTTCTCCC ATTCAGGATG CCCACGGCTG 600
 GAGCTGCCCT TCTCATCCAC TTTCATAATA A

30 Seq ID NO: 336 Protein sequence
 Protein Accession #: NP_002629.1

1 11 21 31 41 51
 35 MRASSELIVV VFLIAGTLVL EAAVTGVVVK GQDTVKGKRP FNGQDPVKQK VSVKGQDKVK 60
 AQEPVKGPFV TKPGSCPIIL IRCAMLNPPN RCLKDTDCPG IKKCEGSGC MACFVPEQ

Seq ID NO: 337 DNA sequence
 Nucleic Acid Accession #: NM_001793.2
 Coding sequence: 71..2560

40 1 11 21 31 41 51
 AAAGGGGCAA GAGCTGAGCG GAACACCGGC CGGCCGTGCG GCAGCTGCT TCACCCCTCT 60
 CTCTGCAGCC ATGGGGCTCC CTCTGGGACC TCTCGCGTCT CTCCTCTTTC TCCAGGTTTG 120
 45 CTGCGCTCAG TCGCGCGCGT CGAGCCCGTG CGGGCGGTC TTCAGGGAGG CTGAAGTGAC 180
 CTTGAGGCGG GGAGGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTCTATGG 240
 CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
 TGGCAGAGCA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG GTTGCTCCAA TATCTGTCCC 360
 ATCCAAAGCT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
 50 TGAAATAGGC AAGGTTCCCT TCCCCCAGAG ACTGAATCAG CTCAGTCTA ATAAGATAG 480
 AGACACCAAG ATTTTCTACA GCATCACGGG GCGGGGGGCA GACACCCCC CTGAGGGTGT 540
 CTTCGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
 GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTGAGAG AATGGTGCCT CAGTGGAGGA 660
 CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
 55 GGACACCTTC CGAGGAGGTG TCTTAGAGGG AGTCCATCCA GGTACTTCTG TGATGCAAGT 780
 GACAGCCAGC GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTGT CTTACTCCAT 840
 CCATAGCCAA GAACCAAGG ACCCACACGA CCTCATGTTC ACCATTACCC GGAGCACAGG 900
 CACCATCAGC GTCATCTCCA GTGGCCCTGA CGGGGAAAAA GTCCCTGAGT ACACACTGAC 960
 CATCCAGGCC ACAGACATGG ATGGGGAAGG CTCCACCACC ACGGCAGTGG CAGTAGTGGA 1020
 60 GATCCTTGAT GCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
 GCCTGAGAAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC 1140
 CAACCTACCA CGGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGAGC GGGACCATTT 1200
 TACCATCACC ACCCACCTCT AGAGCAACCA GGGCATCCTG ACAACAGGA AGGTTTGA 1260
 TTTTGAGGCC AAAAACCAGC ACACCTGTGA CGTTGAAGTG ACCAACGAGG CCCCCTTTGT 1320
 65 GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAG GTGGAGGATG TGAATGAGGC 1380
 ACCTGTGTTT GTCCACCTCT CCAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
 GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAGA TCAGTACCG 1500
 CATCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560
 70 TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTTGTGAGG AACACATCT ATGAAGTCAT 1620
 GGTCTTGGCC ATGACAAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680
 ACTGATTGAT GTCAATGACC ATGGCCCACT COCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
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 CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGCGAG AGGTCAACGA 1860
 75 GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT 1920
 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
 GTGCGACTGC CATGGCCATG TCGAAACCTG CCTTGGACCC TGGAAAGGAG GTTTCATCCT 2040
 CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGGTGTCTG TTTTGTGTGT 2100
 GAGAAAGAGG CGGAAGATCA AGGAGCCCTC CTAATCCCA GAAGATGACA CCGGTGACAA 2160
 80 CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
 GCTCCACCGA GGTCTGGAGG CAGGCGCGGA GGTGGTCTCT CGCAATGACG TGGCACCAAC 2280
 CATCATCCCG ACACCCATGT ACGTCTCTCG CCGAGCCAAC CCAGATGAAA TCGGCACTT 2340
 TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCAAC GCCCCGCCCT ACACACCCCT 2400
 CTGTGTGTTT GACTATGAGG GCAGCGGCTC CGAGCGCGCG TCCTGAGCT CCTCACCTC 2460
 CTCGCGCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGGC GCGCTTCAA 2520
 GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG GCGGCTGCTC TGACGGGCTG 2580

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GGGACCAAAC  GTCAGGCCAC  AGAGCATCTC  CAAGGGGTCT  CAGTTCCCCC  TTCAGCTGAG  2640
GACTTCGGAG  CTTGTCAGGA  AGTGGCCGTA  GCAACTTGGC  GGAGACAGGC  TATGAGTCTG  2700
ACGTTAGAGT  GGTTCGCTTC  TTAGCCITTC  AGGATGGAGG  AATGTGGGCA  GTTTGACTTC  2760
AGCACTGAAA  ACCTCTCCAC  CTGGGCCAGG  GTTGCCCTAG  AGGCCAAGTT  TCCAGAAGCC  2820
TCTTACCTGC  CGTAAATGTC  TCAACCTGT  GTCTGGGCC  TGGGCTGCT  GTGACTGACC  2880
TACAGTGGAC  TTTCTCTCTG  GAATGGAACC  TTCTTAGGCC  TCCTGGTGCA  ACTTAATTTT  2940
TTTTTTTAAT  GCTATCTTCA  AAACGTTAGA  GAAAGTTCTT  CAAAAGTGCA  GCCCAGAGCT  3000
GCTGGGCCCA  CTGGCCGTCC  TGCATTTCTG  GTTTCAGAG  OCCAATGCCT  CCCATTGCGA  3060
TGGATCTCTG  CGTTTTTATA  CTGAGTGTGC  CTAGGTGTCC  CCTTATTTT  TATTTTCCCT  3120
GTTGCGTTGC  TATAGATGAA  GGGTGAGGAC  AATCGTGAT  ATGTACTAGA  ACTTTTTTAT  3180
TAAAGAAACT  TTTCCAGAA  AAAAA
  
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Seq ID NO: 338 Protein sequence
Protein Accession #: NP_001784.2

15
20
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1      11      21      31      41      51
|      |      |      |      |      |
MGLPRGPLAS  LLLLQVCNLQ  CAASEPCRAV  FREAEVTLEA  GGAEQEPQQA  LGKVPFGCPG  60
QEPALFSTDN  DDTTVRNGET  VQERRSLKER  NPLKIFPSKR  ILRRHKRDWV  VAPISVPENG  120
KGFFPQRLNQ  LKSNKORDTK  IFYSITGPGA  DSPPEGVFAV  EKETGWLLIN  KPLDREBIK  180
YELFGHAYSE  NGASVEDPMN  ISIIIVTDND  HKPKFTQDTF  RGSVLEGLVP  GTSVMQVTAT  240
DEDDAIYTYN  GVVAYSIIHQ  EPKDPHDLAF  TIHRSTGTIS  VISSGLDREK  VPEYTLTIQA  300
TDMGDGSGTT  TAVAVVEILD  ANDNAPMFPD  QKYEAHVPEN  AVGHEVQRLT  VTDLDAFNSP  360
AWRATYLMIG  GDDGDHFTIT  THPESNQIL  TTRKGLDPEA  KNQHTLYVEV  TNEAPFVLKL  420
PTSTATIVVH  VEDVNEAPVF  VPPSKVVEVQ  EGIPTGEPVC  VYTAEDPDKE  NQKISYRILR  480
DPAGWLAMDP  DSGQVTAAGT  LDREDEQFVR  NNIYEVMLA  MDNGSPFTTG  TGTLLLTLD  540
VNDHGFVPEP  RQITICNQSP  VRQVLNITDK  DLSPTSPPQ  AQLTDDSDIY  WTAEVNEBGD  600
TVVLSLKRFL  KQDTYDVHLS  LSDHGNKEQL  TVIRATVCDC  RGHVETCPGP  WKGGFILFVL  660
GAVLALLFL  LVLLLLVLRK  RKIKEPLLLP  EDDTRDNVYF  YGEGGGSEED  QDYDITQLHR  720
GLEARPEVVL  RNDVAPTITP  TPMYRPRPAN  PDEIGNPIIE  NLKAANTDPT  APPYDTLLVF  780
DYEGSGSDAA  SLSSLTSSAS  DQDQDYDYLN  EWGSRPFKLA  DMYGGGEDD
  
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Seq ID NO: 339 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..672

35
40
45
50

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1      11      21      31      41      51
|      |      |      |      |      |
ATGAGGCTCC  AAAGACCCCG  ACAGGCCCGG  GCGGTGGGA  GCGCGCGGCC  CCGGGGCGGG  60
CGGGGCTCCC  CCTACCGGCC  AGACCCGGGG  AGAGGCGCGC  GGAGGCTGGG  AAGGTTCCAG  120
AAGGCGGGGG  AGGGGGGGCC  GCGCGCTGAC  CCTCCCTGGG  CACCGCTGGG  GACGATGGCG  180
CTGCTCGCCT  TGCTGCTGGT  CGTGCCCTTA  CGCGGGGTGT  GGACAGAGCG  CAACCTGACT  240
GCGAGACAA  GAGATCCAGA  GGACTCCAG  CGAAGCGAGC  AGGGTGACAA  TAGAGTGTGG  300
TGTCATGTTT  GTGAGAGAGA  AAACACTTTC  GAGTGCCAGA  ACCCAAGGAG  GTGCAAAATG  360
ACAGAGCCAT  ACTGCGTTAT  AGCGGCGGTG  AAAATATTTC  CACGTTTTTT  CATGGTTGGG  420
AAGCAGTGCT  CCGCTGGTTG  TGCAGCGATG  GAGAGACCCA  AGCCAGAGGA  GAAGCGGTTT  480
CTCCTGGAAG  AGCCCATGCC  CTTCTTTTAC  CTCAGTGT  GTAAAATTGG  CTACTGCAAT  540
TTAGAGGGGC  CACCTATCAA  CTCATCAGTG  TTCAGAAGAT  ATGCTGGGAG  CATGGGTGAG  600
AGCTGTGGTG  GGCTGTGGCT  GGCCATCCTC  CTGCTGTGG  CCTCCATTGC  AGCGGCGCTC  660
AGCCTGTCTT  GA
  
```

Seq ID NO: 340 Protein sequence
Protein Accession #: Eos sequence

55
60

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1      11      21      31      41      51
|      |      |      |      |      |
MLRQRPRQAP  AGRRRAPRGG  RGSFYRPDPG  RGARRLRRFQ  KGGGAPRAD  PPWAPLGTMA  60
LLALLLVVAL  PRVWTDANLT  ARQRDPEDSQ  RTDEGDNRVN  CHVCHRENTF  BCQNPRRCRW  120
TEPYCVIAAV  KIPPRFFMVA  KQCSAGCAAM  ERPKPEEKRF  LLEBPMPFFY  LKCKIKRYCN  180
LEGPPINSSV  FKEYAGSMGE  SCGGLWLAIL  LLLASIAAGL  SLS
  
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Seq ID NO: 341 DNA sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 53..1576

65
70
75
80

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1      11      21      31      41      51
|      |      |      |      |      |
GCTGCTGGG  CCGCGGCTCC  CGGGTGTCCC  AGGCCCGGCC  GGTGCGCAGA  GCATGGCGGG  60
TGCGGGCCCG  AAGCGGCGCG  CGCTAGCGGC  CGCGGCGGCC  GAGGAGAAGG  AAGAGGCGCG  120
GGAGAAGATG  CTGGCCGCCA  AGAGCGCGGA  CGGCTCGGG  CCGGCAGGCG  AGGGCGAGGG  180
CGTGACCTCG  CAGCGGAACA  TCACGCTGCT  CAACGGCGTG  GCCATCATCG  TGGGGACCAT  240
TATGCGCTCG  GGCATCTTGG  TGACGCCAC  GGGCGTGCTC  AAGGAGGCA  GCTCGCGGG  300
GCTGGCGCTG  GTGGTGTGG  CCGGTGCGG  CGTCTTCTCC  ATCGTGGGG  CGCTCTGCTA  360
CGCGGAGCTC  GGCACCAACA  TCTCCAAATC  GGGCGGCGAC  TACGCTTACA  TGCTGGAGGT  420
CTACGCTCG  CTGCCCGCT  TCCTCAAGCT  CTGGATCGAG  CTGCTCATCA  TCGGCGCTTC  480
ATGCACTAC  ATCGTGGCCC  TGGTCTTGG  CACCTACCTG  CTCAGCGCG  TCTTCCCCAC  540
CTGCCCGGTG  CCGGAGGAGG  CAGCCAAGCT  CGTGGCTGCG  CTCTGGGTGC  TGCTGCTCAC  600
GGCCGTGAAC  TGCTACAGCG  TGAAGGCCGC  CACCGGGTTC  CAGGATGCGT  TTGCGCGCGC  660
CAAGCTCCTG  GCCCTGGCCC  TGATCATCCT  GCTGGGCTTC  GTCCAGATCG  GAAAGGGTGA  720
TGTGTCCAAT  CTGCTATCCA  ACTTCTCAIT  TGAAGGCACC  AAAGTGGATG  TGGGGAACAT  780
TGTGCTGGCA  TTATACAGCG  GCCTCTTGG  CTATGGAGGA  TGAATTACT  TGAATTTGCT  840
CACAGAGGAA  ATGATCAACC  CCTACAGAAA  CTTGCCCTCG  GCCATCATCA  TCTCCCTGCC  900
CATCGTGACG  CTGGTGTACG  TGCTGACCAA  CTTGGCTTAC  TTCACACCC  TGTCCACCGA  960
GCAGATGCTG  TCGTCCGAGG  CCGTGGCCGT  GGACTTGGG  AACTATCACC  TGGGGTTCAT  1020
  
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5
10
GTCCTGGATC ATCCCCGTCT TCGTGGGCTT GTCCTGCTTC GGCTCCGTC A TGCGGTCCCT 1080
GTTTCACATCC TCCAGGCTCT TCTTCGTGGG GTCCCGGGAA GGCCACCTGC CCTCCATCCT 1140
CTCCATGATC CACCCACAGC TCCTCACCCC CGTCCGCTCC CTCGTGTGTC CGTGTGTGAT 1200
GACGCTGCTC TACGCTCTCT CCAAGGACAT CTTCTCGTC ATCAACTTCT TCAGCTTCTT 1260
CAACTGGCTC TGCCTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
TGAGCTTGAG CGGCCATCA AGGTGAACCT GGCCCTGCCT GTGTCTTCA TCCTGGCCTG 1380
CCTCTTCTG ATCGCCGCTCT CCTTCTGGAA GACACCCGTG GAGTGTGGCA TGGCTTCAC 1440
CATCATCTC AGCGGGCTGC CGTCTACTT CTTCCGGGTC TGGTGGAAAA ACAAGCCCA 1500
GTGGCTCTC CAGGGCATCT TCTCCAGAC CGTCTCTGT CAGAGCTCA TGCAGGTGT 1560
CCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTCCGGA GGAGCATGC

Seq ID NO: 342 Protein sequence
Protein Accession #: XP_035292.2

15
20
25
1 11 21 31 41 51
MAGAGPKRRA LAAPAAEKEE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIV 60
GTIIGSGIFV TPTGVLKEAG SPGLALVWVA ACGVFSIVGA LCYABLGTTI SKSGGDYAYM 120
LEVYGSLLPAP LKLWIELLII RPSSQYIVAL VFATYLLKPL FFTCPVPBEA AKLVACLVL 180
LLTAVNCSYV KAATRVQDAF AAAKLLALAL IILLGFVQIG KGDVSNLDPN FSFEGTKLDV 240
GNIVLALYSV LPAYGGWNYL NFVTEEMINP YRNPLALII SLPIVTLVIV LTNLAYFTIL 300
STEQLMSSEA VAVDFGNVHL GVMSWIIPVF VGLSCFSGVN GSLFTSSRLF FVGSREGHLP 360
SILSMIHPLQ LTPVPSLVFT CVMTLIYAFS KDIFSVINFF SFFNMLCVAL AIIGMIWLRH 420
RKPELERPIK VNLALPVFFI LACLFLIAYS FWKTPVECCI GFTIILSGLP VYFFGVWVKN 480
KPKWLLQGIF STTVLQKLM QVVPQET

Seq ID NO: 343 DNA sequence
Nucleic Acid Accession #: NM_005268.1
Coding sequence: 168..989

30
35
40
45
50
1 11 21 31 41 51
TAAAAAGCAA AAGAATTGCG GGCCGCGTCG ACACGGGCTT CCCCAGAAAC CTTCCTCCGCT 60
TCTGGATATG AAATTCAGAC TGCTTGCTGA GTCTATTGC CGGCTGCTGG GAGCCAGGAG 120
AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 180
TCTTTGAGGG ACTCCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
TGCTCTGGT CTTCATCTTC CGCGTGCTGG TGTACTGGT GACGCGCGAG CGTGTGTGGA 300
GTGATGACCA CAAGGACTTC GACTGCAATA CTGCGCAGCC CGGCTGCTCC AACGTCTGCT 360
TTGATGAGTT CTTCCTGTG TCCCATGTGC GCCTCTGGG CCTGCAGCTT ATCCTGGTGA 420
CATGCCCTC ACTGCTCTG GTCATGCAAG TGCCCTACCG GGAGGTTGAG GAGAAGAGGC 480
ACCGAGAAGC CCATGGGAGG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG 540
GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAG GCGAGCGGTG GACATCGCCT 600
TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCTCTCTGTG GTCAAGTGCC 660
ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAACA 720
TTTTCACCTT CTTCATGGTG GCCACAGCTG CCATCTGCAT CTTGCTCAAC CTGCTGGAGC 780
TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCTGGC AGCAAGGAAA GCTCAAGCCA 840
TGTGACACAG TCATCACCCC CACGGTACCA CCTCTCTCTG CAAACAAGAC GACCTCCTTT 900
CGGGTGACCT CATCTTTCTG GGCTCAGACA GTCATCTCC TCTCTTACCA GACCGCCCCC 960
GAGACCATGT GAAGAAACC ATCTGTGTAG GGGCTGCTG GACTGGTCTG GCAGGTTGGG 1020
CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGAGCTC TGGAGGCCAG TTCTAGTCC 1140
TCAACTCCAG CCACCTGCCC CAGCTCGACG GCACTGGGCC AGTTCGCCCT CTGCTCTGCA 1200
GCTCGGTTTC CTTTCTAGA ATGGAATAG TGAGGGCCAA TGC

Seq ID NO: 344 Protein sequence
Protein Accession #: NP_005259.1

60
65
1 11 21 31 41 51
MNWSIFEGLL SGVNKYSTAF GRWLVLVFI PRVLVYLVT A ERVMSDDHKD FDCNTRQPGC 60
SNVCFDEFFP VSHVRLNALQ LILVTCPSLL VVMHAYREV QEKRRHREAHG ENSGRILYNP 120
GKRRGGLWMT VVCSLVFKAS VDIAPLYVPH SFYPKYLPP VVKCHADPCP NIVDCPISKP 180
SEKNIFTLFM VATAICILL NLVELIYLV KRCHECLAAR KAQAMCTGHH PHGTTSSCKQ 240
DILLSGLLIF LGSDSHPLL PDRPRDHVK TIL

Seq ID NO: 345 DNA sequence
Nucleic Acid Accession #: NM_002391.1
Coding sequence: 26..457

70
75
80
1 11 21 31 41 51
CGGGCGAAGC AGCGCGGCA GCGAGATGCA GCACCGAGGC TTCTCTCTCC TCACCTCTCT 60
CGCCCTGCTG CGCTCACTT CCGCGGTGCG CAAAAGAGAA GATAAGGTGA AGAAGGGCGG 120
CCCGGGGAGC GAGTGGCTCT AGTGGGCTG GGGGCCCTGC ACCCCAGCA GCAAGGATTG 180
CGGCGTGGGT TTCCGCGAGG GCACCTGCGG GGGCCAGACC CAGCGCATCC GGTGCAAGGT 240
GCCTGCAAC TGAAGAAGG AGTTTGAGC GAGCTGCAAG TACAAGTTTG AGAAGTGGG 300
TGCGTGTGAT GGGGGCACAG GCACCAAGT CCGCCAAGGC ACCCTGAAGA AGCGCGCTA 360
CAATGCTCAG TGCCAGSAGA CCATCCGCT CACCAAGCCC TGCAACCCCA AGACCAAGC 420
AAGGGCCAAA GCCAAGAAAG GGAAGGGAAA GGACTAGAGC CCAAGCCTGG ATGCCAAGGA 480
GCCCCGTGGT TCACATGGGG CCTGGCCACG CCTCCCTCT CCCAGGCCCG AGATGTGACC 540
CACCAGTGC TTCTGTCTG TCGTTAGCT TAATCAATCA TGCCCTGCTC TGTCCCTCTC 600
ACTCCACAG CCCACCCCTA AGTGGCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT 660
TGAGCCTCCC CCAAGCAAT GTGAGTCCA GAGCCGCTT TGTCTCTCC CCACAATTCC 720
ATTACTAAGA AACACATCAA ATAACTGAC TTTTCCCCC CAATAAAGC TCTCTTTTT 780

TAATAT

Seq ID NO: 346 Protein sequence
Protein Accession #: NP_002382.1

5
1 11 21 31 41 51
MQHRGFLLLT LLALLALTSA VAKKKDKVKK GPGSECAEW AWGPCTPSSK DCGVGFREBT 60
10 CGAQTQIRRC RVPCNWKKEP GADCKYKFEN WGACDGGTGT KVRQGTLLKA RYNAQCQETI 120
RVTKPCTPKT KAKAKAKKKG GKD

Seq ID NO: 347 DNA sequence
Nucleic Acid Accession #: NM_006783.1
Coding sequence: 1..786

15
1 11 21 31 41 51
ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACTATC CACCAGCATC 60
20 GGGAAAGTGT GGATCAGT CATCTTTATT TTCCGAGTCA TGATCCTAGT GGTGGCTGCC 120
CAGGAAGTGT GGGGTGACGA GCAAGAGGAG TTGCTCTGCA ACACACTGCA ACCGGGATGC 180
AAAAATGTGT GCTATGACCA CTTTTCCTCG GTGTCCACA TCCGGCTGTG GGCCTCCAG 240
CTGATCTTG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300
GAAACCACTC GCAAGTTCAG GCGAGGAGAG AAGAGGAATG ATTTCAAGA CATAGAGGAC 360
ATTAAAAAGC ACAAGGTTCG GATAGAGGGG TCGCTGTGTG GGACGTACAC CAGCAGCATC 420
25 TTTTCCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCCT TTACAATGGG 480
TAACACCTGC CCGGTGTGT GAAATGTGGG ATTGACCCCT GCCCAACCT TGTGACTGTC 540
TTTATTTCTA GGCCACAGA GAAGACCGTG TTTACCATTT TTATGATTTC TGCCTCTGTG 600
ATTTCATGC TGCTTAAGCT GGCAGAGTGT TGCTACCTGC TGCTGAAAGT GTGTTTAGG 660
30 AGATCAAGA GAGCACAGC GCAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
CAGAATGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780
AGCTAA

Seq ID NO: 348 Protein sequence
Protein Accession #: NP_006774.1

35
1 11 21 31 41 51
MDWGLHTFI GGVNKHSTSI GKVVITVIPI FRVMILVVAA QEVWGDQED FVCNTLQPGC 60
40 KNVCYDHPFP VSHRLWALQ LIFVSTPALL VAMHVAYYRH ETTRKPRRGE KRNDFKDIED 120
IKKKVRIEG SLWNTYTSSI FFRITFEAF MYVIFYLYNG YHLPWVLKOG IDPCPNLVDC 180
FISRPTEKTV FTIFMISASV ICMILNVABL CYLLLVKCFR RSKRAQTQKN HPNHALKESK 240
QNEPNELISD SGQNAITGFP S

Seq ID NO: 349 DNA sequence
Nucleic Acid Accession #: NM_002571.1
Coding sequence: 99..587

50
1 11 21 31 41 51
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCTCTCTGC 60
TCACCCCTGG GCTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC 120
AGGACCTGGA GCTCCCAAAG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180
ACATCTCCCT CATGGGACA CTGAAGGCC CTTCTGAGGT CCACATCACC TCACTGTGTC 240
CCACCCCGGA GGACAACTTG GAGATCGTTC TGACAGATG GGAGAACAC AGCTGTGTTG 300
55 AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360
TGGCAACGA GGCCACGCTG CTGATAGTGT ACTACGACAA TTTCTGTGTT CTCTGCTTAC 420
AGGACACCA CACCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCTGGTGG 480
AGGACGATGA GATCATGCAG GGATTCATCA GGGCTTTCAG GCCCTGCCC AGGCACCTAT 540
GGTACTTGCT GGACTTGAAA CAGATGGAAG AGCGGTGCCG TTTCTAGCTC ACCTCCGCT 600
60 CCAGGAAGAC CAGACTCCCA CCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCTGCTCC 660
TTTCAAGAA TAACCAAGC TCAGAAAGAG ATGAAGTGT CATCTGTGTC GCCATCCCT 720
TCCTGCTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCTGGGGGC AGAGTCTCTG 780
GCAGAGGTTA TTAATAAACC CTGGAGCAT G

Seq ID NO: 350 Protein sequence
Protein Accession #: NP_002562.1

70
1 11 21 31 41 51
MDIPQTKQDL ELPLAGTWE SMAMATNNIS LMATLKAPLR VHITSLLPTP EDNLEIVLHR 60
WENNSCVERK VLGEKTGNPK KFKINYTVAN EATLLDTDYD NFLFLCLQDT TPIQSMMQ 120
YLARVLVEDD EIMQGFIRAP RPLRHLWYL LDLKQMEPC RF

Seq ID NO: 351 DNA sequence
Nucleic Acid Accession #: NM_006500.1
Coding sequence: 27..1967

80
1 11 21 31 41 51
ACTTGGCTCT GCGCCCTCGG CCAAGCATG GGCCTCCAG GCTGGTCTGC GCCTTCTTGC 60
TCGCGGCTGT CTGCTGCTGT CCTCGCTCG GGGGTGTGCC CGGAGAGGCT GAGCAGCCTG 120
CGCTGAGCT GGTGGAGGTG GAAGTGGCA GCACAGCCT TCTGAAGTGC GGCCTCTCCC 180
AGTCCCAAG CAACCTCAGC CATGTGACT GGTTTTCTGT CCACAAGGAG AAGCGGAGCG 240
TCATCTTCG TGTGCGCCAG GGCCAGGGCC AGAGCGAACC TGGGAGTAG GAGCAGCGG 300

5 TCAGCCTCCA GGACAGAGGG GCTACTCTGG CCCTGACTCA AGTCACCCCC CAAGACGAGC 360
 GCATCTTCTT GTGCCAGGGC AAGGCGCCCTC GGTCCACAGA GTACCGCATC CAGCTCCGCG 420
 TCTACAAGAC TCCGGAGGAG CCAAAACATCC AGGTCAACCC CCTGGGCATC CCTGTGAACA 480
 GTAAGGAGCC TAGGAGAGTC GCTACCTGTG TAGGAGAGAA CGGGTACCCC ATTCTCAAG 540
 TCATCTGGTA CAAGAATGGC CGGCTCTGA AGGAGGAGAA GAACCGGGTC CACATTCACT 600
 CGTCCAGAC TGTTGGAGTC AGTGGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC 660
 TGGTTAAAGA AGACAAAGAT GCCCAGTTTT ACTGTGAGCT CAACTACCGG CTGCCCAGTG 720
 GGAACCATAT GAAGGAGTCC AGGGAAGTCA CCGTCCCTGT TTTCTACCGG ACAGAAAAG 780
 TGTGGCTGGA AGTGGAGCCC GTGGGAATGC TGAAGGAAGG GGACCCGCTG GAAATCAGGT 840
 10 GTTTGGCTGA TGGCAACCCCT CCACACACT TCAGCATCAG CAAGCAGAAC CCCAGCACCA 900
 GGGAGGCAGA GGAAGAGACA ACCAAGACA ACGGGTCCCT GGTGCTGGAG CCTGCCCGGA 960
 AGGAACACAG TGGGCGCTAT GAATGTCAAG CCTGGAACCT GGACACCATG ATATCGCTGC 1020
 TGAGTGAACC ACAGGAAGTC AGCAGCCTCA CCTGACCTG TGAGGCAGAG AGTAGCCAGG 1080
 CCCCTGAGAG ACAGGAAGGC AGCAGCCTCA CCTGACCTG TGAGGCAGAG AGTAGCCAGG 1140
 15 ACCTCGAGTT CCAGTGGCTG AGAGAAGAGA CAGACCAAGT GCTGGAAGG GGGCCTGTGC 1200
 TTCAGTTGCA TGACCTGAAA CGGAGGCGAG GAGGCGGCTA TGCTGCGTG GCGTCTGTGC 1260
 CCAGCATACC CGGCTGAAC CGCACACAGC TGTGTAAGCT GGCCATTTT GGCCCCCTT 1320
 GGATGGCATT CAAGGAGAGG AAGGTGTGGG TGAAGAGAAA TATGTTGTG AATCTGTCTT 1380
 GTGAAGCTC AGGGCACCCC CGGCCACCA TCTCTGGAA CGTCAACGGC ACGGCAAGTG 1440
 20 AACAGACCA AGATCCACAG CGAGTCTGA GCACCTGAA TGTCTCGTG ACCCGGAGC 1500
 TGTGGAGAC AGGTGTTGAA TGCACGGCT CCAACGACCT GGGCAAAAC ACCAGCATCC 1560
 TCTTCTGGA GCTGGTCAAT TTAACACCC GAGCCACAG CACTCCACA GAGAGAAAGC 1620
 TCAGCACTC CACTGCCAGT CCTCATACCA GAGCCACAG CACTCCACA GAGAGAAAGC 1680
 TGCGGAGCC GAGGAGCGG GGGTGGTCA TCGTGGCTG GATTGTGTG ATCTGTGTC 1740
 25 TGGCGTGCT GGGCGCTGTC CTCTATTTC TCTATAAGAA GGGCAAGCTG CCGTGCAGGC 1800
 GGTCAAGGAA GCAGGAGATC ACGCTGCCCC CGTCTGTGTA GACCGAACTT GTAGTTGAAG 1860
 TTAAGTCAGA TAAGCTCCCA GAAGAGATG GCGTCTGTA GACCGAACTT GTAGTTGAAG 1920
 GGGCTCCGGG AGACCAAGGA GAGAAATACA TCGATCTGAG GCATTAGCCC CGAATCACTT 1980
 CAGCTCCCTT CCTGCTGCG ACCATTCCCA GCTCCCTGCT CACTCTCTC TCAGCCAAAG 2040
 30 CCTCAAGG GACTAGAGAG AAGCCTCCTG CTCCTCTAC CTGCACACCC CCTTTCAGAG 2100
 GGCCACTGGG TTAGGACCTG AGGACCTCAC TTGGCCCTGC AAGCCGCTT TCAGGGAACA 2160
 GTCCACCACC ATCTCTCCA CGTTGAGTGA AGCTCATCCC AAGCAAGGAG CCCAGTCTC 2220
 CGAGCGGGT AGGAGAGTTT CTTCAGAAC GTGTTTTTC TTTACACACA TTATGGCTGT 2280
 35 AAATACCTG CTCCTGCCAG CAGCTGAGCT GGGTAGCCTC TCTGAGCTG TTTCTGCCC 2340
 CAAAGGCTG CTTCACCAT CCAGGTGCAC CACTGAAGT AGGACACACC AGCGGCATCC 2400
 GCCTGCTCAT GTTGAAGTGC GCTGTTACA CCGCTCCCG AGAGCACCCC AGCGGCATCC 2460
 AGAAGCAGCT GCAGTGTGTC TGCCACCAAC TGGTGTGATT CCTTAAAGA TACGTGCCG 2520
 ACATTTTTC TTTGGTCAGA AGCCAGGAAC GCGTGAATC CCAGCACTT GGGAGGCCGA 2580
 40 GGCCAGGTGT GGTGGCTCAC GCGTGAATC CCAGCACTT GGGAGGCCGA GCGGCCGA 2640
 TCACAAAGT AGGACGAGAC CATCTGGCT AACACGGTGA AACCTGTCT CTAATAAAA 2700
 TACAAAAAA AATTAGTAGT GGTAGTGGT TGGCACCTAT AGTCCAGCT ACTCGGAAGG 2760
 CTGAAGCAGG AGAATGGTAT GAATCCAGGA GGTGGAGCTT GCACTGAGCC GAGACCGTGC 2820
 CACTGCACCT CAGCCTGGGC AACACAGCGA GACTCCGCT CGAGGAAAAA AAAAGAAAAA 2880
 45 ACGCTACCT GCGGTGAGGA AGCTGGGCGC TGTTTTCGAG TTCAGGTGAA TTAGCTCAA 2940
 TCCCGTGTT CACTGCTCC CATAGCCCTC TTGATGGATC ACGTAAAACT GAAAGGCAGC 3000
 GGGAGCAGA CAAAGTAGG GTCTACACTG TCCTTACATG GGATTAAAGC TATGTTTATA 3060
 TTAGCACCAA ACTTTCACAA ACCAAGCTCA GGGCCCCAAC CCTAGAAAGG CCCAATGAG 3120
 AGAATGGTAC TTAGGGATGG AARACGGGGC CTGGCTAGAG CTTGGGGTGT GTGTGTCTGT 3180
 50 CTGTGTGTAT GCATACATAT GTGTGTATAT ATGGTTTTGT CAGGTGTGTA AATTGCAAA 3240
 TTGTTTCTT TATATATGTA TATATATATA TATATGAAA TATATATATA TATGAAAAA 3300
 AAAGCTTAAT TGTCCAGAA AATCATACAT TGCTTTTITA TTCTACATGG GTACCACAGG 3360
 AACTGGGGG CCGTGAAAC TACAACCAA AGGCACACAA AACCGTTCC AGTTGGCAGC 3420
 AGAGATCAGG GGTACCTCT GCTTCTGAGC AAATGGCTCA AGCTCTACCA GAGCAGACAG 3480
 55 CACCTACT TTTACAGCAG AAAACGTCCT GTATGAAGCA GCAGGAAGG CCTGCCAGC 3540
 TGTAGCAGG AGCTATGTCC CTTCTATGCT TTTCCGTCCA CTT

Seq ID NO: 352 Protein sequence
 Protein Accession #: NP_006491.1

60 1 11 21 31 41 51
 GLPRLVCAFL LAACCCCPRV AGVPGEAEQP APELVEVEVG STALLKCGLS QSQGNLSHVD 60
 WFSVHEKERT LIFRVRQGG QSEPGYEYQR LSLQDRGATL ALTQVTPQDE RIFLOQGRKP 120
 65 RSQYRIQLR VYKAPPEPNI QVNPLGIPVN SKEPEEVATC VGRNGYPIQ VIWYKNGRPL 180
 KEEKNRVHIQ SSQTVESSGL YTLQSLKAQ LVKEDKDAQ YCELNYRLPS GNMKESREV 240
 TVPVFPFEK VWLEVEPVGM LKEGDRVEIR CLADGNPPPH PSISKQNPST REABEETND 300
 NGVLVLEPAR KEHSGRYECQ AMNLDTMISL LSEPQELLVN YVSDVRVSPA APERQEGSSL 360
 TLTCREASSQ DLBPQWLREE TDQVLERGFV LQLHDLKREA GGGYRCVASV PSIPGLNRTQ 420
 70 LVKLAIFGPP WMAPKERVN VKENMVLNLS CEASGHPRPT ISNNVNGTAS EQDQDPQVRL 480
 STLNLVTPPE LLETGVECTA SNDLGRNTSI LFLBLVNLIT LTPDSNTTIG LSTSTASPH 540
 RANSTSTERR LPEPESRGVV IVAVIVCILV LAVLGAVLYF LYKKGKLPKR RSGKQBITLP 600
 PSRRTLELVE VKSDKLPEEM GLLQSSGDK RAPDQGEKY IDLRH

75 Seq ID NO: 353 DNA sequence
 Nucleic Acid Accession #: NM_003183.3
 Coding sequence: 165..2639

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 TCGAGCCTGG CGGTAGAATC TTCCCACTAG GCGGCGCGGG AGGGAAAAA GGATTGAGG 60
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Seq ID NO: 354 Protein sequence
 Protein Accession #: NP_003174.2

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Seq ID NO: 356 Protein sequence
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 TGCAAGGCCCT GCCTGGCACT TCTCCGCTGC TGCAACCGAG GTCAATGGT GGGCTTTAAG 2400
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 25 GGGCTGTCTT TGCGCTGCTC CCGCCTTTC ACCGAGAACC TGCTGAAGCC TGACACTCGG 2640
 GAGTGCAGCCC AGCTGCGCCA GGAGGTGGAG GAGAACCTGA ACGAGGTCTA CAGGCAGATC 2700
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 30 GGCTACTACA CCTTCACTGC AGACCAAGAC GCGCGGGGCA TGGTGGAGTT CCAGGAGGCG 2940
 GTGGAGCTGG TGGAGCTAGC GGTGCCCTTC TTTATCCGCG CTGAGGATGA CGACGAGAG 3000
 CAGCTGTCTG TGGAGGCCAT CGACGTGCCC GCAGGCACTG TGCTCTTTGA GCAGCTGAG 3060
 GTAAACATCA CCATCATCAA GGAGCAAGCC AGAGAGTGG TGCTCTTTGA GCAGCTGAG 3120
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 35 GCGCGGAAGT CCCAGGTCTC CTACCGCACA CAGGATGGCA CCGCGCAGGG CAACCGGAGC 3240
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 65 TTCACTGCCC TGAGCCAGA CTGCTGCTG CTGAGCTGG AGCGGCCAG GAGGCCAAT 4920
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 75 GCGGCTTCCC TCACCGGCA GTGACCCAG GAGTTTGTGA GCGGCACT GACCAACAG 5340
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 TACTG

Seq ID NO: 360 Protein sequence
 Protein Accession #: NP_000204.1

75 1 11 21 31 41 51
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 80 EVFEPLESPV DLYILMDPSN SMSDDLNLK KMQNLARVL SGLTSDVTIG FGKFDKVSF 180
 PQDMRPEKL KEFNPNSDPP PSFKNVISLT EDVDFRNLK QGERISGNLD APEGGFDAIL 240
 QTAVCRTDYG WRPDSTHLV FSTESAFHYE ADGANVLAGI MSRNDERCHL DTTGTYYQYR 300
 TDYPSVPTL VRLLAHNL PIFAVINYSY SYERKLHTYF PVSSGLVQLE DSSNIVELLE 360
 EAFNRIRENL DIRALDSPRG LRTEVTSKMF QRTRGSPHI RRGVEGIYQV QLRALHVDG 420

5 THVCQLPEDQ KGNHLKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV 480
 CSEGWGQTC NCSTGSLSDI QPCLREGEDK PCSGRGSCQC GHVCYCEGR YEGQFCBYDN 540
 FQCPRTSGFL CNDRGRCSMG QCVCEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCEGR 600
 CHCQOQSLYT DTICBINYSA IHPGLCEDLR SCVQCQANGT GEKKORTCEE CNPKVQMVDE 660
 10 LKRAEVEVVR CSFRDEDDDC TYSYTMEDG AFGPNSTVLV HKKDCPPGS FWNLIPLLLL 720
 LLPLLLALLL LCMKYCACCK ACLALLPCCN RGHMVGPKEO HYMLRENMA SDHLDTPMLR 780
 SGNLKGKRVV RNKVTNNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTRC 840
 AQLRQVEVEN LNEVYRQISG VHKLQOTKFR QQPNAGKKQD HTIVDTVLMA PRSAKPALLK 900
 15 LTERQVEQRA FHDLVKVPYG YTLTADQDAR GMVEFQEGVE LVDVVRVPLFI RPEDDDEKQL 960
 LVERAIDVPAG TATLGRRLVN ITIIEQDARD VVSFEQPEFS VSRGDQVARI FVIRRVLDGG 1020
 KSQSVYRTQD GTAQGNRDYI PVEGELLFQP GEAMKELQVK LLELQEVDSL LRGRQVRRFH 1080
 VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SPTSQMLSSQ PPPHGDLAGP QNPNKAAGS 1140
 RKIHFNLPP SGKPMGYRVK YNIQDSESE AHLLDSKVPS VELTNLYPYC DYEMKVCAYG 1200
 AQGEGFYSSL VSCRTHQEVV SEPGRLAFNV VSSTVTQLSW AEPATNGEI TAYEVCYGLV 1260
 20 NDDNRPIGPM KKVLDVDPKN RMLLIENLRE SQPYRYTVKA RAGAGWGPFR BAIINLATOP 1320
 KRPMISIPPI DIPIVDAQSG EDYDSPLMYS DDVLRSPSGS QRPVSDDTE HLVNRMDFP 1380
 PFGSTNSLHR MTTTSAAYG THLSPHVPHR VLSTSTLTR DYNLSLRSEH SHSTTLPRDY 1440
 STLTSSVSHD SRLTAGVPDT PTRLVPSALG PTLRLVSWQE PRCEPLQGY SVEYQLLNGG 1500
 25 ELHRLNIPNP AQTGTVVEDL LPNHSYVFRV RAQSQEGWGR EREGVITIES QVHPQSPLC 1560
 LPGAFTLST PASGPLVFT ALSPDSLQLS WERPRPRMNG IVGYLVTCM AQGGGPATAP 1620
 RVDGDSPEER LTVPGLENV PYKFKVQART TEGFPEREG IITIESQDGG PFPQLGSRAG 1680
 LFQHPLOQSEY SSITTTHTSA TEFPLVDGPT LGAQHLEAGG SLTRHVTOEF VSRTLTISGT 1740
 LSTHMDQOFF QT

25 Seq ID NO: 361 DNA sequence
 Nucleic Acid Accession #: NM_013332.1
 Coding sequence: 1..63

30 1 11 21 31 41 51
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 35 GCAGAGGAGT AGGTCTCTT CAGCCATGAA GCATGTGTTG AACCTCTACC TGTTAGGTGT 240
 GGTACTGACC CTACTCTCA TCTTCGTTAG AGTGATGAG TCCCTAGAAG GCTTACTAGA 300
 GAGCCCATCG CCTGGGACCT CCTGGACCAC CAGAAGCCAA CTAGCCAACA CAGAGCCACC 360
 CAAGGGCCTT CCAGACCATC CATCCAGAAG CATGTGATAA GACCTCCTTC CATACTGGCC 420
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 40 TGAGCACCGT TGTAACAGA GAACCTATTAC TAGGCCTTGA AGAACCTGTC TAACTGGATG 540
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 CACTTTGGGA GGCTGAGGTG GGTGGATCAC CTGAGGTGAG GAGTTGAGAG CCAGCCTCGC 660
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 GGCTGTAAAT CCAGTTCTCT TGGGAGGCTG AGGCGGGAGA ATTGCTTGAA CCGGGGGACG 780
 45 GAGGTTGCG TGAACCGAGA TGCCACTGCT GTACCCAGCC TGGGCCACAG TGCAAGACTC 840
 CATCTCAAAA AAAAAAAGAA AAAAAAAGC CTGTTTAATG CACAGGTGTG AGTGGATTGC 900
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 TCCTCAGCAG TATGGCTCTG ACATCTCTTA GATGTCCCAA CTTCACTGTG TGGGAGATGG 1020
 TGATATTTTC AACCTTACTT CCTAAACATC TGTCTGGGGT TCCTTTAGTC TTGAATGTCT 1080
 50 TATGCTCAAT TATTTGGTGT TGAGCCTCTC TTCCACAAGA GCTCCTCCAT GTTTGGATAG 1140
 CAGTTGAAGA GGTGTGTGG GTGGGCTGTT GGGAGTGAGG ATGGAGTGTG CAGTGGCCAT 1200
 TTCTCATTTT ACATTTTAAA GTCGTCTCTC CAACATAGTG TGTATTGTCT TGAAGGGGGT 1260
 GGTGGGATCG CAAAGCCTGC TCAAGTTATG GACATTGTGG CCACCATGTG GCTTAAATGA 1320
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55 Seq ID NO: 362 Protein sequence
 Protein Accession #: NP_037464.1

60 1 11 21 31 41 51
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 MKRVLNLYLL GVVLTLLSIF VRVMESEGLL LESPSPGTSM TTRSQLANTE PTKGLPDHPS 60
 RSM

65 Seq ID NO: 363 DNA sequence
 Nucleic Acid Accession #: NM_023915.1
 Coding sequence: 250..1326

70 1 11 21 31 41 51
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 GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA 180
 CCGACGCTTC AATCGTCCC AAGTGTTTCC TGACAAGCAT CTTTGCTTAC AGTGATCAC 240
 AACTGAAGAA TGGGGTTCAA CTTGACGCTT GCAAAATTAC CAAATAAAGA GTCGACGGC 300
 CAAGAGAGTC ACAATTACAG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCCTTAC 360
 75 AATGAATTGG ACACAATTGT CTTGCGGGT CTTTATCTCA TTATATTGT GGCAGCATC 420
 TTGCTGAATG GTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAAC CAGCTTCATA 480
 TTCTATCTCA AAAACATAGT GGTTCAGAC CTCATAATGA CGCTGACATT TCCATTTCGA 540
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 80 GATCGCTATC TGAAGTGTGT CAAGCCATT GGGGACTCTC GGAATGACAG CATTAACCTTC 720
 ACGAAGGTTT TATCTGTTTG TGTTTGGGTG ATCATGCGTG TTTTGTCTTT GCCAAACATC 780
 ATCTGCACAA ATCGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAAA ACTTAAAGT 840
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 GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960

5
 AGGCAATTCA TAAGTCAGTC AAGCCGAAAG CGAAAAACATA ACCAGAGCAT CAGGGTTGTT 1020
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 TGTAGGTCAAT TTCAAGAAG GCTGTTCAAA AAATCAATA TCAGAACCAG GAGTGAAAGC 1260
 ATCAGATCAC TGCAAGGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACACTGAT 1320
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 TTCATTATCC TTAATAAAAA AA

10
 Seq ID NO: 364 Protein sequence
 Protein Accession #: NP_076404

15
 1 11 21 31 41 51
 MGFNLTAKL PNNEHGGES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN 60
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 FYANMTSIV FLGLISIDRY LKVVKPFQDS RMYSTPTKV LSCVWVIMA VLSLPNIILT 180
 NGQPTEDNIH DCSKLSPLG VKWHTAVTVV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
 ISQSSRKRRH NQSIKRVVAV FFTCFLEPHL CRIPFTFSLH DRLLDESAQK ILYYCKEITL 300
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 FLSACNVCLD PIYFFMCRS PSRLFLKXSN IRTSRBSIRS LQSVRRSEVR IYDYDTDV

25
 Seq ID NO: 365 DNA sequence
 Nucleic Acid Accession #: NM_005365.1
 Coding sequence: 1..948

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 TCCTCTGACA GCAAGGAGGA GGAGGTGTCT GCTGCTGGGT CATCAAGTCC TCCCCAGAGT 180
 CCTCAGGGAG GCGCTTCCTC CTCCATTTCG GTCTACTACA CTTTATGGAG CCAATTGGAT 240
 GAGGGCTCCA GCAGTCAAGA AGAGGAAGAG CCAAGCTCCT CGGTGAGACC AGCTCAGCTG 300
 GAGTTCATGT TCCAAGAAGC ACTGAAATTG AAGGTGGCTG AGTTGGTTCA TTCTCTGCTC 360
 CACAAATATC GAGTCAAGGA GCGGTCACA AAGGCAGAAA TGCTGGAGAG CGTCATCAAA 420
 AATTACAAGC GCTACTTTCC TGTGATCTTC GGCAAGCCT CCGAGTTCAT GCAGGTGATC 480
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 CTTGGCCTCT CGTGGCATAG CATGCTGGGT GATGGTCATA GCATGCCCAA GCGCGCCCTC 600
 CTGATCATTT TCTGGGTGT GATCCTAAC AAAGCAACT GCGCCCTGTA AGAGGTTATC 660
 TGGGAAGCGT TGAGTGTGAT GGGGTGTAT GTTGGGAAGG AGCAGATGTT CTACGGGGAG 720
 40
 CCAGGAAGC TGCTCACCCA AGATTGGGTG CAGGAAACT ACCTGGAGTA CCGCAGGTG 780
 CCGCGCAGTG ATCCTGCGCA CTACGAGTTC CTGTGGGGT CCAAGGCCCA CGCTGAAACC 840
 AGCTATGAGA AGGTCATAAA TTATTTGGTC ATGCTCAATG CAAGAGAGCC CATCTGCTAC 900
 CCATCCCTTT ATGAAGAGGT TTTGGGAGAG GAGCAAGAGG GAGTCTGA

45
 Seq ID NO: 366 Protein sequence
 Protein Accession #: NP_005356.1

50
 1 11 21 31 41 51
 MSLEQRSPHC KPDEDLEAQ EDLGLMGAQE PTGEEETTS SSDSKBEEVS AAGSSSPFQS 60
 PQGASSSSIS VYITLWSQPD EGSSSQBEEB PSSSVDPAQL EFMQELKIL KVAELVHFL 120
 RKYRVKEPVT KAEMLESVIK NYKRYFFVIF GKASEFMQVI FGTDVKEVDP AGHSYIIVTA 180
 LQLSCDSMLG DGHSMPPKAL LIIVLGVILT KDNCAPEEVI WEALSVMGVY VGKRMFPYGE 240
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 PRKLLTQDWV QENYLEYRQV PGSDPAHYEF LWGSKAHAET SYEKVINYL VMLNAREPICY 300
 PELYBEVLGE EQEGV

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 Seq ID NO: 367 DNA sequence
 Nucleic Acid Accession #: NM_014400
 Coding sequence: 86..1126

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 1 11 21 31 41 51
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 GATCTGGACT GCAGGCTGGC TGCTGCTGCT GCTGCTTCG GAGGAGCGC AGGCCCTGGA 180
 GTGCTACAGC TGCGTGCAGA AAGCAGATGA CGGATGCTCC CGAACAAGA TGAAGACAGT 240
 GAAGTGGCGG CCGGGCGTGG ACGTCTGCAC CGAGGCCGTG GGGGCGGTGG AGACCATCCA 300
 CGGACCAATC TCGCTGGCAG TGCSGGGTG CGGTTCGGGA CTCCCAGGCA AGAATGACCG 360
 CGGCTTGGAT CTTCAAGGGC TTTCTGGCTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420
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 CTGCAACGCC AAGCTCAACC TCACCTCGCG GCGCTCGAC CCGCAGGTA ATGAGAGTGC 480
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 GGGTACATCG CCGCGGCTGG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGCGTG 600
 CTTGACGCGC AAGCTCACTT TGAAGGCGAG TAATGTGACT GTGTCTCTGC CTGTCCGGGG 660
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 TGGCTCTCTG TGCCAGGGGT CCGGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC 720
 CCCTCGAATC CCACCCCTTG TCGGCTGACC CCTCCAGAG CCCACGACTG TGGCCTCAAC 780
 CACATCTGTC ACCACTTCTA CCTCGGCCCG AGTGAGACCC ACATCCACCA CCACCCCAT 900
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 GCGAGCCGCA ACCAGTCAAG CTCGAGAGCA GGGAGTAGAA CACGAGGCGT CCGGGGATGA 960
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 TCCTGCAAAA GGGGGGCCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080
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 AAATTTCCCT CTCACCTACT TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCTCTGT 1200
 CCCACCACTG GACTGGGCTG GCGGAGCCCC TGTTTTCCA ACATTCCCCA GTATCCCCAG 1260
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GGGTGTTCTA GCTTTTGTAG GACAGCTCCT GTATCCTTCT CATCCTTGTC TCTCCGCTTG 1380
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 AGGATGTCAA GCTTCTACT CACTTCTTCC TAGCCAGCCT GGACTTTGGA GCGTGGGGTG 1500
 GGTGGGACAA TGGCTCCCA CTCTAAGCAC TGCTCCCTCT ACTCCCGGCA TCTTTGGGGA 1560
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 CTTATGCTG TGTGTGATGA GTTTCTGGCA CATAAATGCC TCAATAAAGA TTTAATTACT 1680
 TTGTATAGTG AAAAAAAA

Seq ID NO: 368 Protein sequence
 Protein Accession #: NP_055215

1 11 21 31 41 51
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 SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPFVVS CTNADSHVYK GCFDGNVTLT 180
 AANVTVSLPV RGCVDQDEFCT RDGVTGPGFT LSGSCCGGSR CNSDLRNTKY FSPRIPLVLR 240
 LPPPEPTTVA STTSVTITST AFVRPTSTTK PMPAPTSQTP RQGVHEASR DEEPRLTGGA 300
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Seq ID NO: 369 DNA sequence
 Nucleic Acid Accession #: NM_005329.1
 Coding sequence: 1..1662

1 11 21 31 41 51
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 CACTACTCTG CTTTCGGCCT GTACGGGCGCC ATCCTGGGCC TGACCTGCTC CATTGAGAGC 180
 CTTTTCCTCT TCCTGGAGCA CCGCGCATG CAGGTGCGG GCCAGGCCCT GAAGCTGCCC 240
 TCCCGCGCGC GGGGCTCGGT GGCCTGTGTC ATTGCCGCAT ACCAGGAGGA CCTGACTAC 300
 TTGCGCAAGT GCCTGCGCTC GCGCCAGCGC ATCTCCTTCC CTGACCTCAA GGTGCTCATG 360
 GTGGTGGATG GCAACGCCCA GGAGGACGCC TACATGCTGG ACATCTTCCA CAGGTGCTG 420
 GCGCGCACCG AGCAGGCGCG CTTCTTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG 480
 GGTGAGACGG AGGCCAGCCT GCAGGAGGCG ATGGACCGTG TGGCGGATGT GGTGCGGGCC 540
 AGCACTTCTT CGTGATCATC GCAGAAATGG GGAGGCAAGC GCGAGGTGAT GTACACGGCC 600
 TTCAAGGCCCT TCGCGGATTC GGTGGACTAC ATCCAGGTGT GCGACTCTGA CACTGTGCTG 660
 GATCCAGCCT GCACCATCGA GATGCTTCCA GTCTTGGAGG AGGATCCCCA AGTAGGGGGA 720
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 GTGCGGTACT GTGCGGCTT CAACGTGAGG CCGGCTGCC AGTCTCTACT TGGCTGTGTG 840
 CAGTGTATTA GTGGGCCCTT GGGCATGTAC CGCAACAGCC TCCTCCAGCA GTTCTCTGAG 900
 GACTGTATAC ATCAGAAAGT CCTAGGCAGC AAGTGCAGCT TCGGGGATGA CCGGCACCTC 960
 ACCAACCGAG TCCTGAGCCT TGGCTACCGA ACTAAGTATA CCGCGCGCTC CAAGTGCCTC 1020
 ACAGAGACCC CCCTAAGTA CTTCCGCTGG CTCAACAGC AAACCGCTG GAGCAAGTCT 1080
 TACTTCCGGG AGTGGCTCTA CAACTCTCTG TGGTTCATA AGCACCACCT CTGATGACC 1140
 TACGAGTCAG TGGTCACGGG TTCTTCTCCC TTCTTCTCA TTGCCACCGT TATACAGCTT 1200
 TTCTACCGGG GCGCATCTCG GAACATTCTC CTCTTCTGTC TGACCGGTGA CCGGTGGGCG 1260
 ATTATCAAGG CCACCTACGC CTGCTTCTCT CCGGGCAATG CAGAGATGAT CTTATGCTCC 1320
 CTCTACTCCC TCCTCTATAT GTCCAGCCTT CTGCGCGCCA AGATCTTTCG CATTGCTACC 1380
 ATCAACAAAT CTGGCTGGGG CACCTCTGGC CGAAAAACCA TTGTGGTGAA CTTCTTGGC 1440
 CTCAATCTCT TGTCCATCTG GGTGGCAGTT CTCTGAGAGG GGCTGGGCTA CACAGCTTAT 1500
 TGCCAGAGCC TGTTCAGTGA GACAGAGCTA GCCTTCTCTG TCTCTGGGCG TATACTGTAT 1560
 GGCTGCTACT GGTGGCCCTC CTCTATGCTA TATCTGGCCA TCATGCGCCG GCGATGTGGG 1620
 AAGAAGCCGG AGCAGTACAG CTTGGCTTTT GCTGAGGTGT GA

Seq ID NO: 370 Protein sequence
 Protein Accession #: NP_005320.1

1 11 21 31 41 51
 MPVQLTTALR VVGTSIFALA VLGGILAAYV TGYQFIHTEK HYLSPGLYGA ILGLHLIIQS 60
 LFAPLEHRRM RRAGQALKLP SPRRGSVLAL IAAYQEDPDY LRKCLRSAQR ISFPDLKVV 120
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 STPSCIMQKW GKGREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG 240
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 YFRENLYNSL WFKHHLWMT YESVVTGFFP PFLIATVIQL FYRGRIWNIL LFLITVQLVG 420
 IIKATYACPL RGNABIFMS LYSLLYMSSL LPAKIFALAT INKSGWGTSG RTIIVNFIG 480
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Seq ID NO: 371 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 148-7095

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Seq ID NO: 372 Protein sequence:

Protein Accession #: built from XP_031379

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50 Seq ID NO: 375 DNA sequence
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 Protein Accession #: BOS sequence

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Seq ID NO: 384 Protein sequence
 Protein Accession #: NP_005679.1

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 65 PVVAILGMIV MVIILGPTGF LGSAVFIFLY PAMMFASRLT AYFRKCVAA TDERVQRMNE 360
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 80 RYRENLPVLV KTVSFTIKPK EKIGIVGRTO SKKSSLMAL FBLVELSGGC IKIDGVRI 1260
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Nucleic Acid Accession #: NM_001327.1
Coding sequence: 89..631

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      GACCGGCCAT GCTGATGGCC CAGGAGGCCC TGGCATTCTT GATGGCCAG GGGGCAATGC 180
10     TGGCGGCCCA GGAGAGGCGG GTGCCACGGG CGGCAGAGGT CCGCGGGGCG CAGGGGCAGC 240
      AAGGGCCTCG GGGCGGGGAG GAGGCGCCCC GCGGGTCCG CATGGCGGCG CGGCTTCAGG 300
      GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCCGAG AGCGGCTGC TTGAGTTCTA 360
      CCTGCCATG CCTTTCGCGA CACCCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA 420
      GGATGCCCA CCGCTTCCCG TGCCAGGGGT GCTTCTGAAG GAGTTCAGTG TGTCCGSCAA 480
15     CATACTGACT ATCCGACTGA CTGCTGCAGA CCACGCCCAA CTGCAGCTCT CCATCAGCTC 540
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      GGCTCAGCCT CCCTCAGGGC AGAGGCGCTA AGCCCGCCT GGGCGCCCTT CCTAGGTGAT 660
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Seq ID NO: 386 Protein sequence
Protein Accession #: NP_001318.1

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30 Seq ID NO: 387 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 52..459

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      GGTCCCGGGG GCGCAGGGGC AGCAAGGGCC TCGGGGCCGA GAGGAGCGCG CCGCGGGGT 240
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      GACAGCGCCG TGCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC 360
      ATCAGCTCCT GTCTCCAGCA GCTTTCCTG TTGATGTGGA TCAAGCAGTG CTTTCTGCCC 420
      GTGTTTTGGG CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CGCCCTTCC 480
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45     GCCTGATTGT TTGTCGCTGG AGGAGGACGG CTTACATGTT TGTTCCTGTA GAAATAAAG 600
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Seq ID NO: 388 Protein sequence
Protein Accession #: Eos sequence

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60 Seq ID NO: 389 DNA sequence
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Coding sequence: 90..3671

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      GCTTCTGCTC CTCTCTGCC CAGCGCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA 180
      ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGGAACTTCA CAGACAACT GGTAAATGAT 240
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      GCTTTTACCG GCACAGAGAA AGGGACCGCT GTTGGCCCTG CAATTGTAAC TCCAAGGTT 360
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 Protein Accession #: NP_005553.1

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75 Seq ID NO: 392 Protein sequence
 Protein Accession #: AAD16433.1

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Seq ID NO: 393 DNA sequence
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Seq ID NO: 394 Protein sequence
Protein Accession #: NP_006171.1

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Seq ID NO: 396 Protein sequence
 Protein Accession #: AAL67965.1

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Protein Accession #: BAB61048.1

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Seq ID NO: 401 DNA sequence

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GGGCTCCGCG	CCCGCAGGCC	CTGCCCCCGC	CGAAGGCCCC	CCGCTGTGCC	TGGGCTCCCC	480
CGCGCGCCAC	CTGCGCGGGG	GACGCACGGC	CCGCTGGTGC	AGTGGAAAGG	CCCGGCGGCC	540
CGCGCGCGAG	CCTTCTCGGC	CCGCGCCCCC	GCGGCTGCA	CCCCCATCTG	CTCTTCCCCG	600
CGCGGCGCGG	GCGGCGCGGG	CTGGGGGCCC	GGGCAGCCGC	GCTCGGCGAG	CGGGGGCGGG	660
GGGCTGCGCG	CTGGGCTCGC	AGCTGGTGCC	GCTGCGCGCG	CTCGGCTCGG	GCCACCGCTC	720
CGACGAGCTG	GTGGGTTTCC	GCTTCTCGAG	CGGCTCTGTC	CGCGCGCGCG	GCTCTCCACA	780
CGACCTCAGC	CTGGCCAGCG	TACTGGCGCG	CGGGGCGCTG	CGACCGCCCC	CGGGCTCCCC	840
GCCCGTCAGC	CAGCCCTGCT	GCCGACCCAC	GCGCTACGAA	GCGGTCTCCT	TGATGGACGT	900
CAACAGCACC	TGGAGAACCG	TGGACCGCCT	CTCCGCCACC	GCTCGGCGCT	GCTTGGGCTG	960
AGGGCTCGCT	CCAGGGCTTT	GCAGACTGGA	CCCTTACCGG	TGGCTCTTCC	TGCGTGGGAC	1020
CCTCCCGCAG	AGTCCCACTA	GCCAGCGGCC	TCAGCCAGGG	ACGAGGGCCT	CAAAGCTGAG	1080
AGGCCCCCTAC	CGGTGGGTGA	TGGATATCAT	CCCCGAACAG	GTGAAGGGAC	AACCTGACTAG	1140
CAGCCCCCAGA	GCCCCACCCC	TGCGATATCC	AGCCTAAAGG	ACACAGAGAG	CCTCAGCTAT	1200
GGAGCCCTTC	GGACCCACTT	CTCAGAGACT	CTGGCACTGG	CCAGGCTCTG	AACCTGGGAC	1260
CCCTCTCTCG	ATGAACACTA	CAGTGGCTGA	GGCATCAGCC	CCCCGCCAGG	CCCTGTAGGG	1320
ACAGCATTTG	AAGGACACAT	ATTGCACTTG	CTTGGTTGAA	AGTGCTCTGT	CTGGAAGTGG	1380
CCTGTACTCA	CTCATGGGAG	CTGGCCCC				

Seq ID NO: 402 Protein sequence

Protein Accession #: NP_003967.1

35
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1	11	21	31	41	51	
MELGLGLST	LSHCPWPRRQ	PALWPTLAAL	ALLSSVAEAS	LGSAPRSPAP	REGPPPPVLAS	60
PAGHLPGGRT	ARWCSRRARR	PPPQSRPAP	PPPAPPSALP	RGGRAARAGG	PGSRARAAGA	120
RGCRRLSQLV	PVRALGLGHR	SDELVRFRFC	SGSCRARSFP	HDLSLASILG	AGALRPPPPGS	180
RPVSQPCCRP	TRYEAVSFMD	VNSTWRIVDR	LSATACGCLG			

Seq ID NO: 403 DNA sequence

Nucleic Acid Accession #: NM_057091.1

Coding sequence: 783..1445

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1	11	21	31	41	51	
ACTGGCGGCT	GAGAGAAGAA	TCGGGTGGAG	CAGAGAGCAG	CTGCTGCAGG	GCAGACAGCC	60
GGACCCCAAA	ATCTGCACGT	ACCAGCAGTC	AGCCGCCCCA	CGCAGGGACC	GGCTTACCCC	120
TCGCTCCCGG	CCCTCACTCA	CTTTCTCCCG	CCCTCGGCCC	GGCCTCCCGC	CTCTCTACTT	180
CGCGTGTCTA	CAAACCTAAC	TCCCGGTTTC	CGTGCTCTCT	CACCGCTCGA	GTCTCTACTT	240
CTCCATATCC	GAGGGGGCCC	TCCAGCAGTC	TACCCCCCTC	CCAACCTCGG	GGGACCTAGC	300
CAAGCTAGGG	GGGACTGGAT	CCGACGGGTG	GAGCAGCCAG	GTGAGCCCCG	AAAGGTGGGG	360
CGGGGACGGG	CGCTCCCGAG	CCCCACCCCG	GGATCTGGTG	ACGCTGGGCG	TGGAAATTGA	420
CACCGGACGG	CTGCGCGCGC	GGGCAGGAGG	CTGCTGAGGG	ATGGAGTTGG	GCCCGGCCCC	480
CAGACAAGGC	CGGGGGGCTC	CGCCAGCAGC	AGGTCCCTCG	GGCCCAAGCC	CTCGCTGCCA	540
CCCGGGGCTG	GAGCCCCACA	CCGAGGGGTG	CAGACTGGCT	GCCAAGGCCA	CACTTTGGGC	600
TAAAAGAGGC	ACTGCCAGGT	GTACAGTCTT	GGGCATGGCG	TGTTTGAGCT	TCGGGGGAGA	660
GCCCAGCACT	GGTCCCGGGA	AAGGTGCCTA	GAAGAACAAG	GTGCAGGACC	CGGTGCTGCC	720
TCAACAGAGG	GGTGGGGGAA	CAGCTCAACA	ATGGCTGATG	GGCGCTCCTG	GTGTTGATAG	780
AGATGGAAGT	TGGACTTGGA	GGCTCTCCCA	CGCTGTCCCA	CTGCCCTTGG	CCTAGGCGGC	840
AGCCTGCCTT	GTGGCCACCC	CTGGCGGCTC	TGGCTCTGCT	GAGCAGCGTC	GCAGAGGCCT	900
CCCTGGGCTC	CGCGCCCCGC	AGCCTTGCCC	CCCGGGAAGG	CCCCCGGCTT	GTCTTGGCGT	960
CCCCCGCGGG	CCACCTGCGG	GGGGGACGCA	CGGCGCGCTG	GTGCAGTGGA	AGAGCCCGGC	1020
GGCGCGCGCG	GCAGCTTCTT	CGGCGCGCGC	CCCGCGCGCC	TGCACCCCCA	TCTGCTCTTC	1080
CCCGCGGGGG	CCGCGCGCGG	CGGGCTGGGG	GCCCGGGCAG	CGCGCTCGGG	GCAGCGGGGG	1140
CGCGGGGCTG	CGGCTGCGCG	TCGCAGCTGG	TGCCGCTGCG	CGCGCTCGGC	CTGGGCCACC	1200
GCTCGGACGA	GCTGGTGGGT	TTCGCTTCTT	GCAGCGGCTC	CTGCCGCGCG	GCGCGCTCTC	1260
CACACGACCT	CAGCCTGGCC	AGCCTACTGG	GCGCGGGGCG	CCTGCGGACG	CCCCCGGGCT	1320
CCCGGGCGGT	CAGCCAGCCC	TGCTGCGGAC	CCACGCGCTA	CGAAGCGGTC	TCCTTCATGG	1380
ACGTCAACAG	CACCTGGAGA	ACCGTGGACC	GCCCTCTCCG	CACCGCTTGC	GGTGCCTTGG	1440
GCTGAGGGCT	CGCTCCAGGG	CTTTGCAGAC	TGGACCCCTA	CCGTTGGGCT	TTCCTGCTTG	1500
GGACCTCTCC	CGAGAGTCCC	ACTAGCCAGC	GGCCTCAGCC	AGGGACGAGG	GCTTCAAGGC	1560
TGAGAGGCCC	CTACCGGTGG	GTGATGGATA	TGATCCCGGA	ACAGGTGAAG	GGACAACCTG	1620
CTAGCAGCCC	CAGAGCCCTC	ACCCTGCGGA	TCCAGGCTTA	AAAGACACCA	GAGACCTCAG	1680
CTATGGAGCC	CTTGGGACCC	ACTTCTCACA	GACTCTGGCA	CTGGCCAGGC	CTCGAACCTG	1740
GGACCCCTCC	TCTGATGAAC	ACTACAGTGG	CTGAGGCATC	AGCCCCCGCC	CAGGCGCTGT	1800
AGGACACGCA	TTTGAAGGAC	ACATATTGCA	GTTCCTTGGT	TGAAAGTGCC	TGTGCTGGAA	1860
CTGGCCTGTA	CTCACTCATG	GGAGCTGGCC	CC			

Seq ID NO: 404 Protein sequence

Protein Accession #: NP_003967.1

1 11 21 31 41 51
 5 MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPFVLAS 60
 PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRRARAAGA 120
 RGCRLRSQVL FVRLALGLGHR SDELVRPRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180
 RPPVSPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

10 Seq ID NO: 405 DNA sequence
 Nucleic Acid Accession #: NM_057160.1
 Coding sequence: 1..714

1 11 21 31 41 51
 15 ATGCCCGGCC TGATCTCAGC CGAGGACAG CCCCTCCTTG AGGTCCTTCC TCCCCAAGCC 60
 CACCTGGGTG CCCTCTTTCT CCCTGAGGCT CCACTTGGTC TCTCGCGCA GCCTGCCCTG 120
 TGGCCACACC TGGCCGCTCT GGCTCTGCTG AGCAGCGTCG CAGAGGCCTC CCTGGGCTCC 180
 GCGCCCGCA GCGCTGCCCT CGCGAAGGC CCCCGCCTG TCTTGGGCTC CCCGCGGCG 240
 20 CACCTGCGCG GGGGACGCAC GGCCGCTGG TGCAGTGAA GAGCCCGCG GCGCGCGCG 300
 CAGCTCTTTC GGCCCGCGCC CGCGCGCCT GCACCCCAT CTGCTCTTCC CGCGCGGCG 360
 CGCGCGGCG CGGCTGGGG CGCGGCAGC CGCGCTCGG CAGCGGGGC GCGGGGCTGC 420
 CGCTGCGCT CGCAGCTGGT GCGGTGCGC GCGCTCGGC TGGGCCACG CTCGCAAGAG 480
 CTGGTGCTT TCGCTTCTG CAGCGCTCC TCGCGCGCG CGCGCTCTC ACAAGACCTC 540
 25 AGCCTGGCCA GCTACTGGG CGCGGGGCC CTGCGACCG CCGCGGCTC CGGCGCGCTC 600
 AGCCAGCCCT GCTGCGGACC CAGCGCTAC GAAGCGGCTC CCTTCATGGA CGTCAACAGC 660
 ACCTGGAGAA CCGTGAGCG CCTCTCGGC ACCGCTCGG GCTGCTGGG CTGAGGGCTC 720
 GCTCCAGGCC TTTCAGACT GGACCTTAC CGTGGCTCT TCTGCTGCG GACCTCTCCG 780
 CAGAGTCCA CTAGCCAGG GCTCAGCA GGGACGAAG CCTCAAGCT GAGAGGCCCC 840
 30 TACCGGTGGG TGATGGATAT CATCCCGAA CAGGTGAAG GACAACTGAC TAGCAGCCCC 900
 AGAGCCCTCA CCCTGCGGAT CCCAGCTAA AAGACACAG AGACCTCAGC TATGGAGCCC 960
 TTGGGACCCA CTCTCAGAC ACTTGGCAC TGGCCAGGC TCGAACCTGG GACCTCTCT 1020
 CTGATGAACA CTACAGTGGC TGAGGCATCA GCGCCCGCC AGGCCCTGTA GGGACAGCAT 1080
 TTGAAGACA CATATTGCA TTGCTTGGT GAAAGTGCT GTGCTGGAAC TGGCCTGTAC 1140
 35 TCACTCATGG GAGCTGGCCC C

Seq ID NO: 406 Protein sequence
 Protein Accession #: NP_476501.1

40 1 11 21 31 41 51
 MPGLISARGQ PLLEVLPPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SVAEASLGS 60
 APRSPAPREG PPVLAAPAG HLPGRRTARW CSGRRARPPF QPSRPAPPPF APPSALPRGG 120
 45 RAARAGPGS RARAAGARG RLRSQLVFVR ALGLGHRSD LVRFRFCSGS CRRARSPHDL 180
 SLASLLGAGA LRPPGSRFV SQPCRPTRY EAVSFMDVNS TWRTVDRLSA TACGCLG

Seq ID NO: 407 DNA sequence
 Nucleic Acid Accession #: NM_057090.1
 Coding sequence: 29..715

1 11 21 31 41 51
 50 CTGATGGGGC CTCTGGTGT TGATAGAGAT GGAACITGGA CTGGAGGCC TCTCCACGCT 60
 GTCCCACTGC CCCTGGCCTA GCGGCGAGC TCCACTTGGT CTCTCGCGC AGCCTGCCCT 120
 55 GTGGCCACAC CTGGCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT CCCTGGGCTC 180
 CGGCGCCGCG AGCCCTGCC CCGCGAAGG CCCCCCGCT GTCTGGGCT CCGCGCGCG 240
 CCACCTGCGG GGGGAGCGCA GCGCGGCTG GTGCACTGGA AGAGCCCGC GCGCGCGCG 300
 GCAGCTTCT CGGCGCGCG CCGCGCGCG TGCACCCCA TCTGCTCTC CCGCGCGGG 360
 60 CCGCGCGCG CCGGCTGGG GCGCGGCGC CGCGCTCGG GCAGCGGGG CGCGGGGCTG 420
 CGGCTGCGC TCGCAGCTGG TCGCGGTGG CGCGCTGGC CTGGGCCACC GCTCCGACG 480
 GCTGGTGGT TTCGCTTCT GCAGCGGCTC CTGCGCGCG GCGGCTCTC CACAGCAGCT 540
 CAGCTGGCC AGCCTACTG GCGCGGGGC CCTGCGACG CCGCGGGCT CCGCGCGCGT 600
 CAGCTAGCC TGCTGCGAC CCACGCGTA CGAAGCGGT TCTTTCATG ACCTCAACAG 660
 65 CACCTGGAGA ACCGTGGACC GCTCTCCGC CACCGCTGC GGTGCTGCT GCTGAGGGCT 720
 CGCTCCAGG CTTTGCAGAC TGGACCTTA CGGTGGCTC TTCTGCTG GACCTCTCC 780
 GCAGAGTCCC ACTAGCCAG GGCCTCAGC AGGGAAGAG GCTCAAGC TGAGAGGCC 840
 CTACCGGTGG GTGATGGATA TCATCCCGA ACAGGTGAAG GACAACTGA CTAGCAGCCC 900
 CAGAGCCCTC ACCCTGGGA TCACAGCTA AAAGACACA GAGACCTCA CTATGGAGCC 960
 70 CTTGGGACCC ACTTCTACA GACTCTGGC CTGGCCAGG CTGAACTG GACCTCTCC 1020
 TCTGATGAAC ACTACAGTG CTGAGGCATC AGCCCCGCG CAGGCGCTGT AGGGACAGCA 1080
 TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAAGTGCC TGTGCTGGA CTGGCCTGTA 1140
 CTCACATG GAGCTGGCCC C

75 Seq ID NO: 408 Protein sequence
 Protein Accession #: NP_476431.1

1 11 21 31 41 51
 80 MELGLGGLST LSHCPWPRRQ AFLGLSAQPA LNPPTLAALAL LSSVAEASLG SAPRSPAPRE 60
 GPPFVLASPA GHLPGGRTAR WSGRRARRPP PQPSRPAPPP PAPPSALPRG GRAARAGGPG 120
 SRARAAGARG CRLRSQLVFV RALGLGHRSD ELVRFRFCSG SCRARRSPHD LSLASLLGAG 180
 ALRPPPGSRP VSQPCRPTRY YEAVSFMDVN STWRTVDRLS ATACGCLG

Seq ID NO: 409 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1746

5	1	11	21	31	41	51	
	ATGCCACTGA	AGCATTATCT	CTTTTGTCTG	GTGGGCTGCC	AAGCCTGGGG	TGCAGGGTTG	60
	GCTTACCATG	GCTGCCCTAG	CGAGTGTACC	TGCTCCAGGG	CCTCCCAGGT	GGAGTGCACC	120
	GGGGCAGCGA	TTGTGGCGGT	GCCCACCCCT	CTGCCCTGGA	ACGCCATGAG	CCTGCAGATC	180
10	CTCAACAGCG	ACATCACTGA	ACTCAATGAG	TCCCGTTCC	TCAATATCTC	AGCCCTCATC	240
	GCCTTGAGGA	TTGAGAAGAA	TGAGCTGTGC	CGCATCACGC	CTGGGCGCTT	CCGAAACCTG	300
	GGCTCGCTGC	GCTATCTCAG	CCTCGCCAC	AACAAGCTGC	AGGTTCTGCC	CATCGGCGCTC	360
	TTCCAGGGCC	TGGACAGCCT	TGAGTCTCTC	CTTCTGTCCA	GTAACCACTG	GTTGCAGATC	420
	CAGCGCGCCC	ACTTCTCCCA	GTGCAGCAAC	CTCAAGGAGC	TGCAGTTGCA	CGGCAACCAAC	480
15	CTGGAATACA	TCCCTGACGG	AGCCTTCGAC	CACCTGGTAG	GACTCACGAA	GCTCAATCTG	540
	GGCAAGAATA	GCCTCACCCA	CATCTCACCC	AGGCTCTTCC	AGCACCTGGG	CAATCTCCAG	600
	GTCTCTCCGC	TGTATGAGAA	CAGGCTCAGC	GATATCCCA	TGGGCACCTT	TGATGGGCTT	660
	GTTAACTTGC	AGGAAGTGGC	TCTACAGCAG	AACCAGATTG	GACTGTCTCT	CCCTGGTCTC	720
	TTCCACAACA	ACCAACAACCT	CCAGAGACTC	TACCTGTCCA	ACAACCAAT	CTCCAGCTG	780
20	CCAGCCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACGCTC	TTACTCTCTT	TGGGAATTC	840
	CTGAGGAGGC	TCTCTCTGGG	GATCTTCGGG	CCCATGCCCA	ACCTGGCGGA	GCTTTGGCTC	900
	TATGACAAAC	ACATCTCTCT	TCTACCCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	GTCTGTATTC	TAGCCGCAAA	TCAGATCAGC	TTCATCTCCC	CGGGTGCTTT	CAACGGGCTA	1020
	ACGGAGCTTC	GGGAGCTGTC	CCTCCACACC	AACGCACTGC	AGGACCTGGA	CGGGAATGTC	1080
25	TTCCGATATG	TGGCCAACTT	GCAGAACATC	TCCCTGCAGA	ACAATCCGCT	CAGACAGCTC	1140
	CCAGGGAAATA	TCTTCGCCAA	GCTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACAACCAAG	1200
	CTGGAGAACT	TGCCCTCTGG	CATCTTCGAT	CACCTGGGGA	AAGTGTGTGA	GCTGGCGCTG	1260
	TATGACAAATC	CTGGAGGCTG	TGACTCAGAC	ATCCTTCGCG	TCCGCAACTG	GCTCTGCTCT	1320
	AACCAAGCTTA	GTTTAGGGAC	GGACACTGTA	CCTGTGTGTT	TCAGCCAGC	CAATGTCCGA	1380
30	GGCCAGTCCC	TCAATATCAT	CAATGTCAAC	GTGCTGTTC	CAAGCTTCCA	TGTCCCTGAG	1440
	GTGCTAGATT	ACCCAGAAAC	ACCATGTGAC	CCAGACACAC	CCAGTTACCC	TGACACCAAC	1500
	TCCTGTCTCT	CTACCACTGA	GCTAACCCAG	CCTGTGGAAG	ACTACACTGA	TCTGACTACC	1560
	ATTTCAGGTC	CTGATGACCG	CAGCGTTTGG	GGCATGACCC	AGGCCAGAG	CGGGCTGGCC	1620
	ATTGCGCGCA	TTGTAAATGG	CATTGTGCC	CTGGCTGTCT	CCCTGGCTGC	CTGCTGCGC	1680
35	TGTTGTCTGT	GCAAGAAAG	GAGCCAAAGT	GTCTGTATGC	AGATGAAGGC	ACCCAATGAG	1740
	TGTTAAAGAG	GCAGGCTGGA	GCAGGGCTGG	GGAATGATGG	GACTGGAGGA	CCTGGGAATT	1800
	TCATCTTTCT	GGCTCCACCC	CTGGTCCAT	GGAGCTTCC	CCTGATTGCT	CTTTCTGGCC	1860
	CTAGATAAAG	GTGTGCTTAC	CTCTTCTGTA	CTTGCTGTAT	TCTCCGCTAG	AGAAGCAGGT	1920
40	CGTGCCGGAC	CTTCTTACAA	TCAGGAAGAT	AGATCCAACT	GGCATGGCA	AAAGCCCTGG	1980
	GGATTTCGGA	TTTATACCCC	TGGGCTTCC	TCGAGAGGGC	TCTTCTTCCA	AATCCTCCCC	2040
	ACCTGTCTCT	CAAGAACAGC	CTTCCCTGCG	CCCAGGCCCC	CTCCGGGCTT	CTGTAGACTC	2100
	AGTTAGTCCA	CAGCTGTCTC	ACTTCGTGGG	AATAGTTCTC	CTGTGTTGTG	CTATGGCTTG	2160
45	CCTAAGTATT	ATGTAAGTTG	ATTTCCCTTC	TTTTGTTTCT	CTTGTGTTGT	CTATGGCTTG	2220
	ACCCAGCATG	TCCCTTCAAA	TGAAAGTTCT	CCCCTTGATT	TTCTGCTCCT	GAAGGCAGGG	2280
	TGAGTTCTCT	CCTCAAAGAA	GACTTCAAAAC	CATTTAACCT	GTTTCTTAAG	AGCCGCTCAAT	2340
	CAGCTCGGTT	TTGGGGATGC	TATGAAAGAG	AGAAGGAAAA	TCATGCCGCT	CAGTTCTCTG	2400
50	AGACAGAAGA	GCCTCTATCA	GTGTCTCACT	TGTGATTTTT	ATCTGGAAAA	GGAGAGAAAC	2460
	CCCAGCAGCA	GCAAGCTCAG	CCTTTTAGAG	AAGGATATTT	CCAAACTGCA	AACCTTGCTT	2520
	TGAAAGTTT	AGCCCTTTAA	GGAATGAAAT	CATGTAGAAT	TTTGGACTTC	TAAAAACATT	2580
	AAAATCAGCT	TATTAATACG	GGATAGAGAA	AGAAATCTGG	TGCTGGGGG	TCCCTGTGTT	2640
	CACCCCTAGA	GTTTGTTTTA	AAATTTTAA	TTGAAGCATG	TGAAGTGTAC	STGCAGAAAA	2700
55	GTGGGAACAT	GATAGTGTAT	GGCTTGGTGG	ATTTTCAAA	ACTGAACATA	CTGTGTAAAT	2760
	CAGCATCTAG	ACCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCCTGGGC	TTTTCCAGAA	2820
	GGAGATGGGG	GCTTCTGAAG	ATGGACTTAC	CTGGGACCTG	CCCCCATGA	GCCAGGACGG	2880
	TCCCCCCACA	GTACAGCTGT	GCAAGGGGCC	CGTGGCCAGG	GGTGAGGAG	AATATGTGGG	2940
	TGTGGAGACG	ATGGGAGACT	GTGGCCTGAA	CAGGAGATTT	TATTATATCT	GGAGACCCCT	3000
	AGAGACCCCT	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
60	GTCCGTGACG	CCACACCCCT	TTCCCTGCCA	GCAAGTTGTC	TGCGCTCAT	CGGAGGCCCC	3120
	TCGCGCTGGA	GCCTTCTATG	GACGTGATAT	GCCTGTATCT	GTTTTTAATT	TTCAITCTTC	3180
	ACTTAGGGGA	AGTGAATCG	CTCAGAGATG	AGATCCTTTA	ATTGAAACG	AGTGTAAACG	3240
	GATCTAGTGT	TCTTTCTAAT	GTGGTAAAAA	TCTCCATCAA	CATCACAGTC	AGCTGGCAGC	3300
	TGAACCTTCA	AATCTCACTT	ACAGCAGGCG	ACAAGGGGGT	ACACGATGAG	GTCAACTGG	3360
	GTCTGGGGGC	TCCCTGGAGC	TCTCTCTGCG	TGTGGTCTGG	TTAGGAGTTG	AGTTGTTTGC	3420
65	TCCAGGGTTA	TTCTCTCTCT	CGAGTCAACG	TCACAAGAAAT	ACCTGCCTTC	TCTGGCTTTC	3480
	CTGCTATACA	CATATTACAA	TGGCGCTCAA	GAAGTTAGGC	TCATGGCAAC	GTGTGTCTTT	3540
	CTCTGACAAA	CTGGCCCACT	TTACAGTGAA	ATGGAGAAAT	TCAGGTCTCT	ACGTCTGCCC	3600
	AGGAAGAAG	TTCACTGAGC	TCCACGGGGA	TCTGGAATC	CACGACCAAT	CCGATCCGCG	3660
	TCTTATTAGC	TCCCGCTCC	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	CCATCCCGGA	3720
70	TGGGCTCTTA	TTAGCTCCCC	GCTCCACAAG	ACACCTGTGA	TCTGGAAATC	TACCAACCAAT	3780
	CCGATCCGCG	TCTTATTAGC	TCCCGCTCC	ACAAGACACC	TGTGACATCC	TCCAGGGCCA	3840
	CAGGAGCAGC	TGCTGACCGG	TTTTCCCTTC	CAGTTCTGTC	ACAAAAAGTG	TCCAGAGGGC	3900
	TGTTTGCAAA	CATAGTGA	CTTTGTAGCT	TTTCAACCTC	TGTCACAGG	AATCTAGGAG	3960
	AGATGAGGCC	CGTCAGAGTC	AAGAGATGTC	ATCCCCCAG	GSTCTCCAAG	GCATTTCCAC	4020
75	ACTATTGGTG	GCACCTGGAG	GACATGCACC	AAGGCTTGCC	AGAGCCCAAC	GGAAGTGAGC	4080
	CCAGAGCATG	GCACATGAGC	ATCACCGGCT	GATGGTGGCC	TGCTGTGCTT	GSTGCCAACA	4140
	GGGGCATCCC	GGCCCGTACC	CCTCCAGACA	GGAAGCATGG	GTTTGGCCAC	AGACCTGTCT	4200
	GGTCTCTCTG	TGAGTGGCCT	CCAGATGTCT	TTGTGCATAG	GCACAAGTGG	GCCAGGGCTG	4260
	GAGGGAGGTG	GGAAACCTCA	TCATCCGGTG	GGCCCTGCCA	ATCTTAACCC	AGAACCTTTA	4320
80	GGTATTCCTG	GCAGTGGCCA	TGACATTGGA	GCACTTCTCT	CTCCAGCCAG	AGGCTGACCT	4380
	GAGGGCCACT	GTCTTCAGAT	GACACCAACC	AGGAGCACCC	TAGGTGAGGG	GTGAGGGCCC	4440
	CCTTATGTGA	ACCTCTTGCC	TCTTCTTTTC	TCCCATCAGA	GTGGTTGGAT	GGAGCCATTG	4500
	GCCTCTCTTT	CTTCAGGGGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
	TACTAGAAAA	GCTGAGTGGG	GTCTCTTTTC	CAACAGGATG	ATGCATTGTC	TCAATTCTCA	4620
	GGGCTGGAAT	GAGCCGGCTG	GTCCCCACGA	AAGCTGGAGT	GGGGTACAGA	GTTCAAGTTT	4680

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CCTCTCTGTT TACAGCTCCT TGACAGTCCC ACGCCCATCT GGAGTGGGAG CTGGGAGTTA 4740
GTGTTGGAGA AGAAACAACA AAAGCCAATT AGAACCATA TTTTAAAAA GTGCTTACTG 4800
TGACACAGATA CTCTTCAAGC ACTGGACGTG GATTCTCTCT CTAGCCCTCA GCACCCCTGC 4860
GGTAGGAGTG CGCCTCTAC CCACTTGTGA TGGGTACAG AGGCACTTGC TCTCTGCAT 4920
GGTGTCAAT AGGCTGGGAG TTTTATTAT CTCTTCAAAC TTTGTACAAG AGCTCATGGC 4980
TTGCTTGGG CTTCCTCAT TAAACCAAG GAAATGGAAG CCATTCCCTT GTTGTCTCC 5040
TTAGTCTTGG TCATCAGAAC CTCACTTGGT ACCATATAGA TCAAAAGCTT TGTAAACCACA 5100
GGAAAAATA AACTCTTCCA TCCCTTAAAG AATAGAAATG TTTGTCCCTC TCATGGGAAT 5160
TGGGCTGTAT GTATATTGTT CTTCCTCCTT AGAATTAGA GATACAAGAG TTCTACTTAG 5220
AACTTTTCAT GGACACAATT TCCACAACCT TTCAGATGCT GATGTAGAGC TATTGGGAAA 5280
GAACTTCCAA ACTCAGGAAG TTTGCAGAGA GCAGACAGCT AGAGATAACT CGGAGCCCG 5340
AGTTGGTGA CAGATGTTAG ATGTATCCTA GCTTTTAGCC ATAAACCACT CAAGATTCA 5400
GCCCCAGAT CCCACAGTCA GAACTGAATC TGGTTGTGTG GGAAGCCAGC AGTGGCCTTG 5460
GGAAGGAAGC CATGGCTGTG GTTCAGAGAG GGTGGGCTGG CAAGCCACTT CCGGGGAAAA 5520
CTCCTTCGCG CCCAGGTTTC TTCTTCTCTT AAGGAGATAT TGTCTCACC AACCCGCTGC 5580
CTTCATGCTG CTTTCAAAGC TAGATCATGT TTGCCTTGCT TAGAGAAATTA CTGCAATCA 5640
GCCCCAGTGC TTGGCGATGC ATTTACAGAT TTCTAGGCC TCAGGGTTTT GTAGAGTGTG 5700
AGCCCTGGTG GGCAGGGTGT GGGGGTCTGT CTCTGCTGG ATGCTGCTTG TAATCCATT 5760
GGGTACAGA ATCAACAATA AATAATATAC ATGTAT

Seq ID NO: 410 Protein sequence

Protein Accession #: BAB84587.1

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1 11 21 31 41 51
MPLKHYLLLL VGCQAWGAGL AYHGCPSSECT CSRASQVECT GARIVAVFTP LPWNAMSLQI 60
LNTHITELNE SPFLNISALT ALRIEKNELS RITPGAFLNL GSLRYLSLAN NKLQVLPIGL 120
PQGLDSLESL LLSSNQLLQI QPAHFQSCSN LKELQLHGNH LEYIPDGAPD HLVLTKLNL 180
GKNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTDFGL VNLQELALQQ NQIGLLSPGL 240
PHNNHLQRL YLSNNHISQL PPSIFMQLPQ LNRLTLPQNS LKELSLGIFG PMPNLRRLWL 300
YDNHISLDP NVFNTLRQLQ VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLGNV 360
FRMLANLQNI SLQNNRLRQL PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLGLCLRL 420
YDNFWRCSD ILPLRNWLLL NQPRLGTDTV PFCFSPANVR GQSLIIINVN VAVPSVHVPE 480
VPSYPETPMY PDTPSYDDTT SVSSTTELT S FVEDYDILT IQVTDERSVN GMTQAQSLA 540
IAAIVIGIVA LACSLAACVG CCCCRRSQ VLMQKAPNE C

Seq ID NO: 411 DNA sequence

Nucleic Acid Accession #: XM_098151

Coding sequence: 1..447

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45
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1 11 21 31 41 51
ATGATGCATT TGCTCAATTC TCAGGGCTGG AATGAGCCGG CTGGTCCCCC AGAAAGCTGG 60
AGTGGGGTAC AGAGTTCACT TTTCTCTCTT GTTTACAGCT CCTTGACAGT CCCACGCCCA 120
TCTGGAGTGG GAGCTGGGAG TCAGTGTGG AGAAGAAACA ACAAAGGCCA ATTAGAACCA 180
CTATTTTAA AAAGTGCTTA CTGTGCACAG ATACTCTTCA AGCACTGGAC GTGGATTCTC 240
TCTCTAGCCC TCAGCACCCC TGCGGTAGGA GTGCCGCCCTC TACCACTTG TGATGGGGTA 300
CAGAGGCACT TGCTCTCTG CATGGTGTTC AATAGGCTGG GAGTTTATT TATCTCTTCA 360
AACTTTGTAC AAGAGCTCAT GCGTTGTCTT GGGCTTCTGT CATTAAACCA AAGGAAATGG 420
AAGCCATTCC CCGTTGTCTC TCCTTAG

Seq ID NO: 412 Protein sequence

Protein Accession #: XP_098151

55
60

1 11 21 31 41 51
MMHLLNSQGW NEPAAPPESW SGVQSSVFLS VYSSLIVPRP SGVAGSQCW RRNNKSQLEP 60
LPLKSAICAY ILPKHWTWIL SLALSTPAVG VPPLPTCDGV QRHLLFCMVF NRGVLFISS 120
NFWQELMACL GLSSLNQRKW KPFPCCSP

Seq ID NO: 413 DNA sequence

Nucleic Acid Accession #: NM_002658.1

Coding sequence: 77..1372

65
70
75
80

1 11 21 31 41 51
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CCCCGACCTC GCCACCATGA GAGCCCTGCT GCGCGGCTG CTCTCTGCG TCCTGGTCTGT 120
GAGCGACTCC AAAGGCGACA ATGAACCTCA TCAAGTTCCA TCGAACTGTG ACTGTCTAAA 180
TGGAGGAACA TGTGTGTCCA ACAAGTACTT CTCCAACATT CACTGTGTGA ACTGCCCAAA 240
GAAATTCGGA GGGCAGCACT GTGAAATAGA TAAGTCAAAA ACCTGCTATG AGGGGAATGG 300
TCACTTTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CGGCCCTGCC TGCCCTGGAA 360
CTCTGCCACT GTCTTTCAGC AAACGTACCA TGCCACAGA TCTGATGCTC TTCAGCTGGG 420
CCTGGGAAA CATAATTACT GCAGGAACCC AGACAACCGG AGGCGACCTT GGTGCTATGT 480
GCAGGTGGCG CTAAAGCGCG TTGTCCAAGA GTGCATGGTG CATGACTGCG CAGATGAAA 540
AAAGCCCTCC TCTCTCCAG AAGAAATAAA ATTTCACTGT GGCCAAAGA CTCTGAGGCC 600
CGCTTTTAC ATTATTGGGG GAGAAATCAC CACCATGAG AACCAAGCCCT GTTTTGGCGG 660
CATCTACAGG AGGCACCGGG GGGGCTCTGT CACCTACGTG TGTGGAGGCA GCCTCATCAG 720
CCCTTGCTG GTGATCAGCG CCACACTG CTTCATTGAT TACCAAGA AGGAGGACTA 780
CATGCTCTAC CTGGGTGCGT CAAGGCTTAA CTCCAACAG CAAGGGGAGA TGAAGTTTGA 840
GGTGGAAATC CTCACTCTAC ACAAGGACTA CAGCGCTGAC AGCTTGTCT ACCACAAGA 900
CATTCGCTTG CTGAAGATCC GTTCCAAGA GGGCAGGTGT GCGCAGCCAT CCGGACTAT 960
ACAGACCATC TGCCTGCCCT CGATGTATAA CGATCCCGAG TTTGGACAA GCTGTGAGAT 1020
CACTGGCTTT GGAAAGAGA ATTCTACGA CTATCTCTAT CCGAGCAGC TGAAATGAC 1080

5 TGTGTGAAG CTGATTTCCT ACCGGGAGTG TCAGCAGCCC CACTACTACG GCTCTGAAGT 1140
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 CTGGGGCCGT GGATGTGCCC TGAAGGACAA GCCAGGCGTC TACACGAGAG TCTCACACTT 1320
 ATTACCTCGG ATCCGCGATC ACACCAAGGA AGAGAATGGC CTGGCCCTCT GAGGGTCCCC 1380
 AGGGAGGAAA CGGGCACCAC CCGCTTTCTT GCTGGTGTGC ATTTTTCGAG TAGAGTCATC 1440
 TCCATCAGCT GTAAGAAGAG ACTGGGAAGA TAGGCTCTGC ACAGATGSAAT TTGCTGTGG 1500
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 10 TGTCTTTTTC TGGAGTGAAG CCTGCAGGAG TTAAGGAGG CAGGCGATCT CCTGTGCATG 1680
 GGCTGGAAGG GAGAGCCAGC TCCCGGACC GGTGGGCTAT TGTGAGGCC ATGTTGAGA 1740
 AATGAATAAT TTCCCAATTA GGAAGTGTAA GCAGCTGAGG TCTCTTGAGG GAGCTTAGCC 1800
 AATGTGGGAG CAGCGGTTTG GGGAGCAGAG ACACTAACGA CTTGAGGCA GGGCTCTGAT 1860
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 15 GCTGTGAGTG TAAGTGTGAG TAAGAGCTGG TGTCTGATTG TTAAGTCTAA ATATTTCCTT 1980
 AACTGTGTG GACTGTGATG CCACACAGAG TGGTCTTTCT GGAGAGGTTA TAGGTCATC 2040
 CTGGGGCTTC TTGGGTCCTC CAGTGTGACG TGCCTGGGAA TGTACTTATT CTGCAGCATG 2100
 ACCTGTGACC AGCACTGTCT CAGTTTCACT TTACATAGA TGTCCCTTTC TTGGCCAGTT 2160
 ATCCCTTCCT TTTAGCTAGT TTTATCCAAT CCTCACTGGG TGGGGTGAGG ACCACTCCTT 2220
 20 ACCTGAATA TTTATATTC ACTATTTTAT TTTATATTTT TGTAAATTTA AATAAAGTG 2280
 ATCAATAAAA TGTGATTTT CTGA

Seq ID NO: 414 Protein sequence
 Protein Accession #: NP_002649.1

25 1 11 21 31 41 51
 MRALLARLLL CVLVVSDSKG SNELHQVPSN CDLNGGTCV SNKYPSNIHW CNCPKFGGQ 60
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 30 YCRNPDNRRL PWCVYVGLK PLVQECMVHD CADGKKPSSP PEELKFPQCG KTLRPRFKII 180
 GGEFTTINQ PWFAAIYRRH RGSVTVYVCG GSLISPCWVI SATHCFIDYP KKEDYIVYLG 240
 RSRINSENTQG EMKFEVENLI LHKDYSADTL AHNDIALLLK IRSKEGRCAQ PSRTIQTICL 300
 PSMYNDPQFG TSCBITGPGK ENSTDYLYPE QLRMTVVKLI SHRECCQPHY YGSEVTTKML 360
 CAADPQWKID SCQDGGGFL VCSLQGRMTL TGVSWGRGC ALKDKPGVYT RVSHFLPWIR 420
 35 SHTEKENGILA L

Seq ID NO: 415 DNA sequence
 Nucleic Acid Accession #: NM_024422.1
 Coding sequence: 202..2907

40 1 11 21 31 41 51
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 45 GCTCCGGCGG CGGCCCTCG CCGCGGAGC CCTCCTACCC CGGCCGAGC CTCGCGCGC 180
 GACCTGCCCC GAGCCCTCTC CATGGAGCA GCCCGCCCT CCGGCTCCTG GAACGGAGCC 240
 CTCTCCGGCG TGTCTCTGCT GACCCCTCGC ATCTTAATAT TTGCCAGTGA TGCCTGCAA 300
 AATGTGACAT TACATGTTCC CTCCAACTA GATGCCGAGA AACTTGTGG TAGAGTTAAC 360
 CTGAAGAGT GCTTTACAGC TGCAAACTA ATTCAATCAA GTGATCCTGA CTTCCAAAT 420
 50 TTGGAGGATG GTTCTAGTCTA TACAACAAAT ACTATTCTAT TGTCTCTGGA GAAGAGAAGT 480
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 GAGCATCAAA CAAGAGTCTT AAAGAAAAGA CATACTAAAG AAAAGTTCT AAGGOGGCGC 600
 AAGAGAAGAT GGGCTCCAAT TCCTTGTTCG ATGTAGAAA ACTCCTTGGG TCCTTTTCCA 660
 55 CTCTTCTTTC AACAGTTTCA ATCTGACAG GCCCAAACT ATACCATATA CTATTCCATA 720
 AGAGGTCCTG GAGTTGACCA AGAACCTCG AATTATTTT ATGTGGAGAG AGACACTGGA 780
 AACTGTATT GTACTGTCCT TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC 840
 TTTGCAACAA CTCCAGATGG CCCAATTTT ACAGAAGAAA CTTATCTT TACAATTTT 900
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 GAAATTTGCA GAGTGGGAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCT 1020
 60 GACACGATG ACACACGCT GAAGTACTCC ATCATTGGGC AGGTGCCACC ATCACCACC 1080
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 GAGTTAATTG ACAAGTACCA GTTGAAAATA AAAGTACAAG ACATGGATGG TCAGTATTTT 1200
 GGTCTACAGA CAACTCAAC TTGTATCATT AACATTGATG ATGTAAATGA CCATTTGCCA 1260
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 65 TTACGAGTTA CTGTTGAGGA TAAGGACTTA GTGAATCTG CTAAGTGGAG AGCTAATTAT 1380
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 CAAATTGTGT TAGTTAATGA AGCTCCATT TCCAGAGAGG CTAGTCCAAG ATCAGCCATG 1560
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 70 CCAATACAGA CTGTTGCGAT GAAAGAAAAT GCAGAGTGGG GAACAACAAG CAATGGATAT 1680
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 75 AGCCCATTTA TACCTAAAAA GACAGTATC ATCTGCAAC CCACCATGTC ATCTGCGGAG 1980
 ATTGTTCGGG TTGATCCTGA TGAGCCTATC CATGGCCCAT CCTTTGACTT TAGTCTGGAG 2040
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 CGTCTTTCCT ATCAGAATGA TCCTCCATT GGCTCATATG TAGTACCTAT AACAGTGA 2160
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 80 GAAATGACT GCACACATCG TGTATATCCA AGGATGGCG GTGGAGGAGT ACAACTTGA 2280
 AAGTGGGCCA TCCTTGAAT ATTGTGGGC ATAGCATTGC TAATTCCTGA TGAATTAGCC 2340
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 CAGCAGAAC TAATGTATC AAACACAGAA GCTCCTGAG ATGACAAAGT GTATTCTGCG 2460
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5 TCAGGAATCA AAAACGGAGG TCAGGAGACC ATOGAAATGG TGAAAGGAGG ACACCAGACC 2580
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 ACGGAGGTGG ACAACTGCGAG ATACACTTAC TCGGAGTGGC ACAGTTTATC TCAGCCCCGT 2700
 CTGGGTGAAA AAGTGTATCT GTGTAATCAA GATGAAATC ACAAGCATGC CCAAGACTAT 2760
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 10 TGGGGGTTTT TCTCTCATT TTTGGATGGA ATCTCTTGG TCAATGCAC ATTTACAGAG 3060
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 15 AATTAAGTGT TCATCTGGTG CTGGGAAACT GTTGTTTTCC TGAACATCTA AAGTGTGTAG 3360
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 TTTCTAGCCA GGCATTGACT ATTACAATTT CATT

Seq ID NO: 416 Protein sequence
 Protein Accession #: NP_077740.1

20 1 11 21 31 41 51
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 25 ANLIHSSDPD PQILEDGSVY TWTILLSSE KRSFTILLSN TENQKKKIP VFLEHQTQVL 120
 KKRHTKEKVL RRAKRWRAP PCSMLENSLG PFPLFLQVQ SDTAQNYTIY YSIRGPGVDQ 180
 EPRNLFYVER DTGNLYCTRP VDREQYESPE IIAFATTPDG YTPLEPLPLI IKIEDENDMY 240
 PIFTEETTF TIFENCRVGT TVGQVCATDK DEPTDMHRL KYSIIQGVFP SPTLFSMHP 300
 TGVITTTSSQ LDRELIDKYQ LKIKVQDMQG QYFGLQTTST CIINIDVDND HLPFTFRTSY 360
 30 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKNE NGNFKIVTDA KINEGVLCVV 420
 KPLNYEEKQK MILQIGVVNE APFSREASPR SAMSTATVTV NVEDQDEBPGE CNPPIQTVRM 480
 KENARVGTTS NGKAYDPET RSSSGIRYK LTDPGWNVTI DENTGSIKVF RSLDREAETI 540
 KNGIYNTVL ASDQGGRTCT GTLGIILQDV NDNSPPIPK TVIICKPTMS SAEIVAVDPD 600
 EPIHGPPPDF SLESSTSEVQ RMWRLKAIND TAARLSYQND PPFGSYVVP I TVRDLQMS 660
 35 VTSLDVTLCD CITENDCTHR VDPRIQGGGV QLGKMAILAI LLGIALLFICI LFTLVCGASG 720
 TSKQPKVIPD DLAQQNLIVS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVGSGIKNGG 780
 QETIEMVKGG HQTSBSSCRGA GHHHTLDSR GGHTEVDNCR YTYSEWSHPT QPRLGEKVYL 840
 CNQDENHKHA QDVVLTYNTE GRGSVAGSVG CCSERQEEDG LEFLDNLEPK FRTLAEACMK 900
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Seq ID NO: 417 DNA sequence
 Nucleic Acid Accession #: NM_004949.1
 Coding sequence: 202..2745

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 GCTCCGCGCG CGGCGCTGCG CCGCGGAGGC CCTCTACCC CGGCGCGAGC CTCGGCCCGC 180
 50 GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCCCGCCCCCT CCGGCTCCTG GAAACGAGCC 240
 CTCTGCGCGC TGCTCTCTGT GACCTCGCG ATCTTAATAT TTGCCAGTGA TGCCCTGCAA 300
 AATGTGACAT TACATGTTC CTCCAAACTA GATGCGGAGA AACTTGTGTG TAGAGTTAAC 360
 CTGAAGAAGT GCTTTACAGC TGCAAACTCA ATTCATTCAA GTGATCCTGA CTTCCAAATT 420
 TTGGAGGATG GTTCAGTCTA TACAACAAAT ACTATTCTAT TGCTCTCGGA GAAGAGAAGT 480
 55 TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTGG 540
 GAGCATCAAA CAAAGGCTCT AAAGAAAAGA CATACTAAAG AAAAAGTTCT AAGGCGCGCC 600
 AAGAGAAGAT GGGCTCCAAT TCCTTGTTCG ATGCTAGAAA ACTCCTTGGG TCCTTTTCCA 660
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 AGAGGTCTCT GAGTTGACCA AGAAGCTCGG AATTATTTTT ATGTGGAGAG AGACACTGGA 780
 60 AACTTGTATT GTACTGTGTC TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC 840
 TTTGCAACAA CTCAGATGG GTATACTCCA GAACCTCCAC TGCCCCTAAT AATCAAAATA 900
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 GAAAATGCA GAGTGGGCAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT 1020
 GACACGATGC ACACAGCCT GAAGTACTCC ATCATTTGGC AGGTGCCACC ATCAACCCACC 1080
 65 CTAATTTCTA TGATCTCAAC TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140
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 70 ACCATTTTAA AGGGCAATGA AAATGGCAAT TTTAAAATTG TAACAGATGC CAAAACCAAT 1440
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 CCAATACAGA CTGTTGCGAT GAAAGAAAAT GCAGAGGTGG GAACACAAAG CAATGGATAT 1680
 75 AAAGCATATG ACCCAGAAAC AAGAAGTAGC AGTGGCATAA GGTATAAGAA ATTAACGTAT 1740
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 80 ATTGTTGCGG TTGATCTGTA TGAGCCTATC CATGGCCAC CCTTTGACTT TAGTCTGGAG 2040
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5 CTGGTCTGTG GGGCTTCTGG GACGTCTAAA CAACCAAAAG TAATTCCTGA TGATTAGCC 2400
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 10 AGATGGGCTT GAATTTTGGG ATAATTGGA GCCCAATTT AGGACACTAG CAGAAGCATG 2940
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 15 TCTACAGAGA AATTAAAGTC TGCCTTATT GTTACATTG GGTATAATGA CAACAGCCAA 3240
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 20 ATTATTTTAT TCTGTAAATG TGACCTTTC ACTGTGCAA GGGAGATTTC TAGCCAGGCA 3480
 TTGACTATTA CAATTCATT

Seq ID NO: 418 Protein sequence
 Protein Accession #: NP_004940.1

25 1 11 21 31 41 51
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 30 KKRHTKEKVL RRAKRRWAPI PCSMLENSLG PFLFLQVQV SDTAQNTIY YSRGPGVDQ 180
 EPRNLFYVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YTPLEPLPLI IKIEDENDNY 240
 PIPTEETYP TIFENCRVGT TVGQVCATDK DEPDTHMTRL KYSIIGQVPP SPTLFSMHPT 300
 TGVITTTSSQ LDRELIDKQ LKIKVQDMQ QYFGLQTTST CIINIDVDND HLPFTRTSY 360
 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKNE NGNFKIVTDA KTBEGVLCVV 420
 35 KPLAYEEKQQ MILQIGVNE APFSREASPR SAMSTATTV NVEDQDEGPE CNPPIQTVRM 480
 KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGVMTI DENTGSIKVF RSLDREAEI 540
 KNGIYNITVL ASDGGGTCT GTLGIIQDV NDNSPFIPKK TVIICKPTMS SAEIVAVDP 600
 EPIHGPPFDF SLESSTSEVQ RMWRKAIND TAARLSYQND PPFGSYVVI TVRDLGMSS 660
 VTSLDVLCDD CITENDCTHR VDPRIGGGV QLGKWAIALI LLGIALLFCE LFTLVCGASG 720
 40 TSKQPKVIPD DLAQNLIVS NTEAPGDDKV YSANGFTQT VGASAQGVCG TVGSGIKNGG 780
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 GHTLIK

Seq ID NO: 419 DNA sequence
 Nucleic Acid Accession #: NM_002722.1
 Coding sequence: 14..301

45 1 11 21 31 41 51
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 ACATCAACAT GCTGACCAGG CCTAGGTATG GGAAGAAGCA CAAAGAGGAC ACGCTGGCCT 240
 TCTCGGAGTG GGGTCCCCG CATGCTGCTG TCCCCAGGGA GCTCAGCCCG CTGGACTTAT 300
 55 AATGCCACT TCTGCTCTCT ACGACTCCAT GAGCAGCGCC AGCCAGCTC TCCCTCTGTC 360
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 AAGCC

Seq ID NO: 420 Protein sequence
 Protein Accession #: NP_002713.1

60 1 11 21 31 41 51
 MAAARLCLSL LLLSTCVALL LQPLIGAQGA PLEFVYGDN ATPQMAQYA ADLRRYINML 60
 65 TRPRYGRHK EDTLAFSEWG SPHAAPREL SPLDL

Seq ID NO: 421 DNA sequence
 Nucleic Acid Accession #: NM_032545.1
 Coding sequence: 46..718

70 1 11 21 31 41 51
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 75 CTATCAAGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGGTTG CCACTCAGAA 180
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 CGAGGGCTGG GGGCGGAGG AGCGCTCCCT CTACTCCCGG GCTTTGGGAG AGGGTGGCTC 300
 CGGCGCGCGG CGCTGCTGCA GGAACGGCGG TACCTGCGTG CTGGGCGAGT TCTGCGTGTG 360
 CCGGCGCCAC TTACCGGGCC GCTACTGCGA GCATGACAG AGGCGCAGTG AATGCGGCGC 420
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 80 CCTGCACTGC CTCCCCCTCC AGACGCTGTA CCGCTGTGAC CCGAAGAGT TCTTGGGCTC 540
 CCAAGCTCAC GGGCGAGCG CGGGGGCGCG GCCCAGCTG CTACTCTTGC TGGCTGGCGC 600
 ACTCTGTGAC CGCTCTCTGC GCCCGATGC GCCCGCGCAC CCGGCTGCC TGGTCCCTTC 660
 CGTCTCTCCG CGGGAGCGCG GCCCTGCGG AAGGCGGGA CTTGGGCATC GCCTTTAAT 720
 TTTATGTTG TAAATAATAG ATGTGTTTAC TTTACGTAA GCTGAAGCAC TGGGTGAATA 780

TTTTTATTGG GTAATAAATA TTTTCATGAA AGGCGCAAAA AAAAAAAAAA AAAAAAAAAA 840
AAAAAA

Seq ID NO: 422 Protein sequence
Protein Accession #: NP_115934.1

1 11 21 31 41 51
MTWRHHVRLI FTVSLALQII NLGNSYQREK HNGGREVTK VATQKHROSP LNWTSHPFGE 60
VTGSABGNWP EEPLPYSRAP GEGASARPRC CRNGOTCVLG SFCVCPAHFT GRYCEHDQRR 120
SBOGALEHGA WTLRACHLCR CIFGALHCLP LQTFDRCDPK DFLASHAHGP SAGGAPSILL 180
LLPCALLHRL LRPDAPAFHR SLVPSVLQRE RRPCGRPLGL HRL

Seq ID NO: 423 DNA sequence
Nucleic Acid Accession #: NM_006533.1
Coding sequence: 72..467

1 11 21 31 41 51
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Protein Accession #: XP_069480.1

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 Protein Accession #: FGENESH predicted

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Protein Accession #: NP_009162.1

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1 11 21 31 41 51
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RPFYLYSNG GGAFLIPYAI MLALAGLPLF FLECSLGQFA SLGFSVSWRI LPLFQGVGIT 120
MVLISFVTI YYNVLIAYSL YMFASFQSE LPWKNCSWS DKNCRSPIV THCNVSTVNK 180
GIQEIIQMNK SWVDINNFCT INGSEIYQPG QLPSEQYWNK VALQRSSGMN ETGVIVWYLA 240
LCILLAWLIV GAALFRGIKS SGKVVPYPTAL FPYVVLILL VRGATLEGAS KGISYYIGAQ 300
SNPTKLKBAE VWKDAATQIF YLSVAVGGGL VALSSYNKPK NNCPSDAIVV CLTNCLTSVP 360
AGPAIFSIILG HMAHISGKEV SQVVKSGFDL AFIAYPEALA QLPGGPFWSI LFFFMILLTLG 420
LDSQFASLET ITTTIQDLFP KVMKMRVPI TLGCLLVFL LGLVCVTOAG IYVHLIDHF 480
CAGWGLILAA ILELVGIWI YGGNRFIEDT EMGIGAKRMI FWLHWRACWF VITPILLIAI 540
FWSLVQFHR PNYGAIPYPD WGVALGWHMI VPCIWIPIIM AIKIIQAKG NIPQRLISCC 600
RPASNWGPYL EQHRGERYKD MVDPKKEADH EIPTVSGSRK PE

Seq ID NO: 435 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 51..1085

75
80

1 11 21 31 41 51
GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
CCTCAGCCCC TCCTCTGAGA TTGCATGCC CCTGGAAGGA GGTCTGTCTC ACAGCCTCAC 120
TTCTAACTT CTGGAACCCA CCCACACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
ATGTCGAGA GGGGAAGGAG GTTCTTTTAC TCGCCCAAA CCTGCCCCAG AATCGTATTG 240
GTACACAGTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
TAGGAATCA ACAAGCTACC CCAGGCCCCG CATAAGTGG TCGAGAGACA ATATACCCCA 360
ATGCATCCCT GCTGATCCAG AACGTACCC AGAATGACAC AGGATTTCTAT ACCCTACAAG 420
TCATAAAGTC AGATCTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGAGAC 480
TGCCCAAGCC CTCCATCTCC AGCAACAAC CCAACCCCTT GGAGGACAAG GATGCTGTGG 540

CCTTCACCTG TGAACCTGAG GTTCAGAAACA CAACCTACCT GTGGTGGGTA AATGGTCAGA 600
 GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCTTC ACTCTACTCA 660
 GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720
 ACCGCACTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCT 780
 CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCTGCCAC GCAGCCTCTA 840
 ACCCACTGCG ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960
 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020
 TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080
 TATAGCAGCC CTGGTGTATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCTT 1140
 GAATTCCTCT AGCTCCTCCA ATCCCAITTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200
 CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAATTT TAAAGGGAAA 1260
 ACCCTCAGCG CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAAC 1320
 GCMAACCATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380
 AACAGAGCTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTGTTCCT TGCCTATGCC 1440
 TGCCCTCTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500
 GGGTAACCTA ACAGAGTGTC AGATCTATCT TGTCAATCCC AACGTTTAC ATAAAAAAG 1560
 AGATCCCTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTAAACACAG CCGTGTGTTC 1620
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 TTTAATTCAG CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740
 GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGAAACAT GGCTAAATAC AATGGGTATC 1800
 GCTGAGACTA AGTTGTAGAA ATTAACAAT GTGCTGCTTG GTTAAATGG CTACACTCAT 1860
 CTGACTCATT CTCTATTCTA TTTAGTTGG TTTGTATCTT GCTAAGGTG CGTAGTCCAA 1920
 CTCTGGTAT TACCCTCTTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
 CTCTAAAAGC TTTAAATGTC TGCAATGAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040
 GGCTGGAATT ACAAACTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100
 ATAAAGCCCC CAATGGTGG TAACGTATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160
 TCTCACTTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
 GTTAAGGAAG AAGATAGATC CAATTAATAA AAATTAATAA CAATTTAAAA AAAAAAAGA 2280
 ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCTCT TACTTTAACT 2340
 TTTCAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATT TCTGTGGTTC 2400
 TGTTCCTCTG TTCCAATTG ACAAACCCA CTGTTCTGT ATTGTATTGC CCAGGGGAG 2460
 CTATCACTGT ACTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
 TAGCTCTATA ACT

Seq ID NO: 436 Protein sequence
 Protein Accession #: AAA59907.1

1 11 21 31 41 51
 MGPPSAPPCCR LHVFWKEVLL TASLLTFWNP PITAKLTIES TPFNVABGKE VLLLAHNLPO 60
 NRIGYSWYKG ERVDGNSLIV GYVIGTQOAT PGPAYSGRET IYENASLLIQ NVTQNDTGYF 120
 TLQVIKSLDLV NEBATQGFHV YPELKPSPIS SMNSNPVEDK DAVAFTECEP VQNTTYLWVW 180
 NGQSLFVSER LQLSNGNMTL TLSSVKRND A GSYECIQNP ASANRSDPVT LNVLYGPDVP 240
 TISPSKANYR PGENLNLSC AASNPPAQYS WFINGTFQQS TQELFIPNIT VNSGSGYMCQ 300
 AHSNATGLMR TTVTMITVSG SAFPVLSAVAT VGITIGVLAR VALI

Seq ID NO: 437 DNA sequence
 Nucleic Acid Accession #: M18728.1
 Coding sequence: 1355..1657

1 11 21 31 41 51
 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
 CCTCAGCCCC TCCTCGAGA TTGCATGTCC CCTGGAAGGA GGTCTGCTC ACAGCCTCAC 120
 TTCTAACCCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCAATTCA 180
 ATGTCCGAGA GGGGAAGGAG GTTCTTCTAC TCGCCACCAA CCTGCCCCAG AATCGTATTG 240
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
 TAGGAACCTA ACAAGCTACC CCAGGGCCCG CATAAGTGG TCGAGAGACA ATATACCCCA 360
 ATGCATCCCT GCTGATCCAG AACGTCAACC AGAATGACAC AGGATTCTAT ACCCTACAAG 420
 TCATAAAGTC AGATCTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGAGC 480
 TGCCCAAGCC CTCCTCTCC AGCAACAAC CCAACCCCGT GGAGGACAAG GATGCTGTGG 540
 CTTTCACTG TGAACCTGAG GTTCAGAAACA CAACCTACCT GTGGTGGGTA AATGCTCAGA 600
 GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCTTC ACTCTACTCA 660
 GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720
 ACCGCACTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCT 780
 CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCTGCCAC GCAGCCTCTA 840
 ACCCACTGCG ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960
 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020
 TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080
 TATAGCAGCC CTGGTGTATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCTT 1140
 GAATTCCTCT AGCTCCTCCA ATCCCAITTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200
 CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAATTT TAAAGGGAAA 1260
 ACCCTCAGCG CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAAC 1320
 GCMAACCATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380
 AACAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTGTTCCT TGCCTATGCC 1440
 TGCCCTCTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500
 GGGTAACCTA ACAGAGTGTC AGATCTATCT TGTCAATCCC AACGTTTAC ATAAAAAAG 1560
 AGATCCCTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTAAACACAG CCGTGTGTTC 1620
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 GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGAAACAT GGCTAAATAC AATGGGTATC 1800
 GCTGAGACTA AGTTGTAGAA ATTAACAAT GTGCTGCTTG GTTAAATGG CTACACTCAT 1860

5 CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG OGTTAGTCCAA 1920
 CTCTTGGTAT TACCCCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
 CTCTAAAGGC TTTAAATGTC TGCAATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040
 GGCTGGAATT ACAAACCTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100
 ATAAAGCCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160
 TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATAGTC CAACTGAAAT 2220
 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAATAA CAATTTAAAA AAAAAAAGA 2280
 ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCTTC TACTTTAACT 2340
 10 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATT TCTGTGGTTC 2400
 TGTTCCTCTG TTCCAATTG ACAAACCCA CTGTTCTGT ATTGTATTGC CCAGGGGGAG 2460
 CTATCACTGT ACTTGATAG TGGTGTGTCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
 TAGCTCTATA ACT

15 Seq ID NO: 438 Protein sequence
 Protein Accession #: AAA59908.1

1 11 21 31 41 51
 20 MDSPSQDVKT RLLIMIRLLP PFNLSLLMPA SPANQDDAVI SISQEVASEG NLTECQIYLV 60
 NPNVLHKIRD PLVHPVTDIS SIFNTAVCSN VQWSFSELDP

25 Seq ID NO: 439 DNA sequence
 Nucleic Acid Accession #: M18728.1
 Coding sequence: 2370..2501

1 11 21 31 41 51
 30 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
 CCTCAGCCCC TCCTGTCAGA TTGCATGTCC CCTGGAAGGA GGTCTGTCTC ACAGCCTCAC 120
 TTCTAACCTT CTGGAACCCA CCCACCAGTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
 ATGTGCGAGA GGGGAAGGAG GTTCTTCTAC TCGCCACAA CCGCCCCAG AATCGTATTG 240
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GATATGTAA 300
 TAGSAACTCA ACAAGCTACC CCAGGGGCCG CATACAGTGG TCGAGAGACA ATATACCCCA 360
 35 ATGCATCCCT GCTGATCCAG AACGTCAACC AGAATGACAC AGGATTCTAT ACCCTACAAG 420
 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC 480
 TGCCCAAGCC CTCATCTCC AGCAACAAC CCAACCCGT GGAGGACAAG GATGCTGTGG 540
 CCTTCACCTG TGAACCTGAG GTTCAGAAAC CAACCTACCT GTGGTGGGTA AATGGTCAGA 600
 GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCTTC ACTCTACTCA 660
 40 GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAT ACAGAACCCA GCGAGTGCCA 720
 ACCGCAAGTA CCAGTCAACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCT 780
 CCTCAAGGCC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCTGCCAC GCAGCCTCTA 840
 ACCCACTGCG ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960
 45 CAGCCACTGG CTCGAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020
 TCCTCTCAGC TGTGGCCACC GTGCGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080
 TATAGCAGCC CTGGTGTATT TTCGATATT CAGGAAGACT GGCAGATTGG ACCAGACCTT 1140
 GAATCTCTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200
 CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACCT AATGAAAAAT TAAAGGGAAA 1260
 50 ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACATAGAGA CAGTCAAACT 1320
 GCAAAACCAT GTGAGAAATT GACGACTTCA CACTATGGAG AGCTTTTCCC AAGATGTCAA 1380
 AACAAAGCTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTGTCTCT TGCTTATGCC 1440
 TGCCTCTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAG TAGCTTCAGA 1500
 GGGTAACCTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTAC ATAAATAAG 1560
 55 AGATCCTTTA GTGACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTT 1620
 AAATGTACAG TGGTCTCTTT CAGAGTTGGA CTCTAGACT CACCTGTCTC CACTCCCTGT 1680
 TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740
 GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGAAACAT GGCTAAATAC AATGGGTATC 1800
 GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATAGG CTACACTCAT 1860
 60 CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG OGTTAGTCCAA 1920
 CTCTTGGTAT TACCCCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
 CTCTAAAGGC TTTAAATGTC TGCAATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040
 GGCTGGAATT ACAAACCTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100
 ATAAAGCCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160
 65 TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAATAA CAATTTAAAA AAAAAAAGA 2280
 ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCTTC TACTTTAACT 2340
 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATT TCTGTGGTTC 2400
 TGTTCCTCTG TTCCAATTG ACAAACCCA CTGTTCTGT ATTGTATTGC CCAGGGGGAG 2460
 70 CTATCACTGT ACTTGATAG TGGTGTGTCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
 TAGCTCTATA ACT

75 Seq ID NO: 440 Protein sequence
 Protein Accession #: AAA59909.1

1 11 21 31 41 51
 80 MLTNVPISV LPPCSNLTKP TVLVLYCPGG AITVLVEMCC FNS

80 Seq ID NO: 441 DNA sequence
 Nucleic Acid Accession #: NM_002381.2
 Coding sequence: 64..1524

1 11 21 31 41 51

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	ACCATGCCGC	GCCCCGCCCC	CGCGCGCCGC	CTCCGCGGAC	TCCTCCTGCT	GCTCTGGCCG	120
5	CTGCTGCTGC	TGCCCTCCGC	CGCCCCCGAC	CCCGTGGCCC	GCCCGGGCTT	CCGGAGGCTG	180
	GAGACCCGAG	GTCCCGGGGG	CAGCCCTGGA	CGCCGCCCCC	CTCCTGCGGC	TCCCCACGGC	240
	GGCCCCGCTT	CGGGGACCAG	CGAGCCTGGC	CGCGCCCGCG	GTGCAGGTGT	TTGCAAGAGC	300
	AGACCCCTTG	ACCTGGTGT	TATCATTGAT	AGTTCTCGTA	GCGTACGGCC	CCTGGAATTC	360
	ACCAAAGTGA	AAACTTTTGT	CTCCCGGATA	ATCGACACTC	TGGACATTGG	GCCAGCCGAC	420
	ACGCGGGTGG	CAGTGGTGAA	CTATGCTAGC	ACTGTGAAGA	TCGAGTTCCA	ACTCCAGGCC	480
10	TACACAGATA	AGCAGTCCCT	GAAGCAGGCT	GTGGGTGCAA	TCACACCCCT	GTCAACAGGC	540
	ACCATGTGAG	GCCTAGCCAT	CCAGACAGCA	ATGGAACGAG	CCTTCACAGT	GGAGGCAGGG	600
	GCTCGAGAGC	CCTCTTCTAA	CATCCCTAAG	GTGGCCATCA	TTGTTACAGA	TGGGAGGCCG	660
	CAGSACCAGG	TGAATGAAGT	GGCGGCTCGG	GCCCAAGCAT	CTGTATTGTA	GCTCTATGCT	720
	GTGGGGGTGG	ACCGGGCAGA	CATGGCGTCC	CTCAAGATGA	TGGCCAGTGA	GCCCTAGAG	780
15	GAGCATGTTT	TCTACGTGGA	GACCTATGGG	GTCAATTGAGA	AACTTTCCTC	TAGATTCCAG	840
	GAAACCTTCT	GTGCGCTGGA	CCCCTGTGTG	CTTGGAACAC	ACCAGTGCCA	GCACGCTGCG	900
	ATCAGTGAAT	GGGAAGGCAA	GCACCACTGT	GAGTGTAGCC	AAGGATACAC	CTTGAATGCC	960
	GACAGAAAAA	CGTGTTCAGC	TCTTGATAGG	TGTGCTCTTA	ACACCCACGG	ATGTGAGCAC	1020
	ATCTGTGTGA	ATGACAGAA	TGGCTCTTAT	CATTGTGAGT	GCTATGAAGG	TTATACCTTG	1080
20	AATGAAGACA	GGAAAACTTG	TTCAAGCTCAA	GATAAATGTG	CTTTGGGTAC	CCATGGGTGT	1140
	CAGCACATTT	GTGTGAATGA	CAGAACAGGG	TCCCATCATT	GTGAATGCTA	TGAGGGCTAC	1200
	ACTCTGAATG	CAGATAAAAA	AACATGTTCA	GTCCGTGACA	AGTGTGCCCT	AGGCTCTCAT	1260
	GGTTGCCAGC	ACATTTGTGT	GAGTGTGGGG	GCCGCATCCT	ACCAGTGTGA	TTGCTATCCT	1320
25	GGCTACACCT	TAAATGAGGA	CAAGAAAAACA	TGTTACGCCA	CTGAGGAAGC	ACGAAGACTT	1380
	GTTTCCACTG	AAGATGCTTG	TGGATGTGAA	GCTACACTGG	CATTCCAGGA	CAAGTCCAGC	1440
	TCGTATCTTC	AAGAGCTGAA	CACATAACTT	GATGACATTT	TGGAGAAGTT	GAAAAATAAT	1500
	GAATATGGAC	AAATACATCG	TTAAATTGCT	CCAATTTCTC	ACCTGAAAAA	GTGGACAGCT	1560
	TGTTGTACTT	AATACCTATG	CATCTCTTTG	CACACCTGTT	ATTGCCAATG	TTCTGCTATA	1620
	TAATTTGCCA	TTATCTGTAT	TAATGCTTGA	ATATTACTGG	ATAAATTGTA	TGAAGATCTT	1680
30	CTGCAGAAAT	AGCATGATTT	TTCCAAGGAA	ATACATATGC	AGATACTTAT	TAAGAGCAAA	1740
	CTTTAGTGTG	TCTAAGTTAT	GACTGTGAAA	TGATTTGGTAG	GAAATAGAAT	GAAAAAGTTA	1800
	GTGTTTCTTT	ATCTACTAAT	TGAGCCATTT	AATTTTAAAA	TGTTTATATT	AGATAACCAT	1860
	ATTACAAATG	GAAACTTTAG	GTCTAGTTTC	TTTTGATAGT	ATTATATAAT	TAAATCAATC	1920
35	TTATTACTGA	GAGTGCAAA	TGTACAAAGT	ATTTACACAT	ACAACCTCAT	ATAACTGAGA	1980
	TGAATGTAAT	TTTGAACGTG	TAAACACTTT	TTGTTTTTTG	CTTATTTTGT	TGGAGTATTA	2040
	TTGAAGATGT	GATCAATAGA	TTGTAATACA	CATATCTAAA	AATAGTTAAC	ACAGATCAAG	2100
	TGAACATTAC	ATTCGCATTT	TTAATTCATT	CTGGTCTTTG	AAAGAAATGT	ACTACTAAAG	2160
	AGCACTAGTT	GTGAATTAG	GGTGTAAAC	TTTTTACCAA	GTACAAAAAT	CCCAAAATCA	2220
40	CTTTATTAAT	TTGCTTCAGG	ATCCAAGTGA	CAAAGTTATA	TATTATATAA	ATTGCTATAA	2280
	ATCGACAAAA	TCTAATGTTG	TCTTTTAAAT	GTTAGTGATC	CACCTGCCTC	AGCCTCCCAA	2340
	AGTGCTGGGA	TTACAGGCTT	GAAAGTCTAA	CTTTTTFTTA	CTTATATATT	TGATACATAT	2400
	AATTCALDRC	GCTTTTGAAC	TTGCAACTTT	GAGAACAAAA	CAGTCCTTTA	AATTTTGCAC	2460
	TGCTCAATTC	TGTTTTTCGT	TTGCAATGTC	TTAATATATA	TAAAGTTTAT	TACCTTTACA	2520
45	TATTATCATG	TCTATTTTGT	ATGACTCATC	AATTTTGTCT	ATTAAAGATA	TTTCTTTAAA	2580
	TTAAAAAAA	AAAAAAA					

Seq ID NO: 442 Protein sequence
Protein Accession #: NP_002372.1

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50	MPRPAPARRL	PGLLLLLLWPL	LLLPAAADP	VARPGFRRL	TRGPGGSPGR	RPSAPADGA	60
	PASGTSEPR	ARGAGVKSR	PLDLVFIIDS	SRSVRLPFT	KVKTIVSRII	DTLDIGPADT	120
	RVAVNYAST	KIEPQLQAY	TDKSLKQAV	GRITPLSTGT	MSGLAIQTAM	DEAFTVBAGA	180
55	REPSSNIPKV	AIIVTDGRPQ	DQVNEVAARA	QASGIELYAV	GVDRADMASL	KMMASEPLEE	240
	HVFYVETVGV	IEKLSSRFQE	TFCALDPCVL	GTHQCQHVCI	SDGEGKHECE	CSQGYTLNAD	300
	KKTCALDRG	ALMTGCEHI	CVNDRSGSYH	CECYEGYTLN	EDRKTCASQD	KCALGTHGCG	360
	HICVNDRTGS	HHCECYEGYT	LNADKKTCVS	RDKCALGSHG	CQHICVSDGA	ASYHCDYCPG	420
	YTLNEDKKTC	SATEEARLV	STEDACGCEA	TLAFQDKVSS	YLQRLNTRLD	DILEKLKINE	480
60	YGQIHR						

Seq ID NO: 443 DNA sequence
Nucleic Acid Accession #: NM_016639.1
Coding sequence: 40..429

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65	GCGGCGGGGG	CAGACAGCGG	CGGGCGCAGG	ACGTGCACTA	TGGCTCGGGG	CTCGCTCGGC	60
	CGGTTGCTGC	GGCTCCTCGT	GCTGGGGCTC	TGGCTGGCGT	TGCTGCGCTC	CGTGGCGGGG	120
70	GAGCAAGCGC	CAGGACACGC	CCCTGCTCC	CGCGGAGCT	CCTGGAGCGC	GGACCTGGAC	180
	AAGTGCATGG	ACTGCGCGTC	TTGCGGGCGG	CGACCGCACA	GCGACTTCTG	CCTGGGCTGC	240
	GCTGCAGCAC	CTCTGCGCCC	CTTCCGGCTG	CTTTGGCCCA	TCCTTGGGGG	CGCTCTGAGC	300
	CTGACCTTCG	TGCTGGGGCT	GCTTCTGGCG	TTTTTGCTCT	GGAGACGATG	CCGACGAGGA	360
	GAGAGTTTCA	CCACCCCAT	AGAGGAGACC	GGCGGAGAGG	GCTGCCACGC	TGTGGCGCTG	420
75	ATCCAGTGAC	AATGTGCCCC	CTGCCAGCGG	GGGCTCGCCC	ACTCATCATT	CATTATCCCA	480
	TTCTAGAGCC	AGTCTCTGCC	TCCAGACGCG	GGCGGAGGCC	AAGCTCCTCC	AACCAACAGG	540
	GGGGTGGGGG	GCGGTGAATC	ACCTCTGAGG	CCTGGGCCCA	GGGTTCAGGG	GAACCTTCCA	600
	AGGTGTCTGG	TTGCCCTGCC	TCTGGCTCCA	GAACAGAAAG	GGAGCTCAC	GCTGGCTCAC	660
80	ACAAAACAGC	TGACACTGAC	TAAGGAACCTG	CAGCATTTGC	ACAGGGGAGG	GGGGTCCCTT	720
	CCTTCTCTAG	GACCTGGGGG	CCAGGCTGAC	TTGGGGGCGA	GACTTGACAC	TAGGCCCCAC	780
	TCACTCAGAT	GTCTGAAAT	TCCACCAAGG	GGGTCACTCT	GGGGGGTTAG	GGACCTATT	840
	TTAACACTAG	GGGCTGGCCC	ACTAGGAGGG	CTGGCCCTAA	GATACAGACC	CCCCCAACTC	900
	CCCAAGCGCG	GGAGGAGATA	TTTATTTTGG	GGAGAGTTTG	GAGGGGAGGG	AGAATTTATT	960

AATAAAGAA TCTTTAACTT TAAAAAATA AAAAAAA

Seq ID NO: 444 Protein sequence
 Protein Accession #: NP_057723.1

5
 1 11 21 31 41 51
 | | | | |
 MARGSLRLRL RLLVLGLWLA LLRSVAGEQA PGTAPCSRGS SWSADLDKCM DCASCRRAPH 60
 10 SDFCLGCAAA PPAPFRLWLP ILGGALS LTP VLGLLSGFLV WRCRRREKFP TTPIEETGGE 120
 GCPAVALIQ

Seq ID NO: 445 DNA sequence
 Nucleic Acid Accession #: AF322916.1
 Coding sequence: 50..4300

15
 1 11 21 31 41 51
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 GCACTCCGCA GCCTTTAAGG TTGCGCGCGG GGCCAGGCAA GAGTTAGCCA TGAAGAGCCT 60
 20 CAAGTCCCGC CTGAGGAGGC AGGACGTGCC CGGCCCGCGC TCGTCTGGCG CCGCGCGCGC 120
 CAGGCGGCAT GCAGCAGATT GGAATAAATA TGTATGCCGA TTGATGAAG CAGCAGAAAG 180
 GGGGATGTA GAAAAAGTGA CCTCAATCCT TGCTAAAAAG GGGGTCAATC CAGGCAAACT 240
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 GAATGCCATC CTATATACAT GAGTTGATAT TACAACCCAGT GACACTGCAG GGAGAAATGC 360
 25 TCTTCCACTG GCTGCTAAGT ATGGACATGC ATTGTGCTTA CAAAACTTC TACAGTACAA 420
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 CATGCTAGGT TGCAGATATG GTTGACAGAG TGCAGTAGAA GTCTTAATTA AAAATGGTGC 720
 30 TGATATAAGC TTGCTGGATG CGCTTGGCCA TGATAGTTCT TACTATGCAA GAATGGTGA 780
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 35 AGATTGAAA GAGAGGTTGA GAAAAATTCA GCAAGAACAA AGAATACTTT TGGATAAAGT 1020
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 45 GAGGATGTAT GAGTCAGAAG GTAAAGTTAA ACNAATGCAG ACCCATTTTC TTGCCCTTAA 1620
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 50 GAAAGGAAGA AAGGTCACAG AGATGGAAG CCAGGCAAAA GAATGTGTCG CGAAGTTGGC 1920
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 55 GATCACTGAG TTAACATTGA AAAATCAGAC ACTACAAAAG GAAATTGAAA AAGTTTATTT 2220
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 70 ACTAAAGAC CAGTTATCAG AGCAGACACA AAGTATAGT GTCAAGTAAG AAGAAGTCAA 3120
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5 GCTTAATGAT GTGGAAGAT TAAACAGGC ACTCAATGGC CTTTCCCAAC TCACCTACAC 4080
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 TATCTGTTT ATCTTGCTGG TGCTGAACAT TCTTTGTGCA ACTCCATGGT CTTTCTGGGC 4380
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10 Seq ID NO: 446 Protein sequence
 Protein Accession #: AAG49577.1

1 11 21 31 41 51
 15 MKSLKSLRR QDVPGPASSG AAAASAHAA WNKYDDRLMK AAERGDVEKV TSILAKKGVN 60
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 LQYNCPTEHA DLQRTALQK KAMADCPSSI QLLCDHGASV NAKDVKGRTF LVLATQMSRP 180
 TICQLLIDRG ADVNSRDQKN RTALMLGCEY GCRDAVEVLI KNGADISLLD ALGHDSYYA 240
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 20 ESLRTIEALK NRFPYFESDH LQSGSHFSNR KEDMLLKQGG MYMADSQCTS PGIPAHMQSR 420
 SMLRPLELSL PSQTSYSENE ILKKELEAMR TFCESAKQDR LKLQNELAHK VAECKALALE 480
 CERVKEDSE QIKQLEDALK DVQKRMYESE GKVKQMTHP LALKEHLTSE AASGNHRLTE 540
 ELKDQLDLK VKYEGASAEV GKLRNQIKQN EMIVERFKRD EGKLIENKR LQKELSMCEM 600
 EREKGRKVT EMEGQAKELS AKLALSIPAE KPEMMKSSLS NEVNEKAKKL VEMEREHEKS 660
 25 LSEIRQKRE LENVKAQLA HVKPEEHEQV KSRLEQKSGE LGKKITELTL KNQTLQKEIE 720
 KYYLDNKLK EQAHNLTIEM KHHYVPLKVS EDMKSHDAI IDDLNRKLLD VTQKYTEKKL 780
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 IHALTSENTN LKQMSNQYV PVKTHEEVKM TLNDTLAKTN RELLDVKKFP EDINQEPVKI 900
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 EEVKQKQEN DKLKGIFTL QKDLRDKTVL IEKSHEMERA LSRKTDENKL QLKDLSQKYT 1080
 EVNVKKEKL EENAKQTSEI LAVQNLLQKQ HVPLEQVEAL KKSNGTLEN LKEELKSMQR 1140
 CYEKEQQVT KLHQLLENQK NSSVPLAEHL QIKFAFEKEV GIILASLREK EESQNKMEB 1200
 VSKLQSEVON TKQALKLET REVVDLSKYK ATKSDLETQI SSLNEKLANL NRKYEEVCEE 1260
 35 VLEAKKKEIS AKDEKELLHF SIEQBIKQK EDCDKSLTTI TELQRRIQES AKQIEAKDNK 1320
 ITELLANDVER LKQALNLSQ LTYTSGNPTK RQSQLIDTLQ HQVKSLEQQL ADADRQHQEV 1380
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40 Seq ID NO: 447 DNA sequence
 Nucleic Acid Accession #: NM_003020.1
 Coding sequence: 29..664

1 11 21 31 41 51
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 CCTGACCGG GTCTCAGAAG CAGATATCCA GAGGCTGCTT CATGGTGTTA TGGAGCAATT 180
 GGGCATTGCC AGGCCCCGAG TGGAATATCC AGCTCACCAG GCCATGAATC TTGTGGGCCC 240
 CCAGAGCATT GAAGGTGGAG CTCATGAAGG ACTTCAGCAT TTGGTCCCTT TTGGCAACAT 300
 50 CCCCAACATC GTGGCAGAGT TGACTGGAGA CAACATTCCCT AAGGACTTTA GTGAGGATCA 360
 GGGGTACCCA GACCTCCAA ATCCCTGTCC TGTGGGAAAA ACAGATGATG GATGTCTAGA 420
 AAACACCCCT GACACTGCAG AGTTCAGTCG AGAGTTCAG TTGCACCAGC ATCTCTTTGA 480
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 55 GGATAATGTT GTGCAAGAAG AGTCTGTCCC CCATTTTTCG GATGAGGATA AGGATCCAGA 660
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 60 TAAAAATTAA AATGTGAATG TCAACAATAA AAAGCAAGAC TATGAAAGGC TCAGATTCTT 960
 TGCAGTTTAA AATGTGTCT GAGGTGTGAC TATTTTGGCC AAGTCTGTAG AAAGCTGTCA 1020
 TTTGATTTTG ATTAAGTAGT TCATCCAGCC CTTGGGCATT GTTATACACC AGTAAAGAG 1080
 GCTGTACTCA AGAGGAGGAG CTGACACATT TCACCTGGCT GCGTCTTAAT AAACATGAAT 1140
 GCAAGCATTG GC

65 Seq ID NO: 448 Protein sequence
 Protein Accession #: NP_003011.1

70 1 11 21 31 41 51
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 75 SVNPLYQGR LDNVVAKKSV PHPSDEDKDP E

80 Seq ID NO: 449 DNA sequence
 Nucleic Acid Accession #: NM_003816.1
 Coding sequence: 79..2538

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 AGAAGAGAAG CCCTTAGGCC CTATTCAGAA CAAGTATCTT ATGTTATTCA GGCTGAAGGA 300
 AAAGAGCATA TTATTCACIT GGAAGGAAC AAAGACCTTT TGCTGAAGA TTTTGTGGTT 360
 TATACCTACA ACAGGAAGG GACTTTAATC ACTGACCATC CCAATATACA GAATCATTGT 420
 CATTATCGGG GCTATGTGGA GGGAGTTCAT AATTCAATCA TTGCTCTTAG CGACTGTTTT 480
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 AAAGTTAAT AATAGGTTTA TTAATGAAT TTCATTAGTT TTTTAAAGT GTTTTGGTT 3780
 TGTGTATATA TACATATACA AATACACAT TTACAATAAA TAAATACTT GAAATCTCA 3840
 AAAAAAAA AAAAAAAA AAAAA

Seq ID NO: 450 Protein sequence
 Protein Accession #: NP_003807.1

1 11 21 31 41 51
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 EGVNNSIAL SDGFLRGLL HLENASYIE PLONSSHFEH IYRMDVYK EPLKCGVSNK 180
 DIKKTAKDE EEEPPSMTQL LRRRAVLPO TRYVELPIV DKERYDMGR NQTAVREMI 240
 LLANYLDSMY IMLNIRIVLV GLEIWTNGNL INIVGGAGDV LGNFVQWREK FLITRRRHDS 300
 AQLVLKKGFG GTAGMAPVGT VCSRHAGGI NVFQGITVET PASIVAHELG HNLGMNHDDG 360
 RDCSCAKSC IMNSGASGR NFSSCSAEDF EKLTLNKGW CLLNIPKPE AYSAPSCGNK 420
 LVDAGEBCDC GTPKECELD CCEGSTCKLK SPAECAYGDC CKDCRFLPGG TLRGKSTSEC 480
 DVPEYCNSSG QFQPDVFIQ NGYPCQNNKA YCYNQMCOYY DAQCQVIFGS KAKAAPKDCF 540
 IEVNSKGRFP GNCQPSGNEY KKCATGNALC GKLQCNVQE IPVFGIVPAI IQTPSRGKTC 600
 NGVDPLQGS VPDPMVNEG TKCGAGRICR NFQCVDAVL NYDCDVQKCK EHGHCNENK 660
 NHCENGWAP PNCETKGYG SVDSGPTYNE MNTALRDGLL VFPLIVPLI VCAIPPIKR 720
 DQLWRSYFRK KRSQTVESDG KNQANPSROP GSVPRHVSFV TPPREVPIYA NRPVPTTYAA 780
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WO 03/042661

Seq ID NO: 451 DNA sequence
Nucleic Acid Accession #: NM_016650.1
Coding sequence: 196..789

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CTGCTGCCAT GACAACCATG CAAGGAATGG AACAGGCCAT GCCAGGGTTG GCCTGGTGTG 180
10     CCCCAGCTGG GAAACATGGC TGTACATCAT TCACATCTGT GGAAAGGATT GCAAGAGAAG 240
TTCTTGAGGG GAGAACCCTAA AGTCCTTGGG GTTGTCAGAG TTCTGACTGC CCTGATGAGC 300
CTTAGCATGG GAATAACAAT GATGTGTATG GCATCTAATA CTTATGGAAG TAACCTTATT 360
TCCGTGCATA TCGGGTACAC AATTGGGGG TCAGTAATGT TTATTATTTC AGGATCCTTG 420
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15     ATCACCAGCT CTGTACTGGC TGCATCAGGG ATCTTAATCA ACACATTAG CTGGCGTTT 540
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20     GAGGTTTGGG GCCAACAAAA GATCAACAGA CAAATGCTCC AGAAATCTAT GCTGACTGTG 840
ACACAAGAGC CTCACATGAG AAATTACCAG TATCCAACCT CGATCTGAT AGACGTGTG 900
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AAAATTATGT TCTCATTTT TTCCCTGGAA CTCAATAACT CACTTCAGTG GCTCTTTATC 1020
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Seq ID NO: 452 Protein sequence
Protein Accession #: NP_057734.1

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YTIWGSVMFI ISGSLSIAAG IRTTKGLVRG SLGMNITSSV LAASGILINT FSLAFYSFHH 120
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SHSHMAETAS PTFLENEV

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Seq ID NO: 453 DNA sequence
Nucleic Acid Accession #: NM_002091.1
Coding sequence: 56..503

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AGCGGTCCCG CTGCTGCGCG GCGGAGGGAC CGTCTGACCC AAGATGTACC CGCGCGGCAA 180
45     CCACTGGGCG GTGGGGCACT TAATGGGGAA AAAGAGCACA GGGGAGTCTT CTCTGTGTTT 240
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GGCCTTGGCG AATCAGCAGC CTTCTGTTGG TTCAGAGGAT AGCAGCAACT TCAAGATGT 420
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50     CCCCAGCTG AACCAGCAAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACAAAACCCC 540
TAAGAGACTG AGTTCTGCAA GCATCAGTTC TACGGATCAT CAACAAGATT TCCTTGTGCA 600
AAATATTGTA CTATTCTGTA TCTTTCATCC TTGACTAAAT TCGTGATTTT CAAGCAGCAT 660
CTTCGGTTT AAACITGTTT GCTGTGAACA ATTGTGAAA AGAGTCTTCC AATTATGTCT 720
TTTTTATATC TAGGCTACTT GTTGGTTAGA TTCAAGGCC CGAGCTGTGA CCATTCAACA 780
55     TAAAGCTTA AACACAT

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Seq ID NO: 454 Protein sequence
Protein Accession #: NP_002082.1

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60     1      11      21      31      41      51
|      |      |      |      |      |
MRGSELPLVL LALVLCLAPR GRAVPLPAGG GTVLTMYPR GNHWAUGHLM GKKSTGESSS 60
VSRGSLKQQ LREYIRWEEA ARNILLGLIEA KENRNHQFPQ PKALGNQQPS WDSEDSNFK 120
DVGSKGKVGR LSAFGSQREG RNPQLNQQ

```

Seq ID NO: 455 DNA sequence
Nucleic Acid Accession #: NM_016522.1
Coding sequence: 265..1299

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70     1      11      21      31      41      51
|      |      |      |      |      |
GCGGAAGCAG CAGGAGGGA GCCCCCTTTG GCCGTCTCC GTGGAACCGG TTTTCCGAGG 60
CTGCAAAAGG CCGAGGCTGG ATTTGGGGGA GGAATATTAG ACTCGGAGGA GTCTGCGGCG 120
TTTTCTGCTC CCGCGGCTC CCGGTGCGCG CGGGTTCACC GTCAGTCCC CGCGCTCGCT 180
75     CGCACCCCCA CCCACTTCTT GTGCTGCGCC GGGGGGCGTG TGCGTGGCG CTGCGGAGT 240
TCGGGGAAGT TGTGGCTGTC GAGAATGGGG GTCTGTGGGT ACGTGTCTCT GCCCTGGAAG 300
TGCTCTGTGG TCGTGTCTCT CAGGCTGCTG TTCTGTGTAC CCACAGAGT GCCCGTGGCG 360
AGCGGAGATG CCACCTTCCC CAAAGCTATG GACAACTGTA CGGTCCGGCA GGGGAGAGC 420
GCCACCTCA GGTGCACTAT TGACAACCGG GTCACCCGGG TGGCTGGCT AAACCGCAGC 480
80     ACCATCTCTT ATGCTGGGAA TGACAAGTGG TGCTGGATC CTCGGTGTG CCTTCTGAGC 540
AACACCCAAA CGAGTACAG CATCGAGATC CAGAACGTGG ATGTGTATGA CGAGGGCCCT 600
TACACCTGCT CGGTGACAGC AGACAACCAC CCAAGACCT CTAGGGTCCA CCTCATTGTG 660
CAAGTATCTC CCAAAATGTG AGAGATTCTC TCAGATATCT CCATTAAATGA AGGGAACAT 720
ATTAGCTCA CTGCATAGC AACTGGTAGA CCAGAGCCTA CGGTACTCTG GAGACATC 780

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TCTCCCAAG CGGTTGGCTT TGTGAGTGAA GACGAATACT TGGAAATTCA GGGCATCACC 840
 CGGGAAACAGT CAGGGGACTA CGAGTGCACT GCCTCCAATG ACGTGGCCGC GCCCGTGGTA 900
 CGGAGAGTAA AGGTCAACGT GAACTATCCA CCATACATTT CAGAAGCCAA GGGTACAGGT 960
 5 GTCCCGGTGG GACAAAAGGG GACACTGCAG TGTGAAGCCT CAGCAGTCCC CTCAGCAGAA 1020
 TTCCAGTGGT ACAAGGATGA CAAAAGACTG ATTGAAGGAA AGAAAGGGGT GAAAGTGGAA 1080
 AACAGACCTT TCCTCTCAA ACTCATCTTC TTCAATGTCT CTGAACATGA CTATGGGAAC 1140
 TACACTTGG TGGCTCCAA CAGCTGGGC CACACCAATG CCAGCATCAT GCTATTGGT 1200
 CCAGGCGCG TCAGCGAGGT GAGCAACGGC ACGTCSAGGA GGGCAGGCTG CGTCTGGCTG 1260
 10 CTGCTCTTC TGGTCTTGA CTTGCTTCTC AAATTTTGAT GTGAGTGCCA CTCCCCACC 1320
 CGGGAAAGGC TGCGCCACC ACCACCACCA ACACACAGC AATGGCAACA CCGACAGCAA 1380
 CCAATCAGAT ATATACAAAT GAAATTAGAA GAAACACAGC CTATGGGAC AGAAATTTGA 1440
 GGGAGGGGAA CAAAGAATAC TTTGGGGGGA AAAGAGTTT AAAAAGAAA TTGAAAATTG 1500
 CCTTGAGAT ATTTAGGTAC AATGGAGTTT TCTTTCCCA AACGGGAAGA ACACAGCACA 1560
 15 CCGGCTTGG ACCACTGCA AGCTGCATCG TGCAACCTCT TTGGTGCCAG TGTGGGCAAG 1620
 GGCTCAGCT CTCTGCCAC AGACTGCCCC CAGTGGGAA ATTCTGGAGC TGGCCATCCC 1680
 AAATCAATC AGTCATAGA GACGAACAGA ATGAGACCTT CCGGCCAAG CGTGGGCTT 1740
 CGGGCCCAAG CGTGGGCTG CGGGCACTT GTTAGACTGT GCCACCAAG CGTGTGTGT 1800
 GAAACGTGAA ATAAAAGAG CAAAAAAGG AAAAAAAGG

20 Seq ID NO: 456 Protein sequence
 Protein Accession #: NP_057606.1

1 11 21 31 41 51
 25 MGVCYGLFLP WKCLVVVSLR LLFLVPTGVP VRSGDATFPK AMDNVTVRQG ESATLRCTID 60
 NRVRVAVLNL RSTILYAGND KWCLDPRVVL LSNTQTQYSI BIGNVDVYDE GPYTCVSQTD 120
 NHFKTSRVHL IVQVSPKIVE ISSDISINEG NNISLTICAT GRPEPTVWTR HISPKAVGPFV 180
 SEDEYLEIQG ITRQSGDYB CSASNDVAAP VVRVRKVTN YPPYISEAKG TGVFVGQKGT 240
 30 LQCEASAVPS AEPQWKDDK RLIEGKKGVK VNRPPFLSKL IFFNVSEHDY GNYTCVASNK 300
 LGHTNASIML FGPNAVSEVS NGTSRRAGCV WLLFLVLHL LKLF

35 Seq ID NO: 457 DNA sequence
 Nucleic Acid Accession #: NM_012261.1
 Coding sequence: 203..1045

1 11 21 31 41 51
 40 GATTTGCTCT GCCAGCAGCT GTGGGTGCCG CGCTCGACAC CGAGTCCTAG CTAGGCGCTC 60
 ACAGATATAG CGCTCCCTCC CTCGCCCTTC TCTGTCCCCC GCCTCTCGCT CACCCCGGCC 120
 CACTCCAGCG GCGACTTTGA GGGATTCCCT CTCTGGCGGC CTCTGCAGCA GCACAGCCGG 180
 CCTCATTCGG GGCACGTGGA GTATGGATCT CCAAGGAAGA GGGGTCCCCA GCATCGACAG 240
 ACTTCAGATT CTCTGATGT TGTTCATAC AATGGCTCAA ATCATGGCAG AACAGAAGT 300
 45 GGAATATCTC TCAGGCTTTT CCACTAACCC TGAATAAGAT ATATTGTGG TCGGGGAAA 360
 TGGGAGGAGG TGTCTCATGG CAGAGTTTGC AGCCAAATTT ATTGTACCTT ATGATGTGTG 420
 GGCCAGCAAC TACGATAGTC TGATCAGAGA ACAGGCCGAT ATGCGATTGA CCCGGGGAGC 480
 TGAGGTGAAG GGCGCTGTG GCCACAGCCA GTCGGAGCTG CAAGTGTCTT GGGTGGATCG 540
 CGCATATGCA CTCATAATGC TCTTTGTAAA GGAAGGCCAC AACATGTCCA AGGGACCTGA 600
 GGGGACTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCCACTT 660
 50 CAAAGACGCA GTCACTGCTG GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCCCTGGT 720
 CACCCCGCTT GGAAGTCTCT ATGAGTGTCA AGCTCAACAA ACCATTTCAC TGGCCTCTAG 780
 TGATCGCGAG AAGACGCTCA CCATGATCCT GTCTGGGCTC CACATCCAAC CTTTGTGACAT 840
 TATCTCAGAT TTTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT 900
 GGAAGAAACC TTGCCCTGTA TTTTGGGCTC CATCTTGGGC CTGCTCATCA TGGTAACACT 960
 55 CGCGATTAC CAGTCCACC ACATAATGAC TGCCAAACAG GTGCAGATCC CTCGGGACAG 1020
 ATCCAGTAT AAGCACATGG GCTAGAGGCC GTTAGGCAGG CACCCCTTAT TCCTGCTCCC 1080
 CCAACTGGAT CAGGTAGAAC AACAAAAGCA CTTTTCATC TTGTACAAGA GATACACCAA 1140
 CATAGTACA ATCAAAACAG CTTGGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA 1200
 AACCCAGGGA AGGGGAGAC TCTTTCGGAT TTGTAGGGTG AAATGGCAAT TATTCTCTCC 1260
 60 ATGCTGGGGA GGAGGGGAGG AGGCTCTCAG ACAGCTTTCG TGCTCATGGT GGCTTGGCTT 1320
 TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGGCCCCAA AGTTTAGGGA 1380
 TTGAAACAT GCTTCTTGA GAGGAAACCC CTTTAGGTT CAGAAGAATA TGGGTGCTT 1440
 TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAAAC 1500
 65 TCATGCTCCC TGCAGCAAGA CCGTGAAGAG TGATTATGTC TTCTGGCTGG CATTCTGCAT 1560
 GTTTAGTGAT TGTCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGACT GCAGCACCAG 1620
 AAAACGACTA ATGTAACAT GCAGAGTTGT TTGACTTCT TCCTGTGCCA GGTCCAAGTC 1680
 GGGGACCTG AAGAATCAAT CTGTGTGAGT CTGTTTTTCA AAATGAATA AAACACACTA 1740
 TTCTCTGGC

70 Seq ID NO: 458 Protein sequence
 Protein Accession #: NP_036393.1

1 11 21 31 41 51
 75 MDLQGRGVPS IDRLRVLLML PHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA 60
 EPAAKFIVPY DVNAGSNYVDL ITEQADIALT RGAEEVGRCG HSQSEIQVFW VDRAYALRKL 120
 FVKESHNMMSK GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHHLS ALVTPAGKSY 180
 EQQAQQTISL ASSDPQKTVT MILSAVHIQ FDIISDFVFS BEHKCPVDER EQLEETPLPLI 240
 LGLILGLVIM VTLAIYHVEH KMTANQVQIP RDRSQYKHNG

80 Seq ID NO: 459 DNA sequence
 Nucleic Acid Accession #: NM_001169.1
 Coding sequence: 85..870

1 11 21 31 41 51

WO 03/042661

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	TAGGAGATAA		GAGTATCTTG		CACAGCAGGT		GCAGGTTTCC		CAGCAGCTCA		GGCAAGAGTC	60
	CGATGTTTGT		GCCATCTGAT		CCTGATGTCT		GGAGAGATAG		CCATGTGTGA		GCCTGAATTT	120
	GGCAATGACA		AGGCCAGGGA		GCCGAGCGTG		GGTGGCAGGT		GGCGAGTGTC		CTGGTAGCAA	180
	CGGTTTGTGC		AGCCATGTCT		GGTCGAACCT		CTGGGCTCTG		CTCTCTTCAT		CTTCATCGGG	240
	TGCCTGTGCG		TCATTGAGAA		TGGGACGGAC		ACTGGGCTGC		TGCAGCCGGC		CCTGGCCAC	300
	GGGCTGGCTT		TGGGGCTCGT		GATTGCCACG		CTGGGGAATA		TCAGTGTGGG		ACACTTCAAC	360
	CCTGCCGTGT		CCCTGGCAGC		CATGCTGATC		GGAGGCTCTA		ACCTGGTGAT		GCTCTCCCG	420
	TACTGGGTCT		CACAGTGCTT		CGGGGGGATG		CTCGGGGCTG		CCTTGGCCAA		GGTGTGAGT	480
	CCTGAGGAGA		GGTTCTGGAA		TGCACTCTGG		GCGGCCCTTG		TGACAGTCCA		GGAGCAGGGG	540
	CAGGTGGCAG		GGGCGTTGGT		GGCAGAGATC		ATCCTGACGA		CGCTGTCTGC		CCTGGCTGTA	600
	TGCATGGGTG		CCATCAATGA		GAAGACAAG		GGCCCTCTGG		CCCCGTCTC		CATCGGCTTT	660
	GCGGTACCG		TGGATATCCT		GGCTGGGGGC		CCTGTGTCTG		GAGGCTGCAT		GAATCCCGCC	720
	CGTGCTTTTG		GACCTGGCGT		GFTGGCCAAC		CACCTGGAAT		TCCACTGGAT		CTACTGGCTG	780
	GGCCCACTCC		TGGCTGGCCT		GCTTGTGGA		CTGCTCATTA		GGTGCTTCAT		TGGAGATGGG	840
	AAGACCGGCC		TCATCTCGAA		GGCTCGGTGA		GCAGAGCTCG		TGGGATTCCCT		GCTGCTCCAG	900
	GTGTCCTCAG		CTCAGCTGTC		CCAGACTGAG		GACAGGGGAG		TTCCTGCATT		TCCTGCCAGG	960
	GCAGAGGCC		AGAGAGCGGA		CCCCCTGCTT		CCACTGCTTG		GGCCTGCTTT		CTCAGATAGA	1020
	CTGACTGCTG		AGGAGGCTCT		AGGTCTCTGG		AATTCCTTTG		TGCTCATCAG		AGACCCACAG	1080
	TTGGGGAACA		CGCTGCCCGC		ACTGCCCAGA		GAGCAGTGCA		AACACCAACA		CACAGAGCTG	1140
	TTTCTTGAGA		GGAATGTCCC		CGAGTTGGAC		AAGGAGGCTG		TTTCTGCACA		TCAGCTCATT	1200
	TCCCGCACCC		CATTCTCTGC		TTGATTGCTT		TGTTGGGGGC		CTGGCCACTT		CCTTGTCTCT	1260
	CAAGCTGACA		ATTCTCACTT		TGCAATAAAT		AGTCCAGTGT		TTCCCTCAT			

Seq ID NO: 460 Protein sequence
Protein Accession #: NP_001160.1

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35

	1		11		21		31		41		51	
	MSGEIAMCEP		EPGNDKAREP		SVGGRNRVSW		YERFVQPCLV		ELLGSALFIF		IGCLSVIENG	60
	TDGLLQPAL		AHGLALGLVI		ATLGNISGGH		FNPVSLAAM		LIGGLNLVML		LPYVWSQLLG	120
	GMLGAALAKV		VSPEERFWNA		SGAFAVTQVE		QQVAGALVA		EIILTLALL		AVCMGAINKEK	180
	TKGLAPFPI		GFAVTVDILA		GGFVSGGCMN		PARAFGPAVV		ANHWNFWIY		WLGPLLAGLL	240
	VGLLIRCFIG		DKTRLILKA		R							

Seq ID NO: 461 DNA sequence
Nucleic Acid Accession #: NM_003226.1
Coding sequence: 2..226

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45
50

	1		11		21		31		41		51	
	GATGCTGGGG		CTGGTCTGGG		CCTTGCTGTC		CTCCAGCTCT		GCTGAGGAGT		ACGTGGGCGCT	60
	GTCTGCAAAAC		CAGTGTGCCG		TGCCGGCCAA		GGACAGGGTG		GACTGCGGCT		ACCCCCATGT	120
	CACCCCCAAG		GAGTGCAACA		ACCGGGGCTG		CTGCTTTGAC		TCCAGGATCC		CTGGAGTGCC	180
	TTGGTGTTC		AAGCCCCCTGA		CTAGGAAGAC		AGAATGCACC		TTCTGAGGCA		CCTCCAGCTG	240
	CCCTCGGAT		GCAGGCTGAG		CACCTTGCC		CGCTGTGAT		TGCTGCCAGG		CACGTGTCAT	300
	CTCAGTTTTT		CTGTCCCTTT		GTCGCCGCA		AGCTTTCTGC		TGAAAGTTCA		TATCTGGAGC	360
	CTGATGTCTT		AACGAATAAA		GGTCCCATGC		TCCACCCG					

Seq ID NO: 462 Protein sequence
Protein Accession #: NP_003217.1

55

	1		11		21		31		41		51	
	MLGLVLALLS		SSSAEEYVGL		SANQCAVPAK		DRVDCGYPHV		TPKECNRRGC		CFDSRIPGVP	60
	WCFKPLTRKT		ECTF									

Seq ID NO: 463 DNA sequence
Nucleic Acid Accession #: NM_002993.1
Coding sequence: 64..408

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	1		11		21		31		41		51	
	GGCAGAGGCC		AGTCTCCGGG		CCTCCACCCA		GCTCAGGAAC		CGCGAAACCC		TCTCTTGACC	60
	ACTATGAGCC		TCCCGTCCAG		CCGCGCGGCC		CGTGTCCGGG		GTCTTCCGGG		CTCCTTGTCG	120
	CGGCTGCTCG		CGTGTCTGCT		CCTGCTGACG		CCGCGCGGGC		CCCTGCGCAG		CGCTGGTCTT	180
	GTCTCTGCTG		TGCTGACAGA		GCTGCGTTGC		ACTTGTTTAC		GGGTTAAGCT		GAGAGTAAAC	240
	CCCAAAACGA		TTGGTAAACT		GCAGGTGTTT		CCGCGAGGCC		CGCAGTGCTC		CAAGGTGGAA	300
	TGGTAGCCTT		CCCTGAAGAA		CGGGAAGCAA		GTTTGTCTGG		ACCCGGAAGC		CCCTTTTCTA	360
	AAGAAAGTCA		TCCAGAAAT		TTTGGACAGT		GGAAACAAGA		AAAACCTGAGT		AACAAAAAAG	420
	ACCATGCATC		ATAAAATTGC		CCAGTCTTCA		GCGGAGCAGT		TTTCTGGAGA		TCCCTGGACC	480
	CAGTAAGAAT		AAGAAGGAAG		GGTGTGTTTT		TTTCCATTTT		CTACATGGAT		TCCTACTTTT	540
	GAGAGGTGTG		GGGGAAGGCC		TACGCTTCTC		CCTGAAGTTT		ACAGCTCAGC		TAATGAAGTA	600
	CTAATATAGT		ATTTCACATA		TTTACTGTTA		TTTTACCTGA		TAAGTTATTG		AACCCCTTGG	660
	CAATTGACCA		TATTGTGAGC		AAAGAATCAC		TGGTTATTAG		TCTTTCAATG		AATATTGAAT	720
	TGAAGATAAC		TATTGTATTT		CTATCATACA		TTCTTTAAAG		TCTTACOGAA		AAGGCTGTGG	780
	ATTTCTGATG		GAAATAATGT		TTTATTAGTG		TGCTGTTGAG		GGAGGTATCC		TGTTGTTCTT	840
	ACTCACTCTT		CTCATAAAT		AGGAAATATT		TTAGTTCTGT		TTTCTTGGGG		AATATGTTAC	900
	TCTTTACCTT		AGGATGCTAT		TTAAGTTGTA		CTGTATTAGA		ACACTGGGTC		TGTCATACCG	960
	TTATCTGTGC		AGAATATATT		TCCTTATTCA		GAATTTCTAA		AAATTTAAGT		TCTGTAAGGG	1020
	CTAATATATT		CTCTTCTAT		GGTTTTAGAT		GTTTGATGTC		TTCTTAGTAT		GGCATAATGT	1080
	CATGATTAC		TCATTAAACT		TTGATTTTGT		ATGCTATTTT		TTCACTATAG		GATGACTATA	1140

ATTCTGGTCA CTAATATAC ACITTAGATA GATGAAGAAG CCCAAAAACA GATAAATTC 1200
 TGATGCTAA TTACATAGA AATGTATTCT CTGGTTTTT TAAATAAAAG CAAAATTAC 1260
 AATGATCTGT GCTCTGCAA GTTTTGAAA TATATTGAA CAATTGGAAT ATAAATTCAT 1320
 CATTAGTCC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380
 TTTAAAGGT TTGACCATTT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440
 AAAATGCACT TTTATTTTTT CCTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCAAT 1500
 TGGAGAAACA ATAAAGATT TCTAAACCAA AAAAAA AAAA

Seq ID NO: 464 Protein sequence
 Protein Accession #: NP_002984.1

1 11 21 31 41 51
 MSLPSSRAAR VPGPSGSLCA LLALLLLLTP PGPLASAGPV SAVLTELRCT CLRVTLRVNP 60
 KTIGKLQVFP AGPQCSKVEV VASLKNKQV CLDPEAPFLK KVIQKILDSG NKKN

Seq ID NO: 465 DNA sequence
 Nucleic Acid Accession #: NM_002038.2
 Coding sequence: 108..500

1 11 21 31 41 51
 GAACCGTTTA CTCGCTGCTG TGCCCATCTA TCAGCAGGCT CCGGGCTGAA GATTGCTTCT 60
 CTTCTCTCCT CCAAGGTCTA GTGACGGAGC CCGCGCGGCG CGCCACCATG CGGCAGAAGG 120
 CGGTATCGCT TTCTCTGTGC TACCTGCTGC TCTTCACTTG CAGTGGGGTG GAGGCAGGTA 180
 AGAAAAAGTG CTCGAGAGTG TCGGACAGCG GCTCCGGGTT CTGGAAGGCC CTGACCTTCA 240
 TGGCCGTGCG AGGAGGACTC GCAGTCGCGG GGCTGCCCGC GCTGGCTTTC ACGCGGCGCG 300
 GCATCGCGGC CAACTCGGTG GCTGCCTCGC TGATGAGCTG GTCTGCGATC CTGAATGGGG 360
 GCGCGGTGCC CGCGGGGGGG CTAGTGGCCA CGCTGCAGAG CCTCGGGGCT GGTGGCAGCA 420
 GCGTGTCTAT AGGTAAATAT GGTGCCCTGA TGGGCTACGC CACCCACAGG TATCTGATA 480
 GTGAGGAGGA TGAGGAGTAG CCAGCAGCTC CCAGAACCTC TTCTTCTTTC TTGGCCTAAC 540
 TCTTCCAGTT AGGATCTAGA ACTTGGCTT TTTTTTTTTT TTTTTTTTTT TTTGAGATGG 600
 GTTCTCACTA TATTGTCCAG GCTAGAGTGC AGTGGCTATT CACAGATGCG AACATAGTAC 660
 ACTGCAGCCT CCAACTCTTA GCCTCAAGTG ATCCTCTGTT CTCAACCTCC CAAGTAGGAT 720
 TACAAGCATG CGCGGACGAT GCCCAGAATC CAGAACTTTG TCTATCACTC TCCCCAACAA 780
 CCTAGATGTG AAAACAGAAT AAACCTCACC CAGAAAA

Seq ID NO: 466 Protein sequence
 Protein Accession #: NP_002029.3

1 11 21 31 41 51
 MRQKAVSLFL CYLLFTCSG VEAGKKKCE SSDSGSGFWK ALTFMAVGGG LAVAGLEPALG 60
 FTGAGIAANS VAASLMSWA ILNGGVVPAG GLVATLQSLG AGGSSVVIGN IGALMGYATH 120
 KYLDSSEDEE

Seq ID NO: 467 DNA sequence
 Nucleic Acid Accession #: NM_003469.2
 Coding sequence: 92..1945

1 11 21 31 41 51
 GAAACGGCCC GAGAAGCTCG CCGGAGAAC GGGGAGGAAT ATGCTGTGGA GCTCCTCTGC 60
 CATATAAACA AAAAGAGGAA ATCTTTCAAA CATGCTGAA GCAGAGACC ACTGGCTTGG 120
 AGCAGCCCTG TCTCTTATCC CTTTAATTTT CCTCATCTCT GGGGCTGAAG CAGCTTCATT 180
 TCAGAGAAAC CAGCTGTCTC AGAAGAAACC AGACCTCAGG TTGGAAATG TCCAAAGATT 240
 TCCAGTCTCT GAAATGATCA GGGCTTTGGA GTACATAGAA AACCTCGAC AACAGCTCA 300
 TAAGGAGAA AGCAGCCAG ATTATAATCC CTACCAAGGT GTCTCTGTCC CCCCTCAGCA 360
 AAAAGAAAT GGCATGAAA GCCACTTGCC CGAGAGGGAT TCATGAGTG AAGAGACTG 420
 GATGAGAAAT ATACTCGAAG CTTTGAGACA GGCTGAAAAT GAGCCTCAGT CTGCAACAAA 480
 AGAAATAAG CCTATGCCT TGAATTGAGA AAAGAACTTT CCAATGGACA TGAGTGATGA 540
 TTATGAGACA CAGCAGTGGC CAGAAAGAAA GCTTAAGCAC ATGCAATTCC CTCCTATGTA 600
 TGAAGAGAAT TCCAGGGATA ACCCTTTAA AGGCACAAAT GAAATAGTGG AGGAACAATA 660
 TACTCTCAA AGCCTTGCTA CATTGGAATC TGTCTTCCAA GAGCTGGGGA AACTGACAGG 720
 ACCAAACAAC CAGAAACGTG AGAGGATGGA TGAGGAGCAA AAACCTTATA CGGATGATGA 780
 AGATGATATC TACAAGGCTA ATAACATTGC CTATGAAGAT GTGGTCGGGG GAGAAGACTG 840
 GAACCCAGTA GAGGAGAAAA TAGAGAGTCA AACCCAGGAA GAGGTGAGAG ACAGCAAGA 900
 GAATATAGGA AAAATGAAC AAATCAACGA TGAGATGAAA CGCTCAGGGC AGCTTGGCAT 960
 CCAGGAAGAA GATCTTCGGA AAGAGAGTAA AGACCACTC TCAGATGATG TCTCCAAAGT 1020
 AATTGCCAT TTGAAAGGT TAGTAAATGC TGCAGGAAGT GGGAGGTTAC AGAATGGGCA 1080
 AAATGGGAA AGGGCCACCA GGCTTTTGA GAAACCTCTT GATTCTCAGT CTATTATCA 1140
 GCTGATTGAA ATCTCAAGGA ATTTACAGAT ACCCCAGAA GACTTAATTG AGATGCTCAA 1200
 AACTGGGGAG AAGCGAATG GATCAGTGA ACAGGAGGG GAGCTTGACC TTCCTGTTGA 1260
 CCTAGATGAC ATCTCAGAGG CTGACTTGA CCATCCAGAC CTGTCCAAA ATAGGATGCT 1320
 CTCCAAGAT GGCTACCTTA AACACCTGG TCGTGTGGG ACTGAGGCC TACCAGAGG 1380
 GCTCAGTGTG GAGGATATTT TAAATCTTT AGGGATGGAG AGTGCAGCAA ATCAGAAAAC 1440
 GTGCTATTTT CCCAATCCAT ATAACCAGGA GAAAGTTCTG CCAAGGCTCC CTTATGGTGC 1500
 TGAAGATCT AGATCGAACC AGCTTCCCAA AGCTGCTGG ATTCCACATG TTGAAAACAG 1560
 ACAGATGSCA TATGAAACC TGAACGACAA GGATCAAGAA TTAGGTGAGT ACTTGGCCAG 1620
 GATGCTAGTT AAATACCTTG AGATCATTA TTCAAACCAA GTGAAGCGAG TTCTGGTCA 1680
 AGGCTCATCT GAAGATGACC TGCAGGAAGA GGAACAAATT GAGCAGGCCA TCAAAGAGCA 1740
 TTTGAATCAA GGCAGCTCTC AGGAGACTGA CAAGCTGGCC CGGTGAGCA AAAGTTCC 1800
 TGTGGGGCCC CGAAGAAATG ATGATACCCC AAATAGGCAG TACTGGGATG AAGATCTGTT 1860
 AATGAAAGTG CTGAATACC TCAATCAAGA AAAGGCAGAA AAGGGAAGGG AGCATATTGC 1920

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TAAGAGAGCA ATGGAATAA TGTAAGCTGC TTTCATTAAT TACCCTACTT TCATTCTCTC 1980
 CACCCCAAGC AATCCCAAC ATTTCTCTTC AGTGTGTGA CTTCATCTCT GTTAACACTG 2040
 TAATATCTTT AATGATGTA CAGGCAGATG AAACCAAGTC ACTGGGGAGT CTGCTTCATT 2100
 TCCTCTGAGC TGTATCTTG TGTATGGATA TGTGTAAATG TTATGACTCC TTGATAAAAA 2160
 ATTTATTATG TCCATTATTC AAGAAAGATA TCTATGACTG TGTTTAATAG TATATCTAAT 2220
 GGCTGTGGCA TTGTTGATGC TCACATATGA TAAAAAAGTG TCCTATAATT CTATTGAAAG 2280
 TTTTAAATAT TTATTGAATT ATTTTGTTAC TGTCTGTAGC GTTTGTGGA GACTGTGACC 2340
 AAAAAATAA AGCATTATAA ATATA

Seq ID NO: 468 Protein sequence
 Protein Accession #: NP_003460.1

1 11 21 31 41 51
 15
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MAEAKTHWLG AALSLIPLIF LISGAEEASF QRNQLLQKEP DLRLNVQKF PSPMIRALE 60
 YIENLRQQAQ KEESPDPYNP YQGVSVPLQQ KENGDESHLP ERDSLSEEDW MRILEALRQ 120
 AENEPQSAFK ENKPYALNSE KNFPMDSDD YETQWPERK LKHMQFPMPY EENSNDNFK 180
 RTNEIVEBQY TPQSLATLES VFQELGKLTG FNNQKRERMD EQKLYTDD EDDIYKANNIA 240
 YEDVVGGEW NPVEEKIESQ TQEEVRDSKE NIGKNEQIND EMKRSQGLGI QEEDLRKESK 300
 DQLSDVSKV IAYLKRLLVNA AGSGRLNQNG NGERATRLFE KPLDSQSIYQ LIEISRNLQI 360
 PPEDLIEMLK TGEKPNQSVB PERELDLFVD LDDISEADLD HPDLFQNRML SKSGYPTKTFG 420
 RAGTEALPDG LSVEDILNLL GMESAANQKT SYFPNPYNGE KVLPRLPYCA GRSRSNQLPK 480
 AAMIPHVENR QMAYENLNDK DQELGEYLAR MLVKYPIILN SNQVSRVPGQ GSSEDDLQEE 540
 EQIEQAIEKH LNQSSQETD KLPVSKRFP VGPKNDITP NRQYWEDELL MKVLEYIANQE 600
 KAEKGRHIA KRAMENM

Seq ID NO: 469 DNA sequence
 Nucleic Acid Accession #: NM_006398.1
 Coding sequence: 19..516

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 40
 45

1 11 21 31 41 51
 GGCCCCCTGT CTGCAGAGAT GGCTCCCAAT GCTTCTGCCC TCTGTGTGCA TGTCCGTTCC 60
 GAGGAATGGG ATTTAATGAC CTTTGTATGCC AACCCATATG ACAGCGTGAA AAAAATCAAA 120
 GAACATGTCC GGTCTAAGAC CAAGGTTCTT GTGCAGGACC AGGTTCTTTT GCTGGGCTCC 180
 AAGATCTTAA AGCCACGAGG AAGCCTCTCA TCTTATGGCA TTGACAAGA GAAGACCATC 240
 CACCTTACCC TGAAGTGGT GAAGCCCACTG GATGAGGAGC TGCCCTTGTG TCTGTGGAG 300
 TCAGGTGATG AGGCAAGAGG GCACCTCCTC CAGGTGCGAA GGTCCAGCTC AGTGGCACA 360
 GTGAAGCAA TGATCGAGAC TAAGACGGGT ATAATCCCTG AGACCCAGAT TGTGACTTGC 420
 AATGGAAGA GACTGGAAGA TGGGAAGATG ATGGCAGATT ACGCCATCAG AAAGGGCAAC 480
 TTACTCTTCC TGGCATCTTA TTGTATTGGA GGGTGACCAC CCTGGGGATG GGGTGTGGC 540
 AGGGGTCAA AAGCTTATTT CTTTAAATCT CTACTCAAC GAACACATCT TCTGATGATT 600
 TCCCAAAATT AATGAGAATG AGATGAGTAG AGTAAGATTG GGTGGGATG GTTAGGATGA 660
 AGTATATGTC CCAACTCTAT GTTCTTTGA TTCTAACACA ATTAATTAAG TGACATGATT 720
 TTTACTAATG TATTACTGAG ACTAGTAAAT AAATTTTAA GGCAAAATAG AGCATTTC

Seq ID NO: 470 Protein sequence
 Protein Accession #: NP_006389.1

50
 55

1 11 21 31 41 51
 MAPNASCLCV HVRSEWDLN TFDANPYDSV KKIKEHVRSK TKVPVQDQVL LLGSKILKPR 60
 RLSLSYGIDK EKTILHLTKV VKPSDEELPL FLVESGDEAK RELLOVRRSS SVAQVKAMIE 120
 TKGTIIPETQ IVTCNGKRL E DKKMMADYGI RKGILLFLAS YCIGG

Seq ID NO: 471 DNA sequence
 Nucleic Acid Accession #: XM_094741.1
 Coding sequence: 1..948

60
 65
 70
 75

1 11 21 31 41 51
 ATGAAGGCCA ACTACAGCGC AGAGGAGCGC TTCTCTCTGC TGGGTTCTC CGACTGGCCT 60
 TCCCTGCAGC CGGTCTCTCT CGCCCTTGTC CTCTGTGCT ACCTCTCTGAC CTGAGCGGCG 120
 AACTGGCGCG TGGTGTGCTT GGCCTGTGCG GACCCGCGCC TGCAACAGCC CATGTACTAC 180
 TTCCTCTGCC ACCTGGCCTT GGTAGACGCG GGCTTCACTA CTAGCGTGGT GCCCGCGCTG 240
 CTGCGCAACC TGGCGGAGC AGCGCTCTGG CTGCGCGCA GCCACTGCAC GGCCAGCTG 300
 TGCGCATGCG TGGCTCTGGG TTGCGCGGAA TGGCTCTCTC TGGCGGTGAT GGCTCTGGAC 360
 CGCGCGGCGG CAGTGTGCGG CCCGCTGCGC TATGCGGGG TCGTCTCTCC CGCCTATGT 420
 CGCAGCTGCG CCAGCGCCTC CTGGCTAAGC GGCTCTCAAC ACTCGGTTGC GCAACCGCG 480
 CTCTCTGGCT AGCGCGCGCT GTGCGCGCCC CGCTGCTGCG ACCACTTCAT CTGTGAGCTG 540
 CGCGGTGTGC TCAAGCTGGC CTGCGGAGGC GACGAGAGCA CTACCGAGAA CCAGATGTTT 600
 GCGCGCGCGG TGGTCTCTCT GCTGCTGCGG TTGCGCTCA TCCTGGCCTC CTACGGTGCC 660
 TGTGGTCTCC ACTGACAGC CGTCTGCGCT TTCTACGGCT CGGCCATCTA CACTACCTG 720
 CAGCGCGCGC AGCGCTACAA CCAGGACGCG GGCAAGTTCG TATGCTCTCT CTACACCGTG 780
 GTCACACTCG CTCTCAACCC GCTCATCTAC ACCCTCAGGA ATAAGAAAGT GAAGGGGGCA 840
 GCGAGGAGGC TGCTGCGGAG TCTGGGGAGA GGCCAGGCTG GGCAGTGA 900

80
 Seq ID NO: 472 Protein sequence
 Protein Accession #: XP_094741.1

1 -11 21 31 41 51
 MKANYSABER FLLLGPSDWP SLQFVLFALV LLCYLLTLTG NSALVLLAVR DPLRLTPMY 60

FLCHLALVDA GFTTSVVPPL LANLRGPALW LPRSHCTAQL CASLALGSAE CVLLAVMALD 120
 RAAAVCRPLR YAGLVSPRLC RTLASASWLS GLTNSVAQTA LLAERPLCAP RLLDRHFICEL 180
 PALLKLACGG DGDITFENQMF AARVVILLPL PAVILASYGA VARAVCCMRP SGGRRRAVGT 240
 CGSHLTAVCL FYGSAIYTYL QPAQRYNQAR GKFVSLFYT VTPALNPLIY TLRNKKVKGA 300
 ARRLRLSLGR GQAGQ

Seq ID NO: 473 DNA sequence
 Nucleic Acid Accession #: NM_001062.1
 Coding sequence: 76..1380

1 11 21 31 41 51
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 GCTCTCATT CCTTCTGCC ATCACTTAAT AAATAGCCAG CCAATTCATC AACATTCTGG 60
 TACACTGTGG GAGAGATGAG ACAGTCACAC CAGCTGCCCC TAGTGGGGCT CTTACTGTIT 120
 TCTTTTATTC CAAGCCAACT ATGCGAGATT TGTGAGGTAA GTGAAGAAAA CTACATCCGC 180
 CTAAACCTTC TGTGAATAC AATGATCCAG TCRAACTATA ACAGGGGAAC CAGCGCTGTC 240
 AATGTTGTGT TGTCCCTCAA ACTTGTGGA ATCCAGATCC AAACCCGTAT GCAAAAGATG 300
 ATCCACAAA TCAATACAA TGTGAAAAGC AGATTGTGAC ATGTAAGCTC GGGAGAGCTT 360
 GCCTTGATTA TACTGGCTTT GGGAGTATGT CGTAAOCTG AGGAAACTT AATATATGAT 420
 TACCACCTGA CTGACAGCT AGAAAATAA TTCCAAGCAG AAATTGAAAA TATGGAAGCA 480
 CACAATGCA CTCCTCTGAC TAACACTAC CAGCTCAGCC TGGACGTTT GGCCTTGTGT 540
 CTGTTCAATG GGAATCTACT AACCGCCGAA GTTGTCAACC ACTTCACTCC TGAATAATAA 600
 AACTATTATT TTGGTAGCCA GTTCTCAGTA GATACTGGTG CAATGGCTGT CCTGGCTCTG 660
 ACCTGTGTGA AGAAGATCT AATAATGGG CAGATCAAG CAGATGAAG CAGTTTAAAG 720
 AACATCAGTA TTTATACAAA GTCACTGGTA GAAAAGATT TGTCTGAGAA AAAAGAAAAT 780
 GGTCTCATG GAAACACATT TAGCACAGGA GAAGCCATGC AGGCCCTCTT TGTATCATCA 840
 GACTATTATA ATGAAAATGA CTGGAATTGC CAACAAACT TGAATACAGT GCTCACGGAA 900
 ATTTCTCAAG GAGCATTCAG TAATCCAAAC GCTGCAGCCC AGGTCTTACC TGCCCTGATG 960
 GGAAAGACCT TCTTGGATAT TAACAAGAC TCTTCTGCG TCTCTGCTTC AGGTAACCTC 1020
 AACATCTCG CTGATGAGCC TATAACTGTG ACACCTCTG ACTCACAATC ATATATCTCC 1080
 GTCAATTACT CTGTGAGAA CAATGAAACA TATTTACCA ATGTCACTGT GCTAAATGGT 1140
 TCTGTCTTCC TCAGTGTGAT GGAGAAAGCC CAGAAAATGA ATGATACTAT ATTTGGTTTC 1200
 ACATGGAGG AGCGCTCATG GGGGCCCTAT ATCACTGTA TTCAGGGCCT ATGTGCCAAC 1260
 AATAATGACA GAACCTACTG GAACTTCTG AGTGGAGGC AACCACTGAG CCAAGGAGCT 1320
 GGTAGTTACG TTGTCCGCAA TGGAGAAAC TTGGAGGTTG GCTGGAGCAA ATACTAATAA 1380
 GCCCAAACTT TCCTCAGCTG CATAAAATCC ATTTGCAGTG GAGTTCATG TTTATTGTCC 1440
 TTATGCTTC TTCTCATTT ATCCAGTAC GAGCAGGAGA GTTAATAACC TCCCTTCTC 1500
 TCTCTACATG TTCAATAAAA GTTGTGAAA GATTAAC

Seq ID NO: 474 Protein sequence
 Protein Accession #: NP_001053.1

1 11 21 31 41 51
 | | | | |
 MRQSHQLPLV GLLLFSPIPS QLCEICEVSE ENYIRLKPFL NTMIQSNYNR GTSAVNVVLS 60
 LKLVGIGIQT LMQKMIQIQL YNVKSRSDV SSGELALIL ALGVCNRAEE NLIYDYHLTD 120
 KLENKFAEIL ENMEAHNGTP LTNYQLSLD VLALCLPNGN YSTABVVNHF TPENKNYYFG 180
 SQPSVDTGAM AVLALTCKVK SLINGQIKAD RGLKNISIV TKSLEKILS EKKENGLIGN 240
 TFSTGEAMQA LFFVSSDYNE NDWNCQQLN TVLTEISQGA FSNPNAAQV LPALMGKTFE 300
 DINKDSSCVS ASGNFNISAD EPITVTPPDS QSYISVNVSV RINETYFTNV TVLNGSVFLS 360
 VMEKAQKQND TIFGFTMEER SWGPIYTCIQ GLCANNDRT YWELLSGGEF LSQGAGSVV 420
 RNGENLEVRW SKY

Seq ID NO: 475 DNA sequence
 Nucleic Acid Accession #: NM_004852.1
 Coding sequence: 89..1546

1 11 21 31 41 51
 | | | | |
 GCCCCCGCCC GCCCCGGGCC CTGATGGACT GAATGAAGGC TGCCTACACC GCCTATCGAT 60
 GCGTCACCAA AGACCTAGAA CGTGCGCCAT GAACCGGAG CTGACAATGG AAAGTCTGGG 120
 CACTTTGAC ENCGCGCGCG GCGCGGCGAG TGGCGGGGCG GCGCGGGGGG GCGCGGGGGG 180
 CGCGCGCGGG GCGCGGGGCC ATGAGCAGGA GCTGCTGGCC AGCCCCAGCC CCCACCAAGC 240
 GCGCGCGGCG CGCGTGGCT CGCTCGGGGG CCTTCGCGCG CCTCCACCG CGCACCAGGA 300
 GCTGGGCAAG GCGCGAGCGG CGGCAGCGGC GCGTGGCGGC TCGGCCATGG TCACCAGCAT 360
 GGCTCGATC CTGGAAGCGG GCGACTACCG GCGGAGCTC TCCATCCCG TCACCAAGC 420
 CATGAGCATG TCTTGGACT CGTCTCGCC TGGCATGGGC ATGAGCAACA CCTACACCA 480
 GCTGACACCG CTCCAGCGCG TGCCACCCAT CTCCACCGTG TCTGACAAGT TCCACCAACC 540
 TCACCGCGAC CACCATCCGC ACCACCAACA CCACCAACC CACGAGCGCC TGTCCGGCAA 600
 CGTCAGCGGC AGCTTCACCC TCATGGCGGA GAGGCGGGG CTCCCGGCCA TGAACAACCT 660
 CTACAGTCCC TACAAGGAGA TGCCCGGCAT GAGCCAGAGC CTGTCCCGGC TGGCCGCCAC 720
 GCGCTGGGC AAGCGGCTAG GCGGCTCCA CAACGCGCAG CAGAGTCTGC CCAACTACGG 780
 TCCGCGGGGC CAGCACAATA TGCTCAGCCC CAACCTCGAC GCGCACCACA CTGCCATGCT 840
 GACCGCGGGT GAGCAACACC TGTCCGCGGG CCTGGGCACC CCACTTGGCG CCAATGATGT 900
 GCACCTGAAC GGCCTGCAAC ACCCGGGCCA CACTCAGTCT CAGCGGCGGG TGTGGCACC 960
 CAGTGGCGAG CGGCCACCTC CGTCTCATC GGGCTGCGAG GTGGCCAGT CGGGCCAGCT 1020
 GGAAGAAATC AACACCAAG AGGTGGCCCA GCGCATCACA GCGAGCTGAG AGCGCTACAG 1080
 TATCCCCAG GCGATCTTTG CGCAGAGGGT GCTGTGCGGG TCTCAGGGGA CTCTCTCGA 1140
 CCGTCTCGGG AATCCAAATC CGTGGAGTAA ACTCAATCT GCGAGGGAGA CCTTCGCGAG 1200
 GATGTGGAG TGGCTTCAGG AGCCCGAGTT CCAGGCGATG TCGGCTTAC GCGTGGCAGC 1260
 GTGCAAAAGC AAGAGCAAG AACCAACCA AGACAGGAAC AATTCGCCAG AGAAGTCCCG 1320
 CCTGTGTTC ACTGACCTC AACCGCAAC ACTCTTGGCC ATCTTCAAGG AGAACAAAC 1380
 CCGTCAAG GAGATGCGA TCACCATTTT CCAGCAGCTG GCGCTGGAGC TCACCAACCT 1440
 CAGCACTTC TTATGAAGC CCGCGCGCG CAGCCTGGAG AAGTGGCAAG ACGATCTGAG 1500

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CACAGGGGGC TCCTCGTCCA CCTCCAGCAC GTGTACCAA GCATGATGGA AGGACTCTCA 1560
 CTGGGGCACA AGTCACCTCC AAATGAGGAC AACAGATACC AAAAGAAAAC AAAGGAAAAA 1620
 GACACCGGAT TCCTAGCTGG GGCCTTCAC TGGTG

5 Seq ID NO: 476 Protein sequence
 Protein Accession #: NP_004843.1

1 11 21 31 41 51
 10 MNPELTMESL GTLHGARGGG SGGGGGGGGG GGGGGPGHEQ ELLASPSPHH ARRGPRGSLR 60
 GPPPPPTAHQ ELGTAAAAAA AASRSAMVTS MASILDGGDY RPELSIPLHH AMSMSCDSSP 120
 PGMGMSNTYT TLTPQLPLPP ISTVSDKFHH PHPHHHPHH HHHHHQRLSG NVSGSPILMR 180
 DERGLPAMNN LYSPLYKEMPG MSQSLSPILAA TPLGNLGLGL HNAQSLFNY GPPGHDMLSL 240
 PNFDAHTAM LTRGEQHLRS GLGTTPPAAMM SHLNLGHRPG HTQSHGVPVA PSRERPSSS 300
 15 SSSQVATSGQ LESINTKEVA QRITAEKRY SIPQAIFAQR VLCSQGTLS DLLRNPKPWS 360
 KLKSGRETFR RMWKWLQEPF FORMSALRLA ACKRKEQEPN KDRNNSQKKS RLVPFDLQRR 420
 TLPALFKENK RPSKEMQITI SSQLGLELTT VSNFFMNARR RSLKQWDDL STGSSSTSS 480
 TCTKA

20 Seq ID NO: 477 DNA sequence
 Nucleic Acid Accession #: NM_013271.1
 Coding sequence: 27..809

1 11 21 31 41 51
 25 TCCGGAGCCA GGCCTCGTGG GGCAGCATGG CGGGGTGCGC GCTGCTCTGG GGGCCGCGGG 60
 CCGGGGGCGT CGGCCTTTTG GTGCTGCTGC TGCTCGGCCT GTTTCGGCCG CCCCCCGCGC 120
 TCTGCGCGCG GCGCGTAAGG GAACCCCGCG GCCTAAGCGC AGCGTCTCGC CCCTTGGCTG 180
 AGACTGGCGC TCCTCGCGCG TTCCGGCGGT CAGTGCCTCG AGGTGAGGCG GCGGGGCGCG 240
 30 TGCAGGAGCT GCGCGGCGCG CTGGCGCATC TGCTGGAGGC CGAACGTCAG GAGCGGCGCG 300
 GGGCCGAGCG GCAGGAGGCT GAGGATCAGC AGGCGCGCGT CCTGGCGCAG CTGCTGCGCG 360
 TCTGGGGCGC CCCCCGCAAC GCTCTGCTCC GCGCCCGGCT TGACCTTGCC GCCCTAGCAG 420
 CTGCGAGCGA GCTCGCTGCG GCTCTGCTCC GCGCCCGGCT TGACCTTGCC GCCCTAGCAG 480
 35 CCCAGCTTGT CCGCGCGCGC GTCCCGCGCG CGGCGCTCGC ACCCGGCGCC CCGGTCTACG 540
 ACGACGGCCC CGCGGCGCGC GATGCTGAGG AGGCAGGCGA CGAGACACCC GACGTGAGCC 600
 CCGAGCTGTT GAGGTACTTG CTGGGACGGA TTCTTGCGGG AAGCGCGGAC TCCGAGGGGG 660
 TGGCAGCCCC GCGCGCGCTC CGCGGTGCGC CGACCCAGCA TGTGGGCTCT GAGCTGCCCC 720
 CTGAGGGCGT GCTGGGGGCG CTGCTGCGTG TGAAACGCTT AGAGACCCCG GCGCCCCAGG 780
 TGCTGTCAGC CCGCTCTCTG CCACCTGAG CACTGCGCGG ATCCCGTGCA CCTGGGAGC 840
 40 CAGAAATGCC CCGCCATGCC CGCCACAGG ACTTCTCCCC GCCAGCAGT CCAGAGCAAC 900
 TTACCCCGGC CAGCAGGCC TCTCACCAGA GGATCCCTAC CCGCTGGGCC ACAATAACAT 960
 GATCTGAGC

45 Seq ID NO: 478 Protein sequence
 Protein Accession #: NP_037403.1

1 11 21 31 41 51
 50 MAGSPLWGP RAGVGLLVL LLLGLPRPPP ALCARPVKEP RGLSASPPL AETGAPRRFR 60
 RSVPRGEAAG AVQELARALA HLEAERQER ARAEAQEAED QARVLAQLL RVNGAPRNSD 120
 PALGLDDDFD APAQLARAL LRARLDPAAL AAQLVPAPVP AAALRPRFV YDDGAPGADA 180
 BEAGDETFDV DPELLRYLLG RILAGSADSE GVAAPRRLLR AADHDVGSSEL PPEGVLGALL 240
 RVKRLTPAP QVPARRLLPP

55 Seq ID NO: 479 DNA sequence
 Nucleic Acid Accession #: NM_002214
 Coding sequence: 681..2990

1 11 21 31 41 51
 60 CCCAGAGCGG CTTCCCTCTG TTGCTGGCAT CCGAGCTTTC CTCCCTTGCC AGCCAGSAG 60
 CTGCGGACTT GTCTTTGCCC GCTGCTCCGC AGACGGGGCT GCAAGAGTGC AACTAATGGT 120
 GTTGGCTCCG CTGCCCCACT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTT 180
 65 TCCCTCGAC CTGCGCGCGG TACCCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
 TAGGGTGGTT TCCCCCGCAG CTTCGGGCTT TGTTTGGGTT TGATTTGTTT TGGCTCTTGG 300
 CTAAGCTGAT TTAATGACGA GAAGCCCGAC CGGCTGGAGA GAAACAAAAG CTCCTTTCTT 360
 TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCCGC GCGGGCGCT 420
 TGGCCGTGGA AGGAGGTGCT TCTCGGGAG ACCCGGGGAC CCGCGGTGCC GAGCGGGGAG 480
 70 GGCCTAGGG GCGCTGAGAT GCGAGCGGT GCGGGGGGCC GCTTACCTGC ACGCTTGCT 540
 CCGAGCGCGG GCGTCCGCTT GCTAGGCTGC CGGAAACGCT CTTAGCGACA CTGCCCCGCG 600
 GGCCTCGAGG TCGCCCGGGA GCGCGAGCCC GCGTCCGGAA GGCAGCCAGG CCGCGGGCGC 660
 GGGCGGGGCT GTTTTGCATT ATGTGCGGCT CGGCCCTGGC TTTTTTTACC GCTGCTTTG 720
 TCTGCTGCA AAACGACCGG CGAGGTCCCG CCTGTTCTCT CTGGGAGGCC TGGGTGTTTT 780
 75 CACTTGTGCT TGAAGTGGG CAAGGTGAAG ACAATAGATG TGATCTTCA AATGAGCAT 840
 CTTGTGCCAG GTGCCITGCG CTGGGTCCAG AATGTGGATG GTGTGTTCA GAGGATTTCA 900
 TTTCAAGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTT CAATTTAATA AGCAAGGCT 960
 GCTCAGTTGA TTCAATAGAA TACCATCTG TGATGTTAT AATACCACT GAAATGAAA 1020
 TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCGAAGCTA 1080
 80 ATTTATGCT GAAAGTTCAT CCTCTGAAGA AATATCCTGT GGATCTTTAT TATCTTGTG 1140
 ATGCTCTCAG ATCAATGCAC AATAATAGT AAAAATATAA TTCCGTGGA AACGATTTAT 1200
 CTAGAAAAAT GGCATTTTTC TCCCGTGACT TTGCTCTGG ATTTGGCTCA TACGTTGATA 1260
 AAACAGTTTC ACCATACATT AGCATCCACC CCGAAGGAT TCATATACAA TGCAGTACAT 1320
 ACAATTTAGA CTGATGCTT CCGCATGAT ACATCCATGT GCTGTCTTTG ACAGAGACA 1380
 TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG 1440

5 AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA 1500
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560
 GCAAAATGGC AGGCATAGTG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACAAAGTCT 1620
 ACGTCAATC GACCAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG 1680
 10 ACACACACAT TAATGTCATC TTTGCAGTTC AAGGAAAACA ATTTTCATGG TATAAGGATC 1740
 TTCTACCCCT CTTGCCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA 1800
 ATAATTGGT AGTGGAAGCC TATCAGAAGC TCATTTTCAGA AGTGAAGTT CAGGTGGAAA 1860
 ACCAGGTACA AGGCATCTAT TTTAACATTA COGCCATCTG TCCAGATGGG TCCAGAAAGC 1920
 CAGGCATGGA AGGATGCAGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG 1980
 15 TTACAATGAA AAAATGTGAT GTCACAGGAG GAAAAAACTA TGCAATAATC AAACCTATTG 2040
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 ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACCTTTCT AGATTCCAAAG TGTTCOCAGT 2160
 GTGATGAGAA TAAATGTCTT TTTGATGAAG ATCAGTTTTT TCTGAGAGT TGCAAGTCAC 2220
 20 ACAGGATCA GCGCTTTGCG AGTGGTCTGAG GAGTTTGTGT TGTGGGAAA TGTTCATGTC 2280
 ACAAATTAAG GCTTGGAAAA GTGTATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGTG 2340
 CATATCACC A TGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400
 GCTTCAGTGG CTGGGAAGCT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG 2460
 TCAATTCAA GGGCCAGATG TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520
 25 GCACCGATCC CAGGAGCATC GGCCGCTTCT GTGAACACTG CCCACCTGT TATACAGCCT 2580
 GCAAGGAAAA CTGGAATTGT ATGCAATGCC TTCACCTCA CAATTGTGCT CAGGCTATAC 2640
 TTGATCAGTG CAAAACCTCA TGTGCTCTCA TGGAAACACA GCATTATGTC GACCAAACTT 2700
 CAGAAATGTT CTCCAGGAAA AGCTACTTGA GAATATTTT CATCATTTTC ATAGTTACAT 2760
 TCTTGATTGG GTTGCTTAAA GTCTGTATCA TTAGACAGGT GATACTACAA TGGAAATAGTA 2820
 30 ATAAATTAAG GTCTCTATCA GATTACAGAG TGTCAAGCTC AAAAAAGGAT AAGTTGATTG 2880
 TGCAAGTGT TTGCACAAGA GCAGTCACCT ACCGACGTGA GAAGCCTGAA GAAATAAAAA 2940
 TGGATATCAG CAATTAATAT GCTCATGAAA CTTTCAGGTG CAATCTCTAA AAAAAGATTT 3000
 TTAACACTTT AATGGGAAAT TGGAAATGTT AATAATTGCT CCTAAAGATT ATAATTTTAA 3060
 AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTGTG AACTCGAAC 3120
 35 GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180
 AAAATGTGTC TTACTACTGT TTGAGACTAG TGTGCTGTGA GCATTTTACT GTAATATATA 3240
 ACTTATTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300
 TACCTGTAT CCCTAGCCTT CCCAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATTGTGT 3360
 CACTACAGG GTACAGTAAT CCCTGCACTG GACATGTGAG GAAAAAATA ATCTGGCAAG 3420
 40 TATATTCTAA GGTTCGCAAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG 3480
 ATGAATAAAT GATTGCTGTT TCACCTTTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA 3540
 AAAGATTATT GCTTTTAAAT GTGTGTAGTT TTATGCAATG GTGTTTATGG TTTGCTTATT 3600
 TTGCAAGAT TGATACTAAT TCCAGCATTC TCTCCTCTTT GOCCTTATGT TTTGTTTTCT 3660
 TTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAAT GCTAAGTTAC 3720
 45 TACTGCCATA AAAAATAAT AATACAAAT CACTTTATCA GAATACTAGT TTTAAAGCT 3780
 GAATGTTAA

Seq ID NO: 480 Protein sequence
 Protein Accession #: NP_002205

45 1 11 21 31 41 51
 MCGSALAFPT AAFVCLQND RGPASFLWAA WVPSLVILGL QGEDNRCASS NAASCARCILA 60
 LGPECGMVCQ EDFI6GGSR S ERCDIVSNLI SKGCSVDSIE YPSVHVIPT ENEINTQVTP 120
 50 GEVSQILRPG AEANFMLKVH PLKKYPVDLY YLVDVSASME NNIEKINSVG NDLSRIOAFF 180
 SRDPRLGPGS YVDKTVSPYI SIHPERIHQ CSDYNLDOMP PEGYIHVLSL TENITEFEKA 240
 VHRQISGN I DTPEGGFDAM LQAAVCESHI GWRKEAKRL LVMTDQTSHL ALDSKLAGIV 300
 VPNDGNCHLK NNYYVKSTIM EHPSLGQLS E KLIDNNINVI FAVQGHQPHW YKDLPLPLPG 360
 TLAGIESKA ANLNLVVEA YQKLISEVKV QVENQVQGIY FNITAI CPDG SRKPGMEGCR 420
 55 NVTSNDEL V NVTVMKKCD VTGKNYAI KPIGFNETAK IHIHRNCSCQ CEDNRGPKGK 480
 CVDETFLDSK FDEQPSSES CKSHKQDQVC SGRGVCVGSK CSCHKIKLGK 540
 VYGKYCEKDD FSCPHYHGNL CAGHGECEAG RCQCP8GMEG DRQCP8SAAA QHCVNSKQV 600
 CSGRGTCVCG RCECTDPSI GRFCEHCPTC YTACKENWNC MQLHFNHLS QAILDQCKTS 660
 CALMEQHYV DQTSCEPSSP SYLRIFPIIF IVTFILGLLK VLIIRQVILQ WNSNKIKSSS 720
 60 DYRVASAKD KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETPRCNF

Seq ID NO: 481 DNA sequence
 Nucleic Acid Accession #: NM_003318.1
 Coding sequence: 1..2574

65 1 11 21 31 41 51
 ATGGAATCCG AGGATTAAAG TGGCAGAGAA TTGACAATTG ATTCCATAAT GAACAAAGTG 60
 AGAGACATTA AAAATAAGTT TAAAAATGAA GACCTTACTG ATGAACTAAG CTTGAATAAA 120
 70 ATTTCTGCTG ATACTACAGA TAACTCGGGA ACTGTTAACC AAATTATGAT GATGGCAAAC 180
 AACCCAGAGG ACTGGTTGAG TTTGTTGCTC AAAC TAGAGA AAAACAGTGT TCCGCTAAGT 240
 GATGCTCTTT TAAATAAATT GATTGGTGT TACAGTCAAG CAATTGAAGC GCTTCCCCCA 300
 GATAAATATG GCCAAAATGA GAGTTTGTCT AGAATTCAAG TGAGATTTCG TGAATTAATA 360
 GCTATTCAAG AGCCAGATGA TGCACGTGAC TACTTTCAAA TGGCCAGAGC AAACGTCAAG 420
 75 AATTTGCTTT TTGTTTCATAT ATCTTTTGCA CAATTGGAAC TGTACACAGG TAATGTCAAA 480
 AAAAGTAAAC AACTCTTCCA AAAAGCTGTA GAACTGGAG CAGTACCCT AGAAATGCTG 540
 GAAATTGCC TGGGAAATTT AAACCTCCAA AAAAAGCAGC TGCTTTTCA GAGGAAAAAG 600
 AAGAAATTA GGCATCTAC GGTATTAACT GCCCAAGAAT CATTTTCGGG TTCATTGGG 660
 CATTTACAGA ATAGGAACAA CAGTTGTGAT TCCAGAGGAC AGACTACTAA AGCCAGGTTT 720
 80 TTATATGGAG AGAACATGCC ACCACAGAT GCAGAAATAG GTTACCGGAA TTCATTGAGA 780
 CAAACTAAAC AAACTAAACA GTCATGCCCA TTTGGAAGAG TCCAGTTAA CCTTCTAAAT 840
 AGCCAGATG GTGATGTGAA GACAGATGAT TCAGTTGTAC CTTGTTTTAT GAAAAGACAA 900
 ACCTTAGAT CAGAAATGCC AGATTGTT GTGCCCTGGT CTAACCAAG TGGAAATGAT 960
 TCCTGTGAAT TAAGAAATTT AAAGTCTGTT CAAAATAGTC ATTTCAAGGA ACCTCTGTTG 1020
 TCAGATGAAA AGAGTTCTGA ACTTATTATT ACTGATTCAA TAACCTGAA GAATAAAACG 1080

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5 GAATCAAGTC TTCTAGCTAA ATTAGAAGAA ACTAAGAGT ATCAAGAAC AGAGGTTCCA 1140
 GAGAGTAAC AGAAGACAGT GCAATCTAAG AGAAGTCAG AGTGTTATTA CCAGATCCT 1200
 GCTGCATCTT CAATCACTG GCAGATTCCG GAGTTAGCCC GAAAGTTAA TACAGAGCAG 1260
 AAACATACCA CTTTGTAGCA ACCTGTCTTT TCAAGTTCAA AACAGTCACC ACCAATATCA 1320
 ACATCTAAAT GGTGTGACCC AAAATCTATT TGTAAGACAC CAAGCAGCAA TACCTTGAT 1380
 GATTACATGA GCTGTTTATG AACTCCAGTT GTAAAGAATG ACTTTCACC TGCTGTGAG 1440
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 ACTCCACTTC AAAATTTACA GGTTTAGCA TCTTCTCAG CAATGAATG CATTTCGGTT 1560
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 Protein Accession #: NP_003309.1

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Seq ID NO: 484 Protein sequence
 Protein Accession #: NP_003658.1

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Protein Accession #: Eos sequence

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 GLTGVLSLS ELNLTNCTPT IKLNNTMNAC AVIAALERVK IRPMEHCCCS VRIPCPSPE 180
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 NVPSPIGEIQ PLSPPSPAPI ASSPAIDMFP QSETISSPMP QTHVSGTPPP VKASFSSPTV 300
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 45 SPFDMLAPLA QRLKVVDDI GLQLNFSNTT ISLTSPLSAL AVIRVNASSP NTTTTFVAQDP 420
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 50 WMGLEAFHMY LALVVKFNTY IRKYILKPCI VGMGVPAVVV TIILTISPDN YGLGSYGKPP 720
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 RRYLCCGLRL LAENSDWSKT ATNGLKKQTV NQGVSSSSNS LQSSSNSTNS TTLVNNDCS 900
 VHASGNNGAS TERNGVSPSV QNGDVCLHDF TGKQHPNFK EDSCNKGKRM ALRRTSKRGS 960
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Seq ID NO: 489 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2811

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Seq ID NO: 490 Protein sequence
 Protein Accession #: Eos sequence

30 1 11 21 31 41 51
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 40 QNFETFPAL FQDPSLENLS LISYVSSSV ANLTVRNLR NVTVLKHIN PSQDELTVRC 540
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Seq ID NO: 491 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..3045

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Seq ID NO: 492 Protein sequence
 Protein Accession #: Eos sequence

25 1 11 21 31 41 51
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 30 GEIMFYDRE STVPQNHIT NGTLTGVLSL SELKRSBLNK TLQTLSETYP IMCATAEAS 180
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 PQPSAPIASS PAIDMPPQSE TISSPMPQTH VSGTTPPVKA SFSSPTVSAP ANVNTTSAPP 360
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45 Seq ID NO: 493 DNA sequence
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241..1902

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10 Seq ID NO: 494 Protein sequence
 Protein Accession #: NP_056322

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25 Seq ID NO: 495 DNA sequence
 Nucleic Acid Accession #: NM_003506.1
 Coding sequence: 259..2379

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 AAGAGTGATA TTAGTGAC CAGGCTGGCA CAGAGCAACA ATTTCAGGT CCCAGTTCT 2280
 TCAGAACCAA GCAGSCTCAA AGGTTCACCA TCTCTGCTT TACACCAAGT TTCAGGAGT 2340
 70 AGAAAAGAGC AGGAGGGTGG TTGTCTTCA GATACTGAA GAACATTTT TCTGTTACT 2400
 CAGAAGCAAA TTTGTGTTAC ACTGGAAGTG ACCTATGCA TGTTTGTAA GAATCACTGT 2460
 TACGTTCTT TTTTGCACTT AAAGTTGCAT TGCCTACTGT TATAGTGAA AAAATAGAGT 2520
 TCAAGATAA TATGACTCAT TTACACAAA GGTTAATGAC AACATATAC CTGAAAACAG 2580
 AAATGTGCG GTTAATAATA TTTTAAAT AGTGTGGGAG GACAGAGTTA GAGGAATCTT 2640
 75 CTTTCTCAT TTATGAAGAT TCTACTCTG GTAAGAGTAT TTTAAGATGT ACTATGCTAT 2700
 TTTACCTTTT TGATATAAAA TCAAGATATT TCTTTGCTGA AGTATTTAAA TCTTATCCTT 2760
 GTATCTTTT ATACATATT GAAAAATAGC TTATATGTAT TTGAATTTT TTGAATCCTT 2820
 ATTCAAGTAT TTTTATCATG CTATTGTGAT ATTTTAGCAC TTTGGTAGCT TTTACACTGA 2880
 80 ATTTCTAAGA AAATGTAAA ATAGTCTCT TTTTACTGT AAAAAGAGAT ATACCAAAAA 2940
 GTCTTATAAT AGGAATTTAA CTTTAAAAAC CCACCTATTG ATACCTTACC ATCTAAATG 3000
 TGTGATTTT ATAGTCTCGT TTTAGGAATT TCACAGATCT AAATTATGTA ACTGAATAA 3060
 GGTGCTTACT CAAAGAGTGT CCACATTGTA TTGTATTATG CTGCTCACTG ATCCTTCTGC 3120
 ATATTAAAA TAAATGTCC TAAAGGGTTA GTAGACAAAA TGTAGTCTT TTGTATATTA 3180
 GGCCAAAGTC AATTGACTTC CCTTTTAA TGTTCATGA CCACCAATG ATTGTATTAT 3240

AACCACTTAC AGTTGCTTAT ATTTTGTGTT TTAACCTTTG TTTCTTAACA TTTAGAATAT 3300
TACATTTTGT ATTATACAGT ACCTTTCTCA GACATTTTGT AG

Seq ID NO: 496 Protein sequence
Protein Accession #: NP_003497.1

5
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15
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1 11 21 31 41 51
MEMFTLLTLC IFLPLLRGHS LFTCEPITVP ROMRMAYNMT FFPNLMGHYD QSIAAVEMEH 60
FLPLANLSCS PNIETFLCKA FVPTCIEQIH VVPPCRKLCB KVSYDCKKLI DTPGIRWPEE 120
LECDRLQYCD ETVPVTFDPH TSPLGPQKKT EQVQRDIGFW CPRHLKTSGG QGVKPLGIDQ 180
CAPPCPNMYP KSDELEPAKS FIGTVSIFCL CATLFTFLTP LIDVRRFRYP ERPIIYYSVC 240
YSIVSLMYFI GFLLDGSTAC NKADEKLELG DTVVLGSQNK ACTVLFMLLY PFTMAGTVNM 300
VILTITWFLA AGRKWSCEAI EQKAVWPHAV AWGTPGFLTV MLLALNKKVEG DNISGVCFVG 360
LYDLASRYF VLLPLCLCVF VGLSLLLAGI ISLNHVRQVI QHDGRNQEKI KKFMRIGVFP 420
SGLYLVPLVT LLGCTVYEQV NRITWEITWV SDHCRQYHIP CFYQAKAKAR PELALFMIKY 480
LMTLIVGISA VFWVSGSKTC TEWAGFFKRN KRKDPISER RVLQESCEFF LKHNSKVKKH 540
KKHYKPSSEK LKVISKSMGT STGATANHGT SAVAITSHDY LQGETLLEIQ TSPETSMREV 600
KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD 660
TGLAQSNMLQ VPSSESPSSL KGSTSLLVHP VSGVRKEQGG GCHSDT

Seq ID NO: 497 DNA sequence
Nucleic Acid Accession #: NM_005046
Coding sequence: 16..777

25
30
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45
1 11 21 31 41 51
GGATTTCGGG GCTCCATGGC AAGATCCCTT CTCCTGCCCC TGCAGATCCT ACTGCTATCC 60
TTAGCCTTGG AACTCGCAGG AGAAGAAGCC CAGGGTGACA AGATTATTGA TGGGCCCCCA 120
TGTGCAAGAG GCTCCACACC ATGGCAGGTG GCCCTGCTCA GTGGCAATCA GCTCCACTGC 180
GGAGGCGTCC TGTGCAATGA GCGCTGGGTG CTCCTGCGG CCCACTGCAA GATGAATGAG 240
TACACCGTGC ACCTGGGCAG TGATACGCTG GCGACAGGA GAGCTCAGAG GATCAAGGCC 300
TCGAAGTCAT TCGGCCACCC CGGCTACTCC ACACAGACCC ATGTTAATGA CCTCATGCTC 360
GTGAAGCTCA ATAGCCAGGC CAGGCTGTCA TCCATGGTGA AGAAAGTCA GCTGCCCTCC 420
CGCTGCGAAC CCCCTGGAAC CACCTGTACT GTCTCGGCT GGGGCACTAC CACGAGCCCA 480
GATGTGACCT TTCCTCTGA CCTCATGTGC GTGGATGTCA AGCTCATCTC CCCCCAGGAC 540
TGCAAGGAGG TTACAAAGGA CTTACTGGAA AATTCCATGC TGTGCGCTGG CATCCCGAC 600
TCCAAAGAAA ACGCTGCAA TGTGTACTCA GGGGACCGT TGTGTGCGAG AGGTACCTCG 660
CAAGGTCTGG TGTCTGGGG AACTTCCCT TGGGCGCAAC CCAATGACCC AGGAGTCTAC 720
ACTCAAGTGT GCAAGTTCAC CAAGTGGATA AATGACACCA TGAAAAAGCA TCGTAACGCG 780
CACACTGAGT TAATTAACAT TGTGCTTCCA ACAGAAAAATG CACAGGAGTG AGGACSCCGA 840
TGACCTATGA AGTCAAAATT GACTTTACCT TTCCTCAAAG ATATATTTAA ACCTCATGCC 900
CTGTTGATAA ACCAATCAAA TTGGTAAAGA CCTAAACCA AAACAATAA AGAAACACAA 960
AACCTCAA

Seq ID NO: 498 Protein sequence
Protein Accession #: NP_005037

50
55
1 11 21 31 41 51
MARSLLLPLQ ILLLSLALET AGEBAQGDKI IDGAPCARGS HPWQVALLSG NQLHCGGVLV 60
NERWVLTAAH CMNEYTVHL GSDTLGDRRA QRIKASKSFR HPGYSTQTHV NDLMLVKLNS 120
QARLSSMVKK VRLPSRCEPP GTTCTVSWGNG TTSPDVTFFP SLLMCVDVKL ISPDCTKVY 180
KDLLENSMLC AGIPDSKINA CNGDSGGPLV CRGTLQGLVS WGTFFPGQFN DPGVYTQVCK 240
PTKWINDTMK KHR

Seq ID NO: 499 DNA sequence
Nucleic Acid Accession #: NM_007196
Coding sequence: 182..962

60
65
70
75
80
1 11 21 31 41 51
GTTCCAGAA GCTCCCCAGG CTCTAGTGCA GGAGGAGAAG GAGGAGGAGC AGGAGGTGGA 60
GATTCCCACT TAAAAGGCTC CAGAATCGTG TACCAGGCAG AGAACTGAAG TACTGGGGCC 120
TCCTCCACTG GGTCCGAATC AGTAGGTGAC CCGGCCCCCTG GATTCTGGAA GACTCAACCA 180
TGGGACGCC CCGACCTCGT GCGGCCAAGA CGTGGATGTT CCTGCTCTTG CTGGGGGGAG 240
CCTGGGCAGG ACACTCCAGG GCACAGGAGG ACAAGGTGCT GGGGGGTGAT GAGTGCCAAC 300
CCCATTCGCA GCTTGGCAG GCGGCCTGT TCCAGGGCCA GCAACTACTC TGTGGCGGTG 360
TCCTTGTAGG TGGCAACTGG GTCCCTACAG CTGCGCACTG TAAAAAACCG AAATACACAG 420
TACGCTGGG AGACCACAGC CTACAGAATA AAGATGGCCC AGAGCAAGAA ATACCTGTGG 480
TTCAGTCCAT CCCACACCCC TGCTACAACA GCAGOGATGT GGAGGACCAC AACCATGATC 540
TGATGCTTCT TCAACTGGGT GACCAGGCAT CCCTGGGGTC CAAAGTGAAG CCCATCAGCC 600
TGGCAGATCA TTGCACCCAG CCTGCGCAGA AGTGACCGT CTCAAGCTGG GGCAGTGTCA 660
CCAGTCCCCG AGAGAATTTT CCTGACACTC TCAACTGTGC AGAAGTAAAA ATCTTTCCCC 720
AGAAGAAGTG TGAGGATGCT TACCCGGGCG AGATCAGAGA TGGCATGATC TGTGAGGCA 780
GCAGCAAAAG GGCTGACAGG TGCCAGGGCG ATTCTGGAGG CCCCCTGGTG TGTGATGGTG 840
CACTCCAGGG CATCACATCC TGGGGCTCAG ACCCTGTGG GAGGTCCGAC AAACCTGGCG 900
TCTATACCAA CATTCGCCG TACCTGGACT GGATCAAGAA GATCATAGGC AGCAAGGGCT 960
GATTCTAGGA TAAGCACTAG ATCTCCCTTA ATAACTCAC AACTCTC

Seq ID NO: 500 Protein sequence
Protein Accession #: NP_009127

1 11 21 31 41 51

5 MGRPEPRAAK TWMLLLLG ANAGHSRAQE DKVLGGHECQ PHSQWQAAL FQQQQLLCGG 60
 VLVGGMWVLT AAHCKKPKYT VRLGDHSLQN KDGPEQEPV VQSIPHPCYN SSDVEDENHD 120
 LMLQLRDQA SLGSKVKPIS LADHCTQPGQ KCTVSGWGTV TSPRENFPDT LNCAEVKIFP 180
 QKKCEDAYPG QITDGMVCAQ SSRGADTCQG DSGGPLVCDG ALQGITSWGS DPCGRSDKPG 240
 VYTNICRYLD WIKKIIGSKG

10 Seq ID NO: 501 DNA sequence
 Nucleic Acid Accession #: NM_006103
 Coding sequence: 29..406

15 1 11 21 31 41 51
 CACCTGCACC CCGCCCGGGC ATAGCACCAT GCCTGCTGTG CGCTAGGCC CGTAGCCGC 60
 CGCCCTCCTC CTCAGCCTGC TGCTGTTCGG CTTCACCCCTA GTCTCAGGCA CAGGAGCAGA 120
 GAAGACTGGC GTGTGCCCGC AGCTCCAGGC TGACACGAAAC TGACACGCAAG AGTGCGTCTC 180
 GGACAGCGAA TGCGCCGACA ACCTCAAGTG CTGCAGCGCG GGCTGTGCCA CCTTCTGCCT 240
 TCTCTGCCA AATGATAAGG AGGGTTCTTG CCCCAGGTG AACATTAACT TTCCCAGCT 300
 CGGCTCTGT CGGACACAGT GCCAGGTGGA CAGCCAGTGT CCTGGCCAGA TGAATGCTG 360
 CCGCAATGGC TGTGGGAAGG TGTCTGTGT CACTCCCAAT TTCTGAGTC CAGCCACCAC 420
 CAGGCTGAGC AGTGAGGAGA GAAAGTTTCT GCCTGGCCCT GCATCTGTT CCAGCCACC 480
 TGCCCTCCCC TTTTTCGGGA CTCTGTATTC CCTCTTGGGC TGACCACAGC TTCTCCCTTT 540
 CCAACCAAT AAAGTAACCA CTTTCAGCAA AAAAAAAAAA AAAA

25 Seq ID NO: 502 Protein sequence
 Protein Accession #: NP_006094

30 1 11 21 31 41 51
 MPACRLGFLA AALLLSLLLF GFTLVSGTGA BKTGVCPQLQ ADQNCQECV SDSECADNLK 60
 CCSAGCATFC LLCPNDKEBS CPQVNIINFPQ LGLCRDQCQV DSQCPGQMKC CRNGCGKVSC 120
 VTPNF

35 Seq ID NO: 503 DNA sequence
 Nucleic Acid Accession #: NM_002407
 Coding sequence: 65..352

40 1 11 21 31 41 51
 CCTCCACAGC AACTTCCTTG ATCCCTGCCA CGCAGACTG AACACAGACA GCAGCCGCCT 60
 CGCCATGAAG CTGCTGATGG TCCTCATGCT GCGGCGCCTC CTCCTGCACT GCTATGCAGA 120
 TTCTGGCTGC AAATCTCTGG AGGACATGGT TGAAGAAGACC ATCAATTCCG ACATATCTAT 180
 ACCTGAATAC AAAGAGCTTC TTCAAGAGTT CATAGACAGT GATGCGCTG CAGAGGCTAT 240
 GGGGAATTC AAGCAGTGT TCCTCAACCA GTCACATAGA ACTCTGAAAA ACTTTGACT 300
 GATGATGAT ACAGTGATAG ACAGCATTTG GTGTAATATG AAGAGTAATT AACTTTACCC 360
 AAGGCGTTTG GCTCAGAGGG CTACAGACTA TGGCCAGAAC TCATCTGTTG ATTGCTAGAA 420
 ACCACTTTTC TTCTTTGTGT TGTCTTTTGA TGTGAAACT GCTAGACAAC TGTGAAACC 480
 TCAAAATTCAT TTCCATTICA ATAACCTACT GCAAACT

50 Seq ID NO: 504 Protein sequence
 Protein Accession #: NP_002398

55 1 11 21 31 41 51
 MKLLMVLMLA ALLLHCYADS GCKLLEDMEV KTINSDISIP EYKELLQEFI DSDAAABAMG 60
 KFRQCFLNQS BRTLNKFLML MHTVYDSIWC NMKSN

60 Seq ID NO: 505 DNA sequence
 Nucleic Acid Accession #: NM_014791.1
 Coding sequence: 171..2126

65 1 11 21 31 41 51
 TTGGCGGGCG GAAGCGGCCA CAACCCGGCG ATCGAAAAGA TTCTTAGGAA GCGCGTACCA 60
 GCGCGGTCTC TCAGGACAGC AGGCCCTGT CCTCTGTGCG GGCGCGGCTC AGCGGTGCC 120
 TCCGCCCCCTC AGGTCTCTTT TCTAATTCCA AATAAACTTG CAAGAGGACT ATGAAAGATT 180
 ATGATGAAT TCTCAAATAT TATGAATTAC ATGAAACTAT TGGGACAGGT GGCCTTGCAA 240
 AGGTCAAAT TGCCCTGCCAT ATCCTTACTG GAGAGATGGT AGCTATAAAA ATCATGGATA 300
 AAAACACACT AGGGAGTGAT TTGCCCGGGA TCAAAACGGA GATTGAGGCC TTGAAGAACC 360
 TGAGACATCA GCATATATGT CAACCTTACC ATGTGCTAGA GACAGCCAAC AAAATATTCA 420
 TGGTTCTTGA GTACTGCCCT GGAGGAGAGC TGTTTGACTA TATAATTTCC CAGGATCGCC 480
 TGTCAAGAAG GGAGACCCCG GTTGTCTTCC GTCAGATAGT ATCTGCTGTT GCTTATGTGC 540
 ACAGCCAGGG CTATGCTCAC AGGGACCTCA AGCCAGAAAA TTTGTGTTT GATGAATATC 600
 ATAAATTAAA GCTGATTGAC TTTGGTCTCT GTGCAAAACC CAAGGTAAC AAGGATTACC 660
 ATCTACAGAC ATGCTGTGGG AGTCTGGCTT ATGCAGCACC TGAGTTAATA CRAAGCAAAT 720
 CATATCTGG ATCAGAGGCA GATGTAATG TAATGGCTTT ATACAAGAAG ATTATGAGAG 780
 GTGGATTCT ACCATTGAT GATGATAATG TAATGGCTTT ATACAAGAAG ATTATGAGAG 840
 GAAAATATGA TGTTCCTAAG TGGCTCTCTC CAGTAGCAT TCTGCTTCTT CAACAAATGC 900
 TGCAGGTGGA CCAAGAGAAA CGGATTCTTA TGAAAAATCT ATTGAACCAT CCCTGGATCA 960
 80 TGCAAGATTA CAACTATCTT GTTGAGTGGC AAAGCAAGAA TCCTTTTATT CACCTGGATG 1020
 ATGATTGCGT AACAGAACTT TCTGTACATC ACAGAAACAA CAGGCAACA ATGGAGGATT 1080
 TAATTTCAT GTGGCAGTAT GATCACCTCA CGGCTACCTA TCTTCTGCTT CTAGCCAAGA 1140
 AGGCTCGGG AAAACCAAGT CGTTTAAGGC TTTCTTCTT CTCTGTGGA CAAGCCAGTG 1200
 CTACCCCAT CACAGACATC AAGTCAATA ATTGGAGTCT GGAAGATGTG ACCGCAAGTG 1260

5 ATAAAAATTA TGTGGCGGGA TTAATAGACT ATGATTGGTG TGAAGATGAT TTATCAACAG 1320
 GTGCTGCTAC TCCCGGAACA TCACAGTTTA CCAAGTACTG GACAGAATCA AATGGGGTGG 1380
 AATCTAAATC ATTAACTCCA GCCTTATGCA GAACACCTGC AAATAAATTA AAGAACAAG 1440
 AAAATGTATA TACTCTTAAG TCTGCTGTAA AGAATGAAGA GTACTTTATG TTCTCTGAGC 1500
 CAAAGACTCC AGTTAATAAG AACACGACATA AGAGAGAAAT ACTCACTACG CCAAAATCGTT 1560
 ACACATACCC CTCAAAAGCT AGAAACCACT GCCTGAAAGA AACTCCAATT AAAATACCA 1620
 TAAATTCAAC AGGAACAGAC AAGTTAATGA CAGGTGTCAT TAGCCCTGAG AGGCGGTGCC 1680
 GCTCAGTGGG ATTGGATCTC AACCAAGCAC ATATGAGGGA GACTCCAAAA AGAAAGGGAG 1740
 10 CCAAAGTGTG TGGGAGCCTT GAAAGGGGGT TGGATAAGGT TATCACTGTG CTCACCAGGA 1800
 GCAAAAGGAA GGGTCTCGCC AGAGACGGGC CCAGAGACT AAAGCTTCAC TATAATGTGA 1860
 CTACAAC TAGTGTGAAT CCAGATCAAC TGTGAATGA AATAATGTCT ATTCTTCCAA 1920
 AGAAGCATGT TGACTTTGTA CAAAAGGGTT ATACACTGAA GTGTCAAACA CAGTCAGATT 1980
 TTGGGAAAGT GACAATGCAA TTGTAATTAG AAGTGTGCCA GCTTCAAAAA CCCGATGTGG 2040
 TGGGTATCAG GAGGCAGCGG CTTAAGGGCG ATGCCTGGGT TTACAAAAGA TTAGTGAAG 2100
 15 ACATCCTATC TAGCTGCAAG GTATAATTGA TGGATTCTTC CATCCTGCCG GATGAGTGTG 2160
 GGTGTGATAC AGCCTACATA AAGACTGTGA TGATCGCTTT GATTTTAAAG TTCATTGGAA 2220
 CTACCACTGT GTTCTTAAAG AGCTATCTTA AGACCAATAT CTCTTTGTTT TTAACAAAA 2280
 GATATTATTT TGTGTATGAA TCTAAATCAA GCCCATCTGT CATTATGTGA CTGTCTTTT 2340
 20 TAATCATGTG GTTTGTGTATA TTAATAATG TTAGCTTTCT TAGATTCACT TCCATATGTG 2400
 AATGTAAGCT CTTAACTATG TCTCTTTGTA ATGTGTAAT TCTTTCTGAA ATAAACCAT 2460
 TTGTGAATAT

Seq ID NO: 506 Protein sequence

Protein Accession #: NP_055606.1

25 1 11 21 31 41 51
 MKDYDELLKY YELHETIGTG GFAKVKLACH ILTGEMVAIK IMDKNTLGSD LPRIKTBIEA 60
 LKHLRHHIC QLVHLEETAN KIFMVLEYCP GGBLPDYIIS QDRLESEETR VVFRQIVSAV 120
 30 AYVHSQGYAH RDLKPELLEF DEYHKLKID FGLCAKPKGN KDYHLQTCOG SLAYAAPELI 180
 QGKSYLGSEA DVWSMGILLY VLMCGFLPFD DDNVMAlyk IMRGKYDVPK WLSPPSILL 240
 QQMLQVDPK RISMKNLLNH PWIMQDYNYP VEMQSKNPI HLDLDDCVTEL SVHHRNNRQT 300
 MEDLISLWQY DHLTATYLLL LAKKARGKPV RLRLSSFSOG QASATPPTDI KSNWNSLEDV 360
 TASDKNYVAG LIYDWCEDD LSTGAATPRT SQFTKYWTES NGVESKSLTP ALCRTPANKL 420
 35 KKNENVYTPK SAVKNEEYPM FPEPKTPVKN NQHKREILIT PMRYTTPSKA RNQCLKETPI 480
 KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAKVPSGL ERGLDKVITV 540
 LTRSKRKGSa RDGPRRLKLH YNVTTTRLVN PDQLNLEIMS ILPKKHVDVF QKGYTLKQQT 600
 QSDFGKVTMQ FELEVQQLQK PDVVGIRRRQ LKGDWVYKR LVEDILSSCK V

Seq ID NO: 507 DNA sequence

Nucleic Acid Accession #: NM_000582

Coding sequence: 88..990

45 1 11 21 31 41 51
 GCAGAGCACA GCATCGTCGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA 60
 AAGCCGACCC AAGGAAAACT CACTACCATG AGAATTGCAG TGATTGCTT TTGCTCCTA 120
 GGATCACCT GTGCCATACC AGTTAAACAG GCTGATCTG GAAGTTCTGA GGAAAGCAG 180
 50 CTTTACACA AATACCAGG TGCTGTGGCC ACATGGCTAA ACCCTGACCC ATCTCAGAG 240
 CAGAATCTCC TAGCCCCACA GACCCTTCCA AGTAAGTCCA ACGAAAGCCA TGACCAATG 300
 GATGATATGG ATGATGAAGA TGATGATGAC CATGTGGACA GCCAGGACTC CATTGACTCG 360
 AACGACTGCT ATGATGTAGA TGACACTGAT GATTCTCACC AGTCTGATGA GTCTCACCAT 420
 TCTGATGAAT CTGATGAAT GTTCACTGAT TTTCCCAAGG ACCTGCCAGC AACCGAAGTT 480
 55 TTCACTCCAG TTGTCCCCAC AGTAGACACA TATGATGGCC GAGGTGATAG TGTGGTTTAT 540
 GGACTGAGGT CAAATCTAA GAAGTTTCGC AGACCTGACA TCCAGTACCC TGATGCTACA 600
 GACGAGGACA TCACCTCACA CATGGAAAGC GAGGAGTTGA ATGTGTCATA CAAGGCCATC 660
 CCGGTTGCC AGGACCTGAA CGCGCCTTCT GATTGGGACA GCGGTGGGAA GGACAGTTAT 720
 GAAACGAGTC AGCTGGATGA CCAGAGTCTC GAAACCCACA GCCACAAGCA GTCCAGATTA 780
 60 TATAAGCGGA AAGCCAATGA TGAGAGCAAT GAGCATTCCG ATGTGATTGA TAGTCAGGAA 840
 CTTTCCAAAG TCAGCCGTGA ATTCCACAGC CATGAATTC ACAGCCATGA AGATATGCTG 900
 GTTGTAGACC CCAAAAGTAA GGAAGAAGAT AAACACCTGA AATTTGCTAT TTCTCATGAA 960
 TTAGATAGTG CATCTTCTGA GGTCAATTAA AAGGAGAAAA AATACAATT CTCACTTTGC 1020
 ATTTAGTCAA AAGAAAAAT GCTTTATAGC AAAATGAAAG AGAACATGAA ATGCTTCTTT 1080
 65 CTCAGTTTAT TGGTTGAATG TGTATCTATT TGAGTCTGGA AATACTAAT GTGTTTGATA 1140
 ATTAGTTTAG TTTGTGGCTT CATGGAAACT CCCTGTAAAC TAAAGCTTC AGGTTATGT 1200
 CTATGTTTAT TCTATAGAAG AAATGCAAC TATCACTGTA TTTTAATATT TGTATTCTC 1260
 TCATGAATAG AAATTTATG AGAAGCAAC AAAATACITT TACCCACTTA AAAAGAGAAT 1320
 ATAACATTTT ATGTCACTAT AATCTTTTGT TTTTAAAGTT AGTGATATAT TGTGTGTGAT 1380
 70 TATCTTTTGT TGGTGTGAAT AAATCTTTTA TCTTGAATGT AATAAGAAIT TGGTGGTGTG 1440
 AATTGCTTAT TTGTTTCCG ACGGTTGTCC AGCAATTAAT AAAACATAAC CTTTTTACT 1500
 GCCTAAAAAA AAAAAAAAAA AAAA

Seq ID NO: 508 Protein sequence

Protein Accession #: NP_000573

75 1 11 21 31 41 51
 MRIVICFCL LGITCAIPVK QADSGSSEK QLYNKYPDAV ATWLNPDPSQ KQNLAPQTL 60
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 80 DFPDLDPATE VFTPVVPTVD TYDGRGDSV YGLRSKSKFP RRPDIQYFDA TDEDITSHME 180
 SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES 240
 NESDSVIDSQ ELSKVSREFH SHEPHSHEDM LVVDPKSKEE DHHLKFRISH ELDSASSEVN

Seq ID NO: 509 DNA sequence
Nucleic Acid Accession #: AB051390.1
Coding sequence: 34..2457

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CTGAGCCGGA CTCGGGCACT GCTGGCCCTG GCGCTGCCCC TGGCCGCGGC GCTGGCCTTC 120
TCCGACGAGA CCTTGGACAA AGTGCCCAAG TCAGAGGGCT ACTGCAGCGC TATCTTGGGC 180
GCCAGGGGCA CGCGGCGGGA GGGCTACACC GAGTTCAGCC TCCGCGTGGG GGGCGACCCC 240
GACTTCTACA AGCCGGGAAC CAGCTACCGC GTAACACTTT CAGCTGTCCG TCCCTCTTAC 300
TTCAGAGGAT TCACATTAAAT TGCCCTCAGA GAGAACAGAG AGGGTGATAA GGAAGAAGAC 360
CATGCTGGGA CCTTCCAGAT CATAGACGAA GAAGAACTC AGTTTATGAG CAATTGCCTT 420
GTTGACGTCA CTGAAGGAC TCACGAGGAG AGGACCCGGA TCCAGGTGTT TTGGATAGCA 480
CCACCAAGCG GAACAGGCTG CGTGATTCTG AAGGCCAGCA TCGTACAAA ACGCATTATT 540
TATTTTCAAG ATGAGGGCTC TCTGACCAAG AAACCTTTGTG AACACAGATC CACATTGTAT 600
GGGGTGACTG ACAAAACCAT CTAGACTGCG TGTGCTTGGG GAACCTGCCA GTACAGACTC 660
ACATTTTATG GGAATTGGTC CGAGAAGACA CACCCAAAGG ATTACCTCCG TCGGCGCAAC 720
CACTGTGCTG CGATCATCGG AGGATCCCA TCACAAAGAT ATGTACTGTG GGAATATGGA 780
GGATATGCCA GCGAAGGCGT CAAACAAGTT GCAGAATTGG GCTCACCCTG GAAATGAGAG 840
GAAGAAATTC GACAACAGAG TGATGAGGTC CTCACCGTCA TCACAGCCAA AGCCCAATGG 900
CCAGCTGGGC AGCCTCTCAA CGTGAGAGCA GCACCTTCAG CTGAATTTCG CTGGAGACTG 960
ACGCGCCATT TAATGTCTCT CCGTACCATG ATGGGCCCTA GTCCCGACTG GAACGTAGGC 1020
TTATCTCGAG AAGATCTGTG CACCAAGGAA TGTGGCTGGG TCCAGAGGTT GGTGCAAGAC 1080
CTGATTTCCCT GGGACGCTGG CACCGACAGC GGGGTGACCT ATGAGTCAAC CAACAACCCC 1140
ACCATTTCCC AGGAGAAAAT CCGGCCCTCG ACCAGCCTGG ACCATCTCTA GAGTCTTTTC 1200
TATGACCCAG AGGGTGGGTC CATCACTCAA GTAGCCAGAG TTGTATCGA GAGAATCGCA 1260
CGGAAGGGTG AACAAATGCT TATTGTACCT GACAATGTG ATGATATTGT AGCTGACCTG 1320
GCTCCAGAAG AGAAAGATGA AGATGACACC CCTGAAACCT GCATCTACTC CAATGGTTC 1380
CCATGGTCCG CCGTCAGCTC CTCCACCTGT GACAAAGGCA AGAGGATGCG ACAGGCGATG 1440
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ATGGGCCCTG GCTGCAATGA CGAAGACGGC TCCACCTGCA CCAATGTCGA GTGGATCACC 1560
TGGTCCGCTT GCAGCATCTC CTGCGGCATG GGCATGAGGT CCCGGGAGAG GTATGTGAAG 1620
CAGTTCCCGG AGGACGGCTC CGTGTGCACG CTGCCCACTG AGGAAACGGA GAAGTGCACG 1680
TGCAAGGAGG AGTGCTCTCC CAGCAGCTGC CTGATGACCG AGTGGGCGCA GTGGGACGAG 1740
TGCAAGGCCA CCGTGGGCAT GGGCATGAAG AAGCGGCACC GCATGATCAA GATGAACCCC 1800
CGAGATGGCT CCAATGTCAA AGCGGAGACA TCACAGGCAG AGAAGTGCAAT GATGCCAGAG 1860
TGCCACACCA TCCCATGCTT GCTGTCCCA TGGTCCGAGT GGAGTGACTG CAGCGTGACC 1920
TGCGGGAAGG GCATGCGAAC CCGACAGCGG ATGCTCAAGT CTCTGGCAGA ACTTGGAGAC 1980
TGCAATGAGG ATCTGGAGCA GGTGGAGAA TGATGCTCC CTGAATGCCC CATTGACTGT 2040
GAGCTCACCG AGTGTCTCCA GTGTGCGGAA TGTAACAAGT CATGTGGGAA AGGCCACGTG 2100
ATTGGAACCC GGATGATCCA AATGGAGCCT CAGTTTGGAG GTGCACCTCG CCCAGAGACT 2160
GTGCAAGGAA AAAAGTGCCG CATCCGAAAA TGCCCTCGAA ATCCATCCAT CCAAAAGCTA 2220
CGCTGGAGGG AGGCCCGAGA GAGCCGCGGG AGTGAGCAGC TGAAGGAAGA GTCTGAAGGG 2280
GAGCAGTTCC CAGGTGTGAG GATGCGCCA TGGACGCGCT GGTCAGAATG CACCAAACTG 2340
TGCGGAGGTG GAATTCAGGA ACCTTACATG ACTGTAAAGA AGAGATTCAA AAGCTCCCAG 2400
TTTACCAAGT GCAAGACAA GAAGGAGATC AGAGCATGCA ATGTTTATCC TTGTATGCAA 2460
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GCTTGTATAA GACAATTATA ATTGTGTACG CTAGTTTTCA TTTTTCAGT GTGGTTGCGC 2580
CAGTAGTCTT GTGGATGCCA GAGACATCCT TTCTGAATAC TTCTTGATGG GTACAGGCTG 2640
AGTGGGGGCG CCTCACCTCC AGCCAGCCTC TTCTGCGAGA GAGTAGTGT CAGCCACCTT 2700
GTACTAAGCT AAAACATGTC CCTCTGGAGC TTCCACCTGG CCAGGAGGGA CGGAGACTTT 2760
GACCTACTCC ACATGGAGAG GCAACCATGT CTGGAAGTGA CTATGCTGTA GTCCAGGGGT 2820
GCGGCAGGTA GGAACATTC ACAGATGAAG ACAGCAGATT COCCACATCT TCATCTTTGG 2880
CCTGTCTCAAT GAAACCATGT TTTGCCCATC TCTTCTTGT GGAACCTTAG GTCTCTTTTC 2940
AAGTCTCTCT AGTCATCAAT AGTCTCTGGG GAAAAACAGA GCTGTGAGC TTGAAGAGGA 3000
GCATTGATGT TGGGTGGCTT TTGTCTTTTC ACTGAGAAAT TCGGAATACA TTTGTCTCAC 3060
CCCTGATATT GGTTCCTGAT GCCCCCCCAA CAAAATAAAA TAAATAAATT ATGGCTGCTT 3120
TATTTAAATA TAAGGTAGCT AGTTTTTACA CCGAGATAA ATAATAAGCT TAGAGTGTAT 3180
TTTTCCTGTG CTTTGGGGG TTCAGAGGAG TATGTACAAT TCTCTGGGA AGCCAGCCTT 3240
CTGAACCTTT TGGTACTAAA TCCCTATTGG AACCAAGACA AAGGAAGCAA AATTGGTCTC 3300
TTTAGAGACC AATTTGCCTA AATTTTAAAA TCTTCTTACA CACATCTAGA CGTTCAAGTT 3360
TGCAAAATCA TTTTATGCAA GAAAACATTT TTGCTATACA AACATTTGCG TAAGTCTGCC 3420
CAAGCCCCCC CCAATGCATT CCTTCAACAA AATACAATCT CTGTACTTTA AAGTTATTTT 3480
AGTCATGAAA TTTTATATGC AGAGAGAAAA AGTTACGAG ACAGAAAAACA AATCTAAGGG 3540
AAAGGAATAT TATGGGATTA AGCTGAGCAA GCAATTTCTG TGGAAAGTCA AACCTGTACG 3600
TGCTCCACAC CAGGGCTGTG GTCTCCCGAG ACATGCATAG GAATGGCCAC AGGTTTACAC 3660
TGCTTCCCA GCAATTATA GCACACCAGA TTCAGGGAGA CTGACCACA AGGATAGATG 3720
TAAAGGACA TTTCTCAGT TGGGTCCATC AGCAGTTTTT GTCTTATCCA AATGTGTACC 3780
AACTATTGT TCAATTTCTT CTTTATAGG CTTTATTACT GCTTATTTAA AATGTGTACC 3840
ATTGTGAGA CACATACAA GCTCTGAATA CACTACGAAT TTGTATTAAA CACATCAGAA 3900
TATTTCCAAA TCAACTATAG TATAGTCTG AATATGTAAT TTTAACCAA GAGAGACTAT 3960
TCAATAAAAA TCACTGGGT CTTTCTATGC TTTAAGCTAA GTAAAGTTCT AGAAGTTCT 4020
TTTTATATT GTCTCCACC TCCATCATT TCAATAAAG ATAGGCTTTG TGCTCCCTTG 4080
TTTCTGAGG GACCATTAAT ACATCTCTGA ACTACCTTTG TATCCAACAT GTTTTAAATC 4140
CTTAATGAA TTGCTTTCTC CCAAAAAAAG CACAATATAA AGAAACACAA GATTTAATTA 4200
TTTTCTACT TGGGGGAAA AAAGTCTCA TGTAGAAGCA CCCACTTTTG CAATGTGTTT 4260
CTAAGCTATC TATCTAATC TCAGCCCATG ATAAAGTTCC TTAAGCTGGT GATTCCTAAT 4320
CAAGGACAG CCACCTAGT GTCTCATGTT TGTATTGGT CCGAGTTGGG TACATTTTAA 4380
AATCCTGATT TTGGAGACTT AAAACAGGT TAATGGCTAA GAATGGGTAA CATGACTCTT 4440
GTTGGATTGT TATTTTGTG TTGCAATGGG GAATTTATAA GAGCATCAA GTCTCTTTCT 4500
TACCAAGTC TTGTAGGTG GTTTATAGTT CTTTGGCTA ACAATCATT TTGGAATAA 4560
AGATTTTTTA CTACAAAAAT G

```


Seq ID NO: 510 Protein sequence
Protein Accession #: BAB18461.1

5 1 11 21 31 41 51
| | | | | |
MRLSPAPLKL SRTPALALLA LPLAALAFS DETLDKVPKS EGYCSRILRA QGTRREGYTE 60
FSLRVBGDPD FYKPGTSYRV TLSAAPPSPY RGTTLIALRE NREGDKEDH AGTPQIIDE 120
ETQPMNSCPV AVTESTPRRR TRIQVFWIAP PAGTGCVILK ASIVQKRIIY PQDEGSLTEK 180
LCEQDSTFDG VTDKPIIDCC ACGTAKYRLT FYGNWSEKTH PKDYPRRANH WSAIIGGSHS 240
10 KNYVLWEYGG YASEGVKQVA ELGSPVKMEB EIRQOSDEVL TVIKAKAQWP AWQPLNVRAA 300
PSAEFSVDRT RHLMSFLTWL GPSPDNNVGL SAEDLCTKEC GWVQKVVDL IPWDAGTDSG 360
VTYESPNKPT IPQEKIRPLT SLDHPQSPFY DPEGGSTQV ARVVIERIAR KGEQCNIVPD 420
NVDDIVADLA PEEKEDDTP ETCIYSNWSF WSACSSSTCD KGRMRQRM KAQLDLSVPC 480
15 PDTQDFOPCM GPGCSDSDGS TCTMSEWITW SPCSISCGMG MRSRERYVKQ FPEDGSVCTL 540
PTEETEKCTV NEBCSPSSCL MTENGWDEC SATCGMGKK RHRMIRNPA DGMCKAETS 600
QAEKCMPEC HTIPCLLSPW SEWSDCSVTC GKGMRTQRM LKSLAELGDC NEDLEQVEKC 660
MLPECPIDCE LTWESQWSEC NKSOGKHVI RTRMIQMEPQ FGGAPCPETV QRKKCRIRKC 720
LRNPSIQKLK WREARESRRS EQLKEESEGE QPFCRMRPW TAWSECTKLC GGGIQERYMT 780
VKRFRSSQF TSCKDKKBR ACNVHPC

Seq ID NO: 511 DNA sequence
Nucleic Acid Accession #: NM_003108.1
Coding sequence: 76..1401

25 1 11 21 31 41 51
| | | | | |
GGGCTGGGAG GGGGAGGGGG ACCTCCGCAC GAGACCCAGC GGCCCGGGTT GGAGCGTCCA 60
GCCCTGCAAC GGATCATGTG GCAGCAGGCG GAGAGCTTGG AAGCGGAGAG CAACCTGCC 120
30 CGGGAGGCGC TGGACACGGA GGAGGGCGAA TTCATGGCTT GCAGCCCGGT GGCCCTGGAC 180
GAGAGCGACC CAGACTGGTG CAAGACGCGC TCGGGCCACA TCAAGCGGCC GATGAACGCG 240
TTCATGGTAT GGTCCAAGAT CGAACGCGAG AAGATCATGG AGCAGTCTCC GGCATGAC 300
AACGCGGAGA TCTCCAAGAG GCTGGGCAAG CGCTGGAATA TGCTGAAGGA CAGCGAGAAG 360
ATCCGGTCA TCCGGGAGGC GGAGCGGCTG CGGCTCAAGC ACATGGCCGA CTACCCCGAC 420
35 TACAAGTACC GGCCCGGAA AAGCCCAA ATGGAACCCCT CGGCCAAGCC CAGCGCCAGC 480
CAGAGCCGAG AGAAGAGCGC GGCCGCGGCG GCGGCGGGGA GCGGCGGCG AGGCGCGGCG 540
GGTGCCAGA CCTCAAGGG CTCAGCAAG AATGCGGCA AGCTCAAGGC CCCCAGCGCC 600
GCGGCGGCGC AGGCGGCGCG GGGCAAGCGC GCCAGTCCG GGGACTACGG GGGCGCGGCG 660
GACGACTACG TGCTGGGCGG CTTGCGGCTG AGCGGCTCGG GCGGCGGCG GCGGCGCAAG 720
40 ACGGTCAAGT CGGTGTTTCT GGATGAGAC GACGACGACG ACGACGACGA CGACGAGCTG 780
CAGCTGCAGA TCAACACGGA GCGGAGCGAG GAGGAAGAGG AACCACCGCA CCAGCAGCTC 840
CTGCAGCGCG CGGGGCGAGC GCCGTGCGAG CTGCTGAGAC GCTCAACGCT CGCCAAAGTG 900
CCCGCCAGCC CTAGCTGAG CAGCTCGGCG GAGTCCCGCG AGGGAGCGAG CCTCTACGAC 960
GAGGTGCGCG CCGGCGGCGC CTCGGGCGCC GGGGCGGCG GCGGCTCTTA CTACAGCTTC 1020
45 AAGAACATCA CCAAGCAGCA CCCGCCGCG CTCGCGCAGC CCGCGCTGTC GCCCGGCTCC 1080
TCGCGCTCGG TGTCACCTC CTCGTCCAGC AGCAGCGGCA GCAGCAGCG CAGCAGCGCG 1140
GAGGACCGCG ACGACCTGAT GTTCGACCTG AGCTTGAATT TCTCTCAAG CGCGCACAGC 1200
GCCAGCGAGC AGCAGCTGGG GGGCGGCGCG GCGGCGGCG AACTGTCCT GTGCTGCTG 1260
GATAAGGATT TGATTCGTTT CAGCGAGGGC AGCTGGGCT CCCACTTGA GTTCCCGGAC 1320
50 TACTGACGC CGGAGCTGAG CGAGATGATC GCGGGGCGCT GGTGAGGCG GAACCTCTCC 1380
GACCTGGTGT TCACATATTG AAAGCGCGCC GCTGCTCGCT CTCTCTCTCG GAGGGTGCG 1440
AGCTGGGTTT CTTGGGAGGA AGTTGTAGTG GTGATGATGA TGATGATGAT AATGATGATG 1500
ATGATGGTGG TGTGATGTTT GCGGTGTGTA GGTGAGAGG GAGAGAAGAA GATGCTGATG 1560
55 ATATTGATA GATGTCGTGA CGCAAGAAA TTGAAAACA TGATGAAAT TTTGGTGGAG 1620
TTAAAGTGA ATGAGTAGTT TTTAAACATT TTTCTGTCC TTTTGTGTC CCCCCTCCCT 1680
TCCTTTATCG TGCTCAAGG TAGTTGCATA CCTAGTCTGG AGTTGTGATT ATTTTCCCAA 1740
AAAATGTGTT TTTGTAATTA CTATTCTTT TTCTGAAAT TCGTGATTGC AACAAAGGCA 1800
GAGGGGGCGG CCGGCGGCGG GGGAGGTAGG ACCCGCTCCG GAAGGCGCTG TTTGAAGCTT 1860
60 GTCGCTCTTT GAAGTCTGGA AGAGGACCTT TTTGGCAGCA CAACTGTTAC 1920
TCTAGGGAGT TGTGTGAGAT ATTTTTTTTT CTTAAGAGAA CTTAAAGAAC TGGTGATTTT 1980
TTTTTAACA AAAAAGG

Seq ID NO: 512 Protein sequence
Protein Accession #: NP_003099.1

65 1 11 21 31 41 51
| | | | | |
MVQQAESLEA ESNLPREALD TEEGEFMACS FVALDESDFD WCKTASGHK RPMNAPMVWS 60
KIERRKIMEQ SPDMHNAEIS KRLGKRWMKL KDSEKIPFIR EAERLRLKHM ADYDPYKYRP 120
70 RKKPRMDPSA KPSASQSPSK SAAGGGGSGA GGGAGGAKTS KGSKKCKGL KAPAAAGAKA 180
GAGRAAQSD YGGAGDDYVL GSLRVSGSGG GGAGKTVKCV FLDEDDDDDD DDELQLQIK 240
QEPDEDEEP FHQQLLPFG QPSPQLLRY NVAKVPASPT LSSSAESPEB ASLYDEVRA 300
ATSGAGGSR LYYSFKNITK QHPPLAQA LSPASSRSVS TSSSSSSSGS SSSSGEDADD 360
75 LMFDSLINFQ QSAHSASEQ LGGGAAAGNL SLSLVDKDL SPSGSLGSH PEPDYCTPE 420
LSENIAGDWL EANFSDLVFT Y

Seq ID NO: 513 DNA sequence
Nucleic Acid Accession #: CAT Cluster

80 1 11 21 31 41 51
| | | | | |
GGTGCACCTA AATCTGATAA CTGGCTTATT ATGTAATTTA TTGGTGTAT TATAGTAGAG 60
ATTGGTAACT TACAGTAAGA TTTTCAGTTA GGAATTTGAGA TTATGATAAT AACTAATAGA 120
ATATTCTCAA ATTGGAATTA GAAGATTGTT GTATGACAGA GAGTCAGGAC TTGCCATTG 180

5 GCAAACATCA AAGTCATTGT TTGGTGTGTA ATAGTACAAA ATCATCTTGC TTAACAGAGA 240
AAGGATATCT GTTGTCTCCCG AATGAAACAA TTTTCTGAA ATAGAGGGCC CAGAATTGGT 300
CTCTGACAT TAATAAGAC ATCAAAGATA GCAAATGAT TTTATATCT TAGGGCCAAT 360
ACTACCAAT TAATAATTA AACAAATTCT GTTGAGCTCT GAACCTGGCA GAATTGGTGG 420
CAACATAGAC TTGGGATTTT CCAAATTC CACATAAAAC AAAGGGGATC AACTAGATAG 480
AAAAACCAGA AACCTTTGGA AATATCTGTT TAAAAAATAA AAAAAGTCGA CGCGGGCC

Seq ID NO: 514 DNA sequence
Nucleic Acid Accession #: CAT cluster

10
1 11 21 31 41 51
GGAGCCACAG TGAAAGTCAA GAATGTCAGT GATTCCACAT TTAATATCTA CATTTTGGCA 60
GGGCAGTTAC TCCTTTGTAG TATAACATTG AGCTGATAGC ACATAGTGTG GACAAGTGAA 120
TACAGGATTG TCTGGGTGTG ATTCCCAGAA GTCTGGAGGT CATTTGGATA TTTGTGGGCC 180
CTTGGCTTCA CTCTGACTTG TGTGACACAT AAAAATTGTG ATGAAATGTC CTATAGATGT 240
CCTGCAGGTC TTAAGAAGAC CTITCCAAAC TATGAAACAG CCCAGCAGCA CTGAGTTAGA 300
GGTAAATCTT GAACCCCTGA AACTATAAAC TATTCTAACT GCACATAGAA TTGGCAAGTA 360
GCATTCTATG TCTATGAACA GTATGTCTTT TCTATATAAC AGAGAAAATC TTTTAAAGCA 420
AACTACTCAG TTTAAACCTT AATCTCTCTC ATAATCTCAG TACTTTTGAA TGAAGACATA 480
TCAATGCAAC AGTACACTCT TATTCCAGCA TTTGAAAGAA AGAATTGAGT ACTAGTTTGG 540
TATCAGATAT TATAAATTAG TATGGTTTAG TCTTTGTCTT GAAATCTTAC TTAATTTTGG 600
GACTATAGGT TTAAGAATGT AAGCAGAAAT TCTGCACCAA TCAGAATAAG CTACATTATG 660
CTTGAGTGAC AACTACTGTA ATGACAAAAT ATCAGTGGCT TAATACAATG GTTTTCTCT 720
CATACTTGTG CATAAAGATG CAGCAAGGAC CCTGCTCATT ATGGTCCCTC AGGGACCCAG 780
GGTTGTGGGA AGCTCCACCA TTTTAGATAG CTCCTTTCAG AGTCAGCCAT CTTTGGCAGT 840
CCATGTCCCC CAACAGGCTG GCAAAATTTG GCTCTGGATG GCTTCAAGGA TTGAGCATCG 900
GGCAGTTTAA ATGCTTTCAA CATGGAAGGT GGACACCGGC GGGTTGGGGA ATTGTAATTC 1020
GGGCCAGAAC TAGGTCACTG GGCCCGGACC TAACCTGGGA GGGTTGGGGA ATTGTAATTC 1080
CTCCATGTAC CCAAGTGGGA GAGAAGCCAG ATACTGAGAA ACATCAATAA TGGCTAACAG 1140
AAATCCATTC TACCATTCCC TTTGCCTAAA GTGAAAGATG GAGTACTTTC ATCAATTGTG 1200
AACTGTACT TTTGAAGTAA ATCTGCTAGT CTTCATAGAA TATCATTATT TGATGTAATA 1260
ATATGTAATT TGGGAATGAC ATTCACCTAA GCTCATAGAA TATCATTATT TGATGTAATA 1320
TGCCCTCATT TGCAATACAG GACCAAAATG CACTAACCCAC AAAACCCCCC TCCCCAGGG 1380
GCCCGGGGTC CCTATTCCCC TCCATCCCTT TAAATGAGGC ATTCTATGAT TTGGAATGGA 1440
AGCCCAAGTG TAGTGTAAAG AATTTTACTT AATTCAGAA TTATCTCAC TGAATATGTG 1500
CCAGTTCTGA AAGGAATGCA AAGTCAATTT TTGCATCTTC TTGTCTCAAG GGCCTTAGA 1560
TGTAACAACA CAGACATGAT ACAAGGCTGA CAATGACATT ATGATTAAAT TATGTTAAAC 1620
AATCTATTAA ATTGTGAATC AACAAAAAAT TATGTCTTTT ATTTTATGGT TTTGCATAGT 1680
CCTGACTCAC TGCTACATA CCCCTCTTGT TCTCAGTTC TTATCCCTGA TTTCTTACAG 1740
GATGGCCTAA GACAGCTGTA GATGTTTTTA TTTAGCAAAA AAAAAAATAA AAAAGTCGAG
GGGCCGCGA ATTTAGTAG

Seq ID NO: 515 DNA sequence
Nucleic Acid Accession #: NM_012427
Coding sequence: 43..924

50 1 11 21 31 41 51
CTTGTGGTTC CTCTCTACTT GGGGAAATCA GGTGCAGCGG CCATGGGCTAC AGCAAGACCC 60
CCCTGGATGT GGGTGTCTGT TGCTCTGATC ACAGCCTTGC TTCTGGGGGT CACAGAGCAT 120
GTTCTCGCCA ACAATGATGT TTCTGTGAC CACCCCTCTA ACACCGTGCC CTCTGGGAGC 180
AACCAGGACC TGGGAGCTGG GGCCGGGGAA GAAGCCCGGT CGGATGACAG CAGCAGCCGC 240
ATCATCAATG GATCGACTGT CGATATGCAC ACCCAGCCGT GGCAGGCCGC GCTGTGTCTA 300
AGGCCCAACC AGCTCTACTG CGGGGCGGTG TTGTGTGATC CACAGTGGCT GCTCACGGCC 360
GCCCACTGCA GGAAGAAAGT TTTCAAGTTC CGTCTCGGCC ACTACTCCCT GTCCACAGTT 420
TATGAATCTG GGCAGCAGAT GTTCCAGGGG GTCAAACTGA TCCCCACCCC TGGCTACTCC 480
CACCCCTGGC ACTCTAAGCA CCTCATGCTC ATCAAACTGA ACAGAAGAAT TGGTCCACT 540
AAAGATGTCA GACCCATCAA CGTCTCTCTT CATTGTCCCT CTGCTGGGAC AAAGTGTCTG 600
GTGTCTGGCT GGGGACAAAC CAAGAGCCCC CAAGTGCATC TCCCTAAGGT CCTCCAGTGC 660
TTGAATATCA GGTGTCTAAG TCAGAAAAGG TGCGAGGATG CTTACCCGAG ACAGATAGAT 720
GACACCATGT TCTGCGCCGG TGACAAAGCA GGTAGAGACT CTGCCCAGGG TGATTCTGGG 780
GGGCTGTGGG TCTGCAATGG CTCCCTGCAG GGAAGTGTGT CCTGGGGAGA TTACCTTTGT 840
GCCCGGCCCA ACAGACCGGG TGCTACACG AACCTCTGCA AGTTCACCAA GTGGATCCAG 900
GAAACCATCC AGGCCAATCT CTGAGTCTAT CCAGGACTCA GCACACCGGC ATCCCCACCT 960
GCTGCAGGGA CAGCCCTGAC ACTCCTTTCA GACCTCTATT CCTTCCAGCA GATGTTGAGA 1020
ATGTTACTCT CTCCAGCCCC TGACCCCATG TCTCCTGGAC TCAGGGTCTG CTTCGCCAC 1080
ATTGGGCTGA CCGTGTCTCT CTAGTTGAAC CCTGGGAACA ATTTCCAAA CTGTCCAGGG 1140
CGGGGGTTCG GTCTCAATCT CCCTGGGGCA CTTTCTCCT CAAGCTCAGG GCCCATCCCT 1200
TCTCTGAGC TCTGACCAA ATTTAGTCCC AGAAATAAAC TGAGAAGTGG AAAAAAATAA

Seq ID NO: 516 Protein sequence
Protein Accession #: NP_036559

75 1 11 21 31 41 51
MATARPPMWM VLCAITALL LGVTEHVLN NDVSCDHPN TVPSGSNDL GAGAGEDARS 60
DDSSRIING SDMDMTQPW QAALLRPNQ LYCGAVLVHP QWLLTAHCR KKVFRVRLGH 120
YLSFPVYESG QMFQGVKSI PFGYSHRPH SMDLMLIKL RRIRPTKDV PINVSSHCP 180
AGTKCLVSGW GTTKSPQVHP PKVLQCLNIS VLSQKRCEDA YPRQIDDTMF CAGDKAGRDS 240
CQDGGGPPV CNGSLQGLVS WGDYPCARP RPVVYTNLCK PTKWQBTIQ ANS

1154

1 11 21 31 41 51
5 MLTEVMEVWH GLVIAVVSFL LQACFLTAIN YLLSRHMAHK SEQILKAASL QVPRPSPGHH 60
HPPAVKEMKE TQTERDIPMS DSLYRHSDT PSDSLDSSCS SPPACQATED VDYTQVVFSD 120
PGLKNDSP L DYENIKEITD YVNVNPERHK PSFWYFVNPA LSEPAEYDQV AM

Seq ID NO: 521 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 107..328

1 11 21 31 41 51
15 CTGCTCTGTC TGAGCCAGCG GAATATGATC AAGTGGCCAT GTGAATTCCA AATAITTTTA 60
ATGGGGTCCA GTTCTCTATG GATTCTTACA TTAAATTTGT AGGGAATGTC CATTITTTCCC 120
CCTTAAACAA GGCATGGGCG TCACAAGTCT ATGGAGACAG GCCAAAAAGA ATGTGGAGAA 180
GAAACTGAT AATACACAG AGGTCTCAA GACCATGGA CTCCTGGTCT GTACCCAAA 240
AAGCTGTTG TTCTCAAAA ACRAAAACAA GGCITGGCTG GGAACACAGG CCAATGCCCC 300
GGCAAGAAAG GTTGAGATCA GATGTTAGGA AGAAGTTTCA GGTAAAGTAT GAGAACTATG 360
GAGTCCATCA GCAGAGATAG TAGTGAAGTC TCTCCCAGG GAAAATTTTA AAAAGGTTGA 420
ATCAGCTGTT GTAGAGTTCT ATTTGCAAT CTCATGGTTA AATGACTTCC CTTTGAGCTC 480
TTTAATTATT GGCATAAAC AACTTCTTTA AAGTTTTAA ATAAATAGC AACCCACC 540
A

Seq ID NO: 522 Protein sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
30 MPFFFLKQGM GLTSLWRQAK KNVEKKTDKY TEVLKTHGLL VCTQKSCSPL KNKNKAWLGK 60
QANAPARKVE IRC

Seq ID NO: 523 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 211..1895

1 11 21 31 41 51
40 GGATCTGAGG GGGGCCAGT CACTTCCTCC ACBTCTCTGT GCTGGGCGGG AGGAGCGGAT 60
GGGGCTTGGG AGGCAGCCTG CTCTCCAGTC CCTATCCACC CACAGTMTT TTGGGTGCGA 120
GAGGAATTAT CTGATAAAAT TCCTGGGTTA ATATTTTAA AAACGGAGAG TTTTAAAAA 180
TGATTTTTTT CCCTCGAAAA TGACCTTTT ATGCTTCGAA GCAGTTTGT AACCAGCATA 240
GTGCTTTTTT TTTTCTCTC TTTTCTACG ATAAATGAAA GCATTTCTTC AAGAAAAAGG 300
CACAGTCTCC TTGAACAGCT GGATTCGAT GGCACCATTA CTATAGAGGA GCAGATTGTC 360
CTGTGCTGA AAGCGAAAGT ACAATGTGAA CTCAACATCA CAGCTCACT CCAGGAGGTC 420
GAAGGTAAAT GTTTCCTGA ATGGGATGGA CTCAATTGTT GGCACGAGG AACAGTGGGG 480
AAAATATCGG CTGTTCATG CCTTCCTAT ATTTATGACT TCAACCATAA AGGAGTTGCT 540
TTCGACACT GTAACCCAA TGAACATGG GATTTATGC ACAGCTTAAA TAAACATGG 600
GCCAATTAT CAGATGCGCT TCGCTTCTG CAGCCAGATA TCAGCATAGG AAAGCAAGAA 660
TCTTTGAAC GCCTCTATGT AATGTATACC GTTGGCTACT CCATCTCTTT TGGTTCCTTG 720
GCTGTGGCTA TTCTCATCAT TGGTACTTC AGACGATGTC ATTGCATAG GAATATATC 780
CACATGCACT TATTGTGTC TTTCATGCTG AGAGCTACAA GCATCTTTGT CAAGACAGA 840
GTAGTCCATG CTCACATAGG AGTAAAGGAG CTGGAGTCCC TAATAATGCA GGATGACCCA 900
CAAAATCCA TTGAGGCAAC TTCTGTGGAC AAATCACAAT ATATCGGTTG CAAGATTGCT 960
GTTGTGATGT TTATTACTT CTTGGCTACA AATTATTAT GGATCTCTGT GGAAGGTCTC 1020
TACCTGCATA ATCTCATCTT TGTGGCTTC TTTTCGGACA CCAATACCT GTGGGGCTTC 1080
ATCTGTATAG GCTGGGGGTT TCCAGCAGCA TTTGTTGCG CATGGGCTGT GGCACGAGCA 1140
ACTCTGGCTG ATGCGAGGTT CTGGGAACCT AGTGCTGGAG ACATCAAGTG GATTATCAA 1200
GCACGATCT TAGCAGCTAT TGGGCTGAAT TTTATTCTGT TTCTGAATAC GGTAGAGTT 1260
CTAGCTACCA AATCTGGGA GACCAATGCA GTTGGGCTG ACACAAGGAA GCAATACAGG 1320
AAACTGGCCA AATGACACT GGTCTGCTC CTAGTCTTG GAGTGCRATTA CATCTGTTC 1380
GTATGCTGCT CTCACCTCTT CACTGGGCTC GGGTGGGAGA TCCGATGCA CTGTGAGCTC 1440
TTCTTCACT CCTTCAAGG TTTCTTTGTG TCTATCATCT ACTGCTACTG CAATGGAGAG 1500
GTTCAAGCAG AGGTGAAGAA GATGTGGAGT CGGTGGAATC TCTCGTGGG CTGGAAAAGG 1560
ACACCGCAT CTGGCAGCCG CAGATCGGCG TCAGTGCTCA CCAACGTGAC GCACAGCACC 1620
AGCAGCCAGT CACAGTGGC GGCAGCACA CGCATGGTGC TTATCTCTGG CAAAGCTGCC 1680
AAGATGCGCA GCAGACAGCC TGACAGCCAC ATCACTTTAC CTGGCTATGT CTGAGTAAC 1740
TCAGAGCAGG ACTGCTGCC ACACCTTTC CAGAGGAGA CCAAGGAAGA TAGTGGGAGG 1800
CAGCGAGATG ATATTCTAAT GGAGAAGCCT TCCAGGCTTA TGGATCTAA CCCAGACACT 1860
GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA

Seq ID NO: 524 Protein sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
75 MLRSSLSISI VLFLPSSFST INESISSRKR HRFLEQLDSD GTITIEEQIV LVLKAKVQCE 60
LNIATAQLQEG BGNCFPEWDG LICWPRGTG KISAVPCPPY IYDFNHKGVA FRHCNPNGTW 120
DFMSLAKTW ANYSDCLRLP QPDISIGKE FFERLYVMT VGYISIFGSL AVAILIIGYF 180
RRLHCTRNYI HMHLFVSFML RATSIFVKDR VVHAHIGVKE LESLIMQDDP QNSIEATSD 240
KSQYIGCKIA VVMFIYFLAT NYWILVEGL YLENLIFVAF PSDTKYLWGF ILIGWGFPA 300
FVAWAWARA TLADARCWEL SAGDIKNYQ APILAAGLW FILPLATVRV LATKINETNA 360
VGHDRKQYR KLAKSTLVLV LVFGVHYIVF VCLPHSFTGL GWEIRMHCEL FFNSFQGFV 420
SIICYCNGE VQAEVKMWS RWNLSVDWKR TPPOGSRRCG SVLTTVTHT SSQSQAAS 480

RMVLISGKAA KIASRQPDSDH ITPGVVWSN SEQDCLPHSF HEETKEDSGR QGDDILMEKP 540
SRPMESNPDTEGCGGETEDV L

Seq ID NO: 525 DNA sequence
Nucleic Acid Accession #: NM_005048
Coding sequence: 143..1795

1 11 21 31 41 51
10 GGCCGGTGGC CCGGGCCCCG CCACCCAGC TCGGGTGGT TACTGGGCAC AAGTTTGCTC 60
TGGGCCAGCC AAGTTGGCAA CTGGAAGCT TCTCCCGGC TCTGGAGGAG GGTCCCTGCT 120
TCTTCTACCA GCGGTTCCGG GCATGGCCGG GCTGGGGGG TCGCTCCAGC TCTGGGGTTG 180
GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCAGCTG GATTCTGATG GCACCATTAC 240
TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300
15 AGCTCAACTC CAGGAGGGAG AAGGTAATG TTCCCTGAA TGGGATGGAC TCATTGTGTG 360
GCCGAGGGA ACAGTGGGGA AAATATCGGC TGTTCATGC CCTCCTTATA TTTATGACTT 420
CAACCATAAA GGAGTTGCTT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480
CAGCTTAAAT AAACATGGG CCAATTATTC AGACTGCCTT CGCTTCTGCG AGCCAGATAT 540
CAGCATAGGA AAGCAAGAAT TCTTTGAAAG CCTCTATGTA ATGTATACCG TTGGCTACTC 600
20 CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCAT GTTACTTCA GACGATTGCA 660
TTGCACTAGG AACTATATCC ACATGCACCT ATTTGTGTCT TTCATGCTGA GAGCTACAAG 720
CATCTTTGTC AAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780
AATAATGCAG GATGACCCAC AAAATTCCAT TGAGGCCAAT TCTGTGGACA AATCACAATA 840
TATCGGGTGA AGTATGCTG TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATTATTG 900
25 GATCCTGGTG GAAGGTCTCT ACCTGCATAA TCTCATCTT GTGGCTTCTT TTGGGACAC 960
CAAAATACCTG TGGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TTGTTGCAGC 1020
ATGGGCTGTG GCACGAGCAA CTCTGGCTGA TGGAGGTGC TGGGAACCTA GTGCTGGAGA 1080
CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT 1140
TCTGAATAGC GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAT TTGGGCATGA 1200
30 CACAAGGAAG CAATACAGGA AACTGGCCAA ATGCACACTG GTCTGGTCC TAGTCTTTGG 1260
AGTGCAATAC ATCGTGTTCG TATGCGCTGC TCACCTCTTC ACTGGGCTCG GGTGGGAGAT 1320
CCGCATGCAC TGTGAGCTCT TCTTCAACTC CTTTCAGGCT TTCTTTGTGT CTATCATCTA 1380
CTGCTACTGC AATGAGAGG TTCAAGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT 1440
CTCGTGGAC TGGAAAAGGA CACCGCCATG TGGCAGCGC AGATGCGGCT CAGTGCCTAC 1500
35 CACCGTGACG CACAGCCCA GCAGCCAGTC ACAGGTGGCG GCCAGCACAC GCATGGTGCT 1560
TATCTCTGGC AAAGCTGCCA AGATGGCCAG CAGACAGCCT GACAGCCACA TCACCTTACC 1620
TGGCTATGTC TGGAGTAACT CAGAGCAGGA CTGCGTGGCA CACTCTTTCC ACGAGGAGAC 1680
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40 CATTGTGGC TGACTTTCAT GGGCTGCTCC AATGCTGGT TGTGTGAGAG GGCTTGGCTG 1860
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Seq ID NO: 526 Protein sequence
Protein Accession #: NP_005039

1 11 21 31 41 51
60 MAGLGASLHV MGLMLGSLC LARAQLSDG TITIEBQIVL VLKAKVQCEL NITAIQESGE 60
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NYSDCLEFLQ PDISIGKQEF FERLYVMYTV GYSISFGSLA VAILIIGYFR RLHCTRNYIH 180
MHLFVPSFLR ATSFIFKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKLAV 240
65 VMPFIYFLATN YYWILVEGLY LHNLFVAFV SDTKYLWQFI LIGWGFPAF VAAWAVARAT 300
LADARCWELS AGDIKWIYQA PILAAIGLNF ILPLNTVRVL ATKIWETNAV GHDTRKQYRK 360
LAKSTLVLVL VFGVHYIVFV CLPHSFTGLG WEIRMHCELF FNSFQGFVVS ILYCYNGEV 420
QAEVKMWSR WNLSDVWKRT PFCGRRCGS VLTIVTHSTS SQSQVAASR MVLLISGKAAK 480
70 LASRQPDSDH ITPGVVWSN SEQDCLPHSF HEETKEDSGR QGDDILMEKP SRPMESNPDTE
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Seq ID NO: 527 DNA sequence
Nucleic Acid Accession #: XM_036683
Coding sequence: 38..3655

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80 AATGGTGCAA ATAGATTAC CAATAAAGAG ATATAGAGAG TATGAGCTGG TGACTCCAGT 180
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GGAGTGGCAT GAGACATCTC TGGTGCTTGG GAATATAACC GATCCCATTA ACAACCATCA 420

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5	GGCTCCCAT	GACATGTCCA	AAGACTTCCA	CTACAGAGAG	TGGGACCTGG	AAGGCCTTGA	720
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	CAGACACGCG	GGAGAAAACG	ATTACAATAT	CGAGGTACTG	CTGGGAGTGG	ATGACTCTGT	840
	GGTCCGTTTC	CATGGCAAAG	AGCACGTCCA	AAACTACCTC	CTGACCCCTAA	TGAACATTGT	900
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10	GATAATGCTG	GGATATGCAA	AGTCCATCAG	CCTCATAGAA	AGGGGAAACC	CATCCAGAAG	1020
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	TACCAACAC	CATGTTGTC	CATATGAACA	TCCTGACCCC	AAGAAAAAGT	GCCACCTTTA	1980
	CTGTCACTCC	AAGGAGACTG	GAGATGTTGC	TTACATGAAA	CAACTGGTGC	ATGATGGAAAC	2040
	GCACGTCTCT	TACAAAGATC	CATATAGCAT	ATGTGTGCGA	GGAGAGTGTG	TGAAAGTGGG	2100
	CTGTGATAAA	GAATTTGGTT	CTAATAAGGT	TGAGGATAAG	TGTGGTGTCT	GTGGAGGAGA	2160
30	TAATTTCCAC	TGCGAAACCG	TGAAGGGGAC	ATTTACCAGA	ACTCCCAGGA	AGCTTGGGTA	2220
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	TTCTCTCAT	ATTCCTTGCTA	TTAAGAACCA	GGCTACAGGC	CATTATATTT	TAAATGGCAA	2340
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	GTGGGCTTTG	AAGAGCTGGT	CTCAGTGTTC	CAAAACCTGT	GGTGAGGTTT	TCCAGTACAC	2640
	TAAATATGGA	TGCCGTAGGA	AAAGTGATAA	TAAATGGTTC	CATCGCAGCT	TCTGTAGGGC	2700
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40	CTGGGTAGCA	GAAGAAATGG	AACACTGCAC	CAAAACCTGT	GGAAGTCTCT	GCTATCAGCT	2820
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45	AGCCTGTCAA	CTGCTCCTTT	GTAAATGATGA	ACCATGTTTG	GGAGACAAGT	CCATATTCTG	3120
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	GTCTCTCAGC	AAGCGCAGTA	GCACCCCTGCC	ACCACCATAC	CTTCTAGAAG	CTGCTGAAAC	3240
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	ATCCTTCCCA	CCCACCAAGA	GGGTCCACCT	CAGTTCAGCT	TCACAAATGG	CTGCTGCTTC	3540
	CTTCTTTGCA	GCCAGTGATT	CAATAGGTGC	TTCTTCTCAG	GCAAGAACCT	CAAGAAAGAA	3600
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	CTCAATTACC	AGAATTCAAT	GGAGAAATC	ACCAAGATT	ATTACAAAG	AAAAATATGT	3900
	TGCTAAGATT	GTGTTGGTGG	CTCTCTGAAG	CAGAAAAGGG	ACTGGAACCA	ATTGTGCATA	3960
60	TCAGCTGACT	TTTTGTTTGT	TTTAAAAAG	TTACAGTAAA	AATTAAGAA	AGATAACCAAT	4020
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	AGGGTTTTGT	TGAATCAACA	ATGTGATACG	TAAATTATAG	AAAAAGAAAA	GAAACACAAA	4380
	AGCTATAGAT	ATACAGATAT	CAGCTTACCT	ATTGCCCTCT	ATACTTATAA	TTTAAAGGAT	4440
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	AAGACAAAAC	TGAAACCCCTC	TTTCCAGGAC	CTCAGTAGGC	ACCGTTGAGG	TGTCCTTTGT	4560
70	TTTTGTGTGT	GTGTTTCTT	TTTTAATTTT	CGCAITGTTG	ACAGATACAA	ACAGTTATAC	4620
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	AGCTGAGAAA	AATATCATCA	GTCTAGAATT	GATATTGTAG	TATAGTAGAG	CTTTGGGGCT	4740
	TTGAAAGCAG	GTTCAGAGAA	GCATATGTGG	ATGTTTGAGA	TATTTATTTT	CCATATGGTT	4800
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	ACAGCCAACT	CAAAAGCTAA	AACTGAACAA	ATTTGATGTT	ATGCAAAACAT	CTTGCAATTT	5160
80	TAGTAGTTGA	TATTAAGTTG	ATGACTGTGT	TOCCTTCAAG	GAACATATA	ATTGATGGA	5220
	CTCAGCTAGC	TGTTCAATGA	AATTTGTGAAT	TAGAAACATT	TTTAAAGTTT	TTTGAAGAG	5280
	ATAAGTGCAT	CATGAATTAC	ATGTACATGA	GAGGAGATAG	TGATATCAGC	ATAATGATTT	5340
	TGAGGTGACT	ACCTGAGCTG	TCTAAAAATA	TATTATACAA	ACTAAATGT	AGATGAATTA	5400
	ACCTCTCAAA	GCACGAATG	TGCAAGAACT	TTTGCAATTT	AATCGTTGTA	AACTAACAGC	5460

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 TTAAGTATT GACTCTATAC CTCTAAGAA TTGCTGCTAC TTTGTGCAAG AACTTTGAAG 5520
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10 Seq ID NO: 528 Protein sequence
 Protein Accession #: XP_036683

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 IEPLERGRQM EBEKGRIVHV YKRSVEQAP IDMSKDFHYR ESDLEGLDDL GTVYGNHQQ 240
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Seq ID NO: 529 DNA sequence
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 Coding sequence: 246..980

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70 Seq ID NO: 530 Protein sequence
 Protein Accession #: NP_002765

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 LIQPLPLERD CSANTTSCHI LGWKTADGD PFDTIQAYI HLVSRECEH AYPGQITNM 180
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Seq ID NO: 532 Protein sequence
 Protein Accession #: NP_036284

1 11 21 31 41 51
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 PIYSRSLVLP WTVSNLMAFL IMVVVLYRIY VYVKKRTNVL SPHTSGSISR RRTPMKLMKT 240
 VMTVLGAPVV CWTPLVLL LDGLNCRQCG VQEVKRWFL LALLNSVNP IYSYKDEDM 300
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Seq ID NO: 533 DNA sequence
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 TTGCTGTGA GGTGTAGGCT CCGGGCGCGG TACATGTGTA CTGGCTGCTC GATGGGGCCC 360
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 ACCGGCTGCA GGA CTCTGCGC ACCTTCCAGT GTGTGGCTCG GGATGATGTC ACTGAGAAAG 480
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 CCCAGGACGT GGTAGTAGCG AGGTATGAGG AGGCCATGTT CCATTGCCAG TTCTCAGCCC 900
 AGCCACCCCC GAGCCTCGAG TGGCTCTTTG AGGATGAGAC TCCCATCACT AACCGCAGTC 960
 GCGCCCAACA CCTCGCAGCA GCCACAGTGT TTGCCAACGG GTCTCTGCTG CTGACCCAGG 1020
 TCGGCGCAAG CAATGCAAGG ATCTACCGCT GCATTGGCCA GGGGCGAGGG GGCCCAACCA 1080
 TCATCTGGA AGCCACACTT CACCTAGCAG AGATTGAAGA CATGCCGCTA TTTGAGCCAC 1140
 GGGTGTTCAC AGCTGGCAGC GAGGAGCGTG TGACCTGCTT TCCGCCCAAG GGTCTGCCAG 1200
 AGCCAGCGGT GTGGTGGGAG CACGCGGGAG TCGGCTGCC CACCCATGGC AGGGTCTACC 1260
 AGAAGGGCCA CGAGCTGGTG TTGGCCAATA TTGCTGAAAG TGTGCTGCTG GTCTACACCT 1320
 GCCACGCGCG CAACCTGGCT GGTACGCGGA GACAGGATGT CAACATCACT GTGGCCACTG 1380
 TGCCCTCTCT GCTGAAGAAG CCCCAGACA GCCAGCTGGA GGAGGGCAAA CCCGGCTACT 1440
 TGGATTGCTT GACCCAGGCC ACACCAAAAC CTACAGTTGT CTGGTACAGA AACAGATGC 1500
 TCATCTCAGA GGA CTACAGG TCGAGGCTCT TCAAGATGG GACCTTGGCG ATCAACAGCG 1560
 TGGAGGTGTA TGATGGGACA TGGTACCGTT GTATGAGCAG CACCCAGGCC GGCAGCATCG 1620
 AGGCGCAGAG CCGTGTCCAA GTGTGGAAGA AGCTCAAGTT CACACCACCA CCCCAGCCAC 1680
 AGCAGTGCTT GAGTTTGTAC AAGGAGGCCA CGGTGCCCTG TTCAGCCACA GGCCGAGAGA 1740
 AGCCCACTAT TAAGTGGGAA CCGGCGAGTG GAGCAGGCT CCGAGAGTGG GTGACAGACA 1800
 ACCGCTGGGAC CCTGCATTTT GCGCGGGTGA CTGAGATGA CGCTGGCAAC TACACTTGCA 1860
 TTGCTCTCAA GGGGCGCGAG GCGCAGATTC GTGCCCATGT CCAGTCACT GTGCGAGTTT 1920
 TTATCACCTT CAAGTGGAA CCGAGCGTGA CGACTGTGTA CCAGGGCCAC ACAGCCCTAC 1980
 TGCACTGCGA GCGCCAGGCG GACCCCAAGC CGCTGATTCA GTGGAAGGCG AAGGACCGCA 2040
 TCCTGGACCC CACCAAGCTG GGACCCAGGA TGCACTCTT CCAGATGGC TCCTGGTGA 2100
 TCCATGACGT GGGCCCTGAG GACTCAGGCC GCTACACCTG CATTGAGGC AACAGCTGCA 2160
 ACATCAAGCA CACGAGGCC CCCTCTATG TGTGAGCAA GCCTGTGCGG GAGGAGTCGG 2220
 AGGGCCCTCG CAGCCCTCCC CCCTACAAGA TGTCCAGAC CATTTGGTTG TCGGTGGGTG 2280
 CCGCTGTGCG CTACATCATT GCGTGTCTG GCGCTCATGT CTACTGCAAG AAGCGCTGCA 2340
 AAGCCAAGCG GCTGCAAGAG CAGCCCGAGG GCGAGGAGCG AGAGATGGAA TGCTCAACG 2400
 GAGGCGCTTT GCAGAAAGGG CAGCCCTCAG CAGAGATCCA AGAAGAAGTG GCCTTGACCA 2460
 GCTTGGGCTC CGGCGCCGCG GCCACCAACA AACGCCACAG CACAAGTGAT AAGATGCAT 2520
 TCCCAAGGTC TAGCCTGCGAG CCATCACCA CCGTGGGGAA GAGTGAGTTT GGGGAGGTGT 2580
 TCCTGGCAAA GCCTCAGGCG TTGAGGAGG GAGTGCCAGA GACCCGTGTA CTTGTGAAGA 2640

5
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GCCTGCAGAC GAAGGATGAG CAGCAGCAGC TGGACTTCCG GAGGGAGTTG GAGATGTTTG 2700
GGAAGCTGAA CCAGGCCAAC GTGGTGGGCT TCCTGGGGCT GTGCCGGGAG GCTGAGCCCC 2760
ACTACATGTT GCTGGAATAT GTGGATCTGG GAGACCTCAA GCAGTTTCTG AGGATTTCCTA 2820
AGAGCAAGGA TGAAAAATTG AAGTCACAGC CCCTCAGCAC CAAGCAGAAG GTGGCCCTAT 2880
GCACCCAGGT AGCCCTGGGC ATGGAGCACC TGTCCAACAA CGCTTTGTGT CATAAGGACT 2940
TGGCTGCGCG TAACCTGCGT GTCAGTGCCC AGAGACAAGT GAAGGTGTCT GCCCTGGGCC 3000
TCAGCAAGGA TGTGTACAAC AGTGAGTACT ACCACTTCCG CCAGGCGCTG GTGCGCTGCG 3060
GCTGGATGTC CCCGAGGGCC ATCCCTGGAG GTGACTTCTC TACCAAGTCT GATGTCTGGG 3120
CCTTGGTGT GCTGATGTGG GAAGTGTTTA CACATGGAGA GATGCCCAT GTGGGCGAGG 3180
CAGATGATGA AGTACTGGCA GATTTCAGG CTGGGAAGGC TAGACTTCTT CAGCCCGAGG 3240
GCTGCCCTTC CAAACTCTAT CGCTGATGTC AGCGCTGCTG GGCCTCTCAG CCCAAGGACC 3300
GGCCCTCCTT ATCAGGAGAT GCCAGCGCCC TGGGAGACAG CACCGTGGAC AGCAAGCGGT 3360
GAGGAGGGAG CCCGCTCAGG ATGGCCTGGG CAGGGGAGGA CATCTCTAGA GGAAGGCTCA 3420
CAGCATGATG GGCAGATGCC CTGTCTCTCT GGGCCTCTAG GTGCCCTAGT GCAACAGGCA 3480
TTGCTGAGGT CTGAGCAGGG CCTGGCCTTT CTCTCTCTTC CTCACCTCA TCCTTTGGGA 3540
GGCTGACTTG GACCCAAACT GGGCGACTAG GGCCTTGAGC TGGGCAGTTT CCCTTGCCAC 3600
CTCTTCTCT ATCAGGGACA GTGTGGGTGC CACAGGTAAC CCCAATTCTT GCCTTCAAC 3660
TTCTCCCTT GACCGGGTCC AACTCTGCCA CTCATCTGCC AACTTTGGCT GGGGAGGGCT 3720
AGGCTTGGG TGAGCTGGGT TTGTGGGGAG TTCTTAATA TTCTCAAGTT TGGGCGACAC 3780
AGGGTTAATG AGTCTCTTGC CCACTGGTCC ACTTGGGGGT CTAGACCAGG ATTATAGAGG 3840
ACACAGCAGG TGAGTCTCTC CCACTCTGGG CTGTGTCACA CTGACCCAGA CCCACGTCTT 3900
CCCCCTCCT CTCTCTTTTC CTCATCTTAA GTGCCTGGCA GATGAAGGAG TTTTCAGGAG 3960
CTTTTGACAC TATATAAACC GCCCTTTTGT TATGACCCAC GGGCGGCTTT TATATGTAAT 4020
TGACGCGTGG GGTGGGTGGG CATGGGAGGT AGGGGTGGGC CCTGGAGATG AGGAGGTTGG 4080
GCCATCCTTA CCCCACACTT TTATTGTGTG OGTTTTGTGT TTGTTTGTGT TTTTGTGTGT 4140
TGTTTGTGT TTTACACTCG CTGCTCTCAA TAAATAAGCC TTTTTTA

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Seq ID NO: 534 Protein sequence

Protein Accession #: NP_002812

30
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40
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50

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1 11 21 31 41 51
MGAARGSPAR PRRLPLLSVL LPLLLGGTQT AIVFIKQPSS QDALQRRRL LRCEVEAPGP 60
VHVYWLDDGA PQDTEREFA QGSSLSFAAV DRLQDSGTFQ CVARDDVTGE EARSANASFN 120
IKWIEAGPVV LKHPASEAEI PQQTQVTLRC HIDGHRPTY QWFRDGTPLS DGQSNHTVSS 180
KERNLTLRPA GPEHSGLYSC CAHSAPQAC SSQNFTLSIA DESPARVLLA PQDVVARYE 240
EAMPHCFPSA QPPPSLQWLF EDETPITNRS RPPHLRRATV FANGSLLLTQ VRPRNAGIYR 300
CIGQGQRPFP ILEATLHLA EIEDMLFEP RVFTAGSBER VTCLPFGKLP EPSVWNEHAG 360
VRLPTHGRVY QKGHELVLAN IAEADAGVYT CHAANLAGQR RQDVNITVAT VPSWLKKPQD 420
SQLEEGKFGY LDCLTQATPK PTVVWYRNQM LISEDSRFEV FKNGTLRINS VEYDGTWYR 480
CMSSTPAGSI EAQARVQVLE KLFKTPPPQP QQCMEFDKEA TVPCSATGRE KPTIKNERAD 540
GSSLPFWTMD NAGTLHFARV TRDDAGNYTC IASNGPQGGI RAHVQLTVAV FITFKVEPER 600
TTVYGGHTAL LQCEAQGDPK PLIQWKGRDR ILDPKTLGFR MHIFQNGSLV IHDVAPEDSG 660
RYTCIAGNSC NIKHTEAPLY VVDKPVPEES EGPGSPFPYK NIQTIGLSVG AAVAYIIAVL 720
GLMPYCKKRC KAKRIQKQPE GEBPEMECLN GGPLQNGQPS AEIQEEVALT SLGSGPAATN 780
KRHSTSDIMH FPRSLQPIR TLGKSEFGV FLAKAQGLEE GVAETLVLRK SLQTKDEQQQ 840
LDPRLEWTFD GKLNHANVVR LGLCREAEP HYMVLEYVDL GDLKQFLRIS KSKDEKLKQ 900
FLSTKQKVAL CTQVALGMEH LSNNRPFVKD LAARNCLVSA QRQVKVSAIG LSKDVYNSEY 960
YHFRQAWVPL RWMSPEAILE GDFSTKSDVH AFGVLMWEVF THGEMPHGQQ ADDEVLDLQ 1020
AGKARLPQPE GCPSKLYRLM QRCWALSPIK RPSFSEIASA LGDSTVDSKP

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Seq ID NO: 535 DNA sequence

Nucleic Acid Accession #: NM_013952

Coding sequence: 161..1357

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60
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80

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1 11 21 31 41 51
TTCAGAAAGA GGAGAGACAC GGGGCCAGG GCACCTCTCG GGGGGGGCGG ACCCAAGCAG 60
TGAGGGCCTG CAGCGGGCGG GCCAGGGCAG CGGCAGGCGC GGGCCGAGAC TACGGGAGGA 120
AGCCCGAGGC CCTCGGCGGG CTGCGAGCGA CTCCCGGGCG ATGCCTCACA ACTCCATCAG 180
ATCTGGCCAT GGAGGGCTGA ACCAGCTGGG AGGGGCGCTT GTGAATGGCA GACCTCTGCC 240
GGAAGTGGTC CGCCAGCGCA TCGTAGACCT GGCCCAACAG GGTGTAAGGC CCTGGACAT 300
CTCTCGCCAG CTCGCGTCA GCCATGGCTG GTCAGCAAG ATCCTTGGCA GGTACTACGA 360
GACTGGCAGC ATCGGCCTG GAGTGATAGG GGGCTCCAAG CCCAAGGTGG CCACCCCAA 420
GGTGGTGGAG AAGATTGGGG ACTACAAAGC CCAGAACCTT ACCATGTTTG CTGGGAGAT 480
CCGAGACCGG CTCTCGCTG AGGGCGTCTG TGACAATGAC ACTGTGCCA GTGTCAGCTC 540
CATTAAAGA ATCATCCGGA CCAAAGTGCA GCAACCATC AACCTCCCTA TGGACAGCTG 600
GTTGGCCACC AAGTCCCTGA GTCCCGGACA CAOGCTGATC CCCAGCTCAG CTGTAACCTC 660
CCCGAGTCA CCCAGTGGG ATTCCTTGGG CTCCACCTAC TCCATCAATG GGTCTCTGGG 720
CATCGCTCAG CCTGGCAGCG ACAAGAGGAA AATGGATGAC AGTGATCAGG ATAGCTGCCG 780
ACTAAGCATT GACTCAGAGA GCAGCAGCAG CGGACCCCGA AAGCACCTTC GCACGATGC 840
CTTCAGCCAG CACCACTCG AGCGGCTCGA GTGCCCATTT GAGCGGCAGC ACTACCCAGA 900
GGCTATGCC TCCCCAGGCC ACACCAAGG CGAGCAGGGC CTCTACCCGC TGCCCTTGCT 960
CAACAGCACC CTGAGCAGCG GGAAGGCCAC CCTGACCCCT TCCACACGC CACTGGGGCG 1020
CAACCTCTG ACTCACCAGA CCTACCCGT GTGGCAGCT CGGCCCTTTT GBATCTGCAG 1080
CAAGTGGGCT CCGGGTCCC GCCCTTCAAT GCCTTTCCCC ATGCTGCCTC CGTGTACGGG 1140
CAGTTACCGG GCCAGGCCCT CCTCTCAGGG CGAGAGATGG TGGGGCCAC GCTGCCCGGA 1200
TACCCACCCC ACATCCCCAC CAGCGGACAG GGCAGCTATG CCTCTCTG CAGTCAGGGC 1260
ATGTTGGCAG GAAGTGAATA CTCTGGCAAT GCCTATGGCC ACACCCCTA CTCTCTCTAC 1320
AGCGAGCCCT GGGGCTTCCC CAACTCCAGC TTGCTGAGTT CCCCATATTA TTACAGTTCC 1380
ACATCAAGGC CGAGTGCAAC GCCCACCACT GCCACGGCT TTGACCATCT GTAGTTGCCA 1440
TGGGACAGT G

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Seq ID NO: 536 Protein sequence
Protein Accession #: NP_039246

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5      1      11      21      31      41      51
|      |      |      |      |      |
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK 60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND 120
TVPSVSSINR IIRTKVQPPF NLFMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY 180
SINGLLGIAQ PGSDKRKMD DQDSCRLSI DSQSSSSGPR KHLRTDAPSQ HHLEPLECPF 240
ERQHYPEAYA SPSHTKGBQG LYPLPLNST LDDGKATLTP SNTPLGRNLS THQTYPVVAA 300
PPFWICKSKA PGSRPSMPFP MLPPCTGSSR ARPSQGERW WGRPCPDTHP TSPPADRAAM 360
PPLPSQAMWQ EVNTLAMPMA TPPTPPTARP GASPTPAC

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Seq ID NO: 537 DNA sequence
Nucleic Acid Accession #: NM_003466.1
Coding sequence: 11..1363

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20      1      11      21      31      41      51
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AGGGGCGCTTT GTGAATGGCA GACCTCTGCC GGAAGTGGTC CGCCAGCGCA TCGTAGACCT 120
GGCCCCACGAG GGTGTAAGGC CCTGCGACAT CTCTCGCCAG CTCGCGCTCA GCCATGGTTG 180
CGTCAGCAAG ATCCTTGCCA GGTACTACGA GACTGGCAGC ATCCGCGCTG GAGTGATAGG 240
GGGCTCCAG CCCAAGGTGG CCACCCCAA GGTGGTGGAG AAGATTGGGG ACTACAAAGC 300
CCAGAACCCT ACCATGTTTG CCTGGGAGAT CCGAGACCGG CTCCTGGCTG AGGGGCTCTG 360
TGACAATGAC ACTGTGCCA GTGTGAGCTC CATTAAATGA ATCATCGGA CCAAGTGC 420
GCAACCATTC AACCTCCCTA CTGTAATCC CCGGAGTCA CCCCAGTCG ATTCCTGGG 540
CACGCTGATC CCTCAGCTCAG CTGTAATCC CCGGAGTCA CCCCAGTCG ATTCCTGGG 600
CTCCACTTAC TCCATCAATG GGCTCCTGGG CATCGCTCAG CCTGGCAGCG ACAAGAGGAA 660
AATGGATGAC AGTGATCAGG ATAGCTGCG ACTAAGCAT GACTCACAGA GCAGCAGCAG 720
CGSACCCGGA AAGCACCCTT GCACGGATGC CTTACGCCAG CACCACCTCG AGCCGCTCGA 780
GTGCCCATTT GAGCGGCAGC ACTACCCAGA GGCTATGCC TCCCCAGCC ACACCAAGG 840
CGAGCAGGCG CTCTACCCGC TGCCCTTGCT CAACAGCACC CTGACGACG GGAAGGCCAC 900
CCTGACCCCT TCAACACGCG CACTGGGGCG CAACCTCTCG ACTACCCAGA CCTACCCCGT 960
GGTGGCAGAT CCTCACTCAC CTTTCCCTAT AAGCAGGAA ACCCCGAGG TGTCCAGTTC 1020
TAGCTCCACC CCTTCTCTT TATCTAGTCT CGCCTTTTGT GATCTGCAGC AAGTCGCTC 1080
CGGGGTCGCG CCCTTCAATG CCTTCCCA TGCTGCTTCC GTGTACGGGC AGTTTACGGG 1140
CCAGGCCCTC CTCTCAGGCG GAGAGATGGT GGGGCCACG CTGCCCGGAT ACCCACCCTA 1200
CATCCGCCAC AGCGGACAGG GCAGCTATGC CTCCTCTGCC ATCGCAGGCA TGTGGCAGG 1260
AAGTGAATAC TCTGGCAATG CCTATGGCCA CACCCCTTAC TCCTCTTACA GCGAGGCTG 1320
GCGCTTCCCC AACTCCAGCT TGCTGAGTTC CCCATATTAT TACAGTTCCA CATCAAGGCC 1360
GAGTGCACCG CCCACCACTG CCACGGCCTT TGACCATCTG TAGTTGAAGC TT

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Seq ID NO: 538 Protein sequence
Protein Accession #: NP_003457

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50      1      11      21      31      41      51
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MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK 60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND 120
TVPSVSSINR IIRTKVQPPF NLFMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY 180
SINGLLGIAQ PGSDKRKMD DQDSCRLSI DSQSSSSGPR KHLRTDAPSQ HHLEPLECPF 240
ERQHYPEAYA SPSHTKGBQG LYPLPLNST LDDGKATLTP SNTPLGRNLS THQTYPVVAD 300
PHSPPAIKQE TPEVSSSSST PSSLSAFL DLQVVGSGVP PFNAFFHAAS VYQGTGQAL 360
LSGRENVGPT LPGYPPIPT SGQGSYASSA IAGMVAGSEY SGNAYGHTPY SSYSEAWRFP 420
NSLLSSPIFY YSSTSRPSAP PTTATAFDHL

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Seq ID NO: 539 DNA sequence
Nucleic Acid Accession #: NM_006799
Coding sequence: 19..963

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65      1      11      21      31      41      51
|      |      |      |      |      |
GCGCGCGGAG AGGAGGCCAT GGGCGCGCGC GGGCGGCTGC TGCTGGCGCT GCTGCTGGCT 60
CGGGCTGGAC TCAGGAAGCT GGAGTCGAG GAGGCGCGC CGTTATCAGG ACCATGCGGC 120
CGACGGGTCA TCACGTGCGC CATCGTGGT GGAGAGGACG CCGAACTCGG GCGTTGGCGG 180
TGGCAGGGA GCGTGGCGCT GTGGGATTCC CACGTATGCG GAGTGAGCCT GCTCAGCAC 240
CGCTGGGAC TCACGGCGGC GCACTGCTT GAAACCTATA GTGACCTTAG TGATCCCTCC 300
GGGTGGATGG TCCAGTTTGG CCAGCTGACT TCCATGCCAT CCTTCTGAG CCTGCGAGCC 360
TACTACACCC GTTACTTCGT ATCGAATATC TATCTGAGC CTCGCTACCT GGGGAATTCA 420
CCCTATGACA TTGCTTGGT GAAGCTGTCT GCACCTGTCA CCTACACTAA ACACATCCAG 480
CCCATCTGTC TCCAGGCCTC CACATTGAG TTGAGAACG GGACAGACTG CTGGGTGACT 540
GGCTGGGGT ACATCAAGA GGAAGAGGCA CTGCCATCTC CCAACACCTC CCAGGAAGTT 600
CAGGTCGCCA TCATAAACAA CTCTATGTGC AACCACTCT TCTCAAGTA CAGTTTCCGC 660
AAGGACATCT TTGGAGACAT GGTTTGTGCT GGCAATGCC AAGCGGGAA GGATGCCCTG 720
TTGGTGACT CAGGTGGACC CTGGGCTGT AACAGAAATG GACTGTGTA TCAGATTGGA 780
GTGTTGAGCT GGGGAGTGGG CTGTGGTGG CCAATCGGC CCGGTGTCTA CACCAATATC 840
AGCCACCACT TTGAGTGGAT CCAGAGCTG ATGGCCCGA GTGGCATGTC CCAGCCAGAC 900
CCCTCTGCGC CGCTACTCTT TTCCCTCTT CTCTGGGCTC TCCTACTCT GGGGCGGCTC 960
TGAGCCTACC TGAGCCCATG CAGCCTGGG CCACTGCCAA GTCAGGCCCT GGTCTCTCTC 1020
TGCTTGTGTT GGTAAATAAC ACATTCAGT TGATGCCCTG CAGGGCATTG TCCAAA

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Seq ID NO: 540 Protein sequence
Protein Accession #: NP_006790

1 11 21 31 41 51
 5 MGARGALLLA LLLARAGLRK PESQEAAPLS GPOGRREVITS RIVGGEDAEL GRNFWQGSRLR 60
 LNDSHVCGVS LLSHRWALTA AHCFTYSDL SDPSGWMVQF GQLTSMPSFW SLQAYYTRYF 120
 VSNILSPRY LGNSPYDIAL VKLSAPVTTY KHIOPICLQA STEFENRTD CNVTGNGYIK 180
 EDEALPSPHT LQEVQVAIIN NSMCNHLFLK YSFRKDIFGD MVCAGNAQGG KDACPDSGG 240
 PLACNKNGLN YQIGVVSWGV GCGRPNRPGV YTNISHHFEW IQKLMAQSGM SQPDPSWPLL 300
 FFFLLWALPL LGPV

Seq ID NO: 541 DNA sequence
 Nucleic Acid Accession #: NM_014344
 Coding sequence: 131..1444

1 11 21 31 41 51
 15 GCGGCGCGGA TGGGCGCGAA GCGCCCGAAG CCCCGGAGCC CACAACTGC GGGGCCCGCC 60
 TCGCGCGCGG GACCCGGGTG CCTGGGCTCG GCTTGAAGCG GCGGCGGCGC ACCGGCACAG 120
 CGCGCGGAGC ATGGGCGAGG GATGCGGGG CGCGCGCGCC ACCCGGGGCG TCTGGCTGCT 180
 20 GGCGCTGGGC TCGCTGCTGG CGCTGTGGGG AGGCTCTCTG CGCGCGGGA CCGAGCTGCC 240
 CGCCTCCCGG CCGCCCGAAG ACCGACTCCC ACGGCGCCCG GCCCGGAGCG GCGGCCCGCG 300
 CGCGCGGCGT CGCTTCCCTC TGCCCCCGCC CTGGCGTGG GACGCGCGCG GCGGCTCCCT 360
 GAAAACTTTC CGGCGCTGTC TCACCTTGCG GGCGCGCGCG GACGGCCCGC CCGGCGAGTC 420
 CGGAGCGAGC CCCAGGTGGC ACGTGTGAGC CAGGCGAGCC CGCGCGGAGG AGAGCGCGCG 480
 25 GGTGCAAGGG GGGCTCTTCT GGAGCGCGCG CCTGGAGGAG CAGGTGCCCC CGGGCTTTTC 540
 GGAGGCCAGT GCGGCGGCGT GCGTGGAGGC GGCTCGCGCG GCCCGGATGG TGGCCCTGGA 600
 GCGCGGGGGT TGCGGGCGCA GCTCCAACCG ACTGGCCCGT TTTGCCGAGC GCACCCGCGC 660
 CTGCGTGCOC TAGCGCATCA ACCCGGAGCA GATTGAGGCG GAGGCCCTGT CTTACTATCT 720
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 30 TCGGGGCGCG CAGTGGGCGC AGGTGCGAGG GAGCTGCGC GCTGCGCACT GGACCGAGGG 840
 CAGCGTGGTG AGCCTGACAC GCTGCGTGCC CAACCTCACG GACGTGGTGG TCGCGCGCGC 900
 CTGCGCGCTG GAGGAGCGCC GTCTGCGCCC CCTCGGGAT GCCGGGGGTG AGCTGGCCAA 960
 CCTCAGCCAG GCGGAGCTGG TGGACCTAGT ACAATGGACC GACTTAATCC TTTTGGACTA 1020
 35 CCGTGAAGGC AACTTGGACC GGCTCGTAAG CAACCTCTTC AGCCTGCAGT GGGACCGCGC 1080
 CGTCACTGAG CGTCCACCA GCAACCTGCA CCGCGGTCCG GCGGGGCGCG TGGTCTTTCT 1140
 GGACAATGAG GCGGGCTTGG TGCACGGCTA CCGGGTAGCA GGCATGTGGG ACAAGTATAA 1200
 CGAGCCGCTG TTGCAGTCAG TGTGCGTGTG CCGGAGCGCG ACCCGCGCGC GCGTCTGGA 1260
 GCTGACCCGC GGACAGGAGC CCGCGCGCGC GCTGCTGCGC CTCTACCGGC GCCACGAGCC 1320
 40 TCGCTTCCCG GAGCTGGCGC CCTTGGCAGA CCCCCAGCT CAGCTGCTAC AGCGCGGCT 1380
 CGACTTCTCT GCCAAGCACA TTTTGCCTG TAAGGCCAAG TACGCGCGCC GGTCTGGGAC 1440
 TTAGTGTAC CCGGAGGAAA AGAGAGAGAT CTGGGGCTGG GGTATGGATG ATGGGGGAAA 1500
 GGGCGGTGCG CTCGCGCACT GTGAGGAGCC AGCGCGCCAA CGCCACCCG CAAAGGTGTC 1560
 TAAAACTTC AGCTTTTCAC CCACCTGCCC CTTTCTTCA ATCCCAAGCT GTTCTCTTC 1620
 45 AAAGTTCTG GAGGACGAAC TCACCGAGGC GAGAAGTGA ACATTCTCTC CACCGAGCTT 1680
 ATAAAGGAT TCTTTACTGT GCCAGCACGG GATTGGATC GGAAGAACT GGCTACTGGG 1740
 GTTTGGCCCC CGAGTGGCGC TCCCTGTGGG AGATGCACCC CATTCTTGGG CCCCCCTCAT 1800
 TCCCTTTCCG AAAAAGGAAA ACTTGCCTTT GAGCGGTTGA GCTAATTCTG CAATTTTCTA 1860
 CCAACAGAG CGCTGGTGGC CCGCGAGCAG GGCTGTGACA TTGGCTGTGT GAGCCCTTCT 1920
 50 CTGTGTTCTG GCTTGTGTTCC AGCGCGCGGA TGGTGAGATC ACTGTTCCAA GCAGGGGGAC 1980
 GGCTCGCGAT AGGACAAAGA GAGCAGGACC TCCAGACTCT GGGGAGCCCT GCAGACCTTG 2040
 ACAATTTGCC TGACTCATTC CTGACCTCTT GTCAATTTGG CCTGAAGGCT ACAAAATTCAG 2100
 GGTCACTGT ATGCACTAAG TCAATAATG AATTCTTCC TCCCTCTGCG AACCGACCAA 2160
 AATTTTGACA ACGATGATGT TCACCAGAA GAAAAAATA TCAGTTTAT GCACCTTATT 2220
 55 TGTGTTGAT TTTTATTATT TATTAAGAAA AAATTTTATT TTACAGAAAT TACCTTCTCT 2280
 GTATATATGT GCATAAAGTG TGGTGTAAAT ATACTAAACA AACTTATATT TCAATAAAG 2340
 GGAGTTTAAA ATTTAAAAA AAAAAA

Seq ID NO: 542 Protein sequence
 Protein Accession #: NP_055159

1 11 21 31 41 51
 60 MGRMRGAAA TAGLWLLALG SLLALWGGLL PPRTLPASR PPEDRLPRRP ARSGGPAPAP 60
 RFPLPPLAW DARGGSLKTF RALLTLAAGA DGPPRQSRSE PRWHVBARQP RPESAAVHG 120
 65 GVFWRSGLLE QVPPGFSEAG AAALWLAARG ARMVALERGG CGRSSNRLAR FADGTRACVR 180
 YGINPEQIQG EALSYYLARL LGLQRHVFPF ALARVEARGA QWAQVQEELR AAHWTEGSSV 240
 SLTRNLNLT DUVVPAPWRS EDGRLRPLRD AGGELANLSQ AELVDLVQMT DLILFDYLT 300
 NFDRLVSNLF SLQWDFRVMQ RATSNLHRGP GAGLVFLDNE AGLVHGGRVA GMWDKYNEPL 360
 70 LQSVCFPRER TARRVLELER GDAAAARLLR LYRRHEPRFP ELAALADPHA QLLQRRDLFL 420
 AKHILHCKAK YGRRSGT

Seq ID NO: 543 DNA sequence
 Nucleic Acid Accession #: XM_007652.4
 Coding sequence: 1..1290

1 11 21 31 41 51
 75 ATGGCGCGCT CTGGCGCGTG GAAGCGCGCT AAATCTATGC TAAGGAAGGA TGATGCGCG 60
 CTGTTTTTAA ATGACACCA GCGCTTTGAC TTCTCGGATG AGCGGGGGGA CGAGGGGCTT 120
 80 TCTCGGTACA ACAAACTTC AGTTGTGGTG GCCGATGAG GTTCGGAAG CCGGAAAGG 180
 CCTGTTAAGC GGGCGCACCC GACCTCCAG GCCGAGGAT ATTCTTACT GGACCAAGAC 240
 TTACCTTTGA CCAACAGTCA GCTGAGTTTG AAGGTGGACT CCGTGACAA CTGCAGCAA 300
 CAGAGAGAGA TACTGAAGCA GAGAAAGGTG AAAGCCAGGT TGACCATTCG TGCGGTTCTG 360
 TACTTGCTTT TCAATGATTG AGAATCTGTA GGTGGATACA TTGCAATAG OCTAGCAATC 420

5 ATGACAGATG CACTTCATAT GTTAACTGAC CTAAGCGCCA TCATACTCAC CCTGCTTGCT 480
 TTGTGGCTAT CATCAAAAT ACCAACCAA AGATTACCT TTGGATTTC TCGCTTAGAG 540
 GTTTTGTACG CTATGATTAG TGTGCTGTTG GTGTATATAC TTATGGGATT CCTCTTATAT 600
 GAAGCTGTGC AAAGAACTAT CCATATGAAC TATGAAATAA ATGGAGATAT AATGCTCATC 660
 ACCGAGCTG TTGAGTTGC AGTTAATGTA ATAATGGGGT TTCTGTTGAA CCAGTCTGGT 720
 CACCGTCACT CCCATTCCCA CTCCTGCCT TCAAATTCCT CTACCAGAGG TTCGGGGTGT 780
 GAACGTAAAC ATGGGCAGGA TAGCCTGGCA GTGAGAGCTG CATTGTGACA TGCTTTGGGA 840
 GATTTGGTAC AGAGTGTGG TGTGCTAATA GCTGCATACA TCATACGATT CAAGCCAGAA 900
 10 TACAAGATTG CTGATCCCAT CTGTACATAC GTATTTTCAT TACTTGTGCG TTTTACAACA 960
 TTTCGAATCA TATGGGATAC AGTAGTTATA ATACTAGAAG GTGTGCCAAG CCATTGTAAT 1020
 GTAGACTATA TCAAGAAGC CTGTATGAAA ATAGAAGATG TATATTCACT CGAAGATTTA 1080
 AATATCTGGT CTCTCACTTC AGGAAAATCT ACTGCCATAG TTCACATACA GCTAATTCCT 1140
 GGAAGTTTAT CTAAATGGGA GGAAGTACAG TCCAAGCAA ACCATTTATT ATTGAACACA 1200
 15 TTGGCATGT ATAGATGTAC TATTCAGCTT CAGAGTTACA GGCAAGAAGT GGACAGAACT 1260
 TGTGCAAATT GTCAGATTG TAGTCCCTGA

Seq ID NO: 544 Protein sequence
 Protein Accession #: XP_007652.1

20 1 11 21 31 41 51
 MAGSGAWKRL KSLMRKDDAP LPLNDTSAPD PSDEAGDEGL SRFNKLRRVVV ADDGSEAPER 60
 PVNGAHPTLQ ADDSLLDQD LPLTNSQLSL KVDSCDNCSK QREILKORKV KARLITIAAVL 120
 YLLFMIGELV GGYIANSIAI MTDALHMLTD LSAILITLLA LNLSSKSPTK RPTFGFHRLE 180
 25 VLSAMISVLL VYILMGFLLY EAVQRTIHMN YEINGDIMLI TAAVGVAVNV IMGFLINQSG 240
 HRHSHSHSLP SNSPTRGSGC ERNHGQDSLA VRAAFVHALG DLVQSVGVLI AAYIIRFKPE 300
 YKIADPICTY VFSLLVAFTT FRIIWDTVVI ILEGVPSHLN VDYIKBALMK IEDVYSVEDL 360
 NIWSLTSGKS TAIVHIQLIP GSSSKWEEVQ SKANHLLLNNT FGMYRCTIQL QSVRQEVDR 420
 CANQSSSP

Seq ID NO: 545 DNA sequence
 Nucleic Acid Accession #: AB037765.1
 Coding sequence: 1..2478

35 1 11 21 31 41 51
 ATGTTTTCOG GCTTCAATGT CTTTAGAGTT GGGATCTCTT TTGTCAATAT GTGCATTTTT 60
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 CAACACAGAA AGGCTCTTTT AGCTTATTTT TGTCAAGCTG ATTCGCCAAG AACATCTGTA 180
 40 TTCTTTGAAG AACTGAATGA GGCTGTTAGA CCTCTGCAGG ACTATGGAAT TTCAGTTGCC 240
 AAGGTTAATT GTGTCAAAGA AGAAATATCA AGATACTGTG GAAAAGAAAA GGATTTGATG 300
 AAAGCATATT TATTCAAGGG CAACATATTG CTCAGAGAAT TCCCTACTGA CACCTTGTTT 360
 GATGTGAATG CCATTGTGCG CCATGTTCTC TTTGCTCTTC TTTTATGTA AGTGAATAT 420
 ATTACCAACC TGGAGAGCCT TCAGAACATA GAAATGCTC TGAAGGAAA AGCAATATT 480
 45 ATATTCTCAT ATGTAAGAGC CATTGGAATA CCAGAGCACA GAGCAGTCAT GGAAGCCGCT 540
 TTTGTGTATG GGAATACATA CCAATTGTCT TTAACCAAG AAATTTGCCCT TTTGGAAGT 600
 ATTGGCTCTG AGGATGTGGA ATATGCACAT CTCTACTTTT TTCAATGTAA ACTAGTCTTG 660
 GACTTGACCC AGCAATGTAG AAGAACACTA ATGGAACAGC CATTGACTAC ACTGAACATT 720
 CACCTGTTTA TTAAGACAAT GAAAGCACCT CTGTTGACTG AAGTTGTCTG AGATCCTCAA 780
 50 CAAGTTTCAA CTGTCCATCT CCAACTGGCG TTACCACTGG TTTTATTTGT TAGCCAACAG 840
 GCTACTTATG AAGCTGATAG AAGAACTGCA GAATGGGTTG CTGCGGCTCT TCTGGGAAAA 900
 GCAGGAGTTC TACTCTGTGT AAGGGACTCT TTGGAAAGTGA ACATTCTCTCA AGATGCTAAT 960
 GTGGTCTTCA AAAGAGCAGA AGAGGGAGTT CCAAGTGAAT TTTTGTATT ACATGATGTT 1020
 GATTATTAATA TATCTCATGT GGAAAAATA ATGCACATTG AGGAAATACA AGAAGATGAA 1080
 55 GACAATGACA TGGAAAGTCC AGATATAGAT GTTCAGGATG ATGAAGTGGC AGAACTGTT 1140
 TTCAGAGATA GGAAGAGAAA ATTACCTTTG GAACTTACAG TGGAACTAAC AGAAGAAACA 1200
 TTTAATGCAA CAGTGAATGG TTCTGACAGC ATAGTACTCT TCTATGCTGG TTGGCAAGCA 1260
 GTATCCATGG CATTTTGTGA ATCTATATT GATGTGGCAG TTAACCTGAA AGGCACATCT 1320
 ACTATGCTTC TTACTAGAAT AAAGTGTGCA GATTGTTCTG ATGTATGTAC TAAGCAAAAT 1380
 60 GTTACTGAAT TTCCTATCAT AAAGATGTAC AAGAAAGCGG AGAACCCAGT ATCTTATGCT 1440
 GGAATGTTAG GAACCGAAGA TCTCCTAAAA TTTATCCAGC TCAACAGGAT TTCATATCCA 1500
 GTGAATATAA CATCGATCCA AGAAGCAGAA GAATATTAA GTGGGGAATT ATATAAAGAC 1560
 CTCATCTTGT ATTCTAGTGT GTCAATATTG GGACTATTTA GTCCAAACCAT GAAACACAGA 1620
 ARAGAAGATT TTAGTGAAGC AGGAAACTAC CTAAAAGGAT ATGTTATCAC TGGAAATTAT 1680
 65 TCTGAAGAAG ATGTTTGTCT ACTGTCAACC AAATATGCTG CAAGTCTTCC AGCCCTGCTG 1740
 CTGCGCAGAC ACACAGAAGG CAAAATAGAG AGCATCCAC TAGCTAGCAC ACATGCACAA 1800
 GACATAGTTC AAATAATAAC AGATGCACAT CTGGAATGT TTCCGGAAAT CACTGTGGAA 1860
 AATCTTCCCA GTTATTTCAG ACTTCAGAAA CCAATTATGA TTTTGTTCAG TGATGGCACT 1920
 GTAAATCCTC AGTATAAAAA AGCAATATTG ACCTGGTAA AGCAGAAATA CTTGAGTTCA 1980
 70 TTTACTCCAT GCTGGTTAAA TCTAAAGAT ACTCCAGTGG GGAGAGGAAT CTTGAGGGCA 2040
 TATTTTGATC CTCTGCTCTC CCTTCTCTCT CTGTTTGGG TGAATCTGCA ATTGTGGCTG 2100
 CAAGTATTTG CATTCTCTTC AGACCAAGCT ATAATTGAAG AAAACCTTGT ATTGTGGCTG 2160
 AAGAAATTAG AAGCAGGACT AGAAAATCAT ATCACAATTT TACCTGTCTA AGAATGGAAA 2220
 CCTCTCTTTC CAGCTTATGA TTTTCTAAGT ATGATAGATG CCGCAACATC TCAACGTGGC 2280
 75 ACTAGGAAAG TTCCCAAGTG TATGAAAGAA ACAGATGTGC AGGAGAATGA TAAGGAACAA 2340
 CATGAAGATA AATCGGCACT CAGAAAAGAA CCGATTGAAA CTCTGAGAAAT AAAGCATTTG 2400
 AATAGAAGTA ATTGGTTTAA AGAAGCAGAA AAATCATTTA GACGTGATAA AGAGTTAGGA 2460
 TGCTCAAAG TGAACATA

80 Seq ID NO: 546 Protein sequence
 Protein Accession #: BAA92582.1

1 11 21 31 41 51
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MFSQNFVPRV GISFVIMCIP YMPTVNSLPE LSPQKYPSTL QPKASLAYF CQADSPTS SV 60
FLEELNEAYR PLQDYGISVA KVNCKEBSI RYCGKEDLM KAYLFKGNIL LREFTDTLP 120
DVNAIVAHVL FALLPSEVKY ITNLEDLQNI ENALKGKANI IFSYVRAIGI PEHRAVMEAA 180
FVYGTTYQFV LTTBIALLES IGSEDEVYAH LYFFHCKLVL DLTQCCRRL MSQPLTTLLNI 240
HLFIKTKAP LLTSAVEDPO QVSTVHLQLG LPLVPFVSQQ ATYEADRRTA ESWANRLLGK 300
AGVLLLLRDS LEVNIPODAN VVFKRABECV PVEPLVLADV DLIISHVENN MHIEBIQEDE 360
DNDMEGPDID VQDDEVAETV FRDRKRKLPL ELTVELTEET FNATVMASDS IVLFYAGWQA 420
VSMAPLQSYI DVAVKLKGT S TMLLTRINCA DWSDVCTKQN VTEFPIIKMY KKGEPVSYA 480
GMLGTEDLLK FQLWRISYP VNITSIQEAE EYLSGELYED LILYSSSVSVL GLFSPMTKTA 540
KEDFSEAGNY LKGYVITGIY SEEDVLLST KYAASLPALL LARETEGKIE SIPLASTHAQ 600
DIVQIITDAL LEMFPEITVE NLPSYFRLQK PLLILFSDGT VNPQYKAIL TLVKQRYLDS 660
FTPCNLMLKN TPVGRGILRA YFDPLPPLPL LVLVNLHSGG QVFAFPDQA IIEENLVML 720
KKLEAGLENH ITILPAQEWK PPLPAYDFLS MIDAAATSRG TRKVPKCMKE TDVQENDKEQ 780
HEDKSAVRKE PIETLRKHW NRSNWFKEAB KSFRDRKELG CSKVN

Seq ID NO: 547 DNA sequence
Nucleic Acid Accession #: NM_033102.1
Coding sequence: 1..1662

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1 11 21 31 41 51
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GTCAACCTGC TAACCTTGG CCTGGAGGTG TGTITGGCCG CAGGCATCAC CTATGTGCCG 120
CCTCTGCTGC TGGAAAGTGG GGTAGAGGAG AAGTTTATGA CCATGGTGCT GGGCATTGGT 180
CCAGTGTGCG GCCTGGTCTG TGTCCCGCTC CTAGGCTCAG CCAGTGACCA CTGGCGTGG 240
CGCTATGGCC GCGCGCGGCC CTTCATCTGG GCACTGTCTT TGGGCATCCT GCTGAGCCTC 300
TTTCTCATCC CAAGGGCCGG CTGGCTAGCA GGGCTGCTGT GCGCCGATCC CAGGCCCTG 360
GAGCTGGCAC TGCTCATCCT GGGCGTGGGG CTGCTGGACT TCTGTGGCCA GGTGTGCTTC 420
ACTCCACTGC AGGCCCTGCT CTCTGACCTC TTCGGGACC GGGACCACTG TCGCCAGGCC 480
TACTCTGTCT ATGCTTTCAT GATCAGTCTT GGGGGCTGCC TGGGCTAOCCT CCGCTCTGCC 540
ATTGACTGGG ACACCAAGTG CCTGGCCCCC TACCTGGGCA CCCAGGAGGA GTGCCCTCTT 600
GGCCTGTCTA CCACTCATCTT CCTCACCTGC GTAGCAGCCA CACTGCTGCT GCGTGAGGAG 660
GCAGCGCTGG GCGCCACCGA GCCAGCAGAA GGGCTGTGG CCCCCTCCTT TGCGCCCCAC 720
TGCTGTCCAT GCGCGGCCGG CTGGCTTTC CGGAACCTGG GCGCCCTGCT TCCCGGCTG 780
CACCAGCTGT GCTGCGCAT GCGCCGCACC CTGCGCGCG TCTTCGTGGC TGAGCTGTGC 840
AGCTGGATGG CACTCATGAC CTTCAGCTG TTTTACACGG ATTTCTGTGG CGAGGGGCTG 900
TACCAGGCGG TGCCAGAGC TGAGCGGGCC ACCGAGGCC GAGACACTA TGATGAAGGC 960
GTTCTGGATG GCAGCTGGG GCTGTCTCT CAGTGCGCCA TCTCCCTGCT CTCTCTCTG 1020
GTCTATGACC GGCCTGTGCA GCGATTGCG ACTCGAGCAG TCTATTGGC CAGTGTGGCA 1080
GCTTTCCTCT TGGCTGCCGG TGCCACATGC CTGTCCACA GTGTGGCGCT GGTGACAGCT 1140
TCAGCGCGCC TCACCGGGTT CACCTTCTCA GCGCTGCAGA TCCTGCGCTA CACTGTGCC 1200
TCCCTCTACC ACCCGGAGAA GCAGGTGTTT CTGCCCAAAT ACCGAGGGA CACTGGAGGT 1260
GCTAGCAGT AGGACAGCT GATGACCAG TTCTGCCCAG GCGCTAAGCC TGGAGCTCCC 1320
TTCCCTAATG GACACGTGG TGCTGGAGG AGTGGCTGCT TCCCACTCC ACCCGGCTC 1380
TGCGGGGCTC CTGCTGTGA TGTCTCGTA CGTGTGGTG TGGGTGAGCC CACCGAGGCC 1440
AGSGTGGTTC CGGGCGGGG CATCTGCTG GACCTCGCCA TCCTGGATAG TGCCCTCCTG 1500
CTGTCCAGG TGCCGCCATC CTTGTTATG GGCTCCATTG TCCAGCTCAG CCAGTCTGCT 1560
ACTGCTATA TGGTGTCTG GCGAGGCTG GGTCTGCTG CCATTACTT TGCTACACAG 1620
GTAGTATTTG ACAAGAGCGA CTGGCCAAA TACTCAGGT GA

Seq ID NO: 548 Protein sequence
Protein Accession #: NP_149093.1

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1 11 21 31 41 51
MVQRLVNSRL LRHRKAQLLL VNLITFGLV CLAAAGITYVP PLLLEVGVVE KFMIMVLGIG 60
PVLGLVCPVL LGSASDHWRG RYGRRRPFIW ALSLGILLSL FLIPRAGWLA GLLCPDPRPL 120
ELALLILGVG LLDFOGQVCF TPLEALLSDL FRDPDHCRA YSVYAFMISL GGCLGYLLPA 180
IDWDTALAP YLGTQEECLF GLLTLIFLTC VAATLLVAEE AALGFTEPAE GLSAPSLSPH 240
CCPCRARLAP RNLGALLPRL HQLCCRMPT LRRLFVAELC SWMALMTFTL FYTDFVGEGL 300
YQGVPRAPRG TEARRHYDEG VRMGSLGLFL QCAISLVFSL VMDRLVQRFQ TRAVYLASVA 360
APPVAAATC LSHSVAVVTA SAALTGFTFS ALQILPYTLA SLYHREKQVF LPKYRGDTGG 420
ASSEDSLMTS FLPGPKPGAP PFNGHVAGG GQLLPPPPAL CGASACDVSV RVVVGEPTEA 480
RVVPRGICL DLALDSAPL LSQVAPSLPM GSIVQLSQSV TAYMVSAGL GLVAIYPATQ 540
VVPKSLDLAK YSA

Seq ID NO: 549 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1389

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1 11 21 31 41 51
ATGGGCTACC AGAGGCAGGA GCCTGTCTAT CGCGCGCAGA GAGATTAGTA TGACAGAGAA 60
ACCCTTGTTT CTGAACATGA GTATAAGAG AAAACCTGTC AGTCTGCTGC TCTTTTAAAT 120
GTGTCAACT CGATTATAGG ATCTGGTATA ATAGGATTGC CTATTCAAT GAAGCAAGCT 180
GGGTTTCCCT TGGGAATATT GCTTTTATTC TGGGTTTCAT ATGTACGGA CTTTCCCTT 240
GTTTATTTGA TAAAGGAGG GGGCCCTCTCT GGAACAGATA CCTACCACTG TTTGTCAAT 300
AAACTTTTGG GCTTCCAGG GTATCTGCTC CTCTCTGTTT TCCAGTTTTT GTATCCTTTT 360
ATAGCATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAAGT TTTTCAAAGA 420
ATCCAGGAG TTGATCTCTA AAACGTGTTT ATTGGTCGCC ACTTCATTAT TGGACTTTCC 480
ACAGTACCTT TTACTCTGCC TTTATCCTTG TACCAGAAATA TAGCAAAGCT TGGAAAGGTC 540
TCCCTCATCT CTACAGTTT AACAACTCTG ATTCTGGAA TTGTAATGGC AAGGGCAATT 600
TCACTGGGTC CACACATACC AAAACAGAAA GACGCTGGG TATTTGCAA GCCCAATGCC 660
ATTCAGGCG TCGGGTTTAT GTCTTTTGA TTTATTGGC ACCATAACTC CTTCTTAGTT 720

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TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC 780
GTGATTTCTG TATTTATCTG TATATCTTTT GCTACATGTG GATACTTGAC ATTTACTGGC 840
TTCACCCAAG GGGACTTATT TGAAAATTAC TGCAGAAATG ATGACCTGGT AACATTGGGA 900
AGATTTTGTG ATGGTGTACAC TGTCATTTTG ACATACCCTA TGGAAATGCTT TGTGACAAGA 960
GAGGTAATTG CCAATGTGTT TTTTGGTGGG AATCTTTTCAT CGGTTTTCCTA CATTGTTGTA 1020
ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCACTGC TGATTGATTG CCTCGGGATA 1080
GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCTCA TTTTATCAT TCCATCAGCC 1140
YTTTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTGTC 1200
ATGCTTCCCA TTGGTGTCTG GTGTGATGGT TTTGGATTGG TCATGGCTAT TACAAATACT 1260
CAAGACTGCA CCGATGGGCA GGAATGTTT TACTGCTTTC CTGACAAATT CTCTCTCACA 1320
AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACCTT CTACTTTAAA TATTAGTATC 1380
TTTCAATGA

Seq ID NO: 550 Protein sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
MGYQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIIGSGI IGLPYSMKQA 60
GPFLLGILLFL WVSVTDFSL VLLIKGGALS GTDTYQSLVN KTFGFPGYLL LSVLQFLYPF 120
IAMISYNIIA GDTLSKVFOR IPGVDPENVF IGRHFIIGLS TVTPTLPLSL YRNIKILGKV 180
SLISTGLTTL ILGIVMARAI SLGPHIPKTE DAWVFAKFA IQAVGVMSFA PICHNSFLV 240
YSSLEPTVA KMSRLIHMSI VISVFICIFF ATCGYLFTFG FTQGDLPFENY CRNDDLVTFG 300
RFCYGVTVIL TYPMECFVTR EVIANVFFGG NLSSVFHIVV TVMVITVATL VSLLDCLGI 360
VLELNGVLCA TPLIFIIPSA CYLKLSEPR THSKIMSCV MLPIGAVVMV PGFVMAITNT 420
QDCTHGQEMF YCFPNFSLT NTSSEHVQQT TQLSTLINISI FQ

Seq ID NO: 551 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1284

1 11 21 31 41 51
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AAGCAAGCTG GGTTCCTTTT GGAATATTG CTTTATTCTT GGGTTTCATA TGTACAGAC 120
TTTCCCTTGG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCACTCT 180
TTGGTCAATA AACTTCTGGG CTTCCAGGG TATCTGCTCC TCTCTGTTCT TCAGTTTTTG 240
TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATACTTT GAGCAAAAGT 300
TTTCAAAGAA TCCAGGAGGT TGATCTCGAA AACGTGTTTA TTGGTCGCCA CTTCAATTAT 360
GGACTTTCCA CAGTTACCTT TACTCTGCCT TTATCCTTGT ACCGAAATAT AGCAAAGCTT 420
GGAAGGCTCT CCCTCATCTC TACAGGTTTA ACAACTCTGA TTCTTGAAT TGTAAATGGCA 480
AGGCAATATT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTGGGT ATTGCAAG 540
CCCAATGCCA TTCAAGCGGT CGGGTTATG TCTTTGCTAT TATTGTTCCA CCATAACTCC 600
TTCTTAGTTT ACAGTCTCTT AGAAGAACCC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT 660
ATGTCCATCG TGATTTCTGT ATTTATCTGT ATATTCTTG CTACATGTGG ATACTTGACA 720
TTTACTGGCT TCACCAAGG GGACTTATT GAAATTAAT GCAGAAATGA TGACCTGGTA 780
ACATTTGGAA GATTTTGTGA TGGTGTCACT GTCATTTTGA CATACCTAT GGAATGCTTT 840
GTGACAAGAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTTCATC GGTTTTCCAC 900
ATTGTTGTAA CAGTGATGGT CATCACTGTA GCCACGCTTG TGTCAATGCT GATTGATTGC 960
CTCGGGATAG TTCTAGAACT CAATGGTGTG CTCTGTGCAA CTCCCCTCAT TTTTATCAAT 1020
CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCGA TAAGATTATG 1080
TCTTGTGTC TAATCTCCAT TGGTGTGTTG GTGATGGTTT TTGATTCGT CATGGCTATT 1140
ACAAATACTC AAGACTGCAC CCATGGGCAG GAAATGTTCT ACTGCTTTC TGACAAATTC 1200
TCTCTCACA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260
ATTAGTATCT TTCAACTCGA GTAA

Seq ID NO: 552 Protein sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
MGYQRQEPVI PPQRGLPYSM KQAGFPLGIL LFWVSIVTD FSLVLLIRGG ALSGDTTYQS 60
LVNKTFFGPG YLLSVLQFL YPFIAMISYN IAGDTLSKV FQRIQGVDP NVPFGRHFII 120
GLSTVFTTLP LSLYRNIAKL GKVSLISTGL TTLILGIVMA RAISLGP HIP KTEDAWVFAK 180
PNAIQAVGVM SFAPICHNS FLVYSSLEP TVAKWSRLIH MSIVISVFI IFFATCGYLT 240
FTGFTQGDLE ENYCRNDDL TFGRFYCVT VILTYPMECF VTREIVANVF FGNLSSVFH 300
IVVTVMVITV ATLVSLLDIC LGIVLELNGV LCATPLIFII PSACYLKLSE EPRTHSKIM 360
SCVMLPIGAV VMVPGFVMAI TMTQDCTHGQ EMFYCFPDNF SLTNTSEHV QTTQLSTLN 420
ISIFQLE

Seq ID NO: 553 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1203

1 11 21 31 41 51
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TTTCCAGGCT ATCTGCTCTT CTCTGTTCTT CAGTTTTTGT ATCCTTTTAT AGCAATGATA 180
AGTTACAATA TAATAGCTGG AGATACTTTG AGCAAAGTTT TTCAAAGAAAT CCCAGGAGTT 240
GATCCTGAAA ACGTGTATTG TGGTCGCCAC TTCAATTATT GACTTTCCAC AGTTACCTTT 300
ACTCTGCTCT TATCCTTGTA CGAAATATA GCAAAGCTTG GAAAGGTCTC CCTCATCTCT 360
ACAGGTTTAA CAATCTGAT TCTTGAATT GTAATGGCAA GGGCAATTTT ACTGGGTCCA 420
CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAGC CCAATGCCAT TCAAGCGTC 480

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GGGGTTAAGT CTTTTCATT TATTGGCAC CATAACTCCT TCTTAGTTTA CAGTTCCTTA 540
GAAGAACCCA CAGTAGCTAA GTGGTCCC GCCTATCCATA TGTCATCGT GATTTCGTGA 600
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GACTTATTG AATATTACTG CAGAAATGAT GACCTGGTAA CATTGGGAAG ATTTTGTAT 720
GGTGTCACTG TCAATTTGAC ATACCCCTATG GAATGCTTTG TGACAAGAGA GGTAAATGCC 780
AATGTGTTTT TTGGTGGGAA TCTTTCATCG GTTTCCACA TTGTGTAAAC AGTGATGGTC 840
ATCACTGTAG CCACGCTTGT GTCATTGCTG ATTGATTGCC TCGGGATAGT TCTAGAATCT 900
AATGGTGTGC TCTGTGCAAC TCCCTTCATT TTTATCATT CATCAGCCTG TTAATCTGAAA 960
CTGTCTGAAG AACCAAGGAC ACACCTCCGAT AAGATTATGT CTGTGTGCAT GCTTCCCAT 1020
GGTGTGCTGG TGATGGTTTT TGGATTGCTG ATGGCTATTA CAAATACTCA AGACTGCACC 1080
CATGGGCAGG AATGTCTTCTA CTGCTTTCCT GACAATTCT CTCTCACAAA TACCTCAGAG 1140
TCTCATGTTC AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200
TAA

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Seq ID NO: 554 Protein sequence
Protein Accession #: Eos sequence

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1 11 21 31 41 51
MGYQRQEPVI PPQPSLVLLI KGGALSGTDT YQSLVNKTFG FPGYLLLSVL QFLYPFIAMI 60
SYNIIAGDTL SKVQRIPIGV DPENVFIGRH PIIGLSTVTF TLPLSLYRNI AKLGKVSLLS 120
TGLTTLILGI VMARISLGP HIPKTEDAWV FAKPNAIQAV GVMSFAPICH HNSFLVYSSL 180
EPTVARWNR LIHMSIVISV PICIFFATCG YLFTGTFTQG DLFPNYCRND DLVTFGRFCY 240
GTVILTYPM BCFVTREVI NVFFGGNLS VFIIVVTVMV ITVATLVSL IDCLGIVLEL 300
NGVLCATPLI FIIPSACYLK LSEEPRTSD KIMSCVMLPI GAVVMVPGFV MAINTNQDCT 360
HGQBMFYCFP DNPSLTNTSE SHVQQTQLS TLNISIFQLE

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Seq ID NO: 555 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1140

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1 11 21 31 41 51
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CCAGGGTATC TGCTCCTCTC TGTTCTTCAG TTTTGTATC CTTTATAGC AATGATAAGT 120
TACAATATAA TAGCTGGAGA TACTTTGAGC AAGATTTTTC AAAGAATCCC AGGAGTTGAT 180
CCTGAAAACG TGTATTATGG TCGCCACTTC ATTATTGGAC TTTCCACAGT TACCTTTACT 240
CTGCCCTTAT CCTGTACCG AATATAGCA AAGCTTGGAA AGGTCTCCCT CATCTCTACA 300
GGTTTAAACA CTCGATTCTT TGGAAATTGA ATGGCAAGGG CAATTTCAT GGTCCACAC 360
ATACCAAAAA CAGAAGAGCG TTGGGTATTT GCAAAGCCCA ATGCCATTCA AGCGGTCCGG 420
GTTATGTCTT TTGCATTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480
GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT 540
ATCTGTATAT TCTTGTCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600
TTATTGAAA ATTACTGCAG AATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660
GTCACGTGCA TTTTGACATA CCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720
GTGTTTTTGG GTGGGAATCT TTCATCGGTT TTCCACATTG TTGTAACAGT GATGGTCATC 780
ACTGTAGCCA CGCTGTGTGC ATTGCTGATT GATTGCTCG GGATAGTTCT AGAACTCAAT 840
GGTGTGCTCT GTGCAACTCC CCTCATTTT ATCATTTCCAT CAGCCTGTGA TCTGAAACTG 900
TCTGAAGAAC CAGGACACA CTCGATAAG ATTATGTCTT GTGTATGCT TCCATTGGT 960
GCTGTGGTGA TGTGTTTTGG ATTGCTCATG GCTATTACAA ATACTCAAGA CTGCAACCAT 1020
GGGCAGGAAA TGTCTACTG CTTTCTGAC AATTCTCTC TCACAAATAC CTCAGAGTCT 1080
CATGTTTACG AGACACACA ACTTCTACT TTAAATATTA GTATCTTTCA ACTGAGTAA

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55
Seq ID NO: 556 Protein sequence
Protein Accession #: Eos sequence

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1 11 21 31 41 51
MGYQRQEPVI PPQVNTKTFG PGYLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIPIGV 60
PENVPFIGRH IIGLSTVTFP LPLSLYRNI KLKGVSLIST GLTTLILGIV MARAISLGP 120
IPKTEDAWVF AKPNAIQAVG VMSFAPICH NSFLVYSSLE EPTVARWNR LIHMSIVISV 180
ICIFFATCGY LFTGTFTQG LFPNYCRND LVTFGRFCY VTIIVTYPME CFVTREVIAN 240
VFFGGNLSV FHIIVVTVMV TVATLVSLI DCLGIVLEIN GVLCAATPLI IIPSACYLKL 300
SEEPRTSDK IMSCVMLPI AVVMVPGFVM AINTNQDCTH GQEMPYCFPD NFSLNTSES 360
HVQQTQLST LNISIFQLE

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Seq ID NO: 557 DNA sequence
Nucleic Acid Accession #: XM_057188.1
Coding sequence: 769..4269

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1 11 21 31 41 51
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CTCCCCAAG TCTGTGTCCC TCTCTCTCCC CTAATCTCT GGCCTCTCT TCTGAGTTC 120
CTGCCCTCC CCAATTTCTT TGGTTTTTGC ATCCCCCTCT GCCCTTGGC TCAGTCAAGT 180
CTCCCCGTG TGTCTCTCTC CCCCCGCCCC GGACCTCTGC ACCCCCCAGG TCGTGTCCC 240
TCTGTCCCC TATGGGGGCC TGGGACCGC CTTCTCCCCG CCTCCCGCTT TGGGTCTCC 300
AAGACTCCCC GCCCCCAGA CCTCGCCCCG CCCAGGCTA GGCTGGAAAG TGGAGGATCC 360
GGTTTGCTCT GGGCGGCTCT GGAAGCAGAG CCGCGGAGG GAGCGCCGG GCGCTGGCT 420
GCAGGAGGTT GCGCGGCGG CGGCAGCATG GTGGTCCGG AGAAGGAGCA GAGCTGGATC 480
CCCAAGATCT TCAAGAAGAA GACCTGCACG AGTTTCATAG TTGACTCCAC AGATCCGGGG 540
GATGGGGTCT CGCTCTATTG CCGAGGCTGT TCTCAAACCT CTGGGCTCAA GCAGTCTTTC 600
TGCTTTGACC TCCCAAGATG CTGGATTGT GCCCAGCGT CTTGAAGTT TTGCTCAGAA 660
GAGCAAACTT TCTGGGAAGT AGCTGCAGGT GTTGGAAAGT GCTGCAGGG AACTAGGGGA 720

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5	TTCAAGGATG	GAGCTGAAAT	GGGTGAACGG	ACAAAGTCGG	TAAACTGAAT	GGAGGATGCC	780
	TTCGGGGCAG	CCGTGGTGAC	CGTGTGGGAC	AGCGATGCAC	ACACCAAGCA	GAAGCCACCC	840
	GATGCTTACG	GAGAGCTGGA	CTTCAAGGGG	GCCGGCCGCA	AGCACAGCAA	TTTCTCTCGG	900
	CTCTCTGACC	GAACGGATCC	AGCTGCAGTT	TATAGTCTCG	TCACACGCAC	ATGGGGCTTC	960
	CGTGCCCGGA	ACCTGGTGGT	GTCAGTGCCT	GGGGGATCGG	GGGGCCCCGT	CCTCCAGACC	1020
	TGCTGTCAGG	ACCTGCTGCG	TCGTGGGCTG	GTGCGGGCTG	CCCAGAGCAC	AGGAGCCTCG	1080
	ATTGTCACTG	GGGGTCTGCA	CACGGGCATC	GGCGGGCATG	TTGGTGTGGC	TGTACGGGAC	1140
	CATCAGATGG	CCAGCACTGG	GGGCAACCAAG	GTGGTGCCCA	TGGGTGTGGC	CCCCTGGGGT	1200
	GTGGTTCGGA	ATAGAGACAC	CCTCATCAAC	CCCAAGGGCT	CGTTCCCTGC	GAGGTACCGG	1260
10	TGGCGCGGTG	ACCCGAGGGA	CGGGGTCCAG	TTTCCCCTGG	ACTACAATA	CTCGCCCTTC	1320
	TTCTCTGGTG	ACGACGGCAC	ACACGGCTGC	CTGGGGGGCG	AGAACCGCTT	CGCTTTCGCG	1380
	CTGGAGTCTC	ACATCTCACA	GCAGAAGACG	GGCGTGGGAG	GGACTGGAAT	TGACATCCCT	1440
	GTCTGTCTCC	TCTGTATTGA	TGGTGATGAG	AAGATGTTGA	CGCGAATAGA	GAACGCCACC	1500
	CAGGCTCAGC	TCCCATGTCT	CCTCGTGGCT	GGCTCAGGGG	GAGCTGCGGA	CTGGCTGGCG	1560
15	GAGACCCCTG	AAGACACTCT	GGCCCCAGGG	AGTGGGGGAG	CCAGGCAAGG	CGAAGCCCGA	1620
	GATCGAATCA	GGCGTTTCTT	TCCCAAGGGG	GACCTTGAGG	TCTTGACAGC	CCAGGTGGAG	1680
	AGGATTTCTG	CCCGAAGGGA	GCTCTGACA	GTCTATTCTT	CTGAGGATGG	GTCTGAGGAA	1740
	TTGAGAGCCA	TAGTTTTGAA	GGCCCTTGTG	AAGGCTGTGT	GGAGCTCGGA	GGCCTCAGCC	1800
	TACCTTGGATG	AGCTGCGTTC	GGCTGTGGCT	TGGAACCGCG	TGGACATTGC	CCAGAGTGAA	1860
20	CTCTTTCCGG	GGGACATCCA	ATGGCGGTCC	TTCCATCTCG	AAGCTTCCCT	CATGGAAGCC	1920
	CTGCTGAATG	ACCGGCTGGA	GTTCGTGCGC	TTGCTCATTT	CCCAAGGGCT	CAGCCTGGGG	1980
	CACCTCTGTA	CCCGGATGCG	CCTGGCCCAA	CTCTACAGCG	CGGCGCCCTC	CAACTCGCTC	2040
	ATCGGCAACC	TTTTGGACCA	GGCGTCCAC	AGCGCAGGCA	CCAAAGCCCC	AGCCCTAAAA	2100
	GGGGGAGCTG	CGGAGCTCCG	GCCTCTGAC	GTGGGGCATG	TGCTGAGGAT	GCTGCTGGGG	2160
25	AAGATGTGCG	CGCCGAGGTA	CCCTTCCGGG	GGCGCTGGG	ACCCCTCACC	AGGCCAGGGC	2220
	TTGCGGGAGA	GCATGTATCT	GCTCTGGGAC	AAGGCCACCT	CGCGCTCTCT	GCTGGATGCT	2280
	GGCTCTGGGC	AGGCCCCCTG	GAGCGACCTG	CTTCTTTGGG	CATGTTTGCT	GAACAGGGCA	2340
	CAGATGGCCA	TGTACTTCTG	GGAGATGGGT	TCCAATGCAG	TTTCTCTCAG	TCTTGGGGCC	2400
	TGTTTGTCTG	TCCGGGTGAT	GGCAGCCCTG	GAGCCTGACG	CTGAGGAGGC	AGCACGGAGG	2460
30	AAAGACCTGG	CGTTCAAGTT	TGAGGGGATG	GGCGTTGACC	TCTTTGGCGA	GTGCTATCGC	2520
	AGCAGTGGAG	TGAGGGCTGC	CCGCTCTCTC	CTCCGTGCTG	GCCCGCTCTG	GGGGGATGCC	2580
	ACTTGCTCC	AGCTGGCCAT	GCAAGCTGAC	GCCCGTCCCT	TCTTTGCCCA	GGATGGGGTA	2640
	CAGTCTCTGC	TGACACAGAA	GTGGTGGGGA	GATATGGCCA	GCATACACCC	CATCTGGGCC	2700
	CTGGTTCTCG	CCTTCTTTTG	CCCTCCACTC	ATCTACACCC	GCCTCATCAC	CTTCAGGAAA	2760
35	TCAGAAGAGG	AGCCACACAG	GGAGGAGCTA	GAGTTTGACA	TGATAGTGTG	CATTATGGG	2820
	GAAGGGCCTG	TGCGGAGCGC	GGACCCAGCC	GAGAAGACGC	CGCTGGGGGT	CCCGCGCCAG	2880
	TGCGGCGCTG	GGGTGTGCTG	CGGGGGCCGC	TGCGGGGGCG	GCCGGTCCCT	ACGCGCTGG	2940
	TTCCACTTCT	GGGCGCGGCC	GGTGACCATC	TTTATGGGCA	ACGTGGTTCG	CTACTGCTG	3000
	TTCTGTCTGC	TTTCTCGCGG	GGTGCTGCTC	GTGGATTTC	AGCCGGCGCC	GCCCGGCTCC	3060
40	CTGGAGCTGC	TGCTCTATTT	CTGGGCTTTC	ACGCTGCTGT	GCGAGGAAC	GCGCCAGGGC	3120
	CTGAGCGGAG	GCGGGGGCAG	CCTCGCCAGC	GGGGGCCCGG	GGCTGGGCA	TGCTCTACTG	3180
	AGCCCGCTGC	TGCGCTCTTA	CCTCGCCGAC	AGCTGGAACC	AGTGGGACCT	AGTGGCTCTC	3240
	ACCTGCTTCC	TCTGGGGCT	GGGTGCGCG	CTGACCCCGG	GTTTGTACCA	CCTGGGCCGC	3300
45	ACTGTCTCT	GCATGCACT	CATGGTTTTT	ACGGTGCGGC	TGCTTCACT	CTTCAAGGTC	3360
	AAACAAACAG	TGGGGCCCAA	GATCGTATC	GTGAGCAAGA	TGATGAAGGA	CGTGTCTTTC	3420
	TTCTCTCTCT	TCTCGGGCT	GTGGCTGGTA	GCCTATGGGG	TGGCCACGGA	GGGGCTCTCT	3480
	AGGCCACGGG	ACAGTGAATT	CCCAAGTATC	CTGGCGCGCG	TCTTCTACCG	TCCCTACCTG	3540
	CAGATCTTCG	GGCAGATTCC	CCAGGAGGAC	ATGGAGCTGG	CCCTCATGGA	GCACAGCAAC	3600
50	TGCTCGTGGG	AGCCCGGCTT	CTGGGCACAC	CCTCTGGGG	CCAGGCGGGG	CACCTGGGTC	3660
	TCCCAATATG	CCAACTGGCT	GGTGGTGGTG	CTCTCGTCA	TCTTCTGCT	CGTGCCCAAC	3720
	ATCCTGTGGG	TCAACTTGCT	CATTGCCATG	TTTCAATTCA	CATTGGGCAA	AGTACAGGGC	3780
	AAACAGGATG	TCTACTGGAA	GGGCGAGCGT	TACCGCTCA	TCCGGGAATT	CCACTCTGGG	3840
	CCCGCGCTGG	CCCGGCCCTT	TATCGTATC	TCCCACTTGC	GCCTCTGCT	CAGGCAATTG	3900
55	TGCAGGGCAG	CCCGGAGCCC	CCAGCGCTCC	TCCCGGGCCC	TGAGGCAATT	CCGGGTTTAC	3960
	CTTTCTAAGG	AAGCCGAGCG	GAAGCTGCTA	ACGTGGGAAT	CGGTGCATAA	GGAGAACTTT	4020
	CTGCTGGCAC	GCGCTAGGGA	CAAGCGGGAG	AGCGACTCCG	AGCGTCTGAA	GGCAGCTTCC	4080
	CAGAAGGTGG	ACTTGGCACT	GAACAGCTG	GGACACATCC	GCGAGTACGA	ACAGCGCTGG	4140
	AAAGTGTCTG	AGCGGGAGGT	CCAGCAGTGT	AGCCCGCTCC	TGGGGTGGGT	GGCCGAGGGC	4200
60	CTGAGCGCT	CTGCTTGTCT	GCCCCAGGT	GGGCGGCCAC	CCCTGAGCT	GCCTGGGTCC	4260
	AAAGACTGAG	CCCTGTCTGC	GGACTTCAAG	GAGAAGCCCC	CACAGGGGAT	TTTGTCTCTA	4320
	GAGTAAGGCT	CATCTGGGCC	TGCGCCCCCG	CACCTGGTGG	CCTTGTCTCT	GAGGTGAGCC	4380
	CCATGTCCAT	CTGGGCCACT	GTGAGGACCA	CCTTGGGGAG	TGTATCTCCT	ACAAACCACA	4440
	GCATGCCCGG	CTCTCCCAAG	AACCACTCCC	AGCCTGGGAG	GATCAAGGCC	TGGATCCCGG	4500
65	GCCGTATATC	ATCTGAGGCG	TGCAGGGTCC	TTGGGGTAAC	AGGGACCACA	GACCCCTCAC	4560
	CATCAACAGA	TTCTCTCACAC	TGGGGAATA	AAGCCATTTC	AGAGGAAAAA	AAAAAAAAAA	4620
	AAAAAAAAAA	AAAAAAAAAA	A				

Seq ID NO: 558 Protein sequence
Protein Accession #: XP_057188.1

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	MEDAFGAAVV	TVWDSDAHTT	EKPTDAYGEL	DFTGAGRKHS	NFLRLSDRTD	PAAYVSLVTR	60
	TWGFAPNLV	VSVLGGSGGP	VLQTNLQDLL	RRGLVRAAQS	TGAVITVGGI	HTGIGRHVGV	120
75	AVRDHMAST	GGTKVVMVGV	APWGVVNRD	TLINPKGSFP	ARYRWGDPE	DGVQFPLDYN	180
	YSAPFLVDG	THGCLGGENR	FRRLLESYIS	QKQTVGGTGG	IDIPVLLLLL	DGDEKMLTRI	240
	ENATQAQLPC	LLVAGSGGAA	DCLAETLEDT	LAPGSGGARQ	GEARDRIIRF	FPKGDLEVLQ	300
	AQVERIMTRK	ELLTVYSSSD	GSEEFETIVL	KALVKACGSS	EASAYLDELK	LAVAMNRVDI	360
	AQSELRFDI	QWRSFHLEAS	LMDALLNDP	EPVRLLIHSG	LSLGHFLTPM	RLAQLYSAP	420
80							
	SNSLIRNLID	QASHAGTKA	PALKGGAAEL	RPPDVGHVLR	MLLGRMCAPR	YPSGGWDPH	480
	PGQGFESMY	LLSDKATSP	SLDAGLQAP	WSDLLWALL	LNRAQMAMYF	WEMGSNAVSS	540
	ALGACILLRV	MARLEPDARE	AARRKDLAPK	FEKMGVDLFG	ECYRSSEVRA	ARLLLRRCPL	600
	WGDATCLQLA	MQADARAPFA	QDGVQSLLTQ	KWMDMASTT	PIWALVLAPF	CPFLIYTRLI	660
	TFKRSSEPT	REBLEPDMDS	VINGSGPVGT	ADPAEKTPLG	VPRQSGRPGC	CGRCGGRRC	720

5 LRRWFHFWGA PVTIFMGNVV SYLLFLLLFPS RVLLVDFQPA PPGSLELLLY FWAFTLLCBE 780
 LRQGLSGGGG SLASGGPGPG HASLSQRLRL YLADSWNQCD LVALTCFLLG VGCRLTPGLY 840
 HLGRTVLICD FMVFTVRLHL IPTVNRQLQF KIVIVSKQMK DVFFPLFFLG VWLVAYGVAT 900
 EGLLRPRDSF PPSILRRVYF RPYLQIFGQI PQEDMDVALM EHSNCSSEPG FWAHPPGAQA 960
 GTCVSQYANW LVVLLLVIFL LVANILVNL LIAMFSYTFG KVQNSDLWY KAQRYRLIRE 1020
 FHSRPAALFP FIVISHRLRL LRQLCRRPRS POPSSPALEH FRVYLSKEAE RKLLTWESVH 1080
 KENFLIARAR DKRESDESRL KRTSQKVDLA LKQLGHIREY EQRLKVLERE VQCSRVLGW 1140
 VAEALSRSAI LPPGGPPPPD LPGSKD

10 Seq ID NO: 559 DNA sequence
 Nucleic Acid Accession #: NM_006853.1
 Coding sequence: 26..874

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 CATGAGGATT CTGCAGTTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGGAGAGAC 180
 20 CAGGATCATC AAGGGGTTCG AGTGCAAGCC TCACTCCCAG CCTGGCAGG CAGCCCTGTT 240
 CGAGAAGACG CGGCTACTCT GTGGGGCGAC GCTCATCGCC CCCAGATGGC TCTGACAGC 300
 AGCCCACTGC CTCAGGCCCC GCTACATAGT TCACCTGGGG CAGCACAAAC TCCAGAAGGA 360
 GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCCTTC CCCACCCCG GCTTCAACAA 420
 CAGCCCTCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATCGCCAGT 480
 25 CTCCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCCTCA CGCTGTGTCA CTGCTGGCAC 540
 CAGCTGCCTC ATTTCGGGCT GGGGCGAGAC GTCCAGCCCC CAGTTACGCC TGCCCTCACAC 600
 CTGCGATGC GCCAACATCA CCATCATTGA GCACCAAGAG TGTGAGAAGC CCTACCCCGG 660
 CAACATCACA GACACCATGG TGTGTGCCAG CCGCAGGAA GGGGGCAAGG ACTCTGCCA 720
 GGGTGACTCC GGGGGCCCTC TGGTCTGTAA CCAGTCTCTT CAAGGCATTA TCTCTGGGG 780
 30 CCAGGATCCG TGTGCGATCA CCGGAAAGCC TGGTGTCTAC ACGAAAGTGT GCAAAATATGT 840
 GGACTGGATC CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC 900
 35 ACCCTCATTG TCCACTTGGT GTTTGGTTCC TGTTCACCTT GTTAATAAGA AACCTAAGC 960
 CAAGACCTCT TACGAACATT CTTTGGGCTT CCGGACTTAC AGGAGATGCT GTCACTTAAT 1020
 AATCAACCTG GGGTTCGAAA TCAGTGAGAC CTGGATTCAA ATTCTGCCCT GAAATATTGT 1080
 GACTCTGGGA ATGACAAACAC CTGGTTTGTG CTCTGTGTGA TCCCAGGCC CAAAGACAGC 1140
 TCCTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG

Seq ID NO: 560 Protein sequence
 Protein Accession #: NP_006844.1

40 1 11 21 31 41 51
 MRILQLILLA LATGLVGGET RIIKGFECKP HSQPHQAALF EKTRILLOGAT LIAPRWLLTA 60
 AHCLRPRIYV HLGQHNQKE EGCEQTRTAT ESFPHPGFNN SLFNKDHNRD IMLVKMASPV 120
 45 SITNAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIE HQKCNAYPG 180
 NITDTMVCAS VQEGGKDSQD GDSGGPLVCN QSLQGIISWG QDPCAITRKP GVYTKVCKYV 240
 DWIQBTMKNN

50 Seq ID NO: 561 DNA sequence
 Nucleic Acid Accession #: AY046419.1
 Coding sequence: 1..1743

55 1 11 21 31 41 51
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 GAGCAGAGAA TGGTTGTGAG CTCCTCGTTC ATTGGAGCCC TCCTTGCCCT ACTCACCGGA 180
 GGGGTCTCGA TAGACAGATA TGAAGAAGG ACAGCAATCA TCTTGTCTAT CTGCTGCTT 240
 60 GGACTCGGAA GCTTAGTCTT GATCCTCAGT TTATCTTACA CGGTTCTTAT AGTGGGACGC 300
 ATTGCCATAG GGGTTTCCAT CTCCCTCTCT TCCATTGCCA CTGTGTGTTA CATCGCAGAG 360
 ATTGTCTCTC AACACAGAAG AGGCCTTCTT GTGTCACTGA ATGAGCTGAT GATTGTCTATC 420
 GGCATTCTTT CTGCCATATAT TTCAAATTAC GCATTTGCCA ATGTTTTCOA TGGCTGGAAG 480
 TACATGTTTG GTCTGTGTAT TCCTTGGA GTTTGTCAAG CAATTGCAAT GTATTTTCTT 540
 CCTCCAAGCC CTCGTTTCTT GGTGATGAAA GGACAAGAGG GAGCTGCTAG CAAGGTTCTT 600
 65 GGAAGTTTAA GAGCACTCTC AGATACAAC T GAGGAACTCA CTGTGATCAA ATCCTCCCTG 660
 AAAGATGAAT ATCAGTACAG TTTTGGGAT CTGTTTCGTT CAAAGACAAA CATGCGGACC 720
 CGAATAATGA TAGGACTAAC ACTAGTATTT TTTGTACAAA TCACTGGCCA ACCAAACATA 780
 TTGTTCTATG CATCAACTGT TTTGAAGTCA GTTGGATTTC AAAGCAATGA GGCAGCTAGC 840
 CTCGCTCCA CTGGGTTTGG AGTCGTCAAG GTCAATTAGCA CCATCCCTGC CACTCTTCTT 900
 70 GTAGACCATG TCGGCAGCAA AACATTCCCT TGCAATTGGCT CCTCTGTGAT GGCAGCTTCG 960
 TTGGTGACCA TGGGCATCGT AAATCTCAAC ATCCACATGA ACTTCACCCA TATCTGAGA 1020
 AGCCACAATT CTATCAACCA GTCTTGGAT GAGTCTGTGA TTTATGGACC AGGAAACCTG 1080
 TCAACCAACA ACAATACTCT CAGAGACCAC TTCAAAGGGA TTTCTTCCCA TAGCAGAAGC 1140
 TCACTCATGC CCTCGAGAAA TGATGTGGAT AAGAGAGGGG AGAGGACCTC AGCATCCTTG 1200
 75 CTAAATGCTG GATTAAAGCCA CACTGAATAC CAGATAGTCA CAGACCTCGG GGAAGTCCCA 1260
 GCTTTTTTGA AATGGCTGTG CTTAGCCAGC TTGCTTGTAT ATGTTGCTGC TTTTTCAAAT 1320
 GGTCTAGGAC CAATGCCCTG GCTGGTCTC AGCGAGATCT TTCCTGGTGG GATCAGAGGA 1380
 CGAGCCATGG CTTTAACTTC TAGCATGAAC TGGGGCATCA ATCTCCTCAT CTCGCTGACA 1440
 80 TTTTGTAGCT TAACGTATCT TATTGGCCTG CCATGGGTGT GCTTTATATA TACAATCATG 1500
 AGTCTAGACT CCTGCTCTTT TGTGTATG TTTATACCTG AGACAAAGGG ATGCTCTTTG 1560
 GAACAAATAT CAATGGAGCT AGCAAAAGTG AACTATGTGA AAAACACAT TTTTATTATG 1620
 AGTCACTACC AAGAGAATTT AGTGCCAAA CAGCCTCAA AAAGAAACCC CCAGGAGCAG 1680
 CTCTGGAGT GTAACAAGCT GTGTGTAGG GGCACATCCA GGCAGCTTTC TCCAGAGACC 1740
 TAA

Seq ID NO: 562 Protein sequence
Protein Accession #: AAL02327.1

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5      1      11      21      31      41      51
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GVLIDRYGRR TAILSSCLL GLGSLVLILS LSYTVLIVGR IAIGVSISLS SIATCVYIAE 120
IAPQERRGLL VSLNELMIVI GILSAYISNY AFANVPHGWK YMFGLVIPLG VLQALAMYFL 180
PPSPRFLVMK QGEGAAASKVL GRRLALSDDT BELTVIKSSL KDEYQYSFWD LFRSKDNMRT 240
10    RIMIGLTLVF FVOITGQFNI LFYASTVLKS VGFQSNAAAS LASTGVGVVK VISTIPATLL 300
VDHVGSKTFL CIGSSVMAAS LVTMGIVNLN IHMFTHICR SHNSINQSLD ESVIYGPNGL 360
STNNNTLRDH FRGIBSSHSRS SLMPLRNDVD KRGETTSASL LNAGLSHTEY QIVTDPGDVP 420
AFLKMSLAS LLVYVAAPSI GLGPMPLVLV SEIPFGGIRG RAMALTSMMN WGINLLISLT 480
15    FLTVTDLIGL PWCFYITIM SLASLLFVVM FIPETKGCSL EQISMELAKV NYVKNNICPM 540
SHRQEELVPK QPQKRKPQEQ LLECNKLCGR GQSRQLSPET

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Seq ID NO: 563 DNA sequence
Nucleic Acid Accession #: XM_059466.1
Coding sequence: 1..894

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20      1      11      21      31      41      51
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CTGCTCTGTC CGGCCATCTT CACCGACCAC TGGTACGAGA CGACCCCGCG GCGCCACAAG 120
25    GAGAGCTGGC AGCGCAGCCG CGCGGGGCGC GACCCCCCGG ACCAGAAGAA CGGCCTGATG 180
CCGCTGTGCG ACCTGCGGCT CGCGGACTCG CCCCCGCTGG GCGCGCGGCT GCTCCCGGGC 240
GGCCCGGGGG GCGCGGACCC CGAGTCTCTG CGCTCGCTCC TGGGGCTCGG CGGGCTGGAC 300
GCCGAGTGGC GCGCGCCCTT CTTGCGCAAC TACTCGGGCC TCTGGAGGAA GTGCTACTTC 360
CTGGGCTACG ACCGGGACAT CGACACCCCT ATCCTGAAAG GTATTGCGCA GCGATGCACG 420
30    GCCATCAAGT ACCACTTTTC TCAGCCCATC CGCTTGGGAA ACATTCTCTT TAATTAAACC 480
AAGACCATAC AGCAAGATGA GTGGCACCTG CTTCAATTAA GAAGAATCAC TGTCTGGCTC 540
CTCGGCTATG CCGTAGCCGT CCTTCTCTGC GGCTGCATTG TGGCCACAGT CAGTTTCTTC 600
TGGGAGGAGA GCTTGACCCA GCACGTGSGT GGACTCTCTG TCCTCATGAC AGGGATATT 660
35    TGCACCATTT CCTCTGTAC TTATGCCGCC AGTATCTCGT ATGATTGAA CCGGCTCCCA 720
AAGCTAATTT ATAGCTGCCC TGCTGATGTG GAACATGGTT ACAGCTGGTC CATCTTTTGC 780
GCCTGGTGCA GTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATCGC TTATCCGTTT 840
ATTAGCCGGA CCAAGATTGC ACAGCTAAAG TCTGGCAGAG ACTCCACGGT ATGA

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Seq ID NO: 564 Protein sequence
Protein Accession #: XP_059466.1

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40      1      11      21      31      41      51
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45    PLSHLPLRDS PPLGRLLPLG GPGRADPESW RSLGLGLGLD AEGRLPLFAT YSGLWRKCYF 120
LGIDRDLDTL ILKGLIAQRCT AIKYHFSQPI RLNRNIPNLT KTIQDEWHL LHLRRITAGF 180
LGMNAVVLIC GCIVATVSFF WEESLTQHVA GLLFLMTGIF CTISLCTYAA SISYDLNRLP 240
KLIYSLPADV EHGYSWSIFC AWCSLGFIVA AGGLCIAYPF ISRTKIAQLK SGRDSTV

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Seq ID NO: 565 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..3315

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ACCCGAGACC TGTACTCCAG CGCGTCTCGG AGCAGAGACT TGTCTTACAG TGAAGCGAC 120
TTGGTGAATT TTATTCAAGC AAATTTTAAG AAACAGAAAT GTGTCTTCTT TACCAAGAT 180
TCCAAGGCCA CGGAGAATGT GTGCAAGTGT GGCTATGCCG AGAGCCAGCA CATGGAAGGC 240
60    ACCCAGATCA ACCAAAGTGA GAAATGGAAC TACAAGAAC ACACCAAGGA ATTTCTTACC 300
GAGCGCTTTC GGGATATTCA GTTTGAGACA CTGGGAAGA AAGGGAAGTA TATACGTCTG 360
TCTTGGGACA CGGACGCGGA AATCCTTTAC GAGCTGCTGA CCCAGCACTG GCACCTGAAA 420
ACACCCACCC TGGTCATTTC TGTGACCGGG GCGGCCAAGA ACTTGCCTCT GAAGCCGCGC 480
ATGCGCAAGA TCTTCAGCCG GCTCATCTAC ATCGCGCAGT CCAAGGTTGC TTGGATTCTC 540
65    ACGGAGGCA CCCATTATGG CCTGATGAAG TACATCGGGG AGGTGGTGAG AGATAACACC 600
ATCAGCAGGA GTTCAGAGGA GAATATTGTG GCCATTGGCA TAGCAGCTTG GGCATGCTC 660
TCCAACCGGG ACACCTCAT CAGGAATTGC GATGCTGAGG GCTATTTTTT AGCCAGTAC 720
CTTATGGATG ACTTCAAGAG AGATCCACTG TATATCTTGG ACAACCAACA CACACATTG 780
70    CTGCTCGTGG ACAAATGGCTG TCATGGACAT CCCACTGTG AAGCAAAGCT CCGGAATCAG 840
CTAGAGAAGT ATATCTCTGA GCGCACTATT CAAGATTCCA ACTATGGTGG CAAGATCCCC 900
ATTGTGTGTT TTGCCCAAGG AGGTGGAATA GAGACTTTGA AAGCCATCAA TACCTCCATC 960
AAAAATAAAA TTCTTGTGTT GGTGGTGGAA GGCTCGGGCC AGATCGCTGA TGTGATCGCT 1020
AGCCTGTGTT AGGTGGAAGA TGCCCTGACA TCTTCTGCCG TCAAGGAGAA GATGATCGCT 1080
75    TTTTATCCCC GCACGCTGTC CCGGCTGCCT GAGGAGGAGA CTGAGAGTTG GATCAAATGG 1140
CTCAAGAAA TTCTGGAATG TTCTCACTTA TTAACAGTTA TTAAGATGGA AGAAGCTGGG 1200
GATGAAATTT TGAGCAATGC CATCTCTTAC GCTCTATACA AAGCCTTCAG CACCACTGAG 1260
CAAGACAAGG ATAACCTGAA TGGGCACTG AAGCTTCTGC TGGAGTGAA CCAGCTGGAC 1320
TTAGCCAATG ATGAGATTTT CACCAATGAC CGCGATGGG AGTCTGCTGA CCTTCAGAA 1380
80    GTCATGTTTA CGSCTCTCAT AAAGGACAGA CCAAGTTTG TCCGCTCTT TCTGGAGAT 1440
GGCTTGAACC TACGGAAGTT TCTACCCAT GATGTCTTCA CTGAACCTT CTCCAACCAC 1500
CTCAGCTTTG TCTGGAAACT GOTTGCGAAC TTCCGAAGAG GCTTCCGGA GGAAGACAGA 1560
AATGGCCGGG ACGAGATGGA CATAGAACTC CACGACGTGT CTCTTATTC TCGCACCC 1620
CTGCAAGCTC TCTTCACTG GGCATTCTT CAGATAAGA AGGAACCTC CAAAGTCATT 1740

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5 TGGGAGCAGA CCAGGGGCTG CACTCTGGCA GCCCTGGGAG CCAGCAAGCT TCTGAAGACT 1800
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 TACGAGACCC GGGCTGTGGA GCTGTTCACT GAGTGTATCA GCAGCGATGA AGACTTGGCA 1920
 GAACAGCTGC TGGTCTATTG CTGTGAAGCT TGGGGTGGAA GCAACTGTCT GGAGCTGGCG 1980
 GTGGAGGCCA CAGACCAGCA TTTCATCGCC CAGCCTGGGG TCCAGAATTT TCTTTCTAAG 2040
 CAATGGTATG GAGAGATTTC CCGAGACACC AAGAACTGGA AGATTATCCT GTGCTGTGTT 2100
 ATTATACCTT TGGTGGGCTG TGGCTTTGTA TCATTTAGGA AGAAAACCTG CGACAAGCAC 2160
 AAGAAGCTGC TTGGTACTA TGTGGCGTTC TTCACTCCCT CCTTCGTGGT CTTCTCCTGG 2220
 10 AATGTGGTCT TCTACATCGC CTTCCTCCTG CTGTTTGCCT ACGTGTGCT CATGGATTTC 2280
 CATTGCTGTC CACACCCCCC CGAGCTGGTC CTGTAAGTGC TGGTCTTTGT CCTCTTCTGT 2340
 GATGAAGTGA GACAGTGGTA CGTAAATGGG GTGAATTATT TTAAGTACCT GTGGAATGTG 2400
 ATGGACACGC TGGGGCTTTT TTACTTCATA GCAGGAATTG TATTTCGGCT CCACCTCTCT 2460
 AATAAAAGCT CTTTGTATTG TGAACGATC ATTTTCTGTC TGGACTACAT TATTTTCACT 2520
 15 CTAAGATTGA TCCACATTTT TACTGTAAAG AGAAACTTAG GACCCAAGAT TATAATGCTG 2580
 CAGAGGATGC TGATCGATGT GTTCTTCTTC CTGTTCTCTT TTGCGGTGTG GATGGTGGCC 2640
 TTGCGGTGCG CCAGGCAAGG GATCCTTAGG CAGAATGAGC AGCGCTGGAG GTGGATATTC 2700
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30 Seq ID NO: 566 Protein sequence
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 Nucleic Acid Accession #: NM_006911.1
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75 Seq ID NO: 568 Protein sequence
 Protein Accession #: NP_008842.1

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 NTAAGVAVVL QDWLSYWAN KQSMNLVTN GGNVTEKLD LNWYLGIIYS LTVAIVLFGI 780
 ARSLVFFVVL VNSSQTLHNK MFESILKAPV LFFDRNPGR ILNRFSKDIG HLLDLLPLTF 840
 LDFIQTLLQV VGVVSVAVAV IPWIAIPVLP LGIIFIFLRR YPLETSRDRV RLESTRSPV 900
 FSHLSSSLQG LWIRAYKAE ERCQELFDAH QDLHSEAWFL FLTTSRFAV RLDAICAMFV 960
 IIVAFGLSLL AKTLIDAGVQ LALSALYALTM GMPQWCVRQS AEVENMMISV ERVIEYTDLE 1020
 KEAPWEYQKR PPPAWPHEGV IIFDNVNFMY SPGGPLVLKH LTALIKSQEK VGIVGRTGAG 1080
 KSSLISALFR LSEPEKIKWI DKILITBEIGL HDLRKMSII PQSFVLFTGT MRKNLDPFKE 1140
 HTDEELWNL QEVQLKETIE DLPKMDTEL AESGSNFSVG QRQLVCLARA ILRKNQILII 1200
 DEATANVDPR TDELIQKKIR EKFAHCTVLT IAHRLNTIID SDKIMVLD SG RLKEYDEPYV 1260
 LLQNKESLFY KMVQQLGKAE AAALTETAKV VYFKRNYPHI GHTDHMTNT SNGQSPSTLTI 1320
 FETAL

Seq ID NO: 573 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1365

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 TTGTGCAAAAT CCTTGACCAT TCGACTTATT AGATGCGGCT ATCATGTGGT CATAGGAAGT 180
 AGAAATCTCA AGTTTGCTTC TGAATTTTTT CCTCATGTGG TAGATGTGAC TCATCATGAA 240
 GAGTCTCTCA CAAAAACAAA TATAATATTT GTTGCTATAC ACAGAGAACA TTACACCTCC 300
 CTGTGGGACC TGAGACATCT GCTTGTGGGT AAAATCCTGA TTGATGTGAG CAATAACATG 360
 AGGATAAACC AGTACCCAGA ATCCAATGCT GAATATTTGG CTTTATTATT CCCGATTCT 420
 TTGATTGTCA AAGGATTTAA TGTGTCTCA GCTTGGGCAC TTCAGTTAGG ACCTAAGGAT 480
 GCCAGCCGGC AGGTTTATAT ATGCAGCAAC AATATTCAAG CGCGACAACA GGTATTGAA 540
 CTTCGCCGCC AGTTGAATTT CATTCCCAIT GACTTGGGAT CCTTATCATC AGCCAGAGAG 600
 ATTGAAATTT TACCCCTAGC ACTCTTACT CTCTGGAGAG GGCAGTGGT GGTAGCTATA 660
 AGCTTGGCCA CATTTTTTTT CCTTTATTC TTTGTGAGAG ATGTGATTCA TCCATATGCT 720
 AGAAACCAAC AGAGTGACTT TTACAAAATT CCTATAGAGA TTGTGAATAA AACCTTACCT 780
 ATAGTTGCCA TTACTTATCT CTCCTAGTA TACCTGCGAG GTCTTCGCGC AGCTGCTTAT 840
 CAACCTTATT ACGGACCCAA GTATAGGAGA TTTCCACCTT GGTGGAACAC TGGTTACAG 900
 TGTAGAAAC AGCTTGGATT ACTAAGTTT TTCTTGCTGA TGGTCCATGT TGCCTACAGC 960
 CTCTGCTTAC CGATGAGAAG GTCAGAGAGA TATTGTTC TCAACATGGC TTATCAGCAG 1020
 GTTCATGCAA ATATTGAAAA CTCTTGAAT GAGGAAGAAG TTTGGAGAAT TGAATGTAT 1080
 ATCTCCTTTG GCATAATGAG CCTTGGCTTA CTCTCCCTCC TGGCAGTCAC TTTCTATCCCT 1140
 TCAGTGAGCA ATGCTTTAAA CTGGAGAGAA TTCAGTTTAA TTCAGTCTAC ACTTGGATAT 1200
 GTCGCTCTGC TCATAAGTAC TTCCATGTT TTAATTTATG GATGGAACAG AGCTTTTGAG 1260
 GAAGAGTACT ACAGATTTTA TACACCACA AACTTGTTC TTGCTCTGT TTTGCCCTCA 1320
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Seq ID NO: 574 Protein sequence
 Protein Accession #: Eos sequence

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1 11 21 31 41 51
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 RINQYFESNA EYLAFLPDS LIVKGFNVVS ANAQLGFKD ASRQVYICSN NIQARQQVIE 180
 LARQLNFIPI DLGSLSSARE IENLPLRLFT LWRGFPVVVAI SLATFFFLYS FVRDVHFLY 240
 RNQSDPYKI PIEIVNKTLP IVAITLLSLV YLAGLLAAAY QLYYGTKYRR FPPWLETWLQ 300
 CRKQLGLLSF FPMVHVAYS LCLPMRRSER YLEFLMAYQQ VHANIENSWN EBEVWRIEM 360
 ISFGIMSLGL LSLAVTSIP SVSNALNWRB FSPIQSTLGY VALLISTFHV LIYGWKRAFE 420
 EKYRYFTFP NFVLALVLPF IVIDLLQLC RYPD

Seq ID NO: 575 DNA sequence
Nucleic Acid Accession #: NM_001873.1
Coding sequence: 3..1721

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GGTGGCGAAC TTGCCGCCCC CAGCAGCGCC GGCAGGCTAA GCCCAGGGCC GGCAGACAA 240
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GCGCGGAAGC CCAGGAGCCC GGGGCGCCCC CGCGGGCAT GAGGCGGCGC CGCGGCTGC 420
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AGGCAGGCTC TCAGCCTGGT GAACCTAAGG ACTGGTTTGT GGGTCGAAGC AATGCCAGG 840
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AAGGTAGTCC AAATATCAT CTGTGAAAA ATATGAAGAA AATTGTGGAT CAAAAACAA 960
AGCTTGTCTC TGAGACCAAG GCTGTCAATC ATTGATTAT GGATATTCCT TTTGTGCTTT 1020
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CATACTCTTC TTTCAAACCG GCCATGTCTG ACCCAATCG GCCACCATGT CGCAAGAAATG 1200
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GCTGTGAGAA GTTCCCACTT GAAGAGACTC TGAAGACCTA CTGGGAGGAT AACAAAACT 1380
CCCTCATTAG CTACCTTGAG CAGATACACC GAGGAGTTAA AGGATTGTCT CGAGACCTTC 1440
AAGGTAACCC AATTGCGAAT GCCACCATCT CCGTGAAGG AATAGACCAT GATGTTACAT 1500
CCGCAAGGGA TGGTGATTAC TGGAGATTGC TTATACCTGG AAATAATAAA CTTACAGCCT 1560
CAGCTCCAGG CTATCTGACA ATAAACAAAG AAGTGGCAGT TCCTTACAGC CCGTCTGCTG 1620
GGGTGTGATT TGAAGTGGAG TCATTTTCTG AAAGGAAAGA AGAGGAGAAG GAAGAATTGA 1680
TGGAAATGCT GAATATGATG TCAGAAACTT TAAATTTTAA AAAAGGCTTC TAGTTAGCTG 1740
CTTTAAATCT ATCTATATAA TGTAGTATGA TGTAAATGCG TCTTTTTTTT AGATTTTGTG 1800
CAGTTAATAC TTAACATGGA TTTATTTTTT AATCATTTAA ATATTAATCA ACTTCCCTTA 1860
AAATAAATAG CCTCTTAGGT AAAAATATAA GAACCTTGATA TATTTCAATC TCATTATAG 1920
TATTCATTTT CTAACCTATA TTACACAAAA AAGTATAGAA AAGATTTAAG TAATTTTGCC 1980
ATCCTAGGCT TAAATGCAAT ATTCTTGCTA TTATTTACAA TGCAAGATTT TTTGAGTAAT 2040
TCTAGCTTTC AAAAAATTAG GAAGTTCTTT TACTGTAATT GGTGACAATG TCACATAATG 2100
AATGCTATTG AAAAGGTTAA CAGATACAGC TCGGAGTTGT GAGCACTCTA CTGCAAGACT 2160
TAAATAGTTC AGTATAAAAT GTGTTTTTTT TCTGTGCTG ACTAAGTATA AGCATGATCT 2220
TGTTAATGCA TTTTGTAGTG GAAGAAAAGG TACATGTTTA CAAAGAGGTT TTATGAAAAG 2280
AATAAAATTT GACTCTCTGC TTGTACATAT AGGAGCAATA CTATTATATT ATGTAGTCCG 2340
TTAACACTAC TTAAGGTTT AGGGTTTTCT CTTGGTTGTA GAGTGGCCCA GAATTGCATT 2400
CTGAATGAAT AAGGTTTAAA AAAAAATCCC CAGTGAAAAA AAA

Seq ID NO: 576 Protein sequence
Protein Accession #: NP_001864.1

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MAGRGGSALL ALGALAAACG WLLGAEAQEP GAPAAGMRER RRLQEDGIS FEYHRYPELR 60
BALVSVNLQC TATSRITYVG RSFEGRELLV IELSDNPVHR EPGEPEPKFY GNMHGNEAVG 120
RELLIFLAGY LCNEYQKNE TIVNLIHSTR IHIMPSLNPD GFELKAASQPG ELKDWPFVGRS 180
NAQIDILNRN FPDLDRIYVY NEKEGGFNNH LLKNNKKIVD QNTKLAPETK AVIHWIMDIP 240
FVLNANLHGG DLVANYPYDE TRSGSAHEYS SSFDDAIFQS LARAYSSFNP AMSDFNRPCC 300
RKNDSSSFV DGTINGGAWY SVPGMQDFN YLSSNCFEIT VELSCKEFPF EETLKTYWED 360
NKNSLISYLE QIHRVKGFPV RDLQGNPIAN ATISVEGIDH DVTSAKGDY WRLLIPGNYK 420
LTASAPGYLA ITRKRVVPYS PAAGVDFELE SFSEKKEEEK EELMEWKKMM SETLNP

Seq ID NO: 577 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..933

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TTCCCTGTGG CCAGCGGCAT CCATTGCATC ATTGTGCTCT TCGGTGCAA TGGGTTTGTG 180
GACTGTCCCG ATGCGACGGA TGAAGAGAAC TGACAGCAA ACCCTCTGCT TTGCTCCACC 240
GCCCGCTACC ACTGCAAGAA CGGCTCTGT ATTGACAAGA GCTTCATCTG CGATGGACAG 300
AATAACTGTC AAGACAACAG TGATGAGGAA AGCTGTGAAA GTTCTCAAGA ACCCGGCAAT 360
GGGCAGGTGT TTGTGACTTC AGAGAACCAA CTGTGTATT ACCCCAGCAT CACCTATGCC 420
ATCATCGGCA GCTCGTCAT TTTGTGCTG GTGGTGGGCC TGCTGGCACT GGTCTTGAC 480
CACCAGCGGA AGCGGAACAA CCTCATGACG CTGCGCGTGC ACCGGCTGCA GCACCTGTG 540
CTGCTGTCCC GCCTGTGGT CCTGGACCAC CCCCACCACT GCAACGTCAC CTACAACTG 600
AATAATGGCA TCCAGTATGT GGCCAGCCAG GCGGAGCAGA ATGCGTGGGA AGTAGGCTCC 660
CCACCTCTCT ACTCGAGGC CTGTGCTGAC CAGAGGCCGT CGTGGTATGA CCTTCTCCA 720
CGGCTCTGCA CTCTGACAC GGAATCTCTG AACCAAGCGG ACCTGCCCCC CTACCGCTCC 780
CGGTCCGGGA GTGCCAACAG TGCCAGCTCC CAGGCAGCCA GCAGCTCTCT GAGCGTGGAA 840
GACACAGGCC ACAGCCCGGG GCAGCCTGGC CCCCAGGAGG GCACTGCTGA GCCCAGGAC 900

TCTGAGCCCA GCCAGGGCAC TGAAGAAGTA TAA

Seq ID NO: 578 Protein sequence
Protein Accession #: Eos sequence

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DCPDGSDEN	CTANPLLCST	ARYHCKNGLC	IDKSFICDQ	NNQDNDSE	SCSSSQEPQS	120
GQVFTSENQ	LVYYPSTIYA	IIGSSVIFVL	VVALLALVLH	HQRKRNLMT	LPVHRLQHPV	180
LLSRLVVDLH	PHHCNVTYNV	NNGIQYVASQ	AEQNASEVGS	PPSYSEALLD	QRPAMYDLPP	240
PPYSSDTESL	NQADLPFYRS	RSGSANSASS	QAASSLLSVE	DTSHSPGQFG	PQEGTAEPRD	300
SEPSQGTTEV						

Seq ID NO: 579 DNA sequence
Nucleic Acid Accession #: AF179274.1
Coding sequence: 1..1125

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TTCCCTACCT	CCTTAAGTGA	CTGCCAAGCG	CCCACCGGCT	GGAATTGCTC	TGGTTATGAT	180
GACAGAGAAA	ATGATCTCTT	CCTCTGTGAC	ACCAACACCT	GTAATTTTGA	TGGGGAATGT	240
TTAAGAATTG	GAGACACTGT	GACTTGCCTC	TGTCACTTCA	AGTGCAACAA	TGACTATGTG	300
CCTGTGTGTG	GCTCCAATGG	GGAGAGCTAC	CAGAATGAGT	GTTACCTGCG	ACAGGCTGCA	360
TGCAAAACAGC	AGAGTGAGAT	ACTTGTGTGT	TCAGAAGGAT	CATGTGCCAC	AGATGCAGGA	420
TCAGGATCTG	GAGATGGAGT	CCATGAAGGC	TCTGGAGAAA	CTAGTCAAAA	GGAGACATCC	480
ACCTGTGATA	TTTGCCAGTT	TGGTGCAGAA	TGTGACGAAG	ATGCCGAGGA	TGCTGTGTGT	540
GTGTGTAATA	TTGACTGTTC	TCAAACCAAC	TTCAATCCCC	TCTGCGCTTC	TGATGGGAAA	600
TCTTATGATA	ATGCATGCCA	AATCAAGAA	GCATCGTGTC	AGAAACAGGA	GAAAATTGAA	660
GTCATGTCTT	TGGGTGCGATG	TCAAGATAAC	ACAACCTACA	CTACTAAGTC	TGAAGATGGG	720
CATTATGCAA	GAACAGATTA	TGCAGAGAA	GCTAACAAAT	TAGAAGAAAG	TGCCAGAGAA	780
CACCAATATC	CTGTGCGGGA	ACATTACAAT	GGCTTCTGCA	TGCATGCGAA	GTGTGAGCAT	840
TCTATCAATA	TGCAGGAGCC	ATCTTGACAG	TGTGATGCTG	GTTTACTGCG	ACAACACTGT	900
GAAAAAAGG	ACTACAGTGT	TCTATACGTT	GTTCCCGGTC	CTGTACGATT	TCAGTATGTC	960
TTAATCGCAG	CTGTGATTGG	AACAATTCAG	ATTGCTGTCA	TCTGTGTGGT	GGTCTCTGTC	1020
ATCACAAGGA	AATGCCCCAG	AAGCAACAGA	ATTACAGAC	AGAAGCAAAA	TACAGGGCAC	1080
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Seq ID NO: 580 Protein sequence
Protein Accession #: NP_057276.2

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CKQQSILVY	SEGSCTADAG	SGSGDGVHEG	SGETSQKETS	TCDICQFGAE	CDEDAEDVWC	180
VCNIDCSQTN	FNPLCASDGR	SYDNACQIKE	ASQCKQEKIE	VMSLGRQDN	TTTTKSEDDG	240
HYATDYAEN	ANKLEESARE	HHIPCPEHYN	GFCMHGKCEH	SINMQEPSCR	CDAGYQOHC	300
EKKDYSVLYV	VGPVRFQYV	LIAAVIGTIQ	IAVICVVVLC	ITRKCPSRNR	IHRQKQNTGH	360
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Seq ID NO: 581 DNA sequence
Nucleic Acid Accession #: S78203.1
Coding sequence: 1..2190

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AACATACCAC	TGAGCATGCG	CTTCATTGTG	GTGAATGAAT	TCTGCGAGCG	CTTTCTCTAT	180
TATGGAATGA	AAGCTGTGCT	GATCCTGTAT	TTCTGTATT	TCTGCACTG	GAATGAAGAT	240
ACCTCCACAT	CTATATACCA	TGCCTTCAGC	AGCCTCTGTT	ATTTTACTCC	CATCCTGGGA	300
GCAGCCATIG	CTGACTCGTG	GTTGGGAAAA	TTCAAGACAA	TCATCTATCT	CTCCTTGGTG	360
TATGTGCTTG	GCCATGTGAT	CAAGTCTTGG	GCTGCTTAC	CAATACTGGG	AGGACAAGTG	420
GTACACACAG	TCTATCAIT	GATGCGCTTG	AGTCTAATAG	CTTTGGGGAC	AGGAGGCATC	480
AAACCTGTG	TGGCAGCTTT	TGGTGGAGAC	CAGTTTGAAG	AAAAACATGC	AGAGGAACGG	540
ACTAGATACT	TCTCAGTCTT	CTACCTGTCC	ATCAATGCCG	GGAGCTTGAT	TTCTACATTT	600
ATCACACCCA	TGCTGAGAGG	AGATGTGCAA	TGTTTGGAG	AAGACTGCTA	TGCATTGGCT	660
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AGGGTACTAT	TCCTTTATAT	CCCATTGCCC	ATGTTCTGGG	CTCTTTTGGG	TCAGCAGGGT	960
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CCGACACAGA	TGCAGTTCT	AAATCCCTTT	CTGGTCTCTA	TCTTCATCCC	GTGTTTGTAC	1080
TTTGTCAATT	ATGCTCTGGT	CTCCTAGTGT	GGAATTAAT	TCTCATCACT	TAGGAAAAATG	1140
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ATAAATGAAA	TGGCCCCAGC	CCAGTCAGGT	CCCCAGGAGG	TTTTCTTACA	AGTCTTGAA	1260
CTGGCAGATG	ATGAGGTGAA	GGTGACAGTG	GTGGGAAATG	AAAAACAATC	TCTGTTGATA	1320
GAGTCCATCA	AATCCCTTCA	GAAAACACCA	CACTATTCCA	AACTGCACCT	GAAAACAAAA	1380
AGCCAGGATT	TTCACCTCCA	CCTGAAATAT	CACAAATTGT	CTCTCTACAC	TGAGCATTCT	1440
GTGCAGGAGA	AGAACTGSTA	CAGTCTTGTC	ATTCGTGAAG	ATGGGAACAG	TATCTCCAGC	1500

5 ATGATGGTAA AGGATACAGA AAGCAAAACA ACCAATGGGA TGACAACCGT GAGGTTTGT 1560
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15 Seq ID NO: 582 Protein sequence
 Protein Accession #: AAB34388.1

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 TRYFSVFYLS INAGSLISTP ITPMLRGDVG CPGEDCYALA PGVPQLLMVI ALVVFPAMGSK 240
 IYNKPPFBNQ IVAQVFKCIW FAISNRFKNR SGDIPKRQHW LDWAAEKYPK QLIMDVKALT 300
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 LADDEVKVTV VGNENSLLI RSIKSPQKTP HYSKLHLKTK SQDFHPLKY HNLSLYTEHS 480
 VQEKMYSLV IREDGNSISS MMVKOTESKT TNGMTTVRFV NTLHKDVNIS LSTDTSLNVG 540
 EDYGVSAIRT VQRGEYPAHV CRTEDKNFSL NLGLLDFGAA YLFVITNNTN QGLQANKIED 600
 IPANKMSIAW QLPQYALVTA GEVMPFSVTGL EFSYSQAPSS MKSVLQAAML LTIAGVNIIV 660
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35 Seq ID NO: 583 DNA sequence
 Nucleic Acid Accession #: NM_032642.1
 Coding sequence: 184..1263

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 ACCATGCCCA GCGTGTCTGT GCTGTTCACG GCTGCTCTGC TGTCCAGCTG GGCTCAGCTT 240
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 GAAAGATGAA AATGGAAGG AAGAGCTTAT TTAAGAGACG CTGGAGATCT CTGAGGAGTG 1440
 GACTTTGTCT GTTCTCTCTT CTGTGTGGGT GGGAGACAGG GCTTTTCTCT TCCCTCTGGC 1500
 65 GAGGACTCTC AGGATGTAGG GACTTGGAAA TATTTACTGT CTGTCCACCA CGGCCTGGAG 1560
 GAGGAGGTT GTGGTGTGAT GGAGGAGATG ATCTTGTCTG GAAGTCTAGA GTCTTTGTGT 1620
 GTTAGAGGAC CCGCTGTGAT CTGGCCACT AGGCCAAGAG GCCCTATGAA GGTGGCGGGA 1680
 ACTCAGCTTC AACCTCGATG TCTTCAGGGT CTTGTCCAGA ATGTAGATGG GTTCGTAAAG 1740
 AGGCCTGGTG CTCTCTTACT CTTTCATCCA CGTGCACTTG TCGGCATCTC GCAGTTTACA 1800
 70 GGAACGGCTC CTTCCTTAAA ATGAGAAGTC CAAGGTCACT TCTGGCCAGG TGACCAACAG 1860
 GAGATCTGCA CCTCCCGGAC TTCAGGCTGT OCTTTCCAGC GAGAAATCTT CATCTCCAC 1920
 GGTTCACAGT CTCTACTCTG AAGAGGAAAAG GGGGCCATTT GACCTGACAT GTCAAGAAAAG 1980
 CCCTAAACTG AATGTTTGGC CCGGGCTGTC AGAAGCCAGG GTGCATGACC AGGCTGCGTG 2040
 GACGTTATAC TGTCTTCCCC CACCCCGCGG GAGGGGAAGC TTGAGCTGCT GCTGTCACTC 2100
 75 CTCACCGAG GAGGCTCTCA CAAACCAAG GACGCTGCAA CGGTCAGGCG TGGCGGGCCC 2160
 GCGGTGCTCA TCATCTCTGC CCGAGGTGTA CGGTTTCTCT CTGACATTAA ATGCCCTTCA 2220
 TGGAAAAAAA AAAAAGAAAA AAAAAAAAAA AA

80 Seq ID NO: 584 Protein sequence
 Protein Accession #: NP_116031.1

1 11 21 31 41 51
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 LQLYQERMA YTGEGAKTGI KECQHQRQR RNHCSTADNA SVFGRVMQIG SRETAFTHAV 120

SAAGVVNAIS RACREBELST CGCSRTARPK DLPRDLWGG CGDNVEYGYR FAKEFVDARE 180
 REKNFARGSE EQGRVLMNLQ NNEAGRRAVY KMADVACKCH GVSQSCSLKT CNLQLABFRK 240
 VQDLRLKEKYD SAAAMRVTRK GRLELVNSRF TQPTPELVY VDPSPDYCLR NESTGSLGTQ 300
 GRLECNKTSSE MDGCBLMCCG RGYNQFKSVQ VERCHCKPHW CCFVRCKKCT EIVDQYICK

5

Seq ID NO: 585 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1479

10 1 11 21 31 41 51
 | | | | |
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 CAACCGGAAA ACCCTATCC CGCACAGCCC ACTGTGGTCC CCCTGTCTA CGAGGTGCAT 120
 COGGCTCAGT ACTACCGGTC CCCCGTGCCC CAGTACGCCC CGAGGGTCCT GACCGAGGCT 180
 15 TCCAACCCCG TCGTCTGCAC GCAGCCCAAA TCCCATCCG GACAGTGTG CACCTCAAAG 240
 ACTAAGAAAG CACTGTGCAT CACCTGACC CTGGGGACCT TCCTCGTGG AGCTGCGCTG 300
 GCCGCTGGCC TACTCTGGAA GTTCATGGGC AGCAAGTGCT CCAACTCTGG GATAGAGTGC 360
 GACTCTCAG GTACCTGCAT CAACCCCTCT AACTGGTGTG ATGGCGTGTG ACACCTGCCC 420
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 20 TACTCATCTC AGAGGAAGTC CTGGCACCCT GTGTGCCAAG ACGACTGGAA CGAGAATAC 540
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 TGTATAGCCT CGGGGTCAA CTGAACTCA AGCCGCCAGA CGAGGATCGT GGGCGGCGAG 780
 25 AGCGCGCTCC CGGGGCGCTG GCCCTGGCAG GTCAGCCTGC ACGTCCAGAA CGTCCACGTG 840
 TGGGAGGCTC CCATCATCAC CCCGAGTGG ATCGTGACAG CCGCCCACTG CGTGGAATAA 900
 CCTCTTAACA ATCCATGGCA TTGGACGGCA TTTGCGGGGA TTTTGAGACA ATCTTTACATG 960
 TTCTATGGAG CCGGATACCA AGTAGAAAA GTGATTTCTC ATCCAAATTA TGACTCCAAAG 1020
 ACCAAGAACCA ATGACATTGC GCTGATGAAG CTGCAGAACG CTCTGACTTT CAACGACCTA 1080
 30 GTGAAACCAAG TGTGTCTGCC CAACCCAGGC ATGATGCTGC AGCCAGAACG GCTCTGCTGG 1140
 ATTTCCGGGT GGGGGGCCAC CGAGGAGAAA GGGAAAGACT CAGAAGTGCT GAACGCTGCC 1200
 AAGGTGCTTC TCATTGAGAC ACAGAGATGC AACAGCAGAT ATGTCTATGA CAACCTGATC 1260
 ACACCAAGCA TGATCTGTGC CGGCTTCTCG CAGGGGAACG TCGATTCTTG CCAGGCTGAC 1320
 AGTGGAGGCG CTCGTGTGTC TCGAAGAAC AATATCTGGT GGCTGATAGG GGATACAAGC 1380
 35 TGGGGTTCTG GCTGTGCCAA AGCTTACAGA CCAGGAGTGT ACGGGAATGT GATGTGATTC 1440
 ACGACTGGA TTTATCGACA AATGAGGGCA GACGGCTAA

Seq ID NO: 586 Protein sequence
 Protein Accession #: Eos sequence

40

1 11 21 31 41 51
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 SNPVVCTQPK SPFGTVCTSK TKKALCITLT LGTFLVGAAL AAGLLMKFMG SKCSNSGIEC 120
 45 DSSGTCINPS NWCQGVSHCP GGEDENRCVR LYGENFILQV YSSQRKSWHP VCQDWNENY 180
 GRAACRDMGY KNNFYSSQGI VDDSGSTSFM KLNTSAGNVD IYKILYHSDA CSSKAVVSLR 240
 CIACQVNLNS SRQSRIVGGE SALPGANFWQ VSLHVQNVHV CGGSIITPEW IVTAACVEK 300
 PLNNFWHTA FAGLLRSFPM FYGAGYQVEK VISHPNYDSK TKNNIDIALMK LQKPLTFNDL 360
 VKPVLCPNP MMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLIIETQRC NSRYVVDNLI 420
 50 TPAMICAGFL QGNVDSQCGD SGGPLVTSKN NIWNLIGDTS WSGCAKAYR PGVYGNVMVF 480
 TDNIYRQMRA DG

Seq ID NO: 587 DNA sequence
 Nucleic Acid Accession #: NM_005656.1
 Coding sequence: 57..1535

55

1 11 21 31 41 51
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 CTTTGAATCT AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAGAACAT GGATACCAAC 120
 CGGAAACCC CTATCCCGCA CAGCCACTG TGGTCCCAC TGTCTACGAG GTGCATCCGG 180
 CTCAGTACTA CCGGTCCCCC GTGCCCGAGT ACGCCCCGAG GGTCTGACG CAGGCTTCCA 240
 ACCCGTCGT CTGCAAGCAG CCCAAATCCC CATCCGGGAC AGTGTGCACC TCAAAGACTA 300
 AGAAAGCACT GTGCATCAC TTAGCCCTGG GGACCTTCTC CGTGGGAGCT GCGCTGGCCG 360
 65 CTGGCTTACT CTGGAAGTTC ATGGGCAGCA AGTGCTCCAA CTCTGGGATA GAGTGGCACT 420
 CCTCAGGTAC CTGCATCAAC CCTCTAACT GGTGTGATGG CGTGTACAC TGCCCCGGCG 480
 GGGAGGACGA GAATCGGTGT GTTCGCTCTC ACGACCAAA CTTCATCCTT CAGATGTACT 540
 CATCTCAGAG GAAGTCTCTG CACCTGTGTG GCCAAGACGA CTGGAACGAG AACTACGGGC 600
 GGGCGGCGCT CAGGGACATG GGCTATAAGA ATAAATTTTA CTCTAGCCAA GGAATAGTGG 660
 70 ATGACAGCGG ATCCACAGC TTTATGAAAC TGAACACAG TGCCGSCAAT GTCGATATCT 720
 ATAAAAAAGT GTACCAAGT GATGCTGTG CTTCAAAAGC AGTGGTITCT TTACGCTGTT 780
 TAGCTTGGCG GGTCAACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGGC GGTGAGAGCG 840
 CGCTCCCGGG GGCTTGGCCC TGGCAGGTCA GCCTGCAGCT CCAGAAGCTC CAGTGTGCG 900
 75 GAGGCTCCAT CTGACCCCC GAGTGGATCG TGACAGCGCG CCACTGGGTG GAAAACCTC 960
 TTAACAACTG ATGGCATTGG ACGGCATTGG CGGGGATTTT GAGACAATCT TTCATGTTCT 1020
 ATGAGACCGG ATACCAAGTA CAAAAAGTGA TTTCTCATCC AAATTATGAC TCCAAGACCA 1080
 AGAACAAATG CATTGCCCTG ATGAAGCTGC AGAAGCTCT GACTTTCAAC GACCTAGTGA 1140
 AACCAAGTGT TCTGCCCAAC CCAGGCATGA TGCTGCAGCC AGAACAGCTC TGCTGGATTT 1200
 CGCGGTGGGG GGCCACCGAG GAGAAAGGGA AGACCTCAGA AGTGTGAACT GCTGCCAAGG 1260
 80 TGCTTCTCAT TGAGACACAG AGATGCAACA GCAGATATGT CTATGACAC CTGATCACAC 1320
 CAGCCATGAT CTGTGCGGCG TTCTGTCAGG GGAACGTGCA TTCTTGCCAG GTGACAGTGG 1380
 GAGGGCTCTT GGTCACTTCG AACCAACAAT TCTGGTGGCT GATAGGGGAT ACAAGCTGGG 1440
 GTTCTGGCTG TGCCAAAGCT TACAGACCAG GAGTGTACGG GAATGTGATG GTATTACCGG 1500
 ACTGGATTTA TCGACAAATG AAGGCACACG GCTAATCCAC ATGGTCTTGG TCCTTGACGT 1560

CGTTTTACAA GAAACAATG GGGCTGGTTT TGCTTCCCCG TGCAATGATT ACTCTTAGAG 1620
 ATGATTACGA GGTCACTTCA TTTTATTAA ACAGTGAACT TGCTGGCTT TGGCACTCTC 1680
 TGCCATACCTG TGCAAGCTGC AGTGGCTCCC CTGCCAGCC TGCTCTCCCT AACCCCTTGT 1740
 CGCAAGGGG TGATGGCCGG CTGGTTGTGG GCATGGGGG TCAATTGTGG AAGGAAGAGG 1800
 GTTGGAGGCT GCCCCCAITG AGATCTTCTT GCTGAGTCTT TCCAGGGGC CAATTTTGGG 1860
 TGAGCATGGA GCTGTCACTT CTCAGCTGCT GATGACTTGG AGATGAAAAA GGAGAGACAT 1920
 GGAAGGGGAG ACAGCCAGGT GGCACCTGCA GGGCTGGCC TCTGGGGCCA CTGGTAGTGT 1980
 TCCCCAGCCT ACTTACAAG GGGATTTTGC TGATGGGTTT TTAGAGCCTT AGCAGCCCTG 2040
 GATGGTGGCC AGAAATAAAG GGACAGCCC TTCATGGGTG GTGACGTGGT AGTCACTTGT 2100
 AAGGGGAACA GAAACATTTT TGTTCCTATG GGGTGAGAAT ATAGACAGTG CCCTTGGTGC 2160
 GAGGGGAAGCA ATTGAAAAGG AACTTGCCCT GAGCACTCTT GGTGACAGTC TCCACCTGCA 2220
 CATTTGGTGG GGCTCTTGGG AGGGAGACTC AGCCTTCTCT CTCATCTCTC CTGACCCCTG 2280
 TCCTAGCACC CTGAGAGAGT AATGCCCTTT GGTCCCTGGC AGGGGCGCAA GTTTGGCACC 2340
 ATGTGGCCTT CTTACGGCTT GATAGTCATT GGAAATTGAG GTCCATGGGG GAAATCAAGG 2400
 ATGCTCAGTT TAAGGTACAC TGTTTCCATG TTATGTTTCT ACACATTGAT GGTGGTGACC 2460
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Seq ID NO: 588 Protein sequence
 Protein Accession #: NP_005647.1

1 11 21 31 41 51
 MALNSGSPFA IGPYYENHGY QPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTQA 60
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 DSSGTCTNPS NWCQGVSHCP GGEDENRCVR LYGPNFILQM YSSQRKSWHP VCQDDWNNY 180
 GRAACRDMGY KNNFYSSQGI VDDSGSTSPM KLNTSAGNVD IYKKLYHSDA CSSKAVVSLR 240
 CLACGVNLNS SRQSRIVGGE SALPGAWFWQ VSLHVQNVHV CGSIIITPEW IVTAAHCVEK 300
 PLNNPWHWTA FAGLLRQSFM FYGAGYQVQK VISHENYDSK TONNDIALMK LQKPLTFNDL 360
 VKPVLNPGW MMLQPEQLCM ISGAGATEBK KGTSEVLNAA KVLLETORC NSRVYVDNLI 420
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 TDWYRQMKK NG

Seq ID NO: 589 DNA sequence
 Nucleic Acid Accession #: NM_001935.1
 Coding sequence: 1..2301

1 11 21 31 41 51
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 AAAACTTACA CTCTAACTGA TTACTTAAAA AATACCTATA GACTGAAGTT ATACTCCTTA 180
 AGATGGATTT CAGATCATGA ATATCTCTAC AAACAAGAAA ATAATATCTT GGTATTCAAT 240
 GCTGAATATG GAAACAGCTC AGTTTTCTTG GAGAACAGTA CATTTGATGA GTTTGGACAT 300
 TCTATCAATG ATTATTCAAT ATCTCCTGAT GGCAGTTTGA TTCTCTTGA ATACAATAC 360
 GTGAAGCAAT GGAGGCATTC CTACACAGCT TCATATGACA TTTATGATT AAATAAAAGG 420
 CAGCTGATTA CAGAAGAGAG GATTCCAAAC AACACACAGT GGTGCACATG GTCAACAGTG 480
 GGTCAATAAT TGGCAATATG TTGGAACAAT GACATTTATG TTAAATTTGA ACCAAATTTA 540
 CCAAGTTACA GAATCACATG GACGGGGAAG GAAGATATAA TATATAATGG AATAACTGAC 600
 TGGGTTTATG AAGAGGAAGT CTTCACTGCC TACTCTGCTC TGTGGTGGTG TCCAACGGC 660
 ACTTTTTAG CATATGCCCA ATTTAACGAC ACAGAAGTCC CACTTATTGA ATACTCCTTC 720
 TACTCTGATG AGTCACTGCA GTACCCAAAG ACTGTACGGG TTCCATATCC AAAGGCAGGA 780
 GCTGTGAATC CAACTGTAAA GTTCTTTGTT GTAAATACAG ACTCTCTCAG CTCAGTCACC 840
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 TGTGATGTGA CATGGGCAAC ACAAGAAAGA ATTTCTTTGC AGTGGCTCAG GAGGATTCAG 960
 AACTATTGGG TCATGGATAT TTGTGACTAT GATGAATCCA GTGGAAGATG GAACTGCTTA 1020
 GTGGCAAGGC AACACATTGA AATGAGTACT ACTGGCTGGG TTGGAAGATT TAGGCCCTTA 1080
 GAACCTCAT TACCTTATG TGGTAATAGC TTCTACAAGA TCATCAGCAA TGAAGAAGGT 1140
 TACAGACACA TTGTCTATTT CCAATAGAT AAAAAGACT GCACATTTAT TACAAAAGGC 1200
 ACCTGGGAAG TCATCGGGAT AGAAGCTCTA ACCAGTGATT ATCTATACTA CATTAGTAAT 1260
 GAATATAAAG GAATGCCAGG AGGAAGGAAT CTTTATAAAA TCCAACCTAG TGACTATACA 1320
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 TTCACTAAG AGGCGAAGTA TTATCAGCTG AGATGTTCCG GTCCTGGTCT GCCCCTCTAT 1440
 ACTCTACACA GCAGCGTGAA TGATAAAGGG CTGAGAGTCC TGGAGACAAA TTCAGCTTTG 1500
 GATAAAATGC TGCAGATGT CCAGATGCCC TCCAATAAAC TGGACTTCAT TATTTTGAAT 1560
 GAAACAAAAT TTTGGTATCA GATGATCTTG CCTCCTCATT TTGATAATC CAAGAAATAT 1620
 CCTCTACTAT TAGATGTGTA TGCAAGCCCA TGTAAGTCAA AAGCAGACAT TGCTCTCAGA 1680
 CTGAACCTGG CCACTTAOCT TGCAAGCACA GAAAACATTA TAGTAGCTAG CTTTGTATGC 1740
 AGAGGAAGTG GTTACCAAGG AGATAAGATC ATGCATGCAA TCAACAGAAG ACTGGGAACA 1800
 TTTGAAGTTG AAGATCAAT TGAAGCAGCC AGACAATTTT CAAAAATGGG ATTTGTGGAC 1860
 AACAAACGAA TTGCAATTTG GGGCTGGTCA TATGGAGGGT ACGTAACCTC AATGGTCTTG 1920
 GGATCGGGAA GTGGCGTGT CAAGTGTGGA ATAGCCGTGG CGCTGTATC CCGTGGGGAG 1980
 TACTATGACT CAGTGTACAC AGAACGTTC ATGGGTCTCC CACTCCAGCA AGACAACCTT 2040
 GACCATTACA GAAATTAAC AGTCATGAGC AGAGCTGAAA ATTTTAAACA AGTTGAGTAC 2100
 CTCCTTATTC ATGGAACAGC AGATGATAAC GTTCACCTTC AGCAGTCAGC TCAGATCTCC 2160
 AAGCCCTGG TCGATGTTGG AGTGGATTTC CAGGCAATGT GGTATCTGA TGAAGACCAT 2220
 GGAATAGCTA GCAGCACAGC ACACCAACAT ATATATACCC ACATGAGCCA CTTCATAAAA 2280
 CAATGTTTCT CTTTACCTTA G

Seq ID NO: 590 Protein sequence
 Protein Accession #: NP_001926.1

1 11 21 31 41 51
 MKTPWKILIG LLGAAALVTI ITVPVLLNKG GTDDATADSR KTYTLTDYLK NTRYRLKLYSL 60

5 RWISDHEYLY KQENNILVFN AEYGNSSVFL ENSTFDEFGH SINDYSISPD GQFILLENY 120
 VKQMRHSTTA SYDIYDLNKR QLITEERIPN NTQMVWSPV GHKLAYVWNN DIYVKIEFNL 180
 PSYRITWTGK EDIIVNGITD WYEEVEVFS YSALMWSFNG TFLAYAQFND TEVPLIEYSF 240
 YSDESQYYPK TVRVYPYKAG AVNPTVKFFV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300
 CDVTWATQER ISLQWLRRIQ NYSVMDICDY DESSGRWNCL VARQHIEMST TGVVGRFRPS 360
 EPHFTLDGNS FYKIIISNEEG YRHICYFQID KKDCTFITKG TWEVIGIEAL TSDYLYIISN 420
 EYKGMPPGGRN LYKIQLSDYT KVTCLSCELN PERCQYYSVS FSKEAKYVQL RCGSGPLPLY 480
 TLHSSVNDKG LRVLEDNSAL DKMLQNVQMP SKKLDPIILN ETKFWYQML PPHFDKSKKY 540
 10 PLLLDVYAGP CSQKADTVFR LNWATYLAST ENIIVASFPG RGSQYQGDKI MHAINRRLGT 600
 FEVEDQIEAA RQFSKMGFVD NKRIAIWNS YGGYVTSMLV GSGSGVFKCG IAVAPVSRWE 660
 YDVSVYTERY MGLFTPEDNL DHYRNSTVMS RAENFKQVEY LLIHGTADDN VHFQOQAQIS 720
 KALVDVGVDV QAMMYTDEDH GIASSTAHQH IYTHMSHFIF QCFSLP

15 Seq ID NO: 591 DNA sequence
 Nucleic Acid Accession #: NM_016077.1
 Coding sequence: 128..667

20 1 11 21 31 41 51
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 ACTGTAGATG CCTCCAAAT CCTTGTGTAT GGAATATTTG GCTCATCCCA GTACACTCGG 180
 CTGGCTGTGT GAGTGTGCTT GTGGCATGTG CCTGGGCTGG AGCCCTTCAG TATGCTTTGG 240
 25 GATGCTCCCC AAAAGCAAGA CGAGCAAGAC ACACACAGAT ACTGAAAGTG AAGCAGCATG 300
 CTGGGAGAG AGCGGGAGT ACAAGATGAT TCTTGTGGTT CGAAATGACT TAAAGATGGG 360
 AAAAGGAAAA GTGGCTGCCC AGTGCTCTCA TGCTGCTGTT TCAGCTTACA AGCAGATTCA 420
 AAGAAGAAAT CCTGAAATGC TCAACAATG GGAATACTGT GCCAGCCCCA AGGTGGTGGT 480
 CAAAGCTCCT GATGAAGAAA CCTGATTGTC ATTATTTGCC CATGCAAAAA TGCTGGGACT 540
 30 GACTGTAAAT TTAATTCAG ATGCTGGAGC TACTCAGATT GCACCAGGCT CTCAAACTGT 600
 CCTAGGGATT GGGCCAGGAC CAGCAGACCT AATTGACAAA GTCACTGGTC ACCTAAACTG 660
 TTACTAGGTG GACTTTGATA TGACAACAAC CCTCCATCA CAAGTGTITG AAGCCTGTGA 720
 GATTCTAACA ACAAAAGCTG AATTCTTCA CCCAACTTAA ATGTTCTTGA GATGAAAAATA 780
 AAACCTATTCT CCATGTTCTA AAAAA

35 Seq ID NO: 592 Protein sequence
 Protein Accession #: NP_057161.1

40 1 11 21 31 41 51
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 DSEYKMLIV VRNDLKMKGK KVAACQSHAA VSAYKQIQR NPEMLKQWEY CGQPKVVVKA 120
 PDEETLIALL AHAKMLGLTV SLIQDAGRTQ IAPGSQTVLG IGPADLID KVTGHLKLY

45 Seq ID NO: 593 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..1896

50 1 11 21 31 41 51
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 CGCGAGTCCG GCGCCCGGCC CGGCGCGGGG CCGCGGAACA CCACCGGTT TGGGCTGGG 180
 GCGCGGGGCG GCAGCGGCGC CTCCAGCTCC AACAGCAGTG GCGACGCTT GGTGACCGCG 240
 55 ATTCCATCCC TCCTCCGCGA CCTACCCACC CTCAAGCGAG CCGTGATGTT GCGGTTCGCC 300
 TTATCACACC TCCTCATGCG CTGCGGCTGC CTGCGGCTCT TCAGGTTCGGG AAAGAGGTTA 360
 AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGG AATGGCGCCA 420
 CTAAATGAAG AGGATGATGA AGATGAGGAC TCACAGTAT TCACATCAA ATACAGAGTG 480
 TCCTTGCGCG CTGCACTGAG ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCCT 540
 60 GTGCCCCAC CCTTCATCCT GCACATGAC CTTCAGCAA GATGCACTG AAGGCTGAT 600
 GGTGGAATCA GACCTGTTAA AACCTGTTTC CCAGCCTGTT GGCATCCTGT GGAAGTTGG 660
 TCAGCTGCAA CCTGGGTGTT GAAGGACTGG ACCTGGAAGC CCTCTTGCT CCGAGGTGTT 720
 GAAACCAAAA CGAACGTTAT GTATAAAAC CCAGCTCCAT CGTGCCTGTC AGGCATCTGC 780
 TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTACACCAA TGGAGTTGCT TCTGCCAACC 840
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 65 CTGAATCTCA TGGAAAAGCT GGATTCTCT GCTTACGCA GAAACACCG GGTCCATCT 960
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 CCTTGGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCTTTACAC ACAAACCATG 1080
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 70 AGAGCAGTGA CTAAGGTTCT CCAGGCTAGC TCTTCTCCA AACAGCTGCG CTGGAAGCCA 1200
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 75 ATCTGTCTCC CTGCTGTGCG CGTGAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500
 GTCTTGTGCT CATTTGAGCA GAGCCCAAA AAGGCAGCTG CTGCCACGG GGAGCCTGTC 1560
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 80 GATGGCAGAT GCCAGAAGAT GGTCTGATG TCTGAGGAAG GCACACCTAG TTTGACAGGA 1800
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Seq ID NO: 594 Protein sequence
 Protein Accession #: FGENESH predicted


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1      11      21      31      41      51
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KKTRKYDIIT TPAERVEMAP LNEEDDEDED STVFDIKYRV SLPAALRRQL PGCOTLLTVP 180
VPPPFILDIID LPARCSGRPD GGIRPGKTCF PAMWHPVESM SAATWGVKDW TWKPCVCGGV 240
ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTTMELLPLP FGHPPFKVPPT STPHGFRQLQ 300
LNLMEKLDSS ALRRNTRAPS ARCLPLVLAE MAAAESDLFN PMWHPSATGS PIKTLTYQTM 360
10  STLGLDVPFG AQQRGTFCED RAVTKVLQGS SPKQLRWKP ALESGFPHEL RLLRECPPLS 420
THFVRLARSR ARGQASLTGR RVFRFRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK 480
ICLPCCAVEH LREAKRSVVT VLASFQSPQ KAAAAGBEFV KRGPFGQLTR BTCPGNGITH 540
ANLQTIPTDT GQSGPREVDV HPGGDLGVA NFYLEEBGPQ DGRGCKMVLN SEGGPPSLTG 600
CERLTGSHKF SSHSKSWSLP SPRQPLFLSR P

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Seq ID NO: 595 DNA sequence
Nucleic Acid Accession #: NM_021614.1
Coding sequence: 1..1740

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GGAGGAGGTG GCGGCGCGTC CTCCCCTCTC GCAGCGCGTG CGCGCGCGCG CGCTGTTCGG 180
25  TCCTCAGCCC CCGAGATCGT GGTGTCTAAG CCGCAGCACA ACAACTCCAA CAACCTGGCG 240
CTCTATGGAA CGGCGGCGCG AGGCAGCACT GGAGGAGCGG GCGGCGGTGG CGGGAGCGGG 300
CACGGCAGCA GCASTGGCAC CAAGTCCAGC AAAAAGAAAA ACCAGAACAT CGGCTACAA 360
CTGGGCGACC GCGGCGCGCT GTTCGAAAAG CGCAAGCGGC TCAGGAGTAA CGCGCTCATC 420
TTGCGCATGT TCGGCATCGT GGTCTATGTC ATCGAGACCG AGCTGTCTGG GGGCGCTAC 480
30  GACAGGCGGT CGCTGTATTC CTAGCTCTG AATGCTCTTA TCAGTCTCTC CAAGATCATC 540
CTGCTGCTGC TGATCATCGT GTACCACGCC AGGGAATATC AGTTGTTTAT GGTGGACAAT 600
GGAGCAGATG ACTGGAGAAAT AGCCATGACT TATGAGCTTA TTTTCTTCAT CTGCTTGGAA 660
ATACTGGTGT GTGCTATTCA TCCCATACCT GGGAAATFATA CATTCACATG GACGGCCCGG 720
CTTGCCCTTC CTATGCCCCC ATCCACAACC ACCGCTGATG TGGATATTAT TTTATCTATA 780
35  CCAATGTTCT TAAGACTCTA TCTGATTGCC AGAGTCATGC TTTTACATAG CAAACTTTTC 840
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RMYCSTEGEW LVPIGKCSGN AGYEERGFMC QACRPGFYKA LDGNMKCAK PPHSSTQEDG 300
SMNCRCEANN FRADKDPFSM ACTRPPSPR NVISINETS VILDWSWELD TGGRKDVTFN 360
IICKKCGWNI KQCEPCSPNV RFLPRQFGLT NTVIVIDL L AHTNTPFID AVNGVSELSS 420
PPRQFAAVSI TTNQAAPSPV LTIKKDRISR NSISLSWQEP EHPNGIILDY EVKYERQEQ 480
ETSYTILRAR GTNVITISLK PDTIYVFQIR ARTAAGYGTN SRKFEPETSP DSFSISGESS 540
QVVMIAISAA VAILLLTVVI YVLIGRFGY KSKGGADEKR LHPGNHGLKL PGLRTYVDPH 600
TYEDPTQAVH EFAKELDATN ISIDKVVAG EPEGVCSGRL KLEPSKKEISV AIKTLKVGYT 660
EKQRDFLGE ASIMQGFDR NIIRLEGVVT KSKPVMIVTE YMENGSLDSF LRKHAQFTV 720
IQLVGLRGI ASGMKYLSDM GYVRDLAAR NILINSNLVC KVSDFGLSKV LEDDPEAAYT 780
TRGGKIPIRW TSPEALAYRK FTSASDVWSY GIVLNEVMSY GERPYWEMSN QDVIVKAVDEG 840
YRLPPFMDCP AALYQLMLDC WQKDRNRPK FEQIVSILDK LIRNPGSLKI ITSAAARPSN 900
LLLDQSNVDI STFRITGDWL NGVRTAKCKE IFTGVEYSSC DTIAKISTDD MKKVGTVTVG 960
PQKXIISIK ALETQSKNPG VPV
  
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Seq ID NO: 603 DNA sequence

Nucleic Acid Accession #: NM_005727.1

Coding sequence: 122..847

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1 11 21 31 41 51
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CATGCAGTGC TTCAGCTTCA TTAAGACCAT GATGATCCTC TTCAATTGTC TCATCTTTCT 180
GTGTGGTGCA GCGCTGTTGG CAGTGGGCAT CTGGGTGTCA ATCGATGGGG CATCCTTTCT 240
GAAGATCTTC GGGCCACTGT CGTCCAGTGC CATGCAGTTT GTCAACGTGG GCTACTTCCT 300
CATCGCAGCC GCGTGTGTGG TCTTTGCTCT TGGTTTCTCG GGCTGCTATG GTGCTAAGAC 360
TGAGAGCAAG TGTGCCCTCG TGACGTCTCT CTTTCATCCT CTCTCATCT TCATTGCTGA 420
GGTTCAGACT GCTGTGTGCG CCTTGGTGTG CACCACAATG GCTGAGCACT TCCTGACGTT 480
GCTGGTAGTG CTTGCCATCA AGAAAGATTA TGGTTCCAGG GAAGACTTCA CTCAGTGTG 540
GAACACCAAC ATGAAAGGGC TCAAGTGCTG TGGCTTCACC AACTATACGG ATTTTGAGGA 600
CTACCCCTAC TTCAAAGAGA ACAGTGCCTT TCCCCATTTC TGTGCAATG ACAACGTGAC 660
CAACACAGCC AATGAAACCT GCACCAAGCA AAAGGCTCAC GACCAAAAAG TAGAGGGTTG 720
CTTCAATCAG CTTTGTGTAT ACATCCGAAC TAATGCAGTC ACCGTGGGTG GTGTGGCAGC 780
  
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5
10
15
20

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TGGAAATGGG GGCTCGAGC TGGCTGCCAT GATTGTGTCC ATGTATCTGT ACTGCAATCT 840
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CCCTGGCAAG CAGCAGTGAT TGGGGGAGGG GACAGGATCT AACAAATGCA CTGGGGCCAG 960
AATGGACCTG CCCTTTCTGC TCCAGACTTG GGGCTAGATA GGGACCACCTC CTTTATAGCG 1020
ATGCGTGAAT TTCTTTCCAT TGGTGGGTGG ATGGGTGGGG GGCATTCCAG AGCCTCTAAG 1080
GTAGCCAGTT CTGTGGCCCA TTCCCCAGT CTATTAAACC CTTGATATGC CCCTAGGCC 1140
TAGTGTGTAT CCCAGTGCTC TACTGGGGGA TGAGAGAAAG GCATTTTATA GCCTGGGCAT 1200
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Seq ID NO: 604 Protein sequence
Protein Accession #: NP_005718.1

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1 11 21 31 41 51
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LVVPAIKRDY GSGEDFTQVM NTTMKGLKCC GFTNYTDFED SPYFKENSAP PFPCCNDNVT 180
NTANETCTEQ KARDQKVEGC FNQLLYDIRT NAVTVGGVAA GIGGLELAAM IVSMYLYCNL 240
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Seq ID NO: 605 DNA sequence
Nucleic Acid Accession #: NM_000729.2
Coding sequence:

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35
40

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1 11 21 31 41 51
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GACGCAAGCG GTGCTCCCGC CAGATCCCGC GGGCTCCGGG CTGCAGCGGG CAGAGGAGGC 180
CGCCCTAGG CAGCTGAGGG TATCGCAGAG AACGATGGC GAGTCCCGAG CGCACCTGGG 240
CGCCCTGCTG GCAAGATACA TCCAGCAGGC CCGGAAAGCT CCTTCTGGAC GAATGTCCAT 300
CGTTAAGAAC CTGCAGAAC TGGACCCCGC CCACAGGATA AGTGACCGGG ACTACATGGG 360
CTGGATGGAT TTTGGCCGTC GCAGTGCCGA GGAGTATGAG TACCCCTCCT AGAGGACCCA 420
GCGGCCATCA GCCCAACGGA AGCAACCTCC CAACCCAGAG GAGGCAGAAT AAGACAACAA 480
TCACACTCAT AACTCATTGT CTGTGGAGTT TGACATTGAA TGTATCTATT TATTAAGTTC 540
TCAATGTGAA AATTGTGTCT GTAAGATTGT CCAGTGCAAC CACACAGCCT CACCAGAAGT 600
TGTGCAAACT GAAGACAAA CTGTTTTCTT CATCTGTGAC TCCTGTTCTG AAAATGTTGT 660
TATGCTATTA AAGTGATTTC ATTCTGCC

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Seq ID NO: 606 Protein sequence
Protein Accession #: NP_000720.1

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1 11 21 31 41 51
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Seq ID NO: 607 DNA sequence
Nucleic Acid Accession #: NM_001423.1
Coding sequence: 219..692

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CAGGGCTGCT GCCAGCACCT GCCACTCAGA GCGCTCTGT CGCTGGGACC CTTCAGAACT 180
CTCTTTGCTC ACAAGTTACC AAAAAAAAAA GAGCCAAAT GTTGTATTG CTGGCTGGTA 240
TCCTTTGTGT CCACATCGCT ACTGTTATTA TGCTATTGT TAGCACCATT GCCAATGTCT 300
GGTTGGTTTC CAATACGGTA GATGCATCAG TAGGTCTTTG GAAAACTGT ACCAACATTA 360
GCTGCAGTGA CAGCCTGTCA TATGCCAGTG AAGATGCCCT CAAGACAGTG CAGGCCCTTC 420
TGATTCTCTC TATCATCTTC TGTGTATTG CCTCTCTGCT CTTCGTGTTT CAGCTCTTCA 480
CCATGGAGAA GGGAAACCGG TTCTTCTCT CAGGGGCCAC CACACTGGTG TGCTGGCTGT 540
GCATTCTGT GGGGGTGTCC ATCTACACTA GTCATTATGC GAATGCTGAT GGAACGCACT 600
ATCACCAAGG CTATTCTTAC ATCTCTGGCT GGATCTGCTT CTGCTTCAGC TTCATCATCG 660
GCGTCTCTTA TCTGCTCTG AGAAAGAAAT AAGGCCGGAC GAGTTCATGG GGATCTGGGG 720
GGTGGGGAGG AGGAAGCCGT TGAATCTGGG AGGGAAGTGG AGGTTGCTGT ACAGGAAAAA 780
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GATGCTCCCT TGATGGGGTC CAGAGAGCCT CCCTGCAGCC ACCAGACTTG GCCTCCAGCT 960
GTTCTTAGTG ACACACACTG TCTGGGGCCC CATCAGCTGC CACAACACCA GCCCCACTTC 1020
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GCTCTTCTG AGTTTCTCTA AAGTCACTAG TGAACAATT GGTGTAATA GTACCAACA 1500
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TCAATGTAGC ACAAATCTAT TACTCTTCTT CTAACATTTT TGAGGAAGTT TTGTCTAATT 1680
ATCAATATTG AGGATCAGGG CTCTAGGCT CAGTGGTAGC TCTGGCTTAG ACACCACTCG 1740
GAGTGATCAC CTCTTGGGGA CCTGCTTAT CCCACTTAC AGGTGAAGCA TGGCAATTCT 1800

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5 GGAAGCTGAT TAAACACAC ATAAACCAA ACCAAACAAC AGGCCCTTGG GTGAAAGGTG 1860
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 GCATTCCAG GAAATACGA AATCCCATG AGATAAATAA AAATATAGGT GATGGGCAGA 1980
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 15 ACCATGATT CCCTTATCTT TACTTTTTT TCTGTGACAT TTATGTCTCA TGTAAATTTC 2640
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20 Seq ID NO: 608 Protein sequence
 Protein Accession #: NP_001414.1

1 11 21 31 41 51
 25 MLVLLAGIFV VHIATVIMLF VSTIANVWL V SNTVDASVGL WNKCTNISCS DLSYASEDA 60
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30 Seq ID NO: 609 DNA sequence
 Nucleic Acid Accession #: NM_004961.2
 Coding sequence: 55..1575

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 40 GACCACAAAC TGCGCCTCTG CATGTGAGAG AAGCCCACTG TGGTCACTGT TGAGATCGCC 360
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 45 CCAATGGATT CTCACCTCTG CCCTCTATCT TTCTTAGCT TTTCTATCC TGAGAATGAG 720
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 60 TACTGAGAG TTGTTTTCOC AGTGACTTTC TTCTCTTCA ATGTGCTCTA CTGGCTTGT 1620
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 70 TCAGATTATT ATGTTCTCAG TTCTCTCTCC CTGCTACCCC TTTCTCTGCA GATAGATAGA 2220
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 75 ACTTTCCAG TGACTTCCC TAGCCCTGAC CCAGSCACTA GGCCTTGGT ACTTCTGGG 2520
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 80 GATAGCCTTG TGACATCTTT AGGCGAGGAT TCTTATCCCC ATTTTGAGA TGAACACCT 2820
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 GGCTGAGGT GCTCAGACTG CCCCAGAT CAAATCTCTC CTGGCTGTAG TAACCCAGT 3060
 GAATGAATTT GGACATGCC CAATGCTCT ATATGCTAAG TGAATCTGT GTCTGTAAT

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Seq ID NO: 610 Protein sequence
Protein Accession #: NP_004952.1

5
1 11 21 31 41 51
10 MLKVLPLVLL GILLILQSRV EGPQTESKNE ASSRDVVYGP QPQPLENQLL SEETKSTETE 60
TGSRVGLKPE ASRLINTILS NYDHKLKPGI GEKPTVVIVE IAVNSLGLPLS ILDMETITDI 120
IFSQTWYDER LCYNDTFBSL VLVGNVVSQ L WIPDTFFRNS KRTHHEBITM PNQMVRIYKD 180
GKVLTYTIRM IDAGCSLHML RFPMDSHSCP LSFSSFSYPE NEMIIKWNF KLEINEKNSW 240
KLFQFDFPTGV SNKTBIIITP VGDFMVMTIF FNVSRFPYV AFQNYVPSV TMLSWVSWF 300
IKTESAPART SLGITSVLTM TTLGTFSRKN FPRVSYITAL DFYIAICFVF CFCALLEFAV 360
15 LNFLIYNQTK ARASPKLRHP RINSRAHART RARSACARQ HQEAFVQIV TTEGSDGER 420
PSCSAQPPPS PGSPGPRSL CSKLACCEWC KRFKKYFCMV PDCEGSTWQQ GRLCIHVYRL 480
DNYSRVVPV TFFFNVLVYV LVCLNL

Seq ID NO: 611 DNA sequence
Nucleic Acid Accession #: NM_021984.1
Coding sequence: 572..1753

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CAGAGAAGTG CTCAAATCAT AAGTGTACAG CTGATGAGTT GTCAAAAAAT GACCACAGCG 180
GTGTAAGAA AGCCAAATCA AGGACCCGAA TGTGAGCAGG ACCTCAGAA CCCCCTTTGT 240
CACTGCTCC CAGCAAAGGC AGCACTATCC GGACTTCTAA CACCATCGGG TCGAGGGACC 300
30 TCAGACTGAA TCAAGAATG AAGCCTCTTC CGTGTATGTT GTCTATGGCC CCGAGCCCCA 360
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35 CCAGACCTGG TACGACGAAC GCCTCTGTTA CAACGACACC TTGTAGTCTC TTGTTCTGAA 660
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40 GATCTACRAG TGGAAAAATT TCAAGCTTGA AATCAATGAG AAGAACTCCT GGAAGCTCTT 960
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45 GGGCACCTTT TCTGTAAGA ATTTCCCGCG TGCTCTCTAT ATCACAGCCT TGGATTCTTA 1260
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55 CCTTAACTTG TAGTACCAG CTGTACCTT GTGGGGCAAC CTCTCCAGT CCCCAGGAGG 1800
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70 CAAGAACTA AGGAAACTCG GCTTTGCAAC AGGCATTACT CGCATTGAT TGGTGCCAC 2700
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75 GTCACAGATT TCTGTGGGAC TGTGATCTC ACTGGAAGCT ATCCAAGAGC CCACTGTAC 3000
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CCTGAGGTGC TCAGACTGCC CCAAGATCA AATCTCTCCT GCGTGTAGTA ACCCACTGGA 3180
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80 TTGGGGGGTG GATAGGTTGG GTCTCCATC TACTTTTTGT CACCATCATC TGAATGGGG 3300
AAATATGTAA ATAAATATAT CAGCAAAGC

Seq ID NO: 612 Protein sequence
Protein Accession #: NP_068819.1

1 11 21 31 41 51
 MEYTIIDIIIFS QTWYDERLCY NDTFESLVLN GNVVSQLWIP DTFERNKRT HEHEITMPNQ 60
 5 MVRIYKDGKV LYTIRMIDTA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWFNFKLE 120
 INEKNSWKLQ QLDFTGVSNN TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTTM 180
 LSWVSWFIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDFY IAIQVFCFCF 240
 ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE AFVQCQIVTTE 300
 GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCEWCKRF KKYFCMVDFC EGSTWQQAARL 360
 10 CIHVYRLDNY SRVVFVTFPF FPNVLYMLVC LNL

Seq ID NO: 613 DNA sequence
 Nucleic Acid Accession #: NM_021987.1
 Coding sequence: 572..1657

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 20 CAGAGAAGTG CTCAAATCAT AAGTGTACAG CTGATGAGTT GTCAAAAAT GACCACAGCG 180
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Seq ID NO: 614 Protein sequence
 Protein Accession #: NP_068822.1

75 1 11 21 31 41 51
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 80 VMTIFFNVSR RFGYVAFQNY VPSSVTTMLS WSPFWIKTES APARTSLGIT SVLMTTLGT 180
 FSRKNFPRVS YITALDFYIA ICFVFCFALC LEFAVLNFI YNQTKAHASP KLRHPRINSR 240
 AHARTRARSR ACARQHQEAF VQIVTTEGS DGEERPSCSA QQPPSPGSPE GPRSLCSKLA 300
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Seq ID NO: 615 DNA sequence
Nucleic Acid Accession #: NM_021990.1
Coding sequence: 1309..2490

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20     TTTTCTCTTA AATAAAGAG TGATCATAAA AGAGGGACAG CATAGAAAGT CCCCAAAGAG 840
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30     GAGTCTCTTG TTCTGAATGG CAATGTGGTG AGCCAGCTAT GGATCCCGGA CACCTTTTTT 1440
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Seq ID NO: 616 Protein sequence
Protein Accession #: NP_068830.1

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MVRIVYDGVV LYTIKMTIDA GCSLHMLRFP MDSHSCPLSF SSPSYPENEM IYKWNFKLE 120
INEKNSWLKQ QPDTGVSNK TEIITPVGD FMVMTIFFNV SRREGVVAFO NYVPSSVTM 180
LSWVSFWIKT ESAPARTSLG ITSVLMTMTL GTPSRKNPPR VSYITALDPY IAICFVPCFC 240

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ALLEFAVLNLF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE AFVCQIVTTE 300
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5 Seq ID NO: 617 DNA sequence
 Nucleic Acid Accession #: NM_004864.1
 Coding sequence: 26..952

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35 Seq ID NO: 618 Protein sequence
 Protein Accession #: NP_004855.1

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 40 HRALPRLSPT ASRSWDVTRP LRRQLSLARP QAPALHLRLS PPSQSDQLL AESSARPOL 180
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45 Seq ID NO: 619 DNA sequence
 Nucleic Acid Accession #: NM_003979.2
 Coding sequence: 254..1357

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10 Seq ID NO: 620 Protein sequence
Protein Accession #: NP_003970.1

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KLVRGRKPLS LLVILGLAVG FSLVQDVIAI EYIVLTHNRT NVNVFSELSA PERNEDFVLL 180
LTYVLFMAL TFLMSSFTFC GSFTGWRKHG AHLYLTMLLS IAIWVANITL LMLPDPDRRW 240
DDTILSSALA ANGWVFLLAY VSPEFWLLTK QRNPMDYFVE DAFCKPQLVK KSYGVENRAY 300
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20 Seq ID NO: 621 DNA sequence
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45 ATGGTGTGAC TGTGCTTAT TCCATCTATG AGCTTTGTCA GTGCGGTAG ATGTCAATAA 1080
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Seq ID NO: 622 Protein sequence
Protein Accession #: NP_002414.1

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55 APGTGLGGDA HFDEDERWTD GSSLGINFLY AATHELHSL GMGHSSDPNA VMYPTYGNDD 240
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60 Seq ID NO: 623 DNA sequence
Nucleic Acid Accession #: NM_031457.1
Coding sequence: 204..956

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CTGTGTGGT GTTGGCACCC CACAATGGTT ATCTCTGTAC CCCAGGAAT ATGTCTCAG 300
TGCCCTGTGA TCCAAACAGC CAGCCGCAAG TCCACTAGT TCCCTGGAAC CCACCTAGTT 360
70 TGTGTTCGAA TGTGAATGGG CAGCCTGTGC AGAAAGCTCT GAAAGAAAGC AAAACCTTGG 420
GGGCCATCCA GATCATCATT GGCCTGGCTC ACATGGGCTC CGGCTCCATC ATGGGACGG 480
TTCTGTAGG GGAATACCTG TCTATTTCAT TCTACGGAGG CTTCCTCTTC TGGGAGGGCT 540
TGTGTTTAT CATTTCAAGA TCTCTCTCG TGGCAGCAGA AATCAGCCA TATTCTTATT 600
GCCTGCTGTC TGGCAGTTTG GGCCTGAACA TCGTCAGTGC AATCTGCTCT GCACTTGGAG 660
75 TCATACTCTT CATACAGAT CTAAATATTC CCCACCCATA TGCTTACCCC GACTATTATC 720
CTTACGCTCG GGTGTGAAC CCTGGAATGG GATTTCTTGG CGTCTGTCTG GTCTCTGCTC 780
TCTGTAGG TGGCATCGTA TGGCATCTT CCCACTTGG CTGCCAGTTG GTCTGCTGTC 840
AATCAAGCAA TGTGAGTGTG ATCTATCCAA ACATCTATGC AGCAAAACCA GTGATCACCC 900
CAGAACCGGT GACCTCACCA CCAAGTTATT CCACTGAGAT CCAAGCAAT AAGTAAGGCT 960
80 ACAGATTCTG GAAGCATCTT TCACTGGGAC CAAAGAAAGT CCTCTCCCT TTCTGGGCTT 1020
CCATAACCCA GGTCTTCTCT GTTCTGACAG CTGAGGAAAC GTCTCTCCCA CTGTTGTGAC 1080
TCTCACCTTC ATTTCTCAAT TCAGTCTAGG AAACCATGCT GTTCTCTAT CAAGAAGGAG 1140
ACAGAGATT TAAACAGATG TTAACCAAGA GGGACTCCCT AGGGACATG CATCAGCACA 1200
TATGTGGGCA TCCAGCTCTT GGGGCTTGG CACACACACA TTGCTGTGCT CTGCTGCATG 1260

TGAGCTTG TG GGTAGAGGA ACAAATATCT AGACATTCAA TCTTCACTCT TTCAATTGTG 1320
CATTATTTA ATAAATAGAT ACTGAGCATT CAAAAA AAAAAA

Seq ID NO: 624 Protein sequence
Protein Accession #: NP_113645.1

1 11 21 31 41 51
| | | | |
MNSMTSAVPV ANSVLVVAPH NGYPVTPGIM SHVPLYPNQ PQVHLVPGNP PSLVSNVNGQ 60
10 PVQKALKKQK TLGAIQIIIG LAHIGLGSIM ATVLVGEYLS ISFYGGFFWF GGLWFIISGS 120
LSVAENQPY SYCLLSGSLG LNIWVAICSA VGVILFITDL SIPHPYAYPD YYPYAWGVNP 180
GMAISGVLLV FCLLEFGIAC ASSHFGCQLV CQSSNVSVI YPNIAANPV ITPEPVTSP 240
SYSSEIQANK

Seq ID NO: 625 DNA sequence
Nucleic Acid Accession #: NM_005221.3
Coding sequence: 1..870

1 11 21 31 41 51
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ATGACAGGAG TGTITGACAG AAGGGTCCCC AGCATCCGAT CCGGGGACTT CCAAGCTCCG 60
20 TTCCAGACGT CCGCAGCTAT GCACCATCCG TCTCAGGAAT CGCCAACTTT GCCCGAGTCT 120
TCAGTACCG ATTCTGACTA CTACAGCCCT ACGGGGGGAG CCGGCACCG CTACTGCTCT 180
CCTACCTCG CTCTCTATGG CAAAGCTCTC AACCCCTACC AGTATCAGTA TCACGGCGTG 240
25 AACGGCTCCG CCGGAGGCTA CCCAGCCAAA GCTTATGCCG ACTATAGCTA CGCTAGCTCC 300
TACCACCACT ACGGCGCGCG CTACAACCCG GTCCCAAGCG CCACCAACCA GCCAGAGAAA 360
GAAGTGACCG AGCCCGAGGT GAGAATGGTG AATGGCAAAC CAAAGAAAAGT TCGTAAACCC 420
AGGACTATTT ATTCCAGCTT TCAGCTGGCC GCATTACAGA GAAGGTTTCA GAAGACTCAG 480
TACCTCGCTT TGCCGGAACG CGCCGAGCTG CGCGCTCCG TGGGATTGAC ACAACACAG 540
30 GTGAAATCT GTTTTCAGAA CAAAAGATCC AAGATCAGA AGATCATGAA AAACGGGAG 600
ATGCCCCCG AGCAGCTCC CAGCTCCAGC GACCCATGCG CGTGTAACCT GCGCGAGTCT 660
CCAGCGGTGT GGGAGCCCCA GGGCTCGTCC CGCTCGCTCA GCCACCAACC TCATGCCAC 720
CCTCCGACCT CCAACCACTC CCCAGCGTCC AGCTACCTGG AGAAGTCTGC ATCCTGGTAC 780
35 ACAAGTGCAG CCAGCTCAAT CAATCCAC CTGCGCGCG CCGGCTCCTT ACAGCACCCG 840
CTGGCGCTGG CTTCCGGGAC ACTCTATTAG

Seq ID NO: 626 Protein sequence
Protein Accession #: NP_005212.1

1 11 21 31 41 51
| | | | |
MTGVFDRRVP SIRSDFQAP FQTSAMHHP SQESPTLPES SATDSYYSP TGGAPHGYCS 60
40 PTSASYGKAL NPQYQYHGV NGSAGSYPAK AYADYSYASS YHQYGGAYNR VPSATNQPEK 120
EVTEPEVRMV NGPKPKVRKP RTIYSSFLQA ALQRRFQKTQ YLALPERAEL AASLGLTQTQ 180
45 VKIWFQNKRS KIKKIMKNGE MPPEHSPSSS DPMACNSPQS PAVNEPQSSS RSLSHHPHAH 240
PPTSNGSPAS SYLENSASWY TSAASSINSH LPPPGSLQHP LALASGTLV

Seq ID NO: 627 DNA sequence
Nucleic Acid Accession #: NM_014420
Coding sequence: 118..792

1 11 21 31 41 51
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55 AGCCTCGCTT TGGTGAAGCA CAGTGCTGGG ACCCTCCAGG AGCCCCGGGA TTGAAGGATG 120
GTGCGGCGCG TCCTGCTGGG GCTGAGCTGG CTCTGCTCTC CCCTGGGAGC TCTGGTCTG 180
GACTTCAACA ACATCAGGAG CTCTGCTGAC CTGCATGGG CCGGGAAGGG CTCACAGTGC 240
CTGTCTGACA CGGACTGCAA TACCAGAAAG TTCTGCCTCC AGCCCCGCGA TGAGAAGCCG 300
TTCTGTGCTA CATGTCGTGG GTTGCAGAG AGGTGCCAGC GAGATGCCAT GTGCTGCCCT 360
60 GGGACACTCT GTGTGAACGA TGTGTGTACT ACGATGGAAG ATGCAACCCC AATATTAGAA 420
AGGCAGCTTG ATGAGCAAGA TGGCACACAT GCAGAAGGAA CAAGTGGGCA CCCAGTCCAG 480
GAAACCAAC CCAAGAGGAA GCCAAGTATT AAGAAATCAC AAGGCAGGAA GGGACAAGAG 540
GGAGAAAGTT GTCTGAGAAC TTGTGACTGT GGCCTGGAC TTTGCTGTGC TGTCTATTT 600
TGGACGAAAA TTGTGAAGCC AGTCTCTTTG GAGGGACAGG TCTGCTCCAG AAGAGGGCAT 660
65 AAAGACACTG CTCAGCTCC AGAAATCTTC CAGCGTTGCG ACTGTGCGCC TGGACTACTG 720
TGTGGAAGCC AATTGACAG CAATCGGCAG CATGCTCGAT TAAGAGTATG CCAAAAAATA 780
GAAAAGCTAT AAATATTTC AATAAAGAA GAATCCACAT TGCAAAAAA AAAAAAATA 840
A

Seq ID NO: 628 Protein sequence
Protein Accession #: NP_055235

1 11 21 31 41 51
| | | | |
MVAALLGLS WLCSPLGALV LDFNNIRSSA DLHGARKGSQ CLSDTDCNTR KFCQLPRDEK 60
75 PFCATCRGLR RRCQRDAMCC PGTLCVNDVC TIMEDATPIL ERQLDEQDGT HAEGTTGHPV 120
QENQPKRKPS IKKSQGRKGQ BGESCLRTFD CGPLCCARH FWTKICKPVL LEGQVCSRRG 180
HKDTAQAPBI FQRCDGPGI LCRSQTLSNR QHARLRCQK IEKL

Seq ID NO: 629 DNA sequence
Nucleic Acid Accession #: NM_002448.1
Coding sequence: 241..1134

1 11 21 31 41 51
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GCGGAGTGC TCCCGGGAAC TCTGCCTGCG CGGCGGCAGC GACCGGAGGC CAGGCCAGC 60
ACGCGCGAGC TGGCCTCTGT GGGAGGGGGG GAGAGGGGCG GCGGGAGGGT CCGCCCGGCC 120
AGGCCCCGGG CCCTCGCAGA GGCOCGGCGC GCTCCAGACC GCGCGGAGC CCATGCGCGG 180
CGGCTGGCCA GTGCTGCGGC AGAAGGGGGG GCGCGGCTCT GCATGGCCCC GGCTGCTGAC 240
ATGACTTCTT TGCCACTCGG TGTCAAAGTG GAGGACTCGG CCTTCGGCAA GCGGCGGGGG 300
GGAGGCGCGG GCCAGGCCCC CAGCGCGGCC GCGGCCACGG CAGCGCGCAT GGGCGGGGAC 360
GAGGAGGGGG CCAAGCCCCA AGTGTCCCTC TCGCTCTGCT CCTTCAGCGT GGAGGCGCTC 420
ATGGCGGACC ACAGGAAGCC GGGGGCCAA GAGAGCGCCC TGGCGCCCTC CGAGGGGCTG 480
CAGGCGGGGG GTGGCTCGGC GCAGCCACTG GCGTCCCGC GGGGTCTGCT GGGAGCCCCG 540
GACGCGCCCT CTTCGCGCGG GCGCTCGGC CATTTCTCGG TGGGGGGACT CCTCAAGCTG 600
CCAGAAGATG CGCTCGTCAA AGCGAGAGGC CCGAGAAAGC CCGAGAGGAC CCGTGGATG 660
CAGAGCCCCC GCTTCTCCCC GCGCGCGGCC AGCGGCTGA GCGCCCGAGC CTGCACCTCT 720
CGCAAAACAC AGACGAACCG TAAGCGCGG ACGCCCTTCA CCACCGGCA GCTGCTGGCG 780
CTGGAGCGCA AGTTCGCCA GAAGCAGTAC CTGTCCATCG CCGAGCGCGC GGAGTTCTCC 840
AGCTCGCTCA GGCTCACTGA GACGCAAGTG AAGATATGTT TCCAGAACCG CCGCGCCAAG 900
GCAGAAAGAG TACACAGGCG AGAGCTGGAG AAGCTGAAGA TGGCCCGCAA GCGCATGCTG 960
CCACCGGCTG CCTTCGGCTT CTCTTCCCTC CTGGCGGGCC CCGCAGCTGT AGCGGCGCGG 1020
GGGGGTGCTT CGCTCTAGGG TGCTCTGGC CCCTTCCAGC GCGCGCGCTC GCTGTGGGG 1080
CCCGTGGGAC TCTACACGGC CCATGTGGGC TACAGCATGT ACCACCTGAC ATAGAGGGTC 1140
CCAGGTCCCC ACCGTGGGGC CAGCGGATTC CTCCAGCCCT GGTGTGTGAC CCGCGACGTG 1200
CTCCCTGCTT CCGCAGCGCC AGCGGCTTTC CCTTTAAACC TCACACTGCT CCACTTTTAC 1260
CTCTTTGCTC CCGAGTTTCA CTCTCGAAG TCTGATCCCT GCCAAAAGT GGTGGAAGA 1320
GTCCCTTAGT ACTCTTCTAG CATTTAGATC TACACTCTCG AGTTAAAGAT GGGGAAACTG 1380
AGGCGAGAGA GGTAAACAGA TTTATCTAGG GTCCCGAGCA GAATTGACAG TTGAACAGAG 1440
CTAGAGGCGA TGTCTCTGCG ATAGCTTTTC CCTGTCTGTA CACCAAGCAA GAAAGCGCA 1500
GAGAAATCGG TGTCTGACGA TTTTGAAAT GAGAACATC TCAAAAAAAA AAAAAAAA 1560
AAAAAAGAAA GAAAGAGAAA AAAAAAGACT AGCCAGCCAG GAAGATGAAT CCTAGCTTCT 1620
TCCATTGGAA AATTTAAGAC AAGTTCAACA ACAAACATT TGCTCTGGGG GGCAGGGAAA 1680
ACACAGATGT GTTGCAAGG TAGGTTGAAG GGA

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Seq ID NO: 630 Protein sequence
Protein Accession #: NP_002439.1

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1 11 21 31 41 51
MTSLPLGVKIV EDSAFGKPAQ GGAGQAPSAA AATAAAMGAD EBGAKPKVSP SLLPFSVEAL 60
MADHRKPGAK ESALAPSEGV QAAGGSAQPL GVPPGSLGAP DAPSPSPRLG HPSVGGLLKL 120
PEDALVKAES PEKPERTPMW QSPRPSPPPA RRLSPFACLT RKHKTNRKPR TPFTTAQLLA 180
LEKRFQKQY LSLAERAEPF SLSLTETQV KIWFQNRRAK AKRLQEALE KLKMAAKPML 240
PPAPFGLSFP LGGPAVAAA AGASLYGASG PFQRAALPVA PVGLYTAHVQ YSMYHLT

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Seq ID NO: 631 DNA sequence
Nucleic Acid Accession #: NM_002557.1
Coding sequence: 13..2049

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1 11 21 31 41 51
CAGACCATTC AGATGTGGAA GCTGTTGCTG TGGGTTGGGC TGGTTCCTGT GCTGAAACAC 60
CAGATGGTG CTGCCATAA ACTCGTGTGT TATTTACCA ACTGGGCACA CAGTCGGCCA 120
GGCCTGCTCT CGATCTTGCC CCATGACCTG GACCCCTTTC TCTGACCCA CCTGATATTT 180
GCCTTTGCTT CAATGAACAA CAATCAGATT GTTGCTAAGG ATCTCCAGGA TGAGAAAATT 240
CTCTACCCAG AGTTCAACAA ACTAAAGGAG AGGAACAGAG AGCTGAAAAC ACTACTGTCC 300
ATCGGCGGGT GGAACCTTGG CACCTCAAGA TTCACCATA TGTGTCCAC ATTTGCCAAC 360
CGTGAAAAGT TTAATGCTTC AGTTATATCC CTCTGAGGA CACATGACTT TGATGTCTCT 420
GACCTTTTCT TCTATATACC TGGACTAAGA GGCAGCCCCA TGCTGACCG GTGGACTTTT 480
CTCTTCTTAA TTGAAGAGCT CCGTTTGGC TTCCGGAAGG AGGCACTGCT CACCATGCGC 540
CGAGGGCTGC TGCTGTCTGC TGCTGTTTCT GGGGTCCAC ACATCGTCCA AACATCCTAT 600
GATGTGCGCT TTCTAGGAAG ACTCCTGGAT TTCACTAATG TCTGTCTTAT TGACTTACAT 660
GGAAGTTGGG AAAGGTTTCA AGGACATAAT AGCCCTCTCT TCTCTCTGCC TGAAGACCCC 720
AAATCTTGGG CATATGCTAT GAATATTGG AGAAAGCTTG GGGCACCCCT AGAGAAGCTC 780
ATCATGGGGA TCCCACTTA TGGACGTACC TTTGCTCTCC TCAAAGCTTC TAAGAATGGG 840
TTGCAGGCCA GAGCGATCGG ACCAGCATCT CCAGGGAAGT ACACCAAGCA AGAAGGCTTC 900
TTGGCTTATT TTGAGATTGG TTCTTTGTC TGGGGAGCGA AGAAGCACTG GATTGATTAC 960
CAGTATGTCC CGATGCGCAA CAAGGGGAAA GAGTGGGTTG GCTATGACAA TGCCATCAGC 1020
TTCACTTACA AGGCATGTTT TATAAGGCGA GAGCATTTTG GGGGGGCCAT GGTGTGGACA 1080
TTGGACATGG ATGACGTGAG GGGCACGTTT TGTGGCACTG GCGCTTCCCT CCTGTCTAC 1140
GTATTGAATG ATATCCTGGT GCGGGCTGAG TTCAGTTCAA CTCTTTTACC ACNATTTTGG 1200
CTGTCTCTG CTGTGAATTC TTCAAGCACT GACCCGAAA GCGTGGCTGT GACCAGGGCA 1260
TGGACCACTG ATAGTAAGAT TTTGCCCCCA GGAGGAGAGG CTGGGGTCAC TGAGATCCAC 1320
GGAAAGTGTG AAAATATGAC TATAACCCCT AGAGGTACAA CTGTGACCCC TACAAAGGAA 1380
ACTGTATCCC TTGGAAGCA CACTGTAGCT CTAGGAGAGA AGACTGAGAT CACTGGGGCA 1440
ATGACCATGA CTCTGTGGG TCATCAGTCC ATGACCCCTG GAGAGAAGGC CCTGACCCCT 1500
GTGGGTCTAT AATCTGTGAC CACTGGACAG AAGACCCCTG CCTCTGTGGG TTATCAGTCT 1560
GTGACCCCTG GGGAAAAGAC CCGAACCCCT GTGGGTATC AGTCTGTGAC CCCTGTGAGT 1620
CATCAGTCTG TGAGCCCTGG AGGAACGACT ATGACCCCTG TCCATTTTCA GACTGAGACC 1680
CTTAGACAGA ATACAGTGCC CCTAGAAGG AAGGCTGTGG CCGGTGAAA GGTGACTGTC 1740
CCCTCCAGAA ACATATCAGT CACCCCTGAA GGGCAGACTA TGCCCTTAA GGGGAGAAAT 1800
TTGACTTCTG AGGTGGGCAC TCACCCCGAG ATGGGTAACT TGGGTCTTCA GATGGAAGCT 1860
GAAAACAGGA TGAATGCTGC CTCCAGCCCC GTCACTCCAG TCCCGGAACA AACTCTCTA 1920
GCTTTTACCA ACGCTTTTGT TCCCATCTAT GAAAACCACT CCTCTGTCAA CTCACTAACC 1980
CCTCAACAAA GTCTCTTTTC TCTAAAAAAA GAAATCCAG AAAACTCTGC TGTGGATGAA 2040
GAAGCCTAAG CCGCTCTGGT GTCAGAAACC AGGGAAGAAC CTGTCTTTT CTCTCAAGTG 2100
ACATGTGGA AGCCTTCTCA TCCCGGGGCA AAGCAGGCAT CAAAACAGAA ATAGGCCAAT 2160

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CTCTTTTCCA TTAAATAAAC TGTAACACA AGAACCCA

Seq ID NO: 632 Protein sequence
 Protein Accession #: NP_002548.1

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1	11	21	31	41	51	
MMKLLLVNVL	VLVLKHHGDA	AHKLVCYFTN	WAHSRPGPAS	ILPHDLDPFL	CTHLIFAFAS	60
MNNNQIVAKD	LQDEKILYPE	FNKLKERNRE	LKTLISIGGW	NFGTSRPTTM	LSTFANREKF	120
IASVISLLRT	HDFFGLDLFF	LVPGLRGSPM	HDRWTFLLFI	EELLFAFRKE	ALLTMRPRLL	180
LSAAVSGVPH	IVQTSYDVRF	LGRLLDFFIN	LSYDLHGWS	RFTGHSPLF	SLPEDPKSSA	240
YAMNYWRKLG	AFSEKLIMGI	PTYGRTFRLL	KASKNGLQAR	AIGPASPGKY	TKQSGFLAYF	300
EICSPVMGAK	KHWIDYQYVP	YANKGKEWVG	YDNAISFSYK	ANFIRREHFG	GAMVWTLDM	360
DVRGTFCGTG	PFPLVYVLND	ILVRAEFSST	SLPQFWLSSA	VNSSSTDFER	LAVTTAWTTD	420
SKILPPGGEA	GVTIHKCE	NMTITPRGTT	VTPTKETVSL	GKHTVALGSK	TEITGAMTMT	480
SVGHQSMTPG	EKALTPVGHQ	SVTTGQKTLT	SVGYQSVTPG	EKTLTPVGHQ	SVTPVSHQSV	540
SPGGTITMFPV	HFQETTLRQN	TVAPRRKAVA	REKVTVPSPN	ISVTPBGQTM	PLRGENLTSE	600
VGTHPRMGNL	GLQMEANRM	MLSSSPVIQL	PEQTPLAFDN	RFVPIYGNHS	SVNSVTPQTS	660
PLSLKKEIPE	NSAVDEEA					

Seq ID NO: 633 DNA sequence
 Nucleic Acid Accession #: NM_003885.1
 Coding sequence: 98..1021

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1	11	21	31	41	51	
AAACTCAGAA	TTTTCGCGGG	CTCGGTGAGC	GGTTTATACC	CTCCGCGCGG	CAGGCTGGGC	60
GCAGGGGGCG	AGCCCCCGCC	CGGCGGCGAG	CAGCACCATG	GGCACGGTGC	TGTCCCTGTC	120
TCCAGCTAC	CGGAAGGCCA	CGCTGTTTGA	GGATGGCGCG	GCCACGGTGG	GCCACTATAC	180
GGCCGTACAG	AACAGCAAGA	ACGCCAAGGA	CAAGAACCTG	AAGCGCCACT	CCATCATCTC	240
CGTGCTGCCT	TGGAAGAGAA	TCGTGGCGGT	GTGCGCCAAG	AAGAAGAACT	CCAAGAAGGT	300
GCAGCCTAAC	AGCAGCTACC	AGAACAACAT	CACGCACCTC	AACAATGAGA	ACCTGAAGAA	360
GTCGTCTGCG	TGCGCCAACC	TGTCCACATT	CGCCAGCCCC	CCACCGCCCC	AGCCGCTGTC	420
ACCCCGGGCC	AGCCAGCTCT	CGGGTTCCCA	GACCGGGGGC	TCCTCCTCAG	TCAAGAAAGC	480
CCCTCACCCCT	GCCGTCACTT	CCGCAGGGAC	GCCCAACGGG	GTCTATGTTCC	AGGCGTCCAC	540
CAGTGAGCTG	CTTCGCTGCC	TGGGTGAGTT	TCTCTGCCGC	CGGTGCTACC	GCCTGAAGCA	600
CCGTGCCCCC	ACGACCCCGG	TGCTCTGGCT	GCGCAGCGTG	GACCGCTGCG	TGCTTCTGCA	660
GGGCTGGCAG	GACCAGGGCT	TCATCAGGCC	GGCCAACGTG	GTCTTCTCTT	ACATGCTCTG	720
CAGGATGTTT	ATCTCCTCCG	AGGTGGGCTC	GGATCACGAG	CTCCAGGCGG	TCCTGCTGAC	780
ATGCTGTATC	CTCTCCTACT	CCTACATGGG	CAACGAGATC	TCCTACCCGC	TCAAGCCCTT	840
CCTGGTGGAG	AGCTGCAAGG	AGGCCTTTTG	GGACCGTTGC	CTCTCTGTCA	TCAACCTCAT	900
GAGCTCAAAG	ATGCTGCAGA	TAAATGCCGA	CCACACTAC	TTCACACAGG	TCTTCTCCGA	960
CCTGAAGAAC	GAGAGCGGCC	AGGAGGACAA	GAAGCGGCTC	CTCCTAGGCC	TGGATCGGTG	1020
AGCACTGTAG	CCTGCGTCAT	GGCTCAAGGA	TTCAATGCAT	TTTTAAGAAAT	TTATTATTAA	1080
ATCAGTTTTC	TGTACAG					

Seq ID NO: 634 Protein sequence
 Protein Accession #: NP_003876.1

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1	11	21	31	41	51	
MGTVLSLSPS	YRKATLFEDG	AATVGHYTA	ONSKNAKDN	LKRHSIISVL	PWKRIIVAVSA	60
KKNSKRVQVP	NSSVQNNITH	LNNENLKSL	SCANLSTFAQ	PPPAQPPAPP	ASQLSGSQTG	120
GSSSVKKAPE	PAVTSAGTPK	RVIVQASTSE	LLRCLGEFLC	RRCYRLKHL	PTDPVLNLR	180
VDRSLLQLGW	QDQGFITPAN	VVFLYMLCRD	VISSEVGSDH	ELQAVLLTCL	YLSYSYMGNE	240
ISYPLKPFV	ESCKEAFWDR	CLSVINLMSS	KMLQINADPH	YFTQVPSDLK	NESGQEDKKR	300
LLGLDLR						

TABLE 79A:

5	Key:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	Seq ID No.:	Sequence identification number linking information in Table 79A to sequences in Table 80			
10	Key	ExAccn	UnigeneID	Unigene Title	Seq ID No.
15	424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	Seq ID No. C1 & C217
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	Seq ID No. C2 & C218
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C3 & C219
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C4 & C220
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	Seq ID No. C5 & C221
20	443646	AI085188	Hs.164226	Thrombospondin 1	Seq ID No. C6 & C222
	409956	AW103364	Hs.727	Inhibin, beta A (activin A, activin AB a	Seq ID No. C7 & C223
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	Seq ID No. C8 & C224
	444381	BE387335	Hs.283713	hypothetical protein BC014245	Seq ID No. C9 & C225
	421582	AI910275	Hs.350470	trifol factor 1 (breast cancer, estroge	Seq ID No. C10 & C226
25	411789	AF245505	Hs.72157	Adican	Seq ID No. C11 & C227
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	Seq ID No. C12
	428698	AA852773	Hs.334838	KIAA1866 protein	Seq ID No. C13 & C228
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	Seq ID No. C14 & C229
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	Seq ID No. C15 & C230
30	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	Seq ID No. C16 & C231
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	Seq ID No. C17 & C232
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	Seq ID No. C18 & C233
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	Seq ID No. C19 & C234
	432179	X75208	Hs.2913	EphB3	Seq ID No. C20 & C235
35	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	Seq ID No. C21 & C236
	409889	AW630041	Hs.56937	suppression of tumorigenicity 14 (colon	Seq ID No. C22 & C237
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/V	Seq ID No. C23 & C238
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/V	Seq ID No. C24 & C239
	411975	AI916058	Hs.144583	3'UTR of: dead ringer (Drosophila)-like	Seq ID No. C25 & C240
40	434206	AW136973	Hs.362915	ESTs, Weakly similar to S69890 mitogen i	Seq ID No. C26 & C241
	423936	U77629	Hs.135639	achaete-scute complex (Drosophila) homol	Seq ID No. C27 & C242
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	Seq ID No. C28 & C243
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	Seq ID No. C29 & C244
	415214	AI445236	Hs.125124	EphB2	Seq ID No. C30 & C245
45	443247	BE614387	Hs.333893	c-Myc target JPO1	Seq ID No. C31 & C246
	422048	NM_012445	Hs.228126	spondin 2, extracellular matrix protein	Seq ID No. C32 & C247
	410418	D31382	Hs.63325	transmembrane protease, serine 4	Seq ID No. C33 & C248
	446342	BE298665	Hs.14846	solute carrier family 7 (cationic amino	Seq ID No. C34 & C249
	411274	NM_002776	Hs.69423	kallikrein 10	Seq ID No. C35 & C250
50	104978	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	Seq ID No. C36 & C251
	422260	AA315993	Hs.105484	regenerating gene type IV	Seq ID No. C37 & C252
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No. C38 & C253
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	Seq ID No. C39 & C254
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	Seq ID No. C40 & C255
55	437935	AW539591	Hs.5940	mucin 13, epithelial transmembrane	Seq ID No. C41 & C256
	422330	D30783	Hs.115263	epiregulin	Seq ID No. C42 & C257
	408908	BE296227	Hs.250822	serine/threonine kinase 15	Seq ID No. C43 & C258
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagonist	Seq ID No. C44 & C259
	437852	BE001836	Hs.256897	putative GPCR	Seq ID No. C45 & C260
60	408243	Y00787	Hs.624	Interleukin 8	Seq ID No. C46 & C261
	426088	AF038007	Hs.168198	ATPase, Class I, type 8B, member 1	Seq ID No. C47 & C262
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	Seq ID No. C48 & C263
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	Seq ID No. C49 & C264
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	Seq ID No. C50 & C265
65	417771	AA804698	Hs.82547	retinoic acid receptor responder (Iazaro	Seq ID No. C51 & C266
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	Seq ID No. C52 & C267
	442006	AW975183	Hs.372210	ESTs, Weakly similar to S72482 hypotheti	Seq ID No. C53 & C268
	413048	M93221	Hs.75182	mannose receptor, C type 1	Seq ID No. C54 & C269
	443324	R44013	Hs.164225	ESTs	Seq ID No. C55 & C270
70	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C56 & C271
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C57 & C272
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	Seq ID No. C58 & C273
	442652	AI005163	Hs.201378	Homo sapiens cDNA FLJ40427 fis	Seq ID No. C59 & C274
	450726	AW204600	Hs.355462	HUMPSFBA Human pulmonary surfactant-asso	Seq ID No. C60 & C275
75	416955	N26223	Hs.160436	MDAC1	Seq ID No. C61 & C276
	442275	AW449467	Hs.64795	Homo sapiens secretoglobulin, family 3A, m	Seq ID No. C62 & C277
	431745	AW972448	Hs.163425	Novel FGENSEH predicted cadherin repeat	Seq ID No. C63 & C278
	431745	AW972448	Hs.163425	Novel FGENSEH predicted cadherin repeat	Seq ID No. C64 & C279
	453142	AA033648	Hs.7473	Homo sapiens gap junction protein, alpha	Seq ID No. C65 & C280
80	421659	NM_014459	Hs.106511	protocadherin 17	Seq ID No. C66 & C281
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	Seq ID No. C67 & C282
	421563	NM_006433	Hs.105806	granulysin	Seq ID No. C68 & C283
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	Seq ID No. C69 & C284
	414991	C17898	Hs.105806	Homo sapiens up-regulated by BCG-CWS (LO	Seq ID No. C70 & C285
	419833	AA251131	Hs.220697	Homo sapiens tryptophanyl-tRNA synthetas	Seq ID No. C71 & C286
	424943	AU077260	Hs.153924	death-associated protein kinase 1	Seq ID No. C72 & C287

5	430890	X54232	Hs.2699	glypican 1	Seq ID No. C73 & C288
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	Seq ID No. C74 & C289
	439180	AJ393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	Seq ID No. C75 & C290
	410407	X66839	Hs.63287	carbonic anhydrase IX	Seq ID No. C76 & C291
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	Seq ID No. C77 & C292
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	Seq ID No. C78 & C293
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	Seq ID No. C79 & C294
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C80 & C295
10	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C81 & C296
	431846	BE019924	Hs.271580	uroplakin 1B	Seq ID No. C82 & C297
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	Seq ID No. C83 & C298
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	Seq ID No. C84 & C299
	428440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	Seq ID No. C85 & C300
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	Seq ID No. C86 & C301
15	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	Seq ID No. C87 & C302
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	Seq ID No. C88 & C303
	457819	AA057484	Hs.35406	FLJ20522 Hypothetical protein FLJ20522	Seq ID No. C89 & C304
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	Seq ID No. C90 & C305
20	418462	BE001596	Hs.85266	integrin, beta 4	Seq ID No. C91 & C306
	439606	W79123	Hs.58551	G protein-coupled receptor 87	Seq ID No. C92 & C307
	407720	AB037776	Hs.38002	immunoglobulin superfamily, member 9	Seq ID No. C93 & C308
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	Seq ID No. C94 & C309
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	Seq ID No. C95 & C310
25	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C96 & C311
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C97 & C312
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C98 & C313
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C99 & C314
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C100 & C315
30	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C101 & C316
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C102 & C317
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C103 & C318
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C104 & C319
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C105 & C320
35	409420	Z15008	Hs.54451	laminin, gamma 2 (necin (100kD), kalini	Seq ID No. C106 & C321
	440659	AF134160	Hs.7327	claudin 1	Seq ID No. C107 & C322
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C108 & C323
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C109 & C324
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C110 & C325
40	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	Seq ID No. C111 & C326
	414774	X02419	Hs.77274	plasminogen activator, urokinase	Seq ID No. C112 & C327
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	Seq ID No. C113 & C328
	453857	AL080235	Hs.35861	Ras-induced senescence 1 (RIS1)	Seq ID No. C114 & C329
	449101	AA205847	Hs.23016	G protein-coupled receptor	Seq ID No. C115 & C330
45	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	Seq ID No. C116 & C331
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	Seq ID No. C117 & C332
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	Seq ID No. C118 & C333
	408482	NM_000676	Hs.45743	adenosine A2b receptor	Seq ID No. C119 & C334
50	426761	AJ015709	Hs.172089	PORIMIN Pro-oncogene receptor inducing me	Seq ID No. C120 & C335
	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfam	Seq ID No. C121 & C336
	430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	Seq ID No. C122 & C337
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	Seq ID No. C123 & C338
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	Seq ID No. C124 & C339
55	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	Seq ID No. C125 & C340
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	Seq ID No. C126 & C341
	428513	BE220806	Hs.184697	plexin C1	Seq ID No. C127 & C342
	430280	AA361258	Hs.237868	interleukin 7 receptor	Seq ID No. C128 & C343
	428486	AW583497	Hs.184604	pancreatic polypeptide	Seq ID No. C129 & C344
60	457489	AI693815	Hs.127179	cryptic gene	Seq ID No. C130 & C345
	432874	W94322	Hs.279551	melanoma inhibitory activity	Seq ID No. C131 & C346
	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C132 & C347
	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C133 & C348
	404682			ortholog of mouse polydomain protein	Seq ID No. C134 & C349
65	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	Seq ID No. C135 & C350
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C136 & C351
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C137 & C352
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C138 & C353
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	Seq ID No. C139 & C354
70	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	Seq ID No. C140 & C355
	432586	AJ224741	Hs.278461	matrilin 3	Seq ID No. C141 & C356
	444006	BE395085	Hs.334762	type I transmembrane protein Fn14	Seq ID No. C142 & C357
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	Seq ID No. C143 & C358
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C144 & C359
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C145 & C360
75	428392	H10233	Hs.2255	secretory granule, neuroendocrine protei	Seq ID No. C146 & C361
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	Seq ID No. C147 & C362
	422109	S73265	Hs.1473	gastrin-releasing peptide	Seq ID No. C148 & C363
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	Seq ID No. C149 & C364
	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	Seq ID No. C150 & C365
80	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	Seq ID No. C151 & C366
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	Seq ID No. C152 & C367
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	Seq ID No. C153 & C368
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	Seq ID No. C154 & C369
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	Seq ID No. C155 & C370

5	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (C)	Seq ID No. C156 & C371
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	Seq ID No. C157 & C372
	416498	U33632	Hs.78351	potassium channel, subfamily K, member 1	Seq ID No. C158 & C373
	413095	AA494359	Hs.30715	potassium voltage-gated channel, Isk-rel	Seq ID No. C159 & C374
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	Seq ID No. C160 & C375
	436729	BE521807	Hs.351316	transmembrane 4 superfamily member 1	Seq ID No. C161 & C376
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	Seq ID No. C162 & C377
	451820	AW058357	Hs.199248	ESTs	Seq ID No. C163 & C378
10	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	Seq ID No. C164 & C379
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	Seq ID No. C165 & C380
	421340	F07783	Hs.1369	decay accelerating factor for complement	Seq ID No. C166 & C381
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C167 & C382
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C168 & C383
15	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	Seq ID No. C169 & C384
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	Seq ID No. C170 & C385
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	Seq ID No. C171 & C386
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	Seq ID No. C172 & C387
	439659	AW970780	Hs.59483	leucine-rich repeat-containing G protein	Seq ID No. C173 & C388
20	411825	AK000334	Hs.352415	solute carrier family 39 (zinc transport	Seq ID No. C174 & C389
	412314	AA825247	Hs.356084	G protein-coupled receptor 27 (GPR27) (S	Seq ID No. C175 & C390
	429150	AF120103	Hs.197368	smoothed (Drosophila) homolog	Seq ID No. C176 & C391
	419073	AW372170	Hs.183918	transmembrane receptor Unc5H2 mRNA	Seq ID No. C177 & C392
	411828	AW161449	Hs.72290	wingless-type MMTV integration site fami	Seq ID No. C178 & C393
25	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C179 & C394
	421779	AI879159	Hs.108219	wingless-type MMTV integration site fami	Seq ID No. C180 & C395
	439668	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	Seq ID No. C181 & C396
	433336	AF017986	Hs.31366	secreted frizzled-related protein 2 (str	Seq ID No. C182 & C397
	436972	AA284679	Hs.25640	claudin 3	Seq ID No. C183 & C398
30	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	Seq ID No. C184 & C399
	416370	N90470	Hs.203697	CD38 antigen (p45)	Seq ID No. C185 & C400
	437052	AA861697	Hs.120591	ESTs	Seq ID No. C186 & C401
	421481	AW391972	Hs.104696	KIAA1324 protein	Seq ID No. C187 & C402
	444151	AW972817	Hs.128749	alpha-methylacyl-CoA racemase	Seq ID No. C188 & C403
35	426174	AA547959	Hs.115838	Homo sapiens similar to Echinoidin (LOC1	Seq ID No. C189 & C404
	410037	AB020725	Hs.58009	KIAA0918 protein	Seq ID No. C190 & C405
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	Seq ID No. C191 & C406
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	Seq ID No. C192 & C407
	418576	AW968159	Hs.302740	Epithelial calcium channel 2, CaT-like A	Seq ID No. C193 & C408
40	419693	AA133749	Hs.301350	FXRD domain-containing ion transport reg	Seq ID No. C194 & C409
	419693	AA133749	Hs.301350	FXRD domain-containing ion transport reg	Seq ID No. C195 & C410
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C196 & C411
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C197 & C412
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C198 & C413
45	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C199 & C414
	430144	AI732722	Hs.98927	ERGL protein; ERGIC-53-like protein	Seq ID No. C200 & C415
	408833	AW612232	Hs.254835	ESTs	Seq ID No. C201 & C416
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	Seq ID No. C202 & C417
50	415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C203 & C418
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C204 & C419
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	Seq ID No. C205 & C420
	425976	C75094	Hs.334514	NG22 protein	Seq ID No. C206 & C421
	432800	BE391046	Hs.278962	AIM-1 protein	Seq ID No. C207 & C422
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	Seq ID No. C208 & C423
55	424339	BE257148	Hs.145416	endoglycan	Seq ID No. C209 & C424
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	Seq ID No. C210 & C425
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	Seq ID No. C211 & C426
	434293	NM_004445	Hs.3796	Eph86	Seq ID No. C212 & C427
	427715	BE245274	Hs.180428	KIAA1181 protein	Seq ID No. C213 & C428
60	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	Seq ID No. C214 & C429
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	Seq ID No. C215 & C430
	422424	AI186431	Hs.296638	prostate differentiation factor	Seq ID No. C216 & C431
	432378	AI493046	Hs.146133	ESTs	Seq ID No. C432 & C433
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No. C434 & C435

TABLE 79B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
414991	1785136_1	D78831 C17898 D78863

TABLE 79C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
------	-----	--------	-------------

5

404682	9797231	Minus	40977-41150
404287	2326514	Plus	53134-53281
404287	2326514	Plus	53134-53281
404287	2326514	Plus	53134-53281

Table 80:

Seq ID NO: C1 DNA Sequence
Nucleic Acid Accession #: NM_005814
Coding sequence: 345..1304

	1	11	21	31	41	51	
5	CTACCCCTTT	GTGAGCAGTC	TAGGACTTTG	TACACCTGTT	AAGTAGGGAG	AAGGCAGGGG	60
10	AGGTGGCTGG	TTTAAGGGGA	ACTTGAGGGA	AGTAGGGAAG	ACTCCTCTTG	GGACCTTTGG	120
	AGTAGGTGAC	ACATGAGCCC	AGCCCCAGCT	CACCTGCCAA	TCCAGCTGAG	GAGCTCACCT	180
	GCCAATCCAG	CTGAGGCTGG	GCAGAGGTGG	GTGAGAAGAG	GGAAAATTGC	AGGGACCTCC	240
	AGTTGGGCCA	GGCCAGAAGC	TGCTGTAGCT	TTAACCAGAC	AGCTCAGACC	TGTCTGGAGG	300
	CTGCCAGTGA	CAGGTTAGGT	TTAGGGCAGA	GAAGAAGCAA	GACCATGGTG	GGGAAGATGT	360
15	GGCCTGTGTT	GTGGACATCT	TGTGCAGTCA	GGGTGACCGT	CGATGCCATC	TCTGTGGAAA	420
	CTCCGACAGA	CGTTCTTCGG	GCTTCGCAGG	GAAAGAGTGT	CACCTTGCCC	TGCACCTACC	480
	ACACTTCAC	CTCCAGTCGA	GAGGGACTTA	TTCAATGGGA	TAAGCTCCTC	CTCACTCATA	540
	CGGAAAGGGT	GGTCACTCTG	COGTTTCAA	ACAAAACCTA	CATCCATGGT	GAGCTTTATA	600
	AGAAATCGGT	CAGCATATCC	AACAATGCTG	AGCAGTCCGA	TGCTTCCATC	ACCAATTGATC	660
20	AGCTGACCAT	GGCTGACAA	GGCACCCTAC	AGTGTCTCTG	CTCGCTGATG	TCAGACCTGG	720
	AGGGCAACAC	CAGTCAAGT	GTCCGCTCTG	TGGTCTCTGT	GCCACCTCTC	AAACCAAGAT	780
	GGGGCTCCAC	GGGAGAGACC	ATAATTGGGA	ACAACTCCCA	GCTGACCTGC	CAATCAAAGG	840
	AGGGCTCACC	AACCCCTCAG	TACAGCTGGA	AGAGGTACAA	CATCTGAAAT	CAGGAGCAGC	900
	CCCTGGCCCA	GCCAGCTCTC	GCTCAGCTCT	TCTCCCTGAA	GAATATCTCC	ACAGACACAT	960
25	CGGTTACTA	CATCTGTACC	TCCAGCAATG	AGGAGGGGAC	GCAGTTCTGC	AACATCACGG	1020
	TGGCCGTGAG	ATCTCCCTCC	ATGAACGTGG	CCCTGTATGT	GGGCTGCGCG	GTGGGCGTGG	1080
	TTGACGGCTT	CATTATCAT	GGCATCATCA	TCTACTGCTG	CTGCTGCCGA	GGGAAGGAGG	1140
	ACAACTCTGA	AGACAGAGAG	GATGCAAGGC	CGAACCGGGA	AGCCTATGAG	GAGCCACCCAG	1200
	AGCAGCTAAG	CAGAACTTCC	AGAGAGAGGG	AGGAGGAGGA	TGACTACAGG	CAAGAAGAGC	1260
30	AGAGGAGCAC	TGGGCGTGAA	TCCCGGAGCC	ACCTCGACCA	GTGACAGGCC	AGCAGCAGAG	1320
	GGCGGGCGAG	GAGGGGTTAG	GGGTTCAATC	TCCCGCTCTC	TGGCCTCCCT	TCTCCTTTCT	1380
	AAGCCCTGTT	CTCCTGTCCC	TCCATCCCAG	ACATTGATGG	GGACATTCTT	TCOCCAGTGT	1440
	CAGCTGTGGG	GAACATGGCT	GGCCTGGTAA	GGGGGTCCCT	GTGCTGATCC	TGCTGACCTC	1500
	ACTGTCTGTT	GAAGTAACCC	CTCCTGGCTG	TGACACCTGG	TGCGGGCCTG	GCCCTCACTC	1560
35	AAGACCAGGC	TGCAGCCTCC	ACTTCCTCTG	TAGTTGGCAG	GAGCTCCTGG	AAGCACAGCG	1620
	CTGAGCATGG	GGGCGTCCCA	CTCAGAACTC	TCCAGGGAGG	CGATGCCAGC	CTTGGGGGGT	1680
	GGGGGCTGTC	CTGCTCACTC	GTGTGCCAG	CACCTGGAGG	GGCACCAGGT	GGAGGGTTTG	1740
	CACCTCCAC	ATCTTTCTTG	AATGAATGAA	AGAAATAGTG	AGTATGCTTG	GGCCCTGCAT	1800
	TGGCCTGGCC	TCCAGCTCCC	ACTCCCTTTC	CAACCTCACT	TCCCGTAGCT	GCCAGTATGT	1860
40	TCCAAACCTT	CCTGGGAAGG	CCACCTCCCA	CTCCTGCTGC	ACAGGCCCTG	GGGAGCTTTT	1920
	GCCCAACAC	TTTCCATCTC	TGCCTGTCAA	TATCGTACCT	GTCCCTCCAG	GCCCATCTCA	1980
	AATCAAGAG	ATTCTCTCTA	CCCTATCCTA	ATTGTCCACA	TACGTGGAAA	CAATCCTGTT	2040
	ACTCTGTCCC	ACGTCCAATC	ATGGGCCACA	AGGCACAGTC	TTCTGAGCGA	GTGCTCTCAC	2100
	TGTATTAGAG	CGCCAGCTCC	TGGGGCAGG	GCCTGGGCGT	CATGGCTTTT	GCTTTCCTTG	2160
45	AAGCCCTAGT	AGCTGGCGCC	CATCCTAGTG	GGCAGTTAAG	CTTAATTGGG	GAAACTGCTT	2220
	TGATTGGTTG	TGCTTCCCTT	TCTCTGTCTT	CCTTGAGATG	ATCGTAGACA	CAGGGATGAT	2280
	TCCCAACCAA	ACCCACGTAT	TCATTCAATG	AGTTAAACAC	GAATTGATTT	AAAGTGAACA	2340
	CACACAAGGG	AGCTTGCTTG	CAGATGGTCT	GAGTTCTTGT	GTCTGGTAA	TTCTCTTCCA	2400
	GGCCAGAATA	ATTGGCATGT	CTCCTCAACC	CACATGGGGT	TCCTGGTGTG	TCCTGCATCC	2460
50	CGATACCTCA	GCCTTGGCCC	TGCCAGCCCC	ATTTGGGGTC	TGGTTTTCTG	GTGGGGCTGT	2520
	CCTGTGCCCC	TCCCAAGGCC	TCCTTCTGTT	TGTGAGCAT	TTCTTCTACT	CTTGAGAGCT	2580
	CAGGCAGGCT	TAGGGCTGCT	TAGGTCTCAT	GGACCACTGG	CTGGTCTCAC	CCAACTGCAG	2640
	TTTACTATTG	CTATCTTTTC	TGGATGATCA	GAAAAATAAT	TCCATAAATC	TATTGTCTAC	2700
	TTGCGATTGT	TTAAAAAATG	TATATTTTTA	TATATATTGT	TAAATCCTTT	GCTTCAATCC	2760
55	AAATGCTTTC	AGTAATAATA	AAATTGTGGG	TGG			2793

Seq ID NO: C2 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..3150

	1	11	21	31	41	51	
60	ATGGGGAGCG	GGAGGCCAGA	GTCCCTCTC	CACGCCGTGC	AGCTGCGCTG	GGGCCCCCGG	60
	CGCCGACCCC	CGCTSSGTGC	GCTGCTGTTG	CTGCTSSGTG	CGCCGCCACC	CAGGGTCCGG	120
65	GGCTTCAACT	TAGACGCGGA	GGCCCCAGCA	GTACTCTCGG	GGCCCCCGGG	CTCCTCTTTC	180
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	CCCAAGGGTA	ATACAGGCCA	GCCAGGAGTG	CTGCAGGGTG	GTGCTGTCTA	CCTCTGTCTT	300
	TGGGGTGCCA	GCCCCACACA	GTGCACCCCC	ATTGAATTTG	ACAGCAAGGG	CTCTGGGCTC	360
	CTGGAGTCC	CAGTGTCCAG	CTCAGAGGGA	GAGGAGCCTG	TGGAGTACAA	GTCTTTCGAC	420
70	TGGTTGCGGG	CAACAGTTGG	AGCCCATGGC	TCCTCCATCT	TGGCATGCGC	TCCACTGTAC	480
	AGCTGGCGCA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACTGTCTA	CCTCTCCACA	540
	GATAAGTTCA	CCCGAATTCT	GGAGTATGCA	COCTGCGGCT	CAGATTTCAG	CTGGGCAGCA	600
	GGACAGGGTT	ACTGCCAAGG	AGGCTTCAAT	GCCGAGTTCA	CCAAGACTGG	COGTGTGGTT	660
	TTAGGTGAGC	CAGGAAGCTA	TTTCTGGCAA	GGCCAGATCC	TGTCTGCCAC	TCAGGAGCAG	720
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	CGCCAGGCCA	GTTCATCTTA	TGATGACAGC	TACCTAGGAT	ACTCTGTGGC	TGTTGGTGAA	840
	TTCAAGTGTG	ATGACACAGA	AGACTTTGTT	GCTGGTGTGC	CCAAAGGGAA	CCTCACTTAC	900
	GGCTATGTCA	CCATCCTTAA	TGGCTCAGAC	ATTGATATCC	TCTACAACCT	CTCAGGGGAA	960
	CAGATGGGCT	CCTACTTTGG	CTATGCAGTG	GGCCACACAG	ACGTCAATGG	GGACGGGCTG	1020
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	GAGGTGGGCA	GGGTCTACGT	CTACCTGCAG	CACCCAGCCG	GCAATAGAGC	CACGCCACCC	1140
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	GACCTGGACC	AGGATGGCTA	CAATGATGTG	GCCATCGGGG	CTCCCTTTGG	TGGGGAGACC	1260
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Seq ID NO: C3 DNA Sequence

Nucleic Acid Accession #: NM_002421.2

Coding sequence: 1..1410

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Seq ID NO: C4 DNA Sequence

Nucleic Acid Accession #: Bos sequence

Coding sequence: 1..1410

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Seq ID NO: C5 DNA Sequence
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Coding sequence: 1..1506

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ACCATCTGGA CGGTGTGTGG GGTCTGTCTA CTATTTGGAG CTTTGTCTTA TGCTGAATTG 300
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Seq ID NO: C6 DNA Sequence
Nucleic Acid Accession #: NM_003246.1
Coding sequence: 112..3624

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75	AATGAATGAA	CTTATGAGAC	AGACCTCGGA	GATCATCAG	TTTGCCGAGT	CAGGAAACAGC				480
	CAGGAAGACG	CTGCACCTTG	AGATTTCCAA	GGAAGGCAGT	GACCTGTCTG	TGGTGGAGCG				540
	TGCAGAGATC	TGGCTCTTCC	TAAAGTCCC	CAAGGCCAAC	AGGACCAAGA	CCTAAGTCTAC				600
	CATCCGCCCT	TTCCAGCAGC	AGAAGCACCC	GCAGGGCAGC	TTGGACACAG	GGGAAGAGCCG				660
	CGAGGAAGTG	GGCTTAAAGG	GGGAGAGGAG	TGAACGTGT	CTCTCTGAAA	AAGTAGTAGA				720
80	CGCTCGGAAG	AGCACTGGC	ATGTCCTTCC	TGCTCCAGC	AGCATCCAGC	GGTTGCTGGA				780
	CCAGGGCAAG	AGCTCCCTGG	ACGTTGGGAT	TGCCTGTGAG	CAGTGCCAGG	AGAGTGGGCG				840
	CAGCTTGGTT	CTCTTGGGCA	AGAAGAAGAA	GAAAGAAGAG	GAGGGGGAAG	AGAAAGAAGA				900
	GGGCGGAGGT	GAAGGTGGGG	CAGGAGCAGA	TGAGGAAAG	GAGCAGTCGC	ACAGACCTTT				960
	CCTCATGCTG	CAGGCCCGGC	AGTCTGAAGA	CCACCTCAT	GCGCGGGCTC	GGCGGGGCTT				1020

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GGAGTGTGAT	GGCAAGGTCA	ACATCTGCTG	TAAGAAACAG	TTCTTTGTCA	GTTTCAAGGA	1080
CATCGGCTGG	AATGACTTGA	TCATTGCTCC	CTCTGGCTAT	CATGCCAACT	ACTGCGAGGG	1140
TGAGTGTCCCG	AGCCATATAG	CAGGCAAGTC	CGGGTCTCTA	CTGTCTCTCC	ACTCAACAGT	1200
CATCAACCCAC	TACCGCATGC	GGGGCCATAG	CCCTTTGGCC	AACCTCAAA	CGTGTGTGT	1260
GCCCCACCAAG	CTGAGACCCA	TGTCCATGTT	GTACTATGAT	GATGGTCAAA	ACATCATCAA	1320
AAAGGACATT	CAGAACATGA	TGTTGGAGGA	GTGTGGGTGC	TCATAGAGTT	GCCAGGCCA	1380
GGGGGAAAGG	GAGCAAGAGT	TGTCCAGAGA	AGACAGTGGC	AAAATGAAGA	AATTTTAAAG	1440
GTCTCTGAGT	TAACCAGAAA	AATAGAAATT	AAAAACAAA	CAAAACAAA	AAAAAACAA	1500
AAAAAACAA	AGTAATAATTA	AAAAACAAAC	TGATGAAACA	GATGAAACAG	ATGAAGGAAG	1560
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TGGGAGGGAA	AGGAGAAATG	GTGTACCTTT	TATTTCTTCT	GAATCAGATC	TGATGACATC	1680
AGTTGTITTA	ACGGGTATTT	GTCTTTTCCC	CCCTTGAGGT	TCCTTTGTGA	GCTTGAATCA	1740
ACCAATCTGA	TCTGCAGTAG	TGTGGACTAG	AACAACCCAA	ATAGCATCTA	GAAAGCCATG	1800
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Seq ID NO: C8 DNA Sequence
Nucleic Acid Accession #: NM_000095.1
Coding sequence: 26..2299

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GCAGATGCTT	CGGGAACCTGC	AGGAAACCAA	CGCGGCGCTG	CAGGACGTGC	GGGACTGGCT	180
GCGGCAGCAG	GTCAAGGAGA	TCACGTTCTT	GAAAAACACG	GTGATGGAGT	GTGACGCGTG	240
CGGGATGCAG	CAGTCAGTAC	GCACCGGCGT	ACCCAGCGTG	CGGCGCTGTC	TCCACTGGCG	300
GCCCGGCTTC	TGCTTCCCGG	CGGTGGCGTG	CATCCAGACG	GAGAGCGCGG	GCCGCTGGCG	360
CCCTTGCGCC	AGCGGCTTCA	CGGGCAACGG	CTGCACTGTC	ACCGAGCTCA	ACGAGTGCAA	420
CGCCCACCCC	TGCTTCCCCC	GAGTCCGCTG	TATCAACACC	AGCCCGGGGT	TCCGCTGCGA	480
GGCTTGCCCG	CGGGGTACAC	CGGGCCCCAC	CCACCAGGGC	GTGGGCTGCG	CTTTCCGCCA	540
GGCCCAACAAG	CAGGTTTGCA	CGGACATCAA	CGAGTGTGAG	ACCGGCCAAC	ATAACTGCGT	600
CCCCAATCTC	GTGTGCATCA	ACACCCGGGG	CTCTTCCAG	TGCGGCGCGT	GCCAGCCCGG	660
CTTGTGGGCC	GACCAGGCGT	CGGCTGCGCA	CGCGGCGCA	CAGCGCTTCT	GCCCCGACGG	720
CTCGCCCAAG	GAGTGCCACG	AGCATGCAGA	CTGCGTCTTA	GAGCGCGATG	GCTCGCGGTC	780
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AGACGGCTTC	CGGACGAGAG	AGCTGCGCTG	CCCGAGCGCG	CAGTGCCTGA	AGGACAACTG	900
CGTGACTGTG	CCCACTCAG	GGCAGGAGGA	TGTGGACCGC	GATGGCATCG	GAGACGCGTG	960
CGATCCGGAT	GCCGACGGGG	ACGGGTCTCC	CAATGAAAAG	GACAACTGCC	CGCTGGTGGG	1020
GAACCCAGAC	CAGCCCAACA	CGGACGAGGA	CAAGTGGGGC	GATGCGTGCG	ACAACTGCGG	1080
GTCCCAAGAG	AACGACGACC	AAAAGGACAC	AGACCAGGAC	GGCGGGGGCG	ATGCGTGGCA	1140
CGACGACATC	GACGCGGACC	GGATCCGCAA	CCAGGCCGAC	AACTGCGCTA	GGGTACCCAA	1200
CTCAGACCAAG	AAGGACAGTG	ATGGCGATGG	TATAGGGGAT	GCCTGTGACA	ACTGTCCCCA	1260
GAAGAGCAAC	CGGATCAGG	CGGATGTGGA	CCACGACTTT	GTGGGAGATG	CTTGTGACAG	1320
CGATCAGAC	CAGGATGGAG	ACGGACATCA	GGACTCTGGG	GACAACTGTC	CCACGTTGCC	1380
TACAGTGGCC	CAGGAGGACT	CAGACCAAGA	TGGCCAGGGT	GATGCTTGCG	ACGACGACGA	1440
CGACATGATC	GGAGTCCCTG	ACAGTGGGGA	CAACTGCGCG	CTGGTGCTTA	ACCCCGGCCA	1500
GGAGGAGCGG	GACAGGGACG	CGGTGGGCGA	CGTGTGCCAG	GACGACTTTG	ATGACAGCAA	1560
GGTGTAGAG	AAGATCGACG	TGTGTCCGGA	GAACGCTGAA	GTCACTCTCA	CCGACTTCAG	1620
GGCCTTCCAG	ACAGTCTGTG	TGGACCCGGA	GGGTGACCGG	CAGATTGACC	CCAACCTGGT	1680
GGTGTCTCAAC	CAGGGAAGGG	AGATCGTGCA	GACAAATGAAC	AGCGACCCAG	GCTCTGGTGT	1740
GGTTTACACT	GCCTTCAATG	CGGTGGACTT	CGAGGGCAGC	TTCCATGTGA	ACACGGTCAAC	1800
GGATGACGAC	TATGCGGGCT	TCTATCTTTG	CTACCAGGAC	AGCTCCAGCT	TCTACGTGGT	1860
CATGTGGGAG	CAGATGGAGC	AAACGTATTG	GCAGGCGAAC	CCCTTCCGTC	CTGTGGCCGA	1920
GCCTGCGATC	CAACTCAAGG	CTGTGAAGTC	TTCCACAGGC	CCCGGGGAAC	AGCTGCGGAA	1980
CGCTCTGTGG	CATACAGGAG	ACACAGAGTC	CCAGGTGCGG	CTGCTGTGGA	AGGACCCGCG	2040
AAACGTGGGT	TGGAAGGACA	AGAAGTCTTA	TGTTGGTTTC	CTGCAGCACCC	GGCCCCAAGT	2100
GGGTACATC	AGGGTGCAGT	TCTATGAGGG	CCCTGAGCTG	GTGGCCGACA	GCAAAGTGGT	2160
CTTGGACACA	ACCATGCGGG	GTGGCCGCTT	GGGGTCTTTC	TGCTTCTCCC	AGGAGAACAT	2220
CATCTGGGCC	AACCTGCGTT	ACCGCTGCAA	TGACACCATC	CCAGAGGACT	ATGAGACCCA	2280
TCAGCTGCGG	CAGGCTTAGG	GACCAAGGTT	AGGACCCGCC	GGATGACAGC	CACCTCACCC	2340
GCGGCTGGAT	GGGGGCTCTG	CACCCAGCCC	AAGGGGTGGC	CGTCTGAGG	GGGAAGTGAG	2400
AAGGGCTCAG	AGAGGACAAA	ATAAAGTGTG	TGTGCAGGG			2439

Seq ID NO: C9 DNA Sequence
Nucleic Acid Accession #: XM_057014
Coding sequence: 143..874

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CGCTGCCCCG	CAGCGCGGAG	CCATGCGACC	CCAGGGCCCC	CGCGCTCTCC	CGCAGCGGCT	180
CGCGGCGCTC	CTGTGCTTCC	TGCTGTGCA	GCTGCGCCCG	CCGTGAGCGC	CCTCTGAGAT	240
CCCCAAGGGG	AAGCAAAAAG	CGCAGCTCCG	GCAGAGGGAG	GTGGTGGACC	TGTATAATGG	300
AATGTGCTTA	CAAGGGCCAG	CAGGAGTGCC	TGGTGGAGAC	GGGAGCCCTG	GGGCGCAATG	360
CATTCCGGGT	ACACCTGGGA	TCCCAGTGG	GGATGGATTG	AAAGGAGAAA	AGGGGGAATG	420
TCTGAGGGAA	AGCTTTGAGG	AGTCTGGAC	ACCCAACTAC	AAGCAGTGTG	CATGGAGTTC	480
ATTGAATAT	GGCATAGATC	TGGGAAAAT	TGCGGAGTGT	ACATTTACAA	AGATGCGTTC	540
AAATAGTCT	CTAAGAATTT	TGTTCACTGG	CTCACTTCGG	CTAAAATGCA	GAAATGCATG	600
CTGTGAGCGT	TGTTATTTCA	CAITCAATGG	AGCTGAATGT	TCAGGACCTC	TTCCCATTTG	660
AGCTATAATT	TATTTGGACC	AAGGAAGCCC	TGAAATGAAT	TCAACAATTA	ATATTCATCG	720

5 CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTTGCTAT 780
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 TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAAGTG GTTCAATAT TTTTITTTAGT 1080
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Seq ID NO: C10 DNA Sequence
 Nucleic Acid Accession #: NM_003225
 Coding sequence: 41..295

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 20 GACAGAGACG TGTACAGTGG CCCCCGTGGA AAGACAGAA TGTGGTTTTC CTGGTGTAC 180
 GCCCTCCGAG TGTGCAATA AGGGCTGCTG TTTGAGCAG ACCGTTCTGT GGGTCCCTCT 240
 GCTCTTCTAT CCTAATACCA TCGACGTCCC TCCAGAAGAG GAGTGTGAAT TTTAGACACT 300
 TCTGCAGGGA TCTGCTTGCA TCTGACGGG GTGCGTCCC CAGCACGGTG ATTAGTCCCA 360
 25 GAGCTCGGCT GCCACCTCCA CCGACACCT CAGACAGCT TCTGAGCTG TGCCTCGGCT 420
 CACAACACAG ATTGACTGCT CTGACTTTGA CTACTCAAAA TTGGCTTAAA AATTAAAGA 480
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Seq ID NO: C11 DNA Sequence
 Nucleic Acid Accession #: NM_015419.1
 Coding sequence: 1..8487

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 TGCACTTCC GATCCCTGGC TTCCGTGCC GCTGGCATTG CTAGACACGT GGAAAGATC 180
 AATTTGGGGT TTAATAGCAT ACAGGCGCTG TCAGAAACCT CATTTCAGG ACTGACCAAG 240
 TTGGAGCTAC TTAATGATCA CGGCAATGAG ATCCCAAGCA TCCCGATGG AGCTTTAAGA 300
 40 GACCTCAGCT CTCTCAGGT TTTCAAGTTC AGCTACAACA AGCTGAGAGT GATCAGAGG 360
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 45 AGCATGCTTC GGAACATGCC GCTTCTGGAG AATCTTACT TGCAAGGAAA TCGTGGGACC 660
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	ATCCACCTTG	TGAAAGTAG	TCTAAGCACT	CAAGACACCT	TACTGATTAA	AAAGGGTATG	3180
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5	AGAAGTTCTG	AGAGTAGAGG	CCAAGAGAGC	AAATCCATCA	CTTTGCCTGA	CTCCACACTG	3300
	GGTATAATGA	GCAGTATGTC	TCCAGTTAAG	AAGCCTGGGG	AAACCACAGT	TGGTACCCCTC	3360
	CTAGACAAAG	ACACCAACAAC	AGTAACAACA	ACACCAGGCG	AAAAAGTTGC	TCCGTCATCC	3420
	ACCATGAGCA	CTCACCCCTC	TCGAAGGAGA	CCCAACGGGA	GAAGGAGATT	ACGCCCAAC	3480
	AAATTCGCC	ACCGGCAAA	GCAAAACCCA	CCCAACAATT	TTGCCCATC	AGAGACTTTT	3540
10	TCTACTCAAC	CAACTCAAGC	ACCTGACATT	AAGATTTCAA	GTCAAGTGGG	GAGTTCTCTG	3600
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	AGAATTCCTC	ATTATTCCAA	TGGAAGACTC	CCCTTCTTTA	CCAACAAGAC	TCCTTCTTTT	5220
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	CAGACTGTGT	CCGTACCCCG	TGAGACAGAC	ACTGTGTTCC	CCTGTGAGGC	AACAGGAAAA	5640
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	CAAGATCGAG	GCCAGTATAT	GTGCAACGCC	AGCAACCTGC	ACGCGCTGGA	CAGGATGGTG	5820
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50	CAAAATTTCT	GGATCTTCCC	TGACAGGAGG	GTGTGGCAAA	CTGTGTCCCC	CGTGGAGAGC	6000
	CGCATCACCC	TGACGAGAAA	CCGGAACCTT	TCCATCAAGG	AGGCGTCCCT	CTCAGACAGA	6060
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Coding sequence: none

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70 Seq ID NO: C13 Protein Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..5001

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Seq ID NO: C15 DNA Sequence
Nucleic Acid Accession #: NM_005940
Coding sequence: 23..1489

70
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AAGCCACGCA GCCCAGGGG GATGCTCC GGCCTGCTG CTCCGACGG CGGCCGCGG 60
CGCCCTCTCG CCCCAGATGC TGCTGCTGCT GCTCCAGCG CGCCGCTGC TGGCCCGGG 120
CTGCGCGCGG GAGTCCACC ACCTCCATGC CGAGAGGAGG GGGCCACAGC CCTGGCATGC 180
AGCCCTGCCC AGTAGCCCG CACCTGCCCC TGCCACGCGA GAAGCCCCC GGCTGCGCAG 240
CAGCCCTCAGG CCTCCCGCT GTGGCGTGCC CGACCATCT GATGGGCTGA GTGCCGCAA 300
CGACAGAGAAG AGGTTCTGTC TTTCTGGCG GCGCTGGGAG AAGACGGACC TCACCTACAG 360
GATCCTCTGG TTCCATGGC AGTTGGTGCA GGAGCAGGTG CGGCAGACGA TGGCAGAGGC 420
CCTAAGAGTA TGAAGGATG TGACGCCACT CACCTTTACT GAGGTGCAOG AGGGCGGTG 480
TGACATCATG ATGCACTTCG CCAGGTACTG GCATGGGAC GACCTGCCGT TTGATGGGCC 540
TGGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC CGAGAAGGGG ATGTCCACTT 600
CGACTATGAT GAGACCTGGA CTATCGGGGA TGACCAGGGC ACAGACCTGC TGCAGTGGC 660
AGCCCATGAA TTTGGCCAG TGCTGGGGCT GCAGCACACA ACAGCAGCCA AGGCCCTGAT 720
GTCCGCTTCT TACACCTTTC GCTACCCACT GAGTCTCAGC CCAGATGACT GCAGGGCGGT 780
TCAACACCTA TATGGCCAGC CTGGCCCACT TGTCACTCC AGGACCCAG CCTGGGCC 840
CCAGGCTGGG ATAGACACCA ATGAGATTGC ACCGCTGGAG CCAGACGCCC CGCCAGATGC 900

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5 CTGTGAGGCC TCCTTTGACG CGGTCTCCAC CATCCGAGGC GAGCTCTTTT TCTTCAAAGC 960
 GGGCTTTTGT TGGCGCTCC GTGGGGGCCA GCTGCAGCCC GGCTACCCAG CATTGGCCCTC 1020
 TGGCCACTGG CAGGGAAGTC CCAGCCCTGT GGACGCTGCC TTGAGGATG CCCAGGGCCA 1080
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 CCCCACCCCT CTCACGAGC TGGGCTGTGT GAGGTTCCCG GTCCATGCTG CCTTGGTCTG 1200
 GGGTCCCGAG AAGAACAAGA TCTACTTCTT CCGAGGCAGG GACTACTGGC GTTCCACCC 1260
 CAGCACCCGG CGGTGAGACA GTCCCGTGCC CCGCAGGGCC ACTGACTGGA GAGGGGTGCC 1320
 CTCTGAGATC GAGCTGCTCT TCCAGGATGC TGATGGCTAT GCCTACTTCC TGGCGGGCCG 1380
 CCTCTACTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCGTCTCTGT 1440
 GGGTCCCTGAT TTCTTTGGCT GTGCCGAGCC TGCCACACT TTCTCTGAC CATGGCTTGG 1500
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 GGGACCCGCT ATGCAAGTCC TGGCAAACT GCGTGCCTGT TCTCATCCCT GTCCCTCAGG 1800
 GTAGACCATG GGCAGGACTG GGGAACTGG AGTGTCTTGT CTGTATCCCT GTTGTGAGGT 1860
 TCCTTCCAGG GGCTGGCACT GAAGCAAGGG TGCTGGGGCC CCATGGCCTT CAGCCCTGGC 1920
 TGAGCAACTG GGCTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGTG AGGTGCTGTC 1980
 ATCTGTCTGC CTCTGGCTGT ACAATCTGGT AAATCTGTTC TCCAGAATCC AGGCCAAAAA 2040
 GTTCAAGTCT AAATGGGGAG GGGTATTCTT CATGCAGGAG ACCCCAGGCC CTGGAGGCTG 2100
 CAACATACCT CAATCTGTCT CCAGGCCGGA TCCTCTGAA GCCCTTTTGG CAGCACTGCT 2160
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 TTTTAAACT GAGGATTGTC ATTAACACA GTTGTCTTCT 2260

25 Seq ID NO: C16 DNA Sequence
 Nucleic Acid Accession #: NM_024022
 Coding sequence: 202..1563

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 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180
 AGAGGTCCTG AAATAGTCA CAGTGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC 240
 35 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCTGTTGAC ACCAGATGCA 300
 GATGCTGTGT CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTTC AATCATCGTC 360
 ATTGGGATCA TTGCATGATG ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
 TCAGGGAAGT ACAGATGTCC CTCACTCTTT AAGTGTATCG AGCTGATAGC TOGATGTGAC 480
 GAGTCTCGGG ATTGCAAGA CCGGAGGAGC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 40 AATGCGGTGC TCAGGTGTTT CACAGCTGCT TCGTGAAGA CCAATGTGCT CGATGACTGG 600
 AAGGGTCACT ACSCAAATGT TGCTGTGGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT GTCCATCGAT 720
 CACCTCTTGC CAGATGACAA GTGACTGCA TTACACCACT CAGTATATGT GAGGAGGGGA 780
 TGTGCTCTG GGCACGTGGT TACCTTGACG TGACAGCCCT GTGGTCAATG AAGGGGCTAC 840
 45 AGCTCAGCA TCGTGGGTGT AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900
 CTTCACTTCC AGGGCTACCA CCTGTGCGGG GGCCTGTGTA TCACGCCCTT GTGGATCATC 960
 ACTGTGACAC ACTGTGTTTA TGACTGTGAC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020
 CTAGTTTCCC TGTGGACAAA TCCAGCCCCA TCCCACTTGG TGGAGAGATG TGTCTACCC 1080
 AGCAGTACA AGCCAAAGAG GCTGGGCAAT GACATGCCCC TTATGAGCTG GGCAGGGCCA 1140
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 GTGTACGGTG GCATCATCTC CCCCCTCATG CTCTGCGCGG GCTACCTGAC GGGTGGGGTG 1380
 GACAGCTGCC AGGGGGACAG CCGGGGGCCC CTGGTGTGTC AAGAGAGGAG GCTGTGGAAG 1440
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 ACCCGTGTCA CCTCTTCTCT GGACTGGATC CACGAGCAGA TGGAGAGAGA CCTAAAAACC 1560
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 TCCCTTGGAC TCCCGTGTAG GAACCTGCAC ACGAGCAGAC ACCCTTGGAG CTCTGAGTTC 1680
 CGGCACCACT AGCAGGCCCG AAAGAGGCAC CCTTCCATCT GATTCCAGCA CAACCTTCAA 1740
 60 GCTGCTTTT GTTTTGTGTT TTTTGTAGGT GGAATCTGCG TCTGTGCCCC AGGCTGAGT 1800
 GCAGTGGGGA AATCCCTGCT CACTGCAGCC TCCGCTTCCC TGGTTCAGGC GATTCTCTTG 1860
 CCTCAGCTTC CCCAGTAGCT GGGACCACAG GTGCCGCCCA CCACACCCAA CTAATTTTGT 1920
 TATTTTGTAG AGAGACAGGG TTTCACCATG TTGGCCAGGC TGCTCTCAAA CCCCTGACCT 1980
 CAAATGATGT GCCTGTCTCA GCCTCCCACT GTGCTGGGAT TACAGGCATG GGCACCAACG 2040
 65 CCTAGCTCA CAGTCCCTTC TGATCTTAC TAAGAACAAA AGAAGCAGCA ACTTGCAGAG 2100
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 AGATAAGCAG TTATGTGACC TCAAGTGCAA AGCCACCAAC AGCCACTCAG AAAAGACGCA 2220
 CCAGCCCAAG AGTGCAAGAC TGCAGTCACT GCAAGTTTTT ATCTCTAGGG ACCAGAACCA 2280
 70 AACCCACCTT TTCTACTTCC AAGACTTATT TTCATGTG GGGAGGTTAA TCTAGGAATG 2340
 ACTGTTTAA GGCCTATTTT CATGATTTCT TTGTAGCAAT TGGTGCCTGA CGTATTATTG 2400
 TCCTTTGATT CCAATAATAA TGTTCCTTC CTCAAAAAA AAAAAAAA AAAAAAAA 2460
 AAAAA 2465

75 Seq ID NO: C17 DNA Sequence
 Nucleic Acid Accession #: NM_003220
 Coding sequence: 63..1376

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 AAATGCTTTG GAAATTGACG GATAATATCA AGTAAGAGGA CTGCGAGGAC CGTCAAGACG 120
 GCACAGCAAA CGGACCGGCA CGGTGCCCC AGCTGGGCAC TGTAGGTCAA TCTCCCTACA 180
 CGAGCGCCCC CGCGTGTCC CACACCCCCA ATGCCGACTT CCAGCCCCCA TACTTCCCCC 240
 CACCTACCA GCCTATCTAC CCCCAGTGGC AAGATCCTTA CTCCACGTC AACGACCCCT 300

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ACAGCCTGAA CCCCCTGCAC GCCCAGCCGC AGCCGCAGCA CCCAGGCTGG CCCGGCCAGA 360
GGCAGAGCCA GGAGTCTGGG CTCTGCACA CGCACCGGGG GCTGCCTCAC CAGCTGTGCG 420
GCCTGGATCC TCGCAGGGAC TACAGGCGGC ACGAGGACCT CCTGCACGGC CCACACGGCG 480
TCAGCTCAGG ACTCGGAGAC CTCTCGATCC ACTCCTTACC TCAGGOCATC GAGGAGGTCC 540
CGCATGTAGA AGACCCGGGT ATTAACATCC CAGATCAAAC TGTAAITTAAG AAAGGCCCGG 600
TGTCCCTGTG CAAGTCCAAC AGCAATGCCG TCTCCGCCAT CCCTATTAAAC AAGGACAACC 660
TCTTCGGCGG CGTGGTGAAC CCCAACGAAG TCTTCTGTTC AGTTCGGGGT CGCCTCTCGC 720
TCCTCAGCTC CACCTCGAAG TACAAGGTCA CGGTGGCGGA AGTCAGCGGG CGGCTCTCAC 780
CACCCGAGTG TCTCAACGCG TCGCTGCTGG GCGGAGTGCT CCGGAGGGCG AAGTCTAAAA 840
ATGGAGGAAG ATCTTTAAGA GAAAAACTGG ACAAATAGG ATTAAATCTG CCTGCAGGGA 900
GACGTAAAGC TGCCACGGTT ACCCTGCTCA CATCACTAGT AGAGGGAGAA GCTGTCCACC 960
TAGCCAGGGA CTTTGGGTAC GTGTGCGAAA CCGAATTTCC TGCCAAAGCA GTAGCTGAAT 1020
TTCTCAACCG ACAACATTCC GATCCCAATG AGCAAGTGAC AAGAAAAAAC ATGCTCCTGG 1080
CTACAAAACA GATATGCAAA GAGTTCACCG ACCTGCTGGC TCAGGACCGA TCTCCCTGG 1140
GGAACCTCAG GCCCAACCCC ATCTGGGAGC CCGGCATCCA GAGCTGCTTG ACCCACTTCA 1200
ACCTCATCTC CCACGGCTTC GGCAGCCCCG CGGTGTGTGC CGCGGTACAG GCCCTGCAGA 1260
ACTATCTCAC CGAGGCCCTC AAGGCCATGG ACAAATGTGA CCTCAGCAAC AACCCCAACA 1320
GCCACAGGGA CAACAACGCG AAAAGCAGTG ACAAAGAGGA GAAGCACAAGA AAGTGAGGCT 1380
CTCTCCCGCG CCCGCCCTC CCACGCCCTCA CCAGCCCCCG GCGCGCCAC CCTCCGGCGG 1440
GTGACAGCTC CGGGATCAGC AACCTTCTCT GCTGCTGCTA CTGCTGTGTC TGCTGCGCGC 1500
GCGCGCGCGG CCGCTGCCCT TGGGTCCCGG CGAGTCTCCG GGAAGTCCCT CTGACTGTTC 1560
AGTGGGGCAG CTTCTCGGAC TCTGCACCGC CCTCGACCTC CCCACCGCTC CCACACCCCC 1620
TGTGCCCCCG GAATTC

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Seq ID NO: C18 DNA Sequence
Nucleic Acid Accession #: NM_002988
Coding sequence: 71..340

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1 11 21 31 41 51
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GCCCAGCATC ATGAAGGGCC TTGCAGCTGC CTCTCTGTG CTGCTGTGCA CCATGGCCCT 120
CTGCTCCTGT GCACAGTTTG GTACCAACAA AGAGCTCTGC TGCTCGTCT ATACCTCCTG 180
GCAGATTCCA CAAAGTTTCA TAGTTGACTA TTCTGAAACC AGCCCCAGT GCCCAAGCC 240
AGGTGTCTAT CTCTTAACCA AGAGAGGCGG GCAGATCTGT GCTGACCCCA ATAAGAAGTG 300
GGTCCAGAAA TACATCAGCG ACCTGAAGCT GAATGCCTGA GGGGCTTGA AGCTGGGAGG 360
GCCCAGTAAA CTTGGTGGGC CCAGGAGGGA ACAGGAGCCT GAGCCAGGGC AATGGCCCTG 420
CCACCCCTGA GGCCACTCTC TCTAAGAGTC CCATCTGCTA TGCCAGGCA CATTAACTAA 480
CTTTAATCTT AGTTTATGCA TCATATTTC TTTTGAATTT GATTCTATT GTTGAGCTGC 540
ATTATGAAT TAGTATTTTC TCTGACATCT CATGACATTG TCTTTATCAT CCTTCCCT 600
TTCCCTTCAA CTCTCTGTAC ATTCAATGCA TGGATCAATC AGTGTGATTA GCTTCTCAG 660
CAGACATTGT GCCATATGTA TCAATGACA AATCTTTAT GAATGGTTT GCTCAGCACC 720
ACCTTTAAT ATATTGGCAG TACTTATAT ATAAAGGTA AACCAGCATT CTCACTGTGA 780
AAAAAAAAA AAAAAAAAAA AAA 803

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Seq ID NO: C19 DNA Sequence
Nucleic Acid Accession #: NM_004063
Coding sequence: 121..2619

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1 11 21 31 41 51
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GAAAGAGACT TTAAACCAAC ATTTTGTGAC TTACAGAAAG GAATTTGAAT AAAGAAAACT 120
ATGATACTTC AGGCCCATCT TCACTCCCTG TGTCTTCTTA TGCTTTATTT GGCAACTGGA 180
TATGGCCAG AGGGGAAGTT TAGTGGACCC CTGAAACCCA TGACATTTTC TATTATGAA 240
GGCCAAGAAC CGAGTCAAAT TATATTCCAG TTAAAGGCCA ATCTCTCTGC TGTGACTTTT 300
GAACAGAGCT TGGAGACAGA CAACATATTT GTGATAGAAC GGGAGGGACT TCTGTATTAC 360
AACAGAGCCT TGGACAGGGA AACCAAGATC ACTCACAATC TCCAGTTTGC AGCCCTGGAC 420
GCTAATGGAA TTATAGTGA GGTCCAGTCC CCTATCACA TAGAAGTGAA GGACATCAAC 480
GACAATCGAC CCAAGTTTCT CCAGTCAAAG TAGAAGGCT CAGTAAGGCA GAACTCTCGC 540
CCAGGAAAGC CCTTCTTGTA TGTCAATGCC ACAGACCTGG ATGATCCGGC CACTCCCAAT 600
GGCCAGCTTT ATTACCAGAT TGTATCCAG CTTCCTCATG TCAACAATGT CATGTACTTT 660
CAGATCAACA ACAAACCGGG AGCCATCTCT CTACCCGAG AGGGATCTCA GGAATTGAAT 720
CCTGTCAAGA ATCTTCTTA TAATCTGGTG ATCTCAGTGA AGGACATGGG AGGCCAGAGT 780
GAGAATTCCT TCACTGATAC CACATCTGTG GATATCATAG TGACAGAGAA TATTGGAAA 840
GCACCAAAAC CTGTGGAGAT GGTGGAAAAC TCAACTGATC CTCACCCCAT CAAATCACT 900
CAGGTGGGT GGAATGATCC CGGTGCACAA TATTCCTTAG TTGACAAAGA GAAGCTGCCA 960
AGATTCCCAT TTTCAATTGA CCAGGAAGGA GATATTTACG TGACTCAGCC CTTGGACCGA 1020
GAAGAAAGG ATGCATATGT TTTTATGCA GTTGCAAAAG ATGAGTACGG AAAACCACTT 1080
TCATATCCCG TGGAAATTC TGTAAAAGTT AAAGATATTA ATGATAATCC ACCTACATGT 1140
CCGTACCCAG TAACCGTATT TGAGGTCCAG GAGAATGAAC GACTGGGTAA CAGTATCGGG 1200
ACCCCTACTG CACATGACAG GGATGAAGAA AATACTGCCA ACAGTTTCTT AAACACAGG 1260
ATTGTGGAGC AAACCTCCAA ACTTCCCATG GATGGACTCT TCCTAATCCA AACCTATGCT 1320
GGAATGTTAC AGTTAGCTAA ACAGTCTTGA AAGAAGCAAG ATACTCTCA GTACAACTTA 1380
ACGATAGAGG TGCTGACAAA AGATTTCAG ACCCTTTGTT TTGTGCAAAAT CAACGTTATT 1440
GATATCAATG ATCAGATCCC CATCTTTGAA AAATCAGATT ATGGAAACCT GACTCTTGCT 1500
GAAGACACAA ACATTGGGTC CACCATCTTA ACCATCCAGG CCACTGATGC TGATGAGCCA 1560
TTTACTGGGA GTTCTAAAA TCTGTATCAT ATCATAAAGG GAGACAGTGA GGGACGCTG 1620
GGGTGTGACA CAGATCCCCA TACCAACACC GGATATGTCA TAATTAATAA GCCTCTTGAT 1680
TTTGAACAG CAGCTGTTTC CAACATTTG TTCAAAGCAG AAAATCCTGA GCCTCTAGT 1740
TTTGGTGTGA AGTACAATGC AAGTTCTTTT GCCAAGTTCA CGCTTATTGT GACAGATGTG 1800
AATGAAGCAC CTCATTTTC CCAACAAGTA TTCCAAGCGA AAGTCAGTGA GGATGTAGCT 1860
ATAGGCACTA AAGTGGGCAA TGTGACTGCC AAGGATCCAG AAGGTCTGGA CATAAGCTAT 1920
TCATGAGGG GAGACACAAG AGTTTGGCTT AAAATTGACC ACGTACTG TGAGATCTTT 1980

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5	AGTGTGGCTC	CATTGGACAG	AGAAGCCGGA	AGTCCATATC	GGGTACAAGT	GGTGGCCACA	2040
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	AATGACAACC	CTCCCAGGCT	AGCCAAGGAC	TACACGGGCT	TGTTCTTCTG	CCATCCCCCTC	2160
	AGTGCACTGT	GAAGTCTCAT	TTTCGAGGCT	ACTGATGATG	ATCAGCACTT	ATTTCGGGGT	2220
	CCCATTTTAA	CATTTTCCCT	CGGCAGTGGG	AGCTTACAAA	ACGACTGGGA	AGTTTCCAAA	2280
	ATCAATGGTA	CTCATGCCCG	ACTGTCTACC	AGGCACACAG	AGTTTGAGGA	GAGGGAGTAT	2340
	GTOGTCTTGA	TCGCGATCAA	TGATGGGGGT	CGGCCACCTT	TGGAAGGCAT	TGTTTCTTTA	2400
	CCAGTTACAT	TCTGCAGTTG	TGTGGAAGGA	AGTTGTTTCC	GGCCAGCAGG	TCACCAGACT	2460
10	GGGATACCCA	CTGTGGGCAT	GGCAGTTGGT	ATACTGTCTG	CCACCTTCTT	GGTGATTGGT	2520
	ATAATTTTAT	CAGTTGTGTT	TATCCGCATA	AAGAAGGATA	AAGGCCAAAG	TAATGTTGAA	2580
	AGTGCTCAAG	CATCTGAAGT	CAACCTCTG	AGAAGCTGAA	TTTGAAGAAG	AATGTTTGAA	2640
	TTTATATAGC	AAGTGCTATT	TCAGCAACAA	CCATCTCATC	CTATTACTTT	TCATCTAACG	2700
	TGCATTATAA	TTTTTTAAAC	AGATATTCCC	TCTTGTCTTT	TAATATTGTC	TAAATATTTC	2760
	TTTTTTGAGG	TGGAGTCTTG	CTCTGTCCGC	CAGGCTGGAG	TACAGTGGTG	TGATCCCAGC	2820
15	TCACGTCAAC	GCCGCTCTCC	TGGGTTTACA	TGATTCTCCT	GCCTCAGCTT	CCTAAGTAGC	2880
	TGGGTTTACA	GGCACCCACC	ACCATGCCCA	GCTAATTTTT	GTATTTTAA	TAGAGACGGG	2940
	GTTTGGCCAT	TGGCCAGGCG	TGGTCTTGAA	CTCTGACGCT	CAAGTGATCT	GCCTGCCTTG	3000
	GTCTCCCAAT	ACAGGCATGA	ACCACTGCAC	CCACCTACTT	AGATATTTCA	TGTGCTATAG	3060
20	ACATTAGAGA	GATTTTTCAT	TTTTCCATGA	CATTTTTCCT	CTCTGCAAA	GGCTTAGCTA	3120
	CTGTGTCTCT	TGGGCTGAAG	GGCAAGACAG	ACTCATTAAG	TATTTCTGAC	ATTTTTCCTT	3180
	TATCAAGGAG	ATATATCAGT	GTGTCTCAT	AGAACTGCCT	GGATTCCATT	TATGTTTTTT	3240
	CTGATTCCAT	CCTGTGTCCC	CTTCATCCTT	GACTCCTTTG	GTATTTCACT	GAATTTCAAA	3300
	CATTGTTCAG	AGAAGAAAAA	CGTGAGGACT	CAGGAAAAAT	AAATAAATAA	AAGAACAGCC	3360
25	TTTTCCCTTA	GTATTAAACAG	AAATGTTTCT	GTGTCATTAA	CCATCTTTAA	TCAATGTGAC	3420
	ATGTTGCTCT	TGGGCTGAAG	TTCTTCAACT	TGGAAATGAC	ACAGACCCAC	AGAAGGTGTT	3480
	CAAAACAAC	CTACTCTGCA	AACCTTGCTA	AAGGAACGAG	TCAGCTGGCC	AGATTTCCTC	3540
	ACTACCTGCC	ATGCATACAT	GCTGCGCATG	TTTTCTTCAT	TCGTATGTTA	GTAAAGTTTT	3600
	GGTTATTATA	TATTTAAACAT	GTGGAAGAAA	ACAAGACATG	AAAAGAGTGG	TGACAAATCA	3660
30	AGAAATAACA	CTGGTTGTAG	TCAGTTTGTG	TTGTTAA			3697

Seq ID NO: C20 DNA Sequence
Nucleic Acid Accession #: NM_004443
Coding sequence: 28..3024

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	CCGCGCGGCT	GCCGGGCGCT	GGAAGAGACC	CTCATGGACA	CAAAATGGGT	AACATCTGAG	180
	TGGCGGTGGA	CATCTCATCC	AGAAAGTGGG	TGGGAAGAGG	TGAGTGGCTA	CGATGAGGCC	240
	ATGAATCCCA	TCCGCACATA	CCAGGTGTGT	AAATGTGGCG	AGTCAAGCCA	GAACAACCTG	300
	CTTGCAACG	GGTTTCTCTG	GCGGCGGGAT	GTGCAAGGCG	TCTACGTGGA	GCTCAAGTTC	360
45	ACTGTGCGTG	ACTGCAACAG	CATCCCAAC	ATCCCGGCT	CCTGCAAGGA	GACCTTCAAC	420
	CTCTTCTACT	ACGAGGCTGA	CAGCGATGTG	GCCTCAGGCT	CCTCCGCTTT	CTGGATGGAG	480
	AACCCCTACG	TGAAAGTGGG	CACCATTGCA	CCCGATGAGA	GCTTCTCGCG	GCTGGATGCC	540
	GGCCGTGTCA	ACACCAAGGT	GCGCAGCTTT	GGGCCACTTT	CCAAGGCTGG	CTTCTACCTG	600
	GCCTTCCAGG	ACCAGGGGCG	CTGCATGTGC	CTCATCTCCG	TGCGCGCTTT	CTACAAGAG	660
50	TGTGATCCA	CAACCGCAGG	CTTGCACTC	TTCCCGGAGA	CCCTCACTGG	GGCGGAGGCC	720
	ACCTGCTGCG	TCAATGCTCC	TGGCACCTGC	ATCCCTAAAG	CCGTGGAGGT	GTGGTGCCA	780
	CTCAAGCTCT	ACTGCAACGG	CGATGGGGAG	TGGATGGTGC	CTGTGGGTGC	CTGCACCTGT	840
	GCCACCGGCC	ATGAGCCAGC	TGCCAAGGAG	TCCCAAGTGC	GCCCTGTGCC	CCCTGGGAGC	900
	TACAAGGCGA	AGCAGGGAGA	GCGGCCCTGC	CTCCCATGTC	CCCCCAACAG	CCGTACCAAC	960
55	TCCCGAGCGG	CCAGCATCTG	CACTGCCAC	AAATACTTCT	ACCGTGCGAG	CTCGGACTCT	1020
	GCGGACAGTG	CTGTATCCAC	CGTGCCATCT	CCACCCGAG	GTGTGATCTC	CAATGTGAAT	1080
	GAAACCTCAC	TGATCTCTGA	GTGGAGTGAG	CCCCGGGACC	TGGGTGGCCG	GGATGACCTC	1140
	CTGTACAATG	TGATCTGCAA	GAAGTGCCAT	GGGGCTGGAG	GGGCCTCAGC	CTGCTCAAGC	1200
	TGTGATGACA	AGTGTGAGTT	TGTGCTCGG	CAGCTGGGCC	TGACGGAGCG	CCGGGTCCAC	1260
60	ATCAGCCATC	TGCTGGCCCA	CACGCGCTAC	ACCTTTGAGG	TGACGGCGGT	CAACGGTGTG	1320
	TGCGGCAAGA	GCCTCTGCCC	GCCTCGTTAT	GCGGCGGTGA	ATATCAACCA	AAACCAAGGT	1380
	GCCCGCTCTG	AAATGCCAC	ACTACGCTTG	CACAGCAGCT	CAGGCAGCAG	CCTCACCTTA	1440
	TCTCTGGCAC	CCCCAGAGCG	GCCCAACGGA	GTCACTCTGG	ACTACGAGAT	GAAGTACTTT	1500
	GAGAAGAGCG	AGGGCATCGC	CTCCACAGTG	ACCAGCCAGA	TGAATCCGTT	GCAGCTGGAC	1560
65	GGGCTTCGGC	CTGACGCGCG	CTATGTGCTC	CAGGTCGCTG	CCCGCAGAGT	AGCTGGCTAT	1620
	GGGCACTACA	GCGCCCTGCG	CGAGTTTGAG	ACCACAAGTG	AGAGAGGCTC	TGGGGCCAG	1680
	CAGCTCCAGG	AGCAGCTTCC	CCTCATCTGT	GGCTCCGCTA	CAGCTGGGCT	TGCTTCTGTT	1740
	GTGGCTGTGG	TGTTTATCTG	TATGCTCTGC	CTCAGGAAGC	AGCGACACGG	CTCTGATTCT	1800
	GAGTACACGG	AGAAGCTGCA	GCAGTACATT	GCTCTGGA	TGAAGGTTTA	TATTGACCTT	1860
70	TTTACCTACG	AGGACCTTAA	TGAGGCTGTT	CGGGAGTTTG	CCAAGGAGAT	CGACGTGTCC	1920
	TGCGTCAAGA	TCGAGGAGGT	GATCGGAGCT	GGGGAATTTG	GGGAAGTGTG	CCGTGGTCTA	1980
	CTGAACACAG	CTGGCGCGCG	AGAGGTGTTT	GTGGCCATCA	AGACGCTGAA	GGTGGGCTAC	2040
	ACCGAGAGGC	AGCGCGGGGA	CTTCTTAAGC	GAGGCTCTCA	TGATGGGTCA	GTTTGATCAC	2100
	CCCAATATTA	TCCGGCTCGA	GGCGGTGGTC	ACCAAAAGTC	GGCCAGTTAT	GATCCTCACT	2160
75	GAGTTCATGG	AAACTGCGCG	CCTGGACTCC	TTCTCTCGCG	TCAACGATGG	GCAGTTCAGG	2220
	GTCACTCCAG	TGTTGGGCAT	GTGCGGGGCG	ATTGCTGCGG	GCATGAAGTA	CTGTCTCGAG	2280
	ATGAACATATG	TGCAACCGGA	CCTGGCTGCT	CGCAACATCC	TTGTCAACAG	CAACCTGGTC	2340
	TGCAAGTCTT	CAGACTTTGG	CCTCTCCGCG	TTCTTGGAGG	ATGACCCCTC	CGATCCTACC	2400
	TACACACAGT	CCCTGGGCGG	GAAGATCCCC	ATCCGCTGGA	CTGCCCCAGA	GGCCATAGCC	2460
80	TATCGGAAGT	TCACTTCTGC	TAGTATGTC	TGGAGCTACG	GAATTGTCTAT	GTGGGAGGTC	2520
	ATGAGCATATG	GAGAGGAGCC	CTACTGGGAC	ATGAGCAACC	AGGATGTCTAT	CAATGCGGTG	2580
	GAGCAGGATT	ACCGGCTGCC	ACCAACCATG	GACTGTCCCA	CAGCACTGCA	CCAGCTCATG	2640
	CTGGACTGCT	GGGTGCGGGA	CCGGAACCTC	AGGCCCAAT	TCTCCAGAT	TGTCAATACC	2700
	CTGGACAAGC	TCACTCGGAA	TGCTGCCAGC	CTCAAGGTCA	TTGCCAGGCG	TCAGTCTGGC	2760
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5 GATTGGCTGG ATGCCATCAA GATGGGGCGG TACAAGGAGA GCTTCGTCAG TGCGGGGTTT 2880
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 AGTTGCCCTT TGCCCCCAG AGACTGACTC TCAGAGCCAG AGATGGGATG TGTGAGTGTG 3660
 15 TGTGTGTGTG TGTGCGCGCG CGCGCGCGTG TGTGTGTGCA CGCACTGGCC TGCAACAGAGA 3720
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20 Seq ID NO: C21 DNA Sequence
 Nucleic Acid Accession #: NM_001804
 Coding sequence: 82..879

25 1 11 21 31 41 51
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 GCGCCGCCCC CGGGCGCCCC GCAGTACCCC GACTTCTCCA GCTACTCTCA CGTGGAGCCG 240
 30 GCGCCCGCGC CCGCGAGGCC CTGGGGGGCG CCTTCCCTG CGCCCAAGGA CGACTGGGCC 300
 GCGGCTACG GCGCGGGCCC CGCGGCCCTT GCGGCCAGCC CAGCTTCTGT GGCATTGCGG 360
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 CAGCCCTCG GGGGCCCGGG CACACCGTCC TGCCCGGAG CGCAGAGGCC GACGCCCTAC 480
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 45 AAGCCCCAAA TGGTTGGGGG AGGGGCGTAG ACAAGGCTCC AGGCCCCACC TCCTCTCCA 1200
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 TTTTCTTCT CTTTCAAA 1699

55 Seq ID NO: C22 DNA Sequence
 Nucleic Acid Accession #: NM_021978
 Coding sequence: 36..2603

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 65 AGCATGGCCC GGGGCGCTGG GTGGTGTCTG CAGCGGTGCT GATCGGCTTC CTCTGTGTTT 240
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 CCACGCGCGG CTTCCTTGAC AGCCCTTACC CCGCTCATGC CCGCTGCGAG TGGGCCCTGC 780
 75 GGGGGGACCG CGACTCAGTG CTGAGCCTCA CCTTCCGCGG CTTTGAACCTT GCGTCTGCG 840
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 80 GGACATTCAA CAGCCCCCTAC TACCCAGGCC ACTACCCACC CAACATTGAC TGCAATGGA 1140
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 TCCACTCAGA TCAGTCTTAC ACCGACACCG GCTTCTTACG TGAATACCTC TCCTACGACT 1380

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GCTGGGGACA CACCCAGTAT GGAGGCACTG GCGCGCTGAT CTGCAAAAG GGTGAGATCC 2340
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GAGCTTGGGA GCCTCTCTAG TGAAGGTGTT GGGGCTGCGG GATCTGGGCT GTGGGGCCCT 3000
TGGGCCACGC TCTTGAGGAA GCCCAGGCTC GGAGGACCTT GGAAACACAG CCGGTCTGAG 3060
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AACATTTTAT TTCTTTTAA AAAAAAATA 3149

Seq ID NO: C23 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2268

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AGCGTCCGGA AAGGGAGCTT TGAAGGTCC AAGCATTTC CCATCAGAT CTGTGACGGT 240
CTGGACATCA GCCCGAGGAG GGTGAGAGTG GAGCATTTC AGTTTCACTT CACTCTCTAT 300
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AGAGGATGCG GCGGAGCCCT TGCGGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG 840
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GTTGCGGGCC CAGCGCTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCACT 1440
GAGGCGGTGC GGGCAGAGCT GGAGGAGATC ACAGGAGCC CAAGCATGT GATGTTCTAC 1500
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TTTGAAGTGA ACCCTGACGT GACACAGGTG GGCCTGTTGG TGTATGGCAG CCAGGTGCAG 1740
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GCCCCCTACC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860
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CCCGGGGATT CCCTGATCCA CGTGGCAGCT TACGCCAGCC TGCGGTACCA CCAGGAGCTG 2100
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Seq ID NO: C24 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2424

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Seq ID NO: C25 DNA Sequence
Nucleic Acid Accession #: XM_097386.3
Coding sequence: 142..795

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Seq ID NO: C26 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 95..2128

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GCTTCTGAAA ACCCACTGGA CCTTGACAA ATATGGGGTC CAGGCAGATG CAAAGCTTCT 360
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 Protein Accession #: NP_005161.1

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 CTCTCAATTT CTCTGCGCCG AAGGGTAAGT GGTGCGTCCA GCTTACAGTA TCTGGAGAT 1920
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70 Seq ID NO: C32 DNA Sequence
 Nucleic Acid Accession #: NM_012445.1
 Coding sequence: 276..1271

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Seq ID NO: C33 DNA Sequence

Nucleic Acid Accession #: E08 sequence

Coding sequence: 1..1314

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CGAGTGGCAG TCGGCTCTC CAAGGACCGA TCCACACTGC AGGTGTCTGA CTGGGCCACA 360
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Seq ID NO: C34 DNA Sequence

Nucleic Acid Accession #: NM_003045.1

Coding sequence: 148..2037

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CAGATGCTGC GCGGGAAGGT GGTGACTGT AGCGGGAGG AGACGCGGCT GTCTGCTGC 240
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GTCTGTGGTG GAGCTGTGGC CCGTGAGAA GCAGGCCCTG CCATTGTCTAT CTCTTCTCTG 360
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CCAGCAGACC AAAATGAATT GCAAGCACC AATGATTCCC AGCTGGGGTT TTTACAGAG 1560
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AGCAAGACCA AGCTCTCATT TAAGGTTCCC TTCTGCCAG TGCTCCCATC CCTGAGCATC 1860
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Seq ID NO: C35 DNA Sequence
Nucleic Acid Accession #: NM_002776.1
Coding sequence: 82..912

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GCCCGGGCTC TGGCGAAGCT GCTGCCGCTG CTGATGGGCG AACTCTGGGC CGCAGAGGCG 180
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Seq ID NO: C36 DNA Sequence
Nucleic Acid Accession #: XM_095088
Coding sequence: 1..4074

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Seq ID NO: C37 DNA Sequence

Nucleic Acid Accession #: NM_032044

Coding sequence: 182..658

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Seq ID NO: C38 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 52..3042

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GACCGGGGCA GAGCCTGCGG GAGCTACCGT GTACGGTTCC TCTGTGGGAA GCCTGTGAGG 180
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CAGCAGCTCG TGGGTCACTA CCGATTACAT TTCCACCTGG CCGGTGATGT AGAOGAAAGG 660
GGAGGTTATG ACCCAACCCAC ATACATCAGG GACCTCTCCA TCCATCATAC ATTCTCTGSC 720
TGCTCACAG TCCATTGGCTC CAATGGCTTG TTGATCAAGG ACGTTGTGGG CTATAACTCT 780
TTGGGCCACT GCTTCTTAC GGAAGATGGG CCGGAGGAAC GCAACACTTT TGACCACTGT 840
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AAGATGATCA CAGGAGACTC CTACCCAGGG TACATCCCCA AGCCCAAGCA AGACTGTCAAT 960
GCTGTGTCCA CCTTCTGGAT GGCCCAATCCC AACCAACAAC TCATCAACTG TGCCGCTGCA 1020
GGATCTGAGG AAACCTGGATT TTGGTTTATT TTTCAACAGG TACCAACGGG CCCCTCGGTG 1080

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	TCTGCCAAGG	ACAAGCGGGC	GTTCCTCTCA	ATCATCTCTG	CCAGATACAG	CCCTCACCAG	1260
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5	AACCGAGACC	ACGGGGCCTG	GCTGCGCGCG	GGGATGTGT	GGCTGGACAG	CTGCCGTTT	1380
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	TCCAAGCAAG	AGATAAAGAA	CAGCTTGT	GTGGGAGAGA	GTGGCAACGT	GGGAGCGGAA	1500
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	ATAGGCCAGA	ATTTTCAAT	TAGAGGAAT	CAGTTATATG	ATGGCCCAT	CAACATCCAA	1620
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	GACGTTCCGA	TACTTCCAG	AGTGTCTTTC	GGAGAGCCTG	GGCCCTGGTT	CAACCAAGCTG	1800
	GACATGGATG	GGGATAAGAC	ATCTGTGTTC	CATGACGTG	ACGGCTCGT	GTCCGAGTAC	1860
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	GTCTTCGTGA	GGACCTTGCA	GATGGACAAA	GTGGAGCAGA	GCTACCTGG	CAGGAGCCAC	2340
	TACTACTGGG	ACGAGGACTC	AGGGCTGTGT	TTCTTGAAGC	TGAAGCTCA	GAACGAGAGA	2400
	GAGAAGTTTG	CTTTCTGCTC	CATGAAAGGC	TGTGAGAGGA	TAAAGATTAA	AGCTCTGATT	2460
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25	GCTGTGCTAG	ACGTGCCGAT	GGCCAAAGAG	CTCTTTGGTT	CTCAGCTGAA	AACAAAGGAG	2580
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	GTGCTGATTG	ACGGGAACCA	AGGGCGCGTG	GTGAGCCACA	CGAGCTTCAG	GAACTCCATT	2760
30	CTGCAGAGCA	TACCATGGCA	GCTTTTCAAC	TATGTGGCGA	CCATCCCTGA	CAATTCCATA	2820
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	AAGCTTGGGG	CAGACAGGGG	TCTCAAGTTG	AAAGAGCAAA	TGGCATTCGT	TGCTTCAAA	2940
	GGCAGCTTCC	GGCCCATCTG	GGTGACACTG	GACACTGAGG	ATCAAAAGC	CAAAATCTTC	3000
	CAAGTTGTGG	CCATCCCTGT	GGTGAAGAAG	AAGAAGTTGT	GAGGACAGCT	GGCGCCCGGT	3060
35	GCCACCTCGT	GGTAGACTAT	GACGGTGA	CTTGGCAGCA	GACCACTGGG	GGATGGCTGG	3120
	GTCCCCCAGC	CCCTGCCAGC	AGCTGCCCTG	GAAGGCCGTG	TTTACGCCCT	GATGGGCCAA	3180
	GGGAAGGCTA	TCAGAGACCC	TGGTGTGCTC	ACCTGCCCTT	ACTCAAGTGT	CTACCTGGAG	3240
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40	GTGCTGACAG	CAAAGATCCA	CTTTGGCAGG	AGCCCTGACC	CAGCTAGGAG	GTAGTCTGGA	3420
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	GAGAAAGAGC	CTTGGCCTTA	AGGAAATCTT	TACTCTGTGA	AGCAAGAGCC	AACCTCACAG	3540
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	TTGCTCAAC	AACCGGCCCC	AGAGTGCCCA	GGCACTCCTG	AGGTAGCTTC	TGGAAATGGG	4500
	GACAAATCCC	CTCGAAGGAA	AGGAAATGAC	TAGAGTAGAA	TGACAGCTAG	CAGATCTCTT	4560
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	GGGCTCGCCA	TGTTTCTGGT	GAGCCAATTT	GGCTGATCTT	GGGTGTCTGA	ACAGCTATTG	4800
	GGTCCACCCC	AGTCCCTTTC	AGCTGTGCTG	TAATGCCCTG	CTCTCTCCCT	GGCCCACTTT	4860
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65	ACGAGGCACC	AGAGTCTCCC	TGGGTCTTGT	GATGAACTAC	ATTIATCCCC	TTTCTGCCCC	4980
	CAACCAACAA	CTCTTTCCTT	CAAAGAGGGC	CTGCTGGGCT	CCCTCCACCC	AACCTGACCC	5040
	ATGAGACTCG	GTCCAAGAGT	CCATTCCCCA	GGTGGGAGCC	AACTGTGAGG	GAGGTCTTTC	5100
	CCACCAACAA	CTTTTCAGCT	GCTGGGAGGT	GACCATAGGG	CTCTGCTTTT	AAAGATATGG	5160
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70	AGGAGAGTTA	AAATGACCTC	ATGTCTTCTT	TGTCCACGGT	TTTGTGAGT	TTTCACTCTT	5280
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	ACCAAGAGCC	AATATCTAGG	CATTTCCTTG	GTAGCCAAAA	TTTTCTTATT	GCTTAGAAAA	5520
75	TGTCTCTCT	TGTTATTCTT	GTGTTAAGA	CTTAAGTGAG	TTAGGTCTTT	AAGGAAGACA	5580
	AGGCTCTCT	GAAATGCTTG	TCTTTTCTT	GTGCGCGAAA	TAGCTGGTCC	TTTTTCGGGA	5640
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	TATATTTTCT	ATTTATTAT	TATATGTGCA	CTTCAAGAA	TCAGTGTGAG	AGAAATAAAG	5760
80	AATGTCTTA	AATGTCAAAA	AAAAA	AAAAA	AAAAA	AAAAA	5808

Seq ID NO: C39 DNA Sequence
Nucleic Acid Accession #: NM_014373
Coding sequence: 322..1338

1 11 21 31 41 51
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 5 GTGGCCCTCGA GGTGGTGGCA GGGCGGCCCC CTGCAGTCGG GAGACGAACG CACGGACCGG 60
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 AAATAACATA ATTGAAGGCA GTAAAAGTGA AATTAAATAG GAAGATCATC AGTCAAGGAA 240
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 10 CAGTTACGTC AAACAAACCA GCCCCTAGAC GTTAACTATC TGCTATTCTT GATCATACTT 420
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 15 CTGACAGCTT GTATAGATTA TTGCTGAAT TTCTCTAAAA CAACCAAGCT TTCATTTAAG 720
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 GTTTTGGGAG ACCCAGCCAT CTACCAAGC CTGAAGGCAC AGAATGCTTA TTCTGTCAC 840
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 TTTGTAGCTT TCATAACCTG TTGGGAAGAA GTTACTACTT TGGTACAGGC TATCAGGATA 960
 20 ACTTCTCTATA TGAATGAAC TATCTTATAT TTCTCTTTTT CATCCCACTC CAGTTTATACT 1020
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 CCATTGTGAC TACTTCAGGT AATCATGTGT TTACTTAAAG TTCAGATTCC AGCATATATT 1140
 GAGATGAATA TTCCTGCTT ATACTTTGTC AATAGTTTTT TCATTGCTAC AGTGATTGG 1200
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 25 TGGAAAGTGT GCTTCATTCC ACTTACATTT CCTAATCTTG AGCAAAATGA AAAGCCTATA 1320
 TCAATAATGA TTTGTTAATA TTATTAAATTA AAAGTTACAG CTGTCTAAG ATCATAATT 1380
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35 Seq ID NO: C40 DNA Sequence
 Nucleic Acid Accession #: BC012089
 Coding sequence: 1..2571

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 45 CAGAAGGCAT ATGAATCCAA AATTGATTAT GACAAGATTG TCTACTATGA AGCAGGGGATT 300
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 75 CAATCACTGA GCACCTATA CCAAGCGCTC AAGTACTTTC AACGCACAGG GAATGGATTG 2100
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Seq ID NO: C41 DNA Sequence

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10	GAAACTGGGA	GCACACAGCA	AAATACACTC	TCTTTCCCAA	CAGCTACTTC	ACTGCTCCCC	240
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15	CAATCTACAG	GGCGTCCAC	TGGCACGCT	TTAATTGGGA	CCAGCACCCCT	AAACAGACAC	540
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	CATAATACAA	GTTTTTCGCT	GTGTTTAGAA	GGGTGATTAT	ACAACTCTTC	TAGCTGTAAG	660
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20	GTATTTGGCA	CAATCTGTTA	TGGACAGACT	GTAAATCTTA	CTGTAAGCAC	ATCTCTGTGA	840
	CCAGATGCTG	AATGCGGTGC	TGATGACAG	TTTGTTAATG	TAACAAATAGT	ACAATTTTGT	900
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25	AGGCTTAACC	CACAGAGCCC	TTTCTGGTGT	GCTTCCAGCT	TGCTCCAGTC	TGATCTGGTC	1140
	AACGCAAGCG	ACAAGCAATG	CTTAATAAAG	AAGAGTGGTG	GGGCGCCCTG	GTGCTGGCTG	1200
	GTCGCCGGCT	ACCAGGAAGA	TGCTAATGGG	AACTGCCCAA	TCAAGTGTCC	TGATCTGGCT	1260
	GGACTGACTG	TGAAGACAA	ATTTCAGCTG	ATCTCACTA	TGTGGGCAC	CATCGCTGCG	1320
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30	AAGCATATTT	AAGAAGAGAA	CTTGATTGAC	GAAAGCTTTC	AAAATCTAAA	ACTGCGGTGC	1440
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35	TTTTTCTTCC	ATTGCAATCT	TGCCAGCCTT	TCTGAATGGA	AGTTGTGAAT	TTTGTGCAAG	1740
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40	GGAGACATAT	GACTCAACTG	TGGAGGTTCC	AGGGGATGAG	AGGGGATACC	CACCACTTT	2040
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	AGACTGGAAA	GAGACATATC	TCTGACTTT	TCTAGGAGCT	GTGCTGGGCT	ATCCAGGAAC	2220
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	AGAGAGGCAA	AGGAAACTGG	TGTGGGGAGA	TCAATTAGAG	AGGAGGCCAC	TGGGATCCAC	2400
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	GAAAGACTGC	TGGGAGAAGG	TTTAAAAACA	AAAATCCAG	GAGTAAGAGC	CTTAGGTGCT	2520
	TTTGAATATG	GAGACAAACT	GTCTGGCAAA	GGGTGGGAGA	GGGAGCTGCT	GCTCAGGAGT	2580
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	CTGTTGACAG	AGGCTCAGCT	TGTGGCCACA	ACACACRACC	ACACACACAC	AACCAACAC	2700
	ACAAATGGGG	GCAACCACTC	CCAGTACAG	CTTTTACAAA	TGTTATTATG	GTCCTTTTGT	2760
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	AAAAAAA						2887

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	TCACTTGCT	GATATTTCCA	GTGTGACAGG	GACACAGCCA	ACGTGGGGTC	CCTTCTAGGC	60
	TGACAGCCGC	TCTCCAGCCA	CTGCOCGACG	CCCGCTCTCT	CCCGCCCTGC	CCGTGCACCT	120
	TCCGCAAGCCG	CCCTCCGCCA	AGCCCCAGAC	CCCGCTCCCA	TGCGCGATGA	CCGCGGGGAC	180
65	GAGGATGAGG	ATGCTCTGTG	CCGCGAGGGT	CCCTCGCGTG	CTGCTCTGCC	TGGGTTTCCA	240
	CTTTCTACAG	CGAGTCTCTA	GTACACACTG	GATTCATCAT	TGTAATCCCA	GAGAGTCCAG	300
	TGATACTGTC	ACAGCTTTAG	TTTCAGACGA	AGACAATCCA	CGTGTGGGTC	AAGTGTCAAT	360
	AACAAGTGT	AGCTCTGACA	TGAATGGCTA	TTGTTTGACT	GGACAGTCCA	CTTCATCTGGT	420
	GGACATGAGT	CAAACTACT	CAGGCTGTGA	ACTGGGTAT	ACTGGTGTCC	GATGTGAACA	480
70	CTCTCTTTTA	ACGTCCAC	AACCTTTAAG	CAAGAAGATG	GTGGCTTTGA	CCGTGATCTT	540
	TATTTATTTT	TTTCTATCAT	CAGCTGTGCG	TTCCACATAT	TATTTCTGCA	GAGTGTACAG	600
	AAATCGAAAA	AGTAAAGAAC	CAAGAAGATG	ATATGAGAGA	GTFACTTCAG	GGGATCCAGA	660
	GTGCGCGCAC	GTCTGAATAT	GAGAGAGATG	CCTCAGGGGA	TCCAGAGTGT	CCGCAAGTCT	720
	GAATGCGCCC	ATCAAACCTA	TGGCGAGGGA	TAAAGCTGTG	CTTGGTAAAT	ATTAAATATC	780
75	CAATTTATTA	ATAAATATTA	TGTTGGGTCA	AGTGTAGGT	CAATAACACT	GATTTTAAAT	840
	GTACTCTAAA	AATGTTTTTA	TTTTTGTTTT	ATTTTTCACA	GACTATTTCG	TAATGTATAA	900
	TGTGCGAGAA	ATATTTAATA	TCAAAGAGAA	ATAGATATT	TTATACAGT	AATTTCCGTA	960
	GCTAAATGCT	TCATTGAAAG	CTCTCAAGTT	TATATGCTGT	GTGCAAGTG	CTTAGAGATA	1020
	AGCAATTCCT	AGGTCATAGC	TCAGAAGATG	TAGCAAAATG	ACAGATTTCT	GTTAGCCAT	1080
80	ATATATAGTC	AAATCGATTT	AGTAAGTATG	TTTTTATGTT	TCTCTAAATC	ATGTAAGTAA	1140
	GGTTTGACTG	TACCATGTTT	TGATATGTAG	TGTGCACAT	GGTATCATAT	ATTAAACAA	1200
	TAATGCAATT	AGAAATTTGGG	AGAAGCAAA	ATAGGTCCTG	TGTTAAACAT	TACACATTTG	1260
	AAACAGAGTA	ACCTCGGGGA	GTCTATGTGTC	TTCTTCACTC	GGTCTCAGCT	ATAATCTGCT	1320
	TATATGAGGG	GCAGTGAGCA	GTTCCCTATG	CCAATCTCAG	ACTCTACAG	GTACTAGTCA	1380

	CTCATCTACC	AGATTCTGCC	TATGTAAAAT	GAATTGAAAA	ACAATTTTCT	GTAATCTTTT	1440
	ATTTAAGTAG	TGGGCATTTC	ATAGCTTCAC	AATGTTCCCT	TTTTGTATAT	TACAACATT	1500
	ATGTGAGGTA	ATTATTGCTC	AACAGACAAT	TAGAAAAAAG	TCCACACTTG	AAGCCTAAAT	1560
5	TTGTGCTTTT	TAAGAATATT	TTTAGACTAT	TTCTTTTAT	AGGGGCTTTG	CTGAATCTA	1620
	ACATTAAATC	ACAGCCCAAA	ATTGTATGGA	CTAATTATTA	TTTTAAATA	TATGAAGACA	1680
	ATAATCTAC	ATGTTGTCTT	AAGATGGAAA	TACAGTTATT	TCATCTTTA	TTCAAGGAAG	1740
	TTTTAACTTT	AATACAGCTC	AGTAAATGGC	TTCTTCTAGA	ATGTAAAGTT	AIGTATTTAA	1800
	AGTTGTATCT	TGACACAGGA	AATGGGAAAA	AACTTAAAAA	TTAATATGGT	GTATTTTTCC	1860
10	AAATGAAAA	TCTCAATTGA	AAGCTTTTAA	AATGTAGAAA	CTTAAACACA	CCTTCCTGTG	1920
	GAGGCTGAGA	TGAAAACTAG	GGCTCATTTT	CCTGACATTT	GTTTATTTTT	TGGAAGAGAC	1980
	AAAGATTTC	TCTGCACTCT	GAGCCCATAG	GTCTCAGAGA	GTTAATAGGA	GTATTTTTGG	2040
	GCTATTGCTAT	AAGGAGCCAC	TGCTGCCACC	ACTTTTGGAT	TTTATGGGAG	GCTCCTTCAT	2100
	CGAATGTCTA	ACCTTTGAGT	AGAGTCTCCC	TGGATCAGAT	ACCAGGTCAG	GGAGGATCTG	2160
15	TTCTTCTCT	ACGTTTATCC	TGGCATGTGC	TAGGGTAAAC	GAAGGCATAA	TAAGCCATGG	2220
	CTGACCTCTG	GAGCAGCAGG	TGCCAGGACT	TGTTCTCCATG	TGTATCCATG	CATTATATAC	2280
	CCTGGTGCAA	TCACACGACT	GTCACTATAA	GTCTGGGCC	TGGCCCTTAC	TATTAGGAAA	2340
	ATAAACGAGC	AAACACAGT	AAATATATAT	GGTCTATAC	ATATTGTATA	TATATTCTA	2400
	TACAAACATG	TATGTATACA	TGACCTTAAT	GGATCATAGA	ATTGCAGTCA	TTTGGTGCTC	2460
20	TGCTAACCAT	TTATATAAAA	CTTAAAAACA	AGAGAAAAGA	AAAAATCAAT	AGATCTAAAC	2520
	AGTTATTTC	GTTCCTTATT	TAATATAGCT	GAAGTCAAAA	TATGTAAAGA	CACATTTTAA	2580
	ATACTCTACT	TACAGTTGGC	CCTCTGTGGT	TAGTTCACCA	TCTGTGGATT	CAACCAACCA	2640
	AGGACGGAAA	AGGCTTAAAA	AATAATACAA	CAACACAAA	AAATACATTA	TAACAACAT	2700
	TTACTTTTTT	TTTTTTCTTT	TTGAGATGGA	GTCTGCTCT	GTTGCCCAGG	TTGGAGTGCA	2760
25	GTGGCAGAT	CTCGGCTCAC	TGCAACCTCA	CCTCCCGGGT	TCAAGAGATC	CTCCTGCCTC	2820
	AGCCTCTCTG	GAGCAGCTGG	CTACAGGCGC	ATGCCACCAT	GCCAGCTAA	TTTTTGATT	2880
	TTTAGTAGAG	GCGGGGTTTC	ACCATGTTGG	CCAGGATGGT	CTCAATCTCC	TAACCTTGAG	2940
	ATCCACGCTC	CACAGCCTCC	CAAACTGCTG	GGATTACAGG	CGTGAGCCAC	CGCAAGTAGC	3000
	ATTTACATTA	GGTATTACAA	GTAATGTAAA	GATGATTTAA	GTATACAGGA	GGATGTGAAT	3060
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	TAGTATGTGC	AGGGGGGGGA	TCTGGGAATC	AGTCCCTGT	GGATACCAAG	GTACAACGT	3180
	ATTTATTAAC	GCTTACTAGA	TGTGAGGAGA	GTCTGAATAT	TTTCAGTGAT	CTTGGCTGTT	3240
	TCAAAAAAAT	CTATTGACTT	TTCAATAAAT	CAGCTGCAAT	CCATTATTTT	CATTACAAA	3300
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35	AAAAACAGT	CATTTTGTGA	TTTTTCTAT	TTAAGAAATG	TTAAAAAGC	TAATCCCTAA	3420
	AATAGTTAGA	TCTTTGTAAA	TGCATATTAA	ATAATAAAGT	ATGACCCACA	TTACTTTTTA	3480
	TGGGTGAAAA	TAAGACAAAA	ATAATAGTTT	TAGTGAGGAT	GGTGCTGAGT	AAACATAAAA	3540
	ACTGATTTC	TCTCAGCTGA	TGTGTCTGT	ACACAGTGGG	AAGATTTTAG	TTCAACCTTA	3600
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40	ATTCAATGTA	TTGAGAACCA	AAGCAACAC	AAATGCATAA	ATGCATAATT	TATGGTCTTC	3720
	AACCAAGGCC	ACATAATAAC	CCAGTTAACT	TACTCTTTAA	CCAGGAATAT	TAAGTTCTAT	3780
	AACTAGTACT	CAAGGTTTAA	CCTTAAATTT	AAGATTTCCT	TAACCTTAA	CTTAAATTTG	3840
	ATATTATGTA	AAACATACAT	AATACAAATG	AACTCCACTG	TTCTCTGAA	TATTTTTCG	3900
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45	CTTAAGTCAG	ATTTTATTTT	ATGAGTCTTT	GAGACTAAAT	TCAATCACC	CCAGGTATCA	4020
	AATCAACTTT	TATGCAGCAA	ATATATGATT	CTAGTGTCTG	ACTTTTGTTA	AATTCAGTAA	4080
	TGCAGTTTTT	AAAAACCTGT	ATCTGACCCA	CTTTGTAAAT	TTTGCTCCAA	TATCCATCT	4140
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	TTCTTGTTC	TATGGGAGAA	GGGGAGTAA	TGACTTGTAC	AAACAGTATT	TCTGGTGTAT	4260
50	ATTTTAATGT	TTTTAAAAAG	AGTAATTTCA	TTTAAATATC	TGTTATTCAA	ATTGTATGAT	4320
	GTTAAATGTA	ATATAATGTA	TTTTCTTTT	ATTTGCACT	CTGTAATGTC	ACTTTTAAAG	4380
	TTTGAAGAGC	CATTTTGTGA	AACGGTTTTT	ATTAAAGATG	CTATGGAACA	TAAAGTTGTA	4440
	TTGCATGCAA	TTTAAAGTAA	CTTATTGAC	TATGAATATT	ATCGATTAC	TGAATGTAT	4500
	CAATTGTGTT	GTGTTCAATA	TCAGCTTTGA	TAATTGTGTA	CCTTAAGATA	TTGAAGGAGA	4560
55	AAATAGATA	TTTACAAGAT	ATTATTAAAT	TTTATTATTT	TTTCTTGGGA	ATTGAAAAAA	4620
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Seq ID NO: C43 DNA Sequence

Nucleic Acid Accession #: AF011468.1

Coding sequence: 257..1468

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	GCGCCTTGG	ATCGCTCCT	GGGACCGAG	GCGCCTGTA	GGATCTGCT	TGTTACTTAT
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	ATCAAAACAG	AAAAATGAAG	AATCAAAAA	GAGGCAGTGG	GCTTTGGAAG	ACTTTGAAAT
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	GCATCAGCTC	AGAAAGAGAG	TAGAAATACA	GTCCCACTT	CGGCATCCTA	ATATTCTTAG
	ACTGTATGGT	TATTTCCATG	ATGCTACCA	AGTCTACCTA	ATTCTGGAAT	ATGCACCACT
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	TTATATAACA	GAATTGGCAA	ATGCCCTGTC	TTACTGTCTA	TGGAAGAGAG	TTATTCTATG
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	TGGGTGGTCA	GTACATGCTC	CATCTTCAC	GAGGACCACT	CTCTGTGGCA	CCCTGGACTA
	CCTGCCCCCT	GAAATGATTG	AAGGTCCGAT	GCATGATGAG	AAGGTGGATC	TCTGGAGCCT
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	AGAAGTACTT	GAACACCCCT	GGATCACAGC	AAATTTCATCA	AAACCATCAA	ATTGCGCAAA	1440
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	GGCTGCCATA	TAACCTGACA	GGAACATGCT	ACTGAAGTTT	ATTTTACCAT	TGACTGCTGC	1560
10	CCTCAATCTA	GAACGCTACA	CAAGAAATAT	TTGTTTACT	CAGCAGGTGT	GCCTTAACCT	1620
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	AATTGTGCTA	CTTATCTG	TTTCAATCT	GGAGGCAAGG	TTGACTGCA	GCGCCCGCT	1740
	CAGCCTGTGC	TAGGCATGGT	GTCTTACAG	GAGGCAATC	CAGAGCCTGG	CTGTGGGGAA	1800
	AGTGACCACT	CTGCCCTGAC	CCCGATCAGT	TAAGGAGCTG	TGCAATAACC	TTCTAGTAC	1860
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	GTGATTCTTT	TAAAGTATGA	AAATAAAGAT	ATATGTACAG	ACTTGTATTT	TTTCTCTGGT	1980
	GGCATTCCCT	TAGGAATGCT	GTGTGTCTGT	COGGCACCCC	GGTAGGCTGT	ATTGGGTTTC	2040
	TAGTCCCTCT	TAACCACTTA	TCTCCATAT	GAGAGTGTA	AAAATAGGAA	CACGTGCTCT	2100
	ACCTCCATTT	AGGGATTGTC	TTGGGATACA	GAAGAGGCCA	TGTGTCTCAG	AGCTGTTAAG	2160
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	CTTCTCTCCT	CCTCTCTACA	ATCCATCTCT	TCTTAAGTTG	ATAGTGACTA	TGTCAGTCTA	1140
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85	GAGTCACTGC	CTGAATCTTT	ATTTTTTAAA	TGGAATGTTT	CTTAAAGGTT	AACATTCTTA	3600

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70 Seq ID NO: C46 DNA Sequence
 Nucleic Acid Accession #: NM_000584.1
 Coding sequence: 75..374

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 GCATAAAGAC ATACTCCAAA CCTTTCCACC CCAAAATTAT CAAAGAACT AGAGTGATTG 240
 AGAGTGGACC ACATCGCGCC AACACAGAAA TTATTGTAAA GCTTTCTGAT GGAAGAGAGC 300
 80 TCTGTCTGGA CCCCAGGAA AACTGGGTGC AGAGGGTGTG GGAGAAGTTT TTGAAGAGGG 360
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CAAAAAACAA CAAATAATTT TAAATATATA GGATTTTCCT AGATATTGCA CGGGAGAATA 660
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Seq ID NO: C47 DNA Sequence
Nucleic Acid Accession #: NM_005603.1
Coding sequence: 1..3756

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Seq ID NO: C48 DNA Sequence
 Nucleic Acid Accession #: XM_044533
 Coding sequence: 238..2751

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Seq ID NO: C49 DNA Sequence
 Nucleic Acid Accession #: NM_007019.1
 Coding sequence: 41..580

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15 Seq ID NO: C50 DNA Sequence
 Nucleic Acid Accession #: NM_014584.1
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 ACTGAACGT AATTTTGGGA GGTTTTCATT AGTGGAGCT CTTCAATTTT AAAGCTATTT 3120
 GAAGGGGTTT AGGAATTTAT ATCAGATGGT AATTGTAGAG AAAAAGAAGC TATATACCTC 3180
 AAAATCGTGC CCTCTTACA TATGCTTAT CAGGTATAAC ATGTTGAAAT GTCACATTAG 3240
 75 TAGTAAAGTG GGGTTTATTT ATATAGTGGT TAAGAAATGT CAGTTTACAC TGCTGTATAC 3300
 TTCTCTCTCT GTGCTCTTAA GGCCTGGTAC AGTGCCAAGC ACATACTTGG TATCCAATAA 3334
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80 Seq ID NO: C51 DNA Sequence
 Nucleic Acid Accession #: NM_002888.1
 Coding sequence: 37..723

1 11 21 31 41 51
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CCCGCTCCCTT GGTGCGGGGCC CAGGGGGCCCG CGCCCCACCG CCCCGCTGCT CGCGCTGCTG 120
CTGTGTGCTCG CCCCGGTGGC GGGCGCCCGCG GGGTCCGGGG GCCCGGACGA CCTCGGGCAG 180
CCTCAGGATG CTGGGGTCCC GGGCAGGCTC CTGCAGCAGA AGGCGCGCGC GGCGCTTCAC 240
TTCTTCAACT TCCGGTCCCG CTGCGCCAGC GGGCTGCGAG TGCTGGCCGA GGTGCAGGAG 300
GGCGCGCGCT GGAATTAATCC AAAAGAGGGA TGTAAAGTTC ACGTGGTCTT CAGCACAGAG 360
CGCTACAACC CAGAGTCTTT ACTTCAGGAA GGTGAGGGAC GTTTGGGGAA ATGTTCTGCT 420
CGAGTGTITT TCAAGAATCA GAAACCCAGA CCAACCATCA ATGTAACTTG TACAAGGCTC 480
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CAGGTGTAC ACTACTACTT GGCACAGCTC ACTAGTGTGA GGCAGTGGGT AAGAAAAACC 720
TGAAAAATTA CTGTGCCAC AAGAGTTACA ATCAAAGTGG TCTCTTTAGA CTGAATTCAT 780
GTGAACCTCT AATTTCATAT CAAGAGTTGT AATCACAATT ATTTCAATAA ATATGTGAGT 840
TCCTGC 846

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Seq ID NO: C52 DNA Sequence
Nucleic Acid Accession #: NM_005409.3
Coding sequence: 94..378

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TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCTT GAAAGAAAAAT 300
AAGAGCAAC GATGCTTAAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAAGTT 360
GAAAGAAAGA ATTTTAAAAA ATATCAAAAC ATATGAAGTC CTGAAAAGG GCATCTGAAA 420
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GGGTGAAAGG ACCAAAAACA GAAATACAGT CTCTCTGAAT GAATGACAAAT CAGAATTCCA 600
CTGCCCAAG GAGTCCAGCA ATTAATATGGA TTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
GGTATACATC GAGTTTACA AAGTGCTTTC ACGTCTTAC TTGTTGTATT ATACATTCT 720
GCAITTTCTAG GCTAGAGAAC CTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
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Seq ID NO: C53 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..609

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CACAGCGCTG CCAAGATCGA GCGCAGCTG GCCAGCAGCC TTTTCCCTCT GGACCACTCC 240
AAAAGCCAGC TCTATTGCGA CTTACACACC CCTGGGAGGT ATGGCAGGGT GATCTCTCTC 300
TCCCAACCG GGGACAATAT TTGCTCCAG GCTGAGGGGA TCCTGCAGAC CCACCGAGCC 360
GTGCTGGAAT TGAAGGTGAA CCAAGAGGGC TATAATTATA CTTTTCCCA TCTGTGTGTG 420
TTGAGAAATC AGGATAAGAA ATGCGTGTCTG GATGATATTA TTTCACTGCT AGAGGATCTC 480
AGGAGGGCTG CCGTCTCCAA TAAGACAACA GCCAGGGTGC AAGTGAAGTA TCCCAACACT 540
AAATTAAGG TATGCTCTCT CTGCATGCTT CTGCCAATTA AAGAGGCAGC ACTTCATTTC 600
TTGCCCTAA 609

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Seq ID NO: C54 DNA Sequence
Nucleic Acid Accession #: NM_002438.1
Coding sequence: 104..4474

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GCCCTCTGCT CCATCAGGAG AAGGAAAGGA TAAACCTCG GCCATGAGGC TACCCCTGCT 120
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AATCTATAAT GAAGATCACA AGCGCTGCGT GGATGCACTG AGTCCAGTGG CCGTCCAAAC 240
CGCAGCTGTC AACCAGGATG CCGAATCACA GAAATTCGGA TGGGTGTCCG AATCTCAGAT 300
TATGAGTGTG GCATTTAAAT TATGCCTGGG AGTGCAATCA AAAACAGACT GGGTTGCTAT 360
CACTCTCTAT GCCTGTGACT CAAAAAGTGA ATTTCAAGAA TGGAGTGC AAAAAAGAC 420
ACTTTTGGGG ATCAAGAGAG AAGATTTATT TTTAACTAC GGCAACAGAC AAGAAAAAG 480
TATTATGCTC TACAAGGGAT CGGGTTTATG GAGCAGGTGG AAGATCTATG GAACCAAGA 540
CAATCTGTGC TCCAGAGGTT ATGAAGCCAT GTATACGCTA CTAGGCAATG CCAATGGAGC 600
AACCCTGTGA TTCCCGTTCA AGTTTGAATA CAAGTGTGAC GCAGATTGCA CGAGTGTG 660
GCGGTGCGAT GGATGGCTCT GGTGCGGAAC CACTACTGAC TATGACACAG ACAAGCTATT 720

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TGGATATTGT CCATTGAAAT TTGAGGGCAG TGAAAGCTTA TGGATAAAG ACCCGCTGAC 780
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 CTGCCAACAA CAGAAGCGTG AGCTCCTGAG CATCACAGAG ATACATGAGC AAACATACCT 900
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 5 CAACAGCGGT TGGCAGTGGG GTGACCGCAG TCCTTTCGGA TATTTGAACCT GGTACCAGG 1020
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 10 GTGGCCGTAT GCCGTCACT GTTACAAGAT TCACAGAGAT GAGAAAAAA TCCAGAGGGA 1260
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 20 TGAACAAGCC TTCTGACTTA GTTTCGTTGG CTTAAGGCTT GAAATAATATT TCTGGACAGG 1800
 ACTTTTCAGAT ATACAACCA AAGGACTTTT TCAGTGGACC ATCGAGGAAG AGGTTGCGTT 1860
 CACCCATCTG AATTCAGATA TGCCAGGCGG AAAGCCAGGG TGTGTTGCCA TGAGAACCGG 1920
 GATTGCAAGG GGGCTTATGG ATGTTTTGAA ATGTGATGAA AAGGCAAAAT TTGTTGTCAA 1980
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 35 ACCTGAGCCA ACACGAGCTC CTCAGACAA TCCACAGTT ACTGAAGATG GGTGGGTTAT 2520
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 40 CACAGGTGAA CCCAATTTTG CAAATGAAGA TGAAACTGT GTGACCATGT ATTCAAATTC 2820
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 70 GAATTTTATA AATTTGTAAC TGAATTTTAA AATTTTGTG TCAATGTGAT TGTTTTCTT 4560
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 75 TTGGCATAAT TTAAGGAGCT CCCAAATGT GTTACCTATT AAATTTGTAAC TCAGCAAGTA 4860
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Seq ID NO: C55 DNA Sequence
 Nucleic Acid Accession #: NM_024574.2
 Coding sequence: 424..2130

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1 11 21 31 41 51
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	CGACCGCGCG	CCGCCCCGCC	TCGCCCCGCT	TTGAAGTTTG	CTGTGCGGAC	CGCAAAGTTG	240
	GGACACTTCA	GGGAGTTGAA	TTTTTCTCTT	TTATCTGCCT	CCGTCCCCGC	CCTCCAGGCT	300
5	TCTCGTTCCT	GGATATTGGT	GCTTAGCATC	TTGGCAGGGT	CCGGGGAAGT	GGACTATTTC	360
	GCACACCACA	CCACGGGGAG	GGATTTTTTT	CTATTTTCCC	TACGAAAAAC	AGATCTTTTT	420
	AAGGATGGTG	CTGCTCCACT	GGTGCTGCT	GTGGCTCCTG	TTTCCACTCA	GCTCAAGGAC	480
	CCAGAAGTTA	CCCACCCGGG	ATGAGGAACT	TTTTCAGATG	CAGATCCGGG	ACAAGGCATT	540
	TTTTCATGAT	TCGTCACTAA	TTCCAGATGG	AGCTGAAATT	AGCAGTTATC	TCITTAGAGA	600
	TACACCTAAA	AGGTATTCTT	TTGTGGTTGA	AGAAGACAAT	ACTCCATTAT	CAGTCACAGT	660
10	GACGCCCTGT	GATGCGCCTT	TGGAGTGGAA	GCTGAGCCTC	CAGGAGCTGC	CAGAGGACAG	720
	GAGCGGGGAA	GGCTCAGGTG	ATCTGGAACC	TCTTGAGCAG	CAGAAGCAGC	AGATCATTTAA	780
	TGAGGAAGGC	ACTGAGTTAT	TCTCCTACAA	AGGCAATGAT	GTGAGTATT	TTATATCGTC	840
	TAGTTCCCCA	TCCGGTTTAT	ATCAGTTGGA	TCTTCTTTCA	ACAGAGAAAG	ACACACATTT	900
15	CAAAGTATAT	GCCACCAAAA	CTCCAGAAATC	TGATCAGCCA	TACCCCTGAGT	TACCCATGAA	960
	CCCAAGAGTA	GATGTGACCT	CACTGGGGCG	CACCAAGGTC	ACTTTGGCCT	GGAAACCAAG	1020
	CCCCACTGCC	TCTTTGCTGA	AACAACCCAT	TCAGTACTGT	GTGGTCATCA	ACAAAGAGCA	1080
	CAATTTCAAA	AGTCTCTGTG	CAGTGGAAAG	AAAACCTGAGT	GCAGATGATG	CTTTTATGAT	1140
	GGCACCGAAA	CCTGGTCTGG	ACTTCAGCCC	CTTTGACTTT	GCCCACTTTG	GAITTCCTTC	1200
	TGATAATTCA	GGTAAAGAAC	GCAGTTTCCA	GGCAAAGCCT	TCTCCAAAAC	TGGGGCGTCA	1260
20	TGTCTACTCC	AGGCCCAAGG	TTGATATTCA	GAAAATCTGC	ATAGGAAACA	AGAACATCTT	1320
	CACCGTCTCT	GATCTGAAAC	CCGACACGCA	GTACTACTTT	GACGTATTTG	TGGTCAACAT	1380
	CAACAGCAAC	ATGAGCACCG	CTTATGTAGG	TACCTTTGCC	AGGACCAAGG	AAGAAGCCAA	1440
	ACAGAAGACA	GTGAGCTCA	AAGATGGGAA	GATAACAGAT	GTATTTGTGA	AAAGGAAGGG	1500
25	AGCAAAGTTT	CTACGGTTTG	CTCCAGTCTC	TTCTCACCAA	AAAGTCACCT	TCTTTATTCA	1560
	CTCTTGTCG	GATGCTGTCC	AAATCCAGT	GAGAAGAGAT	GGGAAACTTC	TCTGTCTCA	1620
	GAAATGTGAA	GGCATTTCAG	AGTTTCAGCT	TAGAGGAAAA	CCTAAAGCTA	AATACCTCGT	1680
	TCGACTGAAA	AGAAACAAGA	AAGGAGCATC	TATGTTGAAA	ATTCTAGCTA	CCACAAGGCC	1740
	TACTAAGCAG	TCAATTCCTT	CTCTTCCTGA	AGACACAAGA	ATCAAAGCCT	TTGACAAGCT	1800
30	CGTAACTGTT	TCCTCGGCCA	CCGTGGCTTG	GCTAGGCAC	CAGGAAGGGA	ACAAAGTTTG	1860
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	CCAATGTCTA	GGACACAGTA	TAAAGGAAGA	GTCAAGAAAG	GTCTCTGTGA	AATATTTCCTA	1980
	CAGTCAAAAC	CTGACAAAAG	CAGTGACCAC	AGAAACAATT	AAAGGTCTTC	AGCCTGGCAA	2040
	ATCTTACCTG	CTGGATGTTT	ATGTCATAGG	ACATGGGGGG	CACCTCTGTA	AGTATCAGAG	2100
35	TAAAGTTGTG	AAAACAGAAA	AGTTCTGTGA	GTACCTCTCT	TATAGAGATA	TATTATGTAG	2160
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	CTGATGCCGG	TTGGTGTCAA	AGATAGAGGG	CTTCTTGAAG	GAACTTGCCA	TTCTTGCTTT	2400
40	TGACCACTGC	ATGAACCTGT	TCTAAATAT	TTTATTACCT	AAAAATTTAA	AATATGCCAT	2460
	TCATTGCACA	CACCCACAAA	TGCCAATCAT	TCCTCTCTAT	AGATGCTAGG	ATATATATAA	2520
	ATTATTTTAT	AAATTCCTGT	TTTAAATGTC	AGTGTTCCTA	TGATGTGAAA	CTATTAAATT	2580
	CTTTCTCTAT	TAAAGTACAG	ATCTAATCTA	AGTATTATTA	AGTTGATAGC	CCTCTAGTCA	2640
	GTTATATTGC	TATTGTAAAT	TCTTGTGTTG	TGAGTAAAT	GTTTAAATAC	TATATGTATC	2700
45	TCATGTACAA	AGTTGACATA	CATTATATTC	ATGTACATAA	AATTAAGAGG	ATTAGATTAT	2760
	ATACTGTTAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	2808

Seq ID NO: C56 DNA Sequence

Nucleic Acid Accession #: BC034229.1

Coding sequence: 373..1422

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	AGTGTTTACA	AATCAGAATA	ACTTTTAGAC	AATATTAAGG	TGGTAATCAT	GAACAGAAAA	180
	GATTTTGTAG	TTCTTCCATG	GGGAAAAACCT	GGAAATCTG	TAAAGCTAAA	ATATAGCAAT	240
	GTAATAATTA	AAACAAAAGT	CTAAGATTGG	AAGAGATAAT	TTGCTTCAGG	ATTTTGTATG	300
60	AAGGCAATG	CTAATTTTAA	AAACCAAGAT	TCGGAGAAGT	ACAAAAGAAA	TAGAAATGCT	360
	CAAGAACTGC	GAATGGAGAA	AGTACAGTTA	GAGTTTGAGA	ACCAAGAGAT	GGAGAAGAAA	420
	CTGCAAGAAAT	TCGATCCAC	AAGAAACAAA	GAAAAGGAAG	ATAGAGAGTC	AAGCGAGTAT	480
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	AAAGGAAATG	TTGTTAAGTT	TTCTGCTGGA	AAAGTGAAT	TAAATTTGCT	GAAGGAACAG	600
	ATTCAGAGC	CAGTGAAACC	AACAGTTAAT	TATAAAATGG	CAAAATCTTC	AGAATGTGAA	660
65	AAACCCAAGA	TAAATGGGAA	AGTTTGTGGA	CAGTGTGAGA	ACAAAGCTGC	TCTACTGGTA	720
	TGCCTTGAAT	GTGGAGAAGA	TTATTGTTCA	GGATGCTTTG	CTAATGTTCA	CCAGAAAGGG	780
	GCATTAAGC	TCCACAGAAC	AACTCTTTTG	CAGGCAAGAT	CTCAAAATAT	ATTCAATGTA	840
	TTGGATGTTG	CCCATCAGTT	TATAAAGGAT	GTTAATCCAG	ATGAACCCAA	AGAGGAGAAAT	900
	AATTCTACAA	AGGAAACCAAG	TAAAATTCAA	CATAAACCCA	AATCTGTACT	TCTCCAGAGG	960
70	AGCAGCTCTG	AGGTAGAAAT	TACAACGATG	AAAAGAGCAC	AACGTACAAA	ACCAAGAAAA	1020
	AGTCTGTGTT	GTGAAGGGTC	ATTGATGAAA	GAAAGCTTCT	CACAGTCCCT	TCAAGGAAGT	1080
	TTAAGTCTGA	GGAGAACCGG	AAATCATGAT	GACAAACAAG	AACAGAAATT	ACATGCAGCA	1140
	GTAAAAGACT	CATTGGAAGA	ATGCGAAGTA	CAGACTAATC	TGAAAATTTG	GAGAGAAACA	1200
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75	CACAGGAGAA	CTCCACAGAA	GCAACTTTTT	AAATGCTACC	AGATACGTTT	CCACATCCAC	1320
	ATGAACACCA	TGTTGATGCA	CAGTGTCTCT	AAAATGAAAA	CGATGAAGAT	AGTGATGGTG	1380
	AGGAGACCAA	AGTACACAC	ACAGCTCTTT	TATTGCCAGT	AGAAACATTA	AACATAGAGA	1440
	GACCTGAACC	ATCTCTGAAG	ATAGTGAAC	TGGATGATAC	TTATGAAGAG	GAATTTGAAG	1500
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80	TGCTTTTCTA	TGATTGTGAG	AAGAATAGCT	TTCCATATGA	AAATGGCATC	CATCAACATC	1620
	ATGTTTTCGA	TAAAGGAAAG	AGAGACTTCT	TAAATCTTTG	TCTGAGAAAC	AGCTCTACTT	1680
	ATTATAAGAA	TAAATCAAAA	GGAGAAACTT	CAACACAGA	TTTTGACAAC	ATCGTGGATC	1740
	CTGATGTGTA	TTCTTCTGAC	ATTGAAAAAA	TTGAGGAAAG	CACCTCCTTT	GAAAGAAATT	1800
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WO 03/042661

5 TTGAAAGCAA GGACACTTTG CTAGGTAGAG ATTTAGAAAA AGCTCCCATI GAGGAGAAAT 1920
 TATCTCAAGA CATCAAGAA TCCITGGAAAT TGAGCAATCT GTATAAGAGG CCAAGCTTTG 1980
 AAGAATCAAA AACTACAAAG TCATCACTGT TGTACAGA AATAGCCTGC AGAAGTAAGC 2040
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 AAGCTCCAG TTGCCTTTCA TCCTCTCATC CTCGATCAAG AAGTGCAGCT GCTCAATCAT 2280
 CATCTAGAGC TGCTTCTGAA ATTTAGAAAA TTGAATATAT TGATATTACT GACCAGAATG 2340
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 10 AAGTGTGAG ATCTCTTGCA GATACTCAG AAAAGCTTTA CAGCTTAACC TCAGAAGAGT 2460
 TCCAGATT CAGCAGCCAA TCACCTGAATA TAAGTCAGAT TTCCACAGAT TTCCTTAAGA 2520
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 AAATTCAGTC TTGCTGTCA CTCTCTGAGA GCAGTACAGA TGAGGAGGAG GAAGATTTTC 2640
 TCAACAGCA ACATGTCATC ACATACCGT GGTCAAAGAG TACTTAAAGA TTATTTGTTT 2700
 15 ATTACTGTT CCATTTTGTA CCCAGAGTAA AGCAAACAC TGAGAAAAGT AACCAAGTGA 2760
 TTACCTATCC AAGTGTGGA GATTTTGATT ACTAATGTCT TTGATGTTT AAGGCTACAA 2820
 ACTAATAAAA GTAAATTTAT AAGTTCAAAA AAATTTTAA AAAAAAAAT AAAAAA 2876

20 Seq ID NO: C57 DNA Sequence
 Nucleic Acid Accession #: NM_024687.1
 Coding sequence: 138..1706

25 1 11 21 31 41 51
 AAAACATGA TGACAACAAG AAACAGAAAT TACATGCAGC AGTAAAGAC TCATTGGAAG 60
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 AAGACATTCT ATCCTATATG GAAAAATAT GGCTTAAAAA ACACAGGAGA ACTCCACAAG 180
 30 AGCAACTTTT TAAAAATGCTA TCAGATACGT TOCCACATCC ACATGAAACC ACTGGTGATG 240
 CACAGTGTTC TCAAAATGAA AACGATGAAG ATAGTGTATG TGAGGAGACC AAAGTACAAC 300
 ACACAGCTCT TTTATTGCCA GTAGAAACAT TAAACATAGA GAGACCTGAA CCATCTCTGA 360
 AGATAGTCGA ACTGATGAT ACTTATGAAG AGGAATTGGA AGAAGCAGAA AATATTGTGC 420
 CTTACAAAGT TAAATTAGCT GATGACAGCA GTCAACGAAG TTGTGCTTT CATGATTGTC 480
 AGAAGAATAG CTTTCCATAT GAAATGTGCA TCCATCAACA TCATGTTTC GATAAGGGAA 540
 35 AGAGAGACTT CTAAATCTT TGTCTGAGAA ACAGCTCTAC TTATTATAAA GATAATTCAA 600
 AAGGAGAAAC TTCAACACA GATTTTGACA ACATCGTGGG TCCTGATGTG TATTCTCTG 660
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 GTTTAGAAAG TAATCAAAAG TCTGATGATT CCTGTGTATC ACTTGAAAGC AAGGACACTT 780
 TGCTAGGTAG AGATTTAGAA AAAGCTCCCA TTGAGGAGAA ATTATCTCAA GACATCAAG 840
 40 AATCCTTGA ATTGAGCAAT CTGTATAAGA GGCCAAGCTT TGAAGAATCA AAACATCAA 900
 AGTCATCACT GTTGTACAA GAAATAGCCT GCAGAAATGA GCCTATAACA AAACATATC 960
 AAGGACTTGA GAGATTCTTT ATTTTGATA CAAATGAAAG ACTCAACTTA CTCCTTCTC 1020
 ATCGTTTGA ATGCAACAT TCCAGTACTA GGATTACACT TGCAGAGAC AGAGAATGGA 1080
 TTCCAGACCA TAGCTTAAGT GAATATGCTG ATAATGCAAT TGTCTTGGGT GTTCTGACGG 1140
 45 GTGCTCAGAG TCCATCATCA AGTAGAAAAC AGCAAAAGAT GGTCTCAGAA TCACAGAGAC 1200
 CTTCAACAGC AAATTTTCCA CTTTCCAAC CTGTAAAGA AAGCTCCAGT TGCCCTTTTCA 1260
 CCTCTCATCC TCGATCAAGA AGTGCAGCTG CTCATCATC ATCTAGAGCT GCTTCTGAAA 1320
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 CACTACCGTG GTCAAGAGT ACTTAAAGAT TATTTGTTC TTAAGTTTC CATTTGTGAC 1740
 55 CCAGAGTAAA GCAAAACACT GAGAAAAGTA ACCAAGTGAT TACCTATCCA AGTGTGGAG 1800
 ATTTTGATTA CTAATGTCTT TGATGTTTCA AGGCTACAAA CTAATAAAG TAAATTTATA 1860
 AGTTCAAAA AAAAAA AAAA

60 Seq ID NO: C58 DNA Sequence
 Nucleic Acid Accession #: NM_005408.1
 Coding sequence: 76..372

65 1 11 21 31 41 51
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 TTCAATTTA CGAGTAAGAA GATCTCCTTG CAGAGGCTGA AGAGCTATGT GATCACACC 240
 70 AGCAGGTGTC CCCAGAGGC TGTCTCTTC AGAACCACAC TGGGCAAGGA GATCTGTGCT 300
 GACCCAAAGG AGAAGTGGGT CCAGAATTAT ATGAAACACC TGGGCGGAA AGCTCACACC 360
 CTGAAGACTT GAATCTGCT ACCCTACTG AAATCAAGCT GGAGTACGTG AAATGACTTT 420
 TCCATTCTCC TCTGGCTTCC TCTTCTATGC TTTGGAATAC TTCTACCATA ATTTTCAAAT 480
 AGGATGCAAT CGGTTTGTG ATTCAAAATG TACTATGTGT TAAGTAATAT TGGCTATTAT 540
 75 TGAATCTGTT GCTGGTTTGG AGTTTATTTG AGTATTGCTG ATCTTTTCTA AAGCAAGGCC 600
 TTGAGCAAGT AGGTTGCTGT CTCTAGCCC CCTTCCCTTC CACTATGAGC TGCTGGCAGT 660
 GGGTTTGTAT TCGGTTTCCA GGGGTTGAGA GCATGCTGTG GGGAGTCAIT GACATGAAGG 720
 GATGCTGCAA TGTAGGAAGG AGAGCTCTTT GTGAATGTGA GGTGTTGCTA AATATGTTAT 780
 TGTGGAAGA TGAATGCAAT AGTAGGACTG CTGACATTTT GCAGAAAATA CATTTTATTT 840
 80 AAAATCTCCA AAAAAA AAAA

Seq ID NO: C59 DNA Sequence
 Nucleic Acid Accession #: AK097746.1
 Coding sequence: 185..2224

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5 CTTTCATGAC AGTAACAAAT CCAAGATTTT GGAAGAGCGC CTAOGATATT TAAATGACCA 60
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ATTTTCCTTT TTATTATGTG CCAATCTTCT TCTGGCAAGG AAAGAGATTG AATACCAGGA 180
ACTGATGTTT CTTTAACTG GAGGAGTAAG TCTTAAAGT GCTGAGAAAA ATCCTGATCC 240
AACTTGGCTA CAGGACAAAA GCTGGGAGGA AATCTGTGG GCAAGTGAAT TTCCTGCCTT 300
CAGAGGACTC AGGCAACATT TTTGTGAACA TATATATGAA TGGCGAGAAA TCTATGACAG 360
10 TAAAGAGCCA CATAATGCTA AATTTCCAGC ACCAATGGAT AAGAACCCTAA ATGAACTACA 420
GAAAAATAA ATCTTCGGT GTTTAAGACC TGATAAGATA ACCCCAGCTA TAACAAACTA 480
TGTAACAGAC AAATAGGGA AAAAGTTTGT AGAGCCTCCA CCATTGATT TGACAAAGAG 540
TTACTTGGAT TCAAAATGCA CCATTCCCTT AATTTTGT CTATCTCCAG GAGCAGATCC 600
TATGGCCAGC CTGCTGAAAT TTGCAATGA TAAATCTATG TCTGGAAATA AGTTTCAAGC 660
15 TATTTCACTG GGACAGGAGC AAGGACCGAT TGCAGCAAAA ATGATTAAAG CAGCAATTGA 720
AGAAGGAACT TGGGTGTGCC TACAGAATTG CCATCTTGCA GTGTCTCGGA TGCCCATGTT 780
GGAAGAAATG TGTGAAGATT TTACCTCTGA AACCTGTAAC TCATCCTTTA GGCTTTGGCT 840
GACAGCTAT CCATCTTCAA AATTCOCAGT AACATTTCTA CAGAATGGAG TAAAAATGAC 900
20 TAATGAACCT CCCACGGGTC TTCGGCTGAA TCTCCTCAA TCATATCTCA CTGATCCAGT 960
TTCTGATCCT GAGTTTTTCA AGGGATGCGG TGGAAAGGAA CTGTTATTTA TCAATGAATA 1020
TGATACAAAT CCATTGGAAG CTATATCTTA CTGACTGGG GAGTGTAAAT ATGGAGGAAG 1080
AGTGACAGAC GTTGGAGACA GACGCTTCTT ATTAACCATG CTGGCTGACT TTTATAATCT 1140
GTACATAGTT GAAAACCTC ATTATAAGTT TTCTCCAGT GGAACCTATT TTGCACTCC 1200
25 TAAAGGCAC TATGAGGACT ACATTGAATT CATTAAGAAA CTTCATTTA CTCAACACCC 1260
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CCTCTTTGAG TCCTTGCTCC TCACCCAGGG AGGCTCCAAA CAGACAGGAG CCTCAGGAAG 1380
TACTGATCAG ATTCTGTTAG AAATTACCAA AGATATCCTC AACACAGCTCC CTAGTGATT 1440
CGACATTGAA ATGCACTAC GGAAGTATCC TGTGAGATAT GAAGAAAGCA TGAATACTGT 1500
30 GTTAGTACAA GAAATGGAAG GATTTAACAA TTTAATTATA ACTATACTGA ACACCTACG 1560
GGACCTGAA AAAGCTATTA AGGGTGTGOT TGTGATGGAT TCTGCAATTG AGGCACTCTC 1620
CAGTAGCTTA CTGTTGGAA AGGTTCAGAA AATATGGGCC AAACGTTTAT ACCCAAGCCT 1680
TAAGCCCTG GAAAGTTACA TCACAGATT CTAGCCCGG TTGAACCTTT TACAGGACTG 1740
GTATAATTCA GGAACCTT GTGTGTTTGT GCTGTCAAGT TTCTTTTCA CTGAGGCTT 1800
35 TTTAAGTGA GCTATGCGA ATTATGCCAG AAAATATACC ACCCTATTG ATTTGCTAGG 1860
ATATGAATT GAGGTTATCC CATCTGATAC ATCTGACACA TCACAGGAG ATGGTGTTTA 1920
TATCCAGCAG CTGTATCTCG ATGGGCGCAG CTGGGACCGA GAAAGTGGAT TGCTTGCTGA 1980
ACCAATATCC AAACCTCTGT TTGACCTGAT GCCATCATA TGGATAAAAC CAACTCAAAA 2040
ATCTCGGATT ATAAAGTCGG ATGCCCTATG CTGTCCCTC TACAAGACAA GTGAACGTAA 2100
40 AGGAACCTT TCCACTACGG GACATTCTAC TAACTTTGTC ATTGCAATGT TGTAAAAAC 2160
AGACCAACCT ACTCGGCACT GGATCAAGCG CGGGTGTGCT TTGCTTTGTC AGTTGGATGA 2220
CTAAATTGGA CAAATTTATA AAACATCCAA AAGTTT 2256

Seq ID NO: C60 DNA Sequence
Nucleic Acid Accession #: J02761.1
Coding sequence: 14..1159

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50 GAATTCGGGT GCCATGGCTG AGTCACACCT GCTGCAGTGG CTGCTGCTGC TGCTGCCAC 60
GCTCTGTGGC CCAGGCACTG CTGCCCTGGAC CACCTCATCC TTGGCCTGTG CCCAGGGCCC 120
TGAGTTCTGG TGCCAAGGCC TGGAGCAAGC ATTGCACTGC AGAGCCCTAG GGCATTGCC 180
ACAGGAAGCT TGGGACATG TGGGAGCCGA TGACCTATGC CAAGAGTGTG AGGACATCG 240
CCACATCTCT AACAAAGATGG CCAAGGAGGC CATTTTCCAG GACACGATGA GGAAGTTCT 300
55 GGAGCAGGAG TGCAACGTC TCCCTTGAA GCTGCTCATG CCCAGTGA CAACAGTGT 360
TGACGACTAG TTCCCTGAG TCATCGACTA CTCCAGAAC CAGACTGACT CAACCGCAT 420
CTGTATGAC CTGGGCTGT GCAAAATCCG CGAGCCAGAG CCAGAGCAGG AGCCAGGGAT 480
GTCAAGCCCC CTGCCAAAC CTCTGCGGGA CCCTCTGCGA GACCTCTGC TGGACAAGCT 540
OGTCTCTCCT GTGCTGCCCG GGGCCCTCCA GGGGAGGCT GGGCTCACA CACAGGATCT 600
60 CTCCGAGCAG CAATTCOCOA TTCTCTCTCC CTATTGCTGG CTCTGCAGGG CTCTGATCAA 660
GCGGATCCAA GCCATGATT CCAAGGGTGC GCTAGCTGTG GCACTGCCCC AGGTGTGCG 720
CGTGTACCT CTGGTGGGCG GCGGCATCTG CCAGTGCTG GCTGAGGCT ACTCCGCTAT 780
CTGTCTGAC ACCTGCTGCG GCGCATGCT GCGCCAGCTG GTCTGCGGCC TCGTCTCCG 840
GTGCTCCATG GATGACAGCG CTGGCCCAAG GTGCGGACA GGAGAATGGC TGCCGCGAGA 900
65 CTCTGATGCG CACCTCTGCA TGTCCGTGAC CACCCAGGCC GGGAACAGCA GCGAGCAGGC 960
CATACCAAG GCAATGCTCC AGGCTGTGT TGGCTCTGCG CTGGACAGGG AAAAGTGCAA 1020
GCAATTTGTG GAGCAGCACA GCGCCAGCT GCTGACCTG GTGCCAGGG GCTGGGATGC 1080
CCACACACCC TGCCAGGCCCT TCGGGGTGTG TGGGAACATG TCCAGCCCTC TCCAGTGTAT 1140
CCACAGCCCC GACCTTTGAT GAGAACTCAG CTGTCCAGCT GCAAGGAAA AGCCAAAGTA 1200
70 GAGGGCTCT GGGACCATGG TGACCAAGCT CTTCCTCTGC TCCCTGGCCC TCGCCAGCTG 1260
CCAGGCTGAA AAGAAGCCTC AGCTCCCA CAAGCCCTCT CACCTCCCTT CCTCGGAGT 1320
CACTTCCACT GGTGGACAC GGGCCCCCAG CCCTGTGTG GCTTGTCTG TCTCAGCTCA 1380
ACCAAGTCT GACACAGAG CCCACTTCCA TCCCTCTGCG TGTGAGGCA AGCGAGGCA 1440
GCATCTGGAG GAGCTCTGCA GCCTCCACAC CTACCAAGGC CTCCAGGGC TGGGCTCAGG 1500
75 AAAAAACAG CACTGCTTTA CAGGACAGGG GGTGGAAGCT GAGCCCCGCC TCACACCCAC 1560
CCCCATGAC TCAAGATTG GATTTTACAG CTACTTGCAA TTCAAAATTC AGAAGAATAA 1620
AAAATGGGAA CATACAGAAC TCTAAAGAT AGACATCAGA AATTGTTAAG TTAAGCTTTT 1680
TCAAAAAATC AGCAATTCCT CAGGATAGTC AAGGGTGGAC ACTGCAAGCT CTGGCATGAT 1740
GGGATGGCGA CCGGCAAGC TTTCTTCTC GTGATGCTCT GCTGCTGAG AGCTATTGCT 1800
80 TTGTTAAGAT ATAAAAAGG GTTCTTTT GTCTTCTGT AAGGTGGACT TCCAGATTTT 1860
GATTGAAAGT CCTAGGTTGA TTCTATTCT GCTGTGATTT ATCTGCTGAA AGCTCAGCTG 1920
GGGTGTGCA AGCTAGGAG CCATTCTGT GTAATACAA GTCTGACCA ATGCTAATAA 1980
AGTCCTATTC TCTTTTAAAA AAAAAAAGG GAATTC 2026

Seq ID NO: C61 DNA Sequence

Nucleic Acid Accession #: NM_139172.1
Coding sequence: 19..552

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   GTTGACATAT GGGACCGGGA GAGCTGTGGG GGCCAGGCGG CCATCGATAG CCCCAACCTC 180
   TGCTGCTGTC TCCGCTGCTG CTACCGCAAT GGGGTCTGCT ACCACGAGCG TCCAGACGAA 240
   AACGTGCGGA GGAAGCACAT GTGGGCGCTG GTCTGGACGT GCAGCGGCTT CCTCCTCTTG 300
   AGCTGCAGCA TCTGCTTGT CTGGTGGGCC AAGCGCCGGG ACGTCTGCA TATGCCCGGT 360
   TTCTGGCGGG GTCCGTGTGA CATGTCCAAG TCCGTCTCGC TGCTCTCCAA GCACCGAGGG 420
   ACCAAGAAGA CGCCGTCCAC GGGCAGCGTG CCAGTCGCCC TGTCCAAAGA GTCCAGGGAT 480
   GTGGAGGGAG GCACCGAGGG GGAAGGGACG GAGGAGGGTG AGGAGACAGA GGGCGAGGAA 540
   GAGGAGGATT AGGGGAGTCC CGGGGGACT GCTCAATACA GATACGGTGG ACG 593
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Seq ID NO: C62 DNA Sequence
Nucleic Acid Accession #: NM_054023.2
Coding sequence: 98..379

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   ATTTTAAAC TCCTGAAAAA TATCCAGAT AACTGTCTATG AAGCTGGTAA CTATCTTCT 120
   GCTGGTGACC ATCAGCCTTT GTAGTTACTC TGCTACTGCC TTCCTCATCA ACAAGTGCC 180
   CCTTCTGTGT GACAAAGTGG CACCTTTACC TCTGGACAAC ATTCTTCCCT TTATGGATCC 240
   ATTAAAGCTT CTCTGAAAAA CTCTGGGCAT TTCTGTGTAG CACCTTGTGG AGGGGCTAAG 300
   GAAGTGTGTA AATGAGCTGG GACCAGAGGC TTCTGAAGCT GTGAAGAAAC TGTGGAGGC 360
   GCTATCACAC TTGGTGTGAC ATCAAGATAA AGAGCGGAGG TGGATGGGGA TGAAGATGA 420
   TGCTCTATC CTCCCTGCTT GAAACCTGTT CTACCAATTA TAGATCAAAAT GCCCTAAAT 480
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   AAAAAAAAAA 550
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Seq ID NO: C63 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..2874

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   TGCACTGACA GAAACTGGCA TGCTGGCAGA ACACGTGGAA TTTGGCTGGG GCAAGTGGAG 180
   GAGAGATGTT CAGATGTGTT CGGAGTTTCT TTCTTCTGGT GGGTTCGTGG TCTGCTGGC 240
   TCAGGAGCGA AGCTGCAGAC CTTCACGCCA GCCCAGGAAG GGGCTCCAC AGTGACGCGG 300
   CAGGCTGAAG CGCTCCTCAA GTGCCGCGAG AGTGGGCGTC CAGGCAGAGG AGGCGCGGAG 360
   AGCGAGCGAG CGAGGGATGC CAGCATGCTG TCACCTCTCA GTGCTGCCAT GCGAAACTAC 420
   CCAAGCTCCT CTACCATCCC TCCAAGAAGA TCCTACTCTC CAACCGAAAT TGCTCACAG 480
   AGTTACTCCT GCAGCCTTCC AGACATGAAA ATCTCCATGG CAGAATCTGG CCGCTCCTTG 540
   GATAGCCTTG ACATTCTGGA GGATGGCGAG TCTGGGTCAC CATTTCTTGT GACTCATTTG 600
   TACTTTCTGG GGGTTGTGAC CACTGGGATG GAACAACCTAG ATTTTGAAC AGGACCAAA 660
   ATATTTGATT TGCAGATTTA TGTGAAGGAT GAGGTTGGTG TCACAGACCT GCAAGTCTG 720
   ACTGTCCAGG TAACAGATGT GAAACGAGCA CCTCAGTTTC AAGGCAACTT GGCAGAGAT 780
   CATCTCCGTG CAGACGAGCC ACATTTCAT GCTCATAGTC ACACGTACGT GAGGATAGTG 840
   GCTACTGCTG TGGCAGGACA CAGGCTTAGA TCTAGCATTG GTTCCCCTT CCTGGGCACC 900
   TTCTGTGTTG TGGTGGGAT GCAGTATTTT CTGATTTCTC CCCCAGAGAG CTTGAGAAAT 960
   TTCCATCTCA TGTGGAGGT GAGGGACAGT GGAGGCGCTC AAGCCTCCAC AGAGCTCCAG 1020
   GTGAACATCG TGAACCTCAA CGACGAAGTC CCTGCTTTA CCAGCCGAC ACAGGTGTAC 1080
   ACAGTCTGCG AGGAACCTGAG TCCAGGAACC ATCGTGGCCA ATATCACAGC GGAGGATCCT 1140
   GATGATGAAG GTTTTCCAG CCACCTCCTC TACAGCATTG CCACTGTAG CAAATATTTT 1200
   ATGATAAATC AGTTGACTGG TACAATCCAA GTGGCCCAAA GGATAGACCG AGATGCAGGT 1260
   GGTCAGGAGA ATCGCATCCA GATACCTTTC ATTGTGGAAG AGTCAACGA CAATCCTGCC 1320
   ACATGCCAAA AGTTACCTT CAGATCCAGT CTCACCCCTG CTCTGTGCTC CAAGACGCTG 1380
   ACCTGGATGG ATACCGTATT AGACTGTTT CATGCTGCTG ATAAAGATAT ACCTGTGACT 1440
   GGGCGATTGA CAAAGAAAG AGGTTTAATT GGACTTACAG TTCCACATGG CTGGGGAAGC 1500
   CTCACATCA TGGCAGAAAG CAAGGAGGAG CAAGTCACAT CTTACATGGA TGGCAGCAGG 1560
   CAAAGAGATA GAGCTGTGT AGGGAAACTC CTCCTTATAA AGGCATCAGA TCTCATGAGA 1620
   CTTAGTCACT ATCAGGAGAA CAACTCAGGA AAGACTTGCC CCCATGATTC CATTCTCTCC 1680
   TACCAGTCC CTCCACAAC ATGTAGGAAT TCAAGAAATC AGGCCACCA CAACGAAGAC 1740
   ACAAGCTCTG TCACGTGTAC TGTGAACATC CTGGAAGAAA ATGATGAAAA GCGCAATTGT 1800
   ACTCCAACT CTTATTCTCT GGGCCTCCCA GTGGATCTGA AAGTTGGCAC AAATATTCTAG 1860
   AATTTCAGC TGACATGTAC CGACCTTGAT TCCAGCCCCA GATCTTTCGG TTATTCCATT 1920
   GGCCGAGGTA AGTCAACAA TCATTTCACC TTCTCTCCCA ATGCTGGTTC CAATGTACA 2040
   CGCCTGCTGC TTACATCTCG CTTTGACTAT GCTGGTGGGT TTGATAGAT CTGGGACTAC 2100
   AAGCTACTTG TCTACGTAA C GACTGACAA TTTGATGCTG ACAGGAAGAA AGCGGAGGCT 2160
   CTGTGTTGGA CAGGAACAGT GACACTGAGT ATTAAGTCA TCCCCACCC AACCATATC 2220
   ATCACCAGCA CCCCAGGCC CAGGGTCACC TATCAGGTCC TGAGGAAAAA CGTTTACTCT 2280
   CCATCTGCAT GGTACGTGCC GTTTGTATC ACTTTGGGCT CCATATGCT TCTGGGTCTC 2340
   CTGCTGTACC TGGTGTCTCT ATTGGCCAAA GCCATCCACA GACACTGCC CTGCAAGACT 2400
   GGGAGAGAACA AGGAACCTCT GACAAAGAAA GGAGAAACGA AAGCCATAGA TCCAGAGCT 2460
   GTGGTGGAAA CTATCCAGAT GAACACTATC TTTGATGGAG AAGCCATAGA TCCAGAGCT 2520
   GAGCAAGCTT CACTCGAGCT CTATGCCCTG CTGCCAGCT GCTGCGACCC TAGTCCAGTA 2580
   ACCCTAAGAA AGGTCAGGT GTGTGGGAG AGTGAAGAGA CCGGTCACTG TTCCGGCCAC 2640
   2700
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ATCACACTTC CCGGCAAGAT TCCAGTCGAT GACCCCAAGGA AACAGGAAAC AGGCCTGCAG 2760
GGTGATTTCG AGGTCTGGAC TCTATGCCCC GCTGTGAAGG TGGTGTAGG CAGCCCTCAA 2820
GCTGAACGGT GCATTGCGATT GGCTCTCAGT CTGAAAAAGT ACAGTTCTGA TTAA 2874

5

Seq ID NO: C64 DNA Sequence
Nucleic Acid Accession #: XM_168571.1
Coding sequence: 155..988

10 1 11 21 31 41 51
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TTCATGATAA ATCAGTTGAC TGGTACAATC CAAGTGGCCC AAAGGATAGA CCGAGATGCA 180
GGTGAATTGA GACAAAATCC CACCATTTCC CTGGAAGTTC TAGTGAAGGA CAGACCATAT 240
15 GGGGGTCAGG AGAATCGCAT CCAGATAACC TTCATTGTGG AAGACGTCAA OGACAATCCT 300
GOCACATGCC AAAAGTTTCC CTTCAGCATT ATGGTGGCCG AAAGAACAGC CAAGGGGACG 360
TGCTTCTCTG ACCTAAACAA GTTCTGCTTT GATGATGACA GTGAGGCACC AAACAACAGA 420
TTCACTTCA CCATGCCATC TGGAGTGGGG AGCGGCAGCA GATTTTACA GGATCCAGCT 480
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20 GCGGCAATA AATATACGGT GATAATCCAG GTGCAGGATG TGGCCCCCCC TTACTATAAA 600
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AGGCCATCTT ATGTATTGTA TGTGTCAGAA AGAAGGCCCG CCCAGGGTCA CCTATCAGGT 720
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CTCCATATTG CTTCTGGGTC TCCTCGTGTA CTGGTCTGTC CTATTGGCCA AAGCCATCCA 840
25 CAGACACTGC CCCTGCAAGA CTGGGAAGAA CAAGGAACCT CTGACAAAGA AAGGAGAAAC 900
GAGACTGCA GAGAGAGACG TCGTGGTGGG AACTATCCAG ATGAACACTA TCTTTGATGG 960
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30 AGAAGATGAG CTGAGTGGCA AAGCGTGGGC TGAGGATGCT GGTCTGGGTT CCAAGAAATGA 1200
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CAAAACACAC CCAGGAAAGT AAACGGGGTC TAAGGAGGGG CCGTCTCAATC ACTGAGATGC 1320
TGCCCTCACC TAAATTTCTAT GGGGATGGTG TGGGCATGGT GTAGGGGGGA AAATGTGGGC 1380
TGAGGGGATT CAGACATCCA GGGTCAACA TGGGATGTTT GACAAATTTT TAAACAAATA 1440
35 GAAAGGGGTT TGATCACATA GTTGCGTGTT CTGAAATGAT ACAGGAACAT TTTCTATCAG 1500
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CTGCCCTCGT TTTAACATCA CCCAGATTTC TTCAGTTATA AATATGCCAT ACACCTTTGT 1740
40 AAGTCACTCC AATCTTCTT CAAAGAAAGC AGAACAGTGA AAAAAACAGA TGAGTAAGTT 1800
AAGAGTTGGT CATCTGGAAA GAAGAAAACCT CAGTAGGCAC CTTCCTTTGT TTTTCTTGT 1860
GGTGTCCGGA TCAGCATCCT GCATGTGAGA TTCATCCAG TTGTCCTGTC TAGCAGTAGT 1920
TCAGTTCTCT TCATGTTTAT GTCTGGTTTC ATTCTATGAT TATATCACAA TTTATCTATT 1980
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45 ACTACAGGCA GGGCATGATG GCTCATGCCT GTAATGCCAG CACTTTGCCA AGGTGGGCAG 2100
ATCACTAAG GTCAGGAGTT CAAGATCAGC CTGGCCTAGA TGGCAAAACC CTGTCTCTAC 2160
TAAAAAATAC AAAAATTAGC TTGGTGTGGT GGTGGGCACA TGTAATCCCA GCTACTTGGG 2220
AGGCTGAGGT AGGGAGAACT GCTTAAACCT GAGAGGTGGA GGTACAGTG AGTTGAGATT 2280
GTGCCACTGC ACTCTAGCCT GGGTGACAAA GCAAGACTCC ATCTCAGAAA AAAAAATAA 2340
50 AAGTGAATTA CAACACT 2357

Seq ID NO: C65 DNA Sequence
Nucleic Acid Accession #: NM_005266.3
Coding sequence: 122..1198

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1 11 21 31 41 51
GGCACGAGGC CATTTTCAAA CAGTCCCTCC TGGGAGAACA CAGACAGGCA GAGGATTACA 60
ACACAAGGCA GCAAGCACTG GGAGACGAAA GTTTTGGCAT CTGTTCCTCT GCTGTGCCAA 120
60 GATGGGCGAT TGGAGCTTCC TGGGAAATTT CCTGGAGGAA GTACACAAGC ACTGACCGT 180
GGTAGGCAAG GTCTGGCTCA CTGTCTCTT CATATTCGGT ATGCTGTGTC TGGGCACAGC 240
TGCTGAGTCT TCCTGGGGGG ATGAGCAGGC TGATTTCGGG TGTGATACGA TTCAGCCTGG 300
CTGCCAAGAT GTCTGTACAG ACCAGGCTTT CCCCCTCTCC CACATTCGCT ACTGGGTGCT 360
GCAGATCATC TTCTGTCTCA CGCCCTCTCT GGTGTACATG GGCACGCCA TGCACACTGT 420
65 GGCATGTCAG GAGAAGCGCA AGCTACGGGA GGCCGAGAGG GCCAAAGAGG TCCGGGGCTC 480
TGGCTCTTAC GAGTACCCGG TGGCAGAGAA GGCAGAACTG TCCTGTCTGG AGGAAGGGAA 540
TGGAAGGATT GCGCTCCAGG GCACTCTGCT CAACACCTAT GTGTGCAGCA TCCTGATCCG 600
CACCACCATG GAGGTGGGCT TCATTGTGGG CCACTACTTC ATCTACGGAA TCTTCTTGAC 660
70 CACCTGTCAT GTCTGCGCA GAGTCCCTG TCCCCACCGG GTCAACTGTT ACGTATCCCG 720
GCCCACAGAG AAGAATGTCT TCATTGTCTT TATGCTGGCT GTGGCTGCAC TGTCCCTCTC 780
CCTTAGCCTG GCTGAATCT ACCACCTGGG CTGGAAGAG ATCAGACAGC GATTGTGCAA 840
ACCGGCGCAG CACATGCGTA AGTGCCAGCT TTCTGGCCCC TCTGTGGGCA TAGTCAGAG 900
CTGCACACCA CCCCOCGACT TTAATCAGTG CCTGGAGAA GGCCTGGGG GAAATTTCTT 960
75 CAATCCCTTC AGCAATAATA TGGCCTCCCA ACMAAACACA GACAACCTGG TCACCGAGCA 1020
AGTACAGAGT GATGAGCAGA CTCTGGGGA AGGTTTCATC CAGGTTGTTT ATGCCAGAA 1080
GCCGTAGGTT CCCAATGGAG TCTCACAGG TCACCGCTT CCCCATGGCT ATCATAGTGA 1140
CAAGCGAAGT CTTAGTAAGG CCAGCAGCAA GGCAAGGTCA GATGACCTAT CAGTGTGACC 1200
CTCCTTTATG GAGGATTCAG GACAGGTGG GAACAAGGA GGCTCAGAGA GGAAGACGT 1260
80 GTCCCTCTG AACTGATGCT TTCTCACTGT CATCACTGCT TGGTCTCTTT GAGCCCGGG 1320
TCTCAATGAC GTTGCTCATT AATTCTAGAA ACTATAACCA GGGCTCTGGG ATAGTAAGAG 1380
AGGTGACAA CCACCCAGAC TGCAATTTCC TCCCCACCT CTACCCAGTA TACGAAGCCT 1440
TTCAGATTAC TCAATGAACA GGGTAGAGGG AAAGAAGGGA AGCATGGCAA AAGCTGGCCT 1500
GGAAGGGATA GCCAGAGGGA TAGAATGACT CTCTCTCTAC ATACCCAGCA CATACCAAT 1560
GGTTCCTTA AGTTCTTACC TCCTTGACCT GATCACCTC CTCTCTCAA GGAAGAGCTC 1620

5 AAAGTTCCCA GCCAATAGAC AGCATGAATC AAGGAACCTG CATTATATGT GCTCTTGAAT 1680
 CTGTGTCTC CATGACCAT TCCTCGAGT AGTGGTGAGA TGGCCTTGGG TTGCCCTTGG 1740
 CTCTCTCTCC CTCTACTCAG CCTTAAAAAG GGCTTCTTGG AACTTTTCCA GCAGCCTCAG 1800
 CTTTACAAT GCCTTGGTAT GTACCTCTGG CAAATGCCCT GSTATGTACC TCTGGCAAT 1860
 GCCCACCTT GGTGATGTTG CAACCTTTCC TTCTGCTAGG GTGTACACCT AGCCTGTGCA 1920
 GGTGTGAGCC CTGCTAGGGA GTCACTGTAC ACACAACTC TACTGGAATT CCTGCCAACA 1980
 TCTGTACCC TGCAGTCTCT TTACAGTTCA ATCCAATGAT AGAAACCATC CCTTCCCTTT 2040
 CTCCCTTGGC TGTTCACCCA GCCATTCCCT GAAGGCCTTA CCAACAGGAA TATCCAAGAA 2100
 CTTGTTGTCC TTCTCGAAC CCTGACCAGA TCATCAGCCA CTGAGGCCAG TGAATTTCC 2160
 10 CCAGGCCTTG TTAACAAAAA AAAAAA 2190

Seq ID NO: C66 DNA Sequence
 Nucleic Acid Accession #: NM_014459.2
 Coding sequence: 738..3407

15 1 11 21 31 41 51
 GTAGATGCG TCCGCCGCC CGCTGCTCT AGCCAGCAAT GCAAGATTAG ATCTCTAAAT 60
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 20 GCTGGGGAAG CTTCAAAATA TATCTGTGAC TCTGTCTTGG TTGCTCTTCA TCCCCTCAA 180
 TTTTACACG GGAGGCGAGC AGCAAGTAAG AATTTCACCT TCGGATCTGC CTAGAGACAC 240
 ACCTCCCTGC TCCCTCCCC ACTCGATGT AGAGTATTC CGGAGTCTCC GGGCGGGAGT 300
 AGATTTGCG CACCTTAGCG GGAGCGAGGA AACCTACTG ATTCTTTAGC TCATTATCAT 360
 CTCTCCAGCA CGAGATTTC TTCTTATCG CTGCCTCATC GCTCAAGTTT GAGCTCCCG 420
 25 AAGTCCGGCG GGGAGAGAGC AAACCCCTGG CTCACCCCA GCGCAGGAA GCCACCGCCT 480
 TGCTCCAGC CCCTGAGCT CTGCTGCACC GCAGCTTCTC ACCCAGTGGC GATGCTGTAG 540
 ATCAACAGT TCAGGAACT TGAGCAGAA AAGAGAGAGC CACCGGTGC CGCAGCTCGG 600
 GTGCAGAGGG AAAAAGGAC CCATAGACTT GTGGCTCGCG TCGCGCGCGC ACGCTGCGCC 660
 AGGGCCCCAG GCTGGCGCGC ACTCCCTCTC TGGCTCTTCC AGTCCGATTG CTCTGCCCC 720
 30 CACCTTACAG GTCTGGGATG TACCTTTCCA TCTGTTGCTG CTTTCTTCTA TGGGCCCCCTG 780
 CCCTCACTCT CAGAACCTC AACTACTCCG TGCCGAGGGA GCAAGGGGCC GGCACGGTGA 840
 TCGGGAACAT CGCAGGGATG GCTCGACTGC AGCCTGGGCT TCCGCTGCA GAGCGCGGG 900
 GCGAGGGGCG CAGCAAGTCG GGTAGTACC GGTGCTGGA GAATCCGCA CCGCACTGCG 960
 35 TGGACGTGGA CGCAGACAGC GGGCTCTCT ACACCAAGCA GCGCATCGAC CGCAGTCCC 1020
 TGTGCGCGCA CAATGCCAAG TGCCAGCTGT CCTCGAGGT GTTCGCCAAC GACAAGGAGA 1080
 TCTGCTGAT CAGGTAGAG ATCCAGGACA TCAACGACAA CGCGCCCTCC TTCTCTCTGG 1140
 ACCAGATCA AATGAGCATC TCGGAGAACG CTGCTCCGGG CACCGCTTCC CCGCTACCA 1200
 GCGCACATGA CCCCAGCCCG GCGAGAAATG GGCTCCGAC CTACCTGTCTC ACGCGGACG 1260
 40 ATCAGCGCTT CTTTGGACTG GACGTTAAGT CCGCGGCGCA CGCACCAAG TTCCAGAAC 1320
 TGGTATCCA GAAGGCTCTG GACCGGAGC AACAGAAATCA CCATACGCTC GTGCTGACTG 1380
 CCCTGGAGCG TGGCGAGCTT CCACGTTCCG CCACCGTACA GATCAACGCTG AAGGTGATTG 1440
 ACTCCAACGA CAACAGCCCG GTCTTCGAGG CGCATCTCTA CTTGGTGGAA CTGCCGAGA 1500
 ACGCTCCGCT GGTGACATG GTCATCGATC TGAACGCCAC CGACGCGATG GAAGTCCCA 1560
 45 ATGGTAGAGT GCTCTACTCT TTCAGCAGCT ACGTGCCTGA CCGCGTGGCG GAGCTCTTCT 1620
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 50 GGGTCACTGA CCGGACTCTT GGCAGAAAG GACAGCTGCA GTGTGGGTCT CTAGGGGAG 1920
 GAGGACGCGG CGCGCGCGGG GGCTGGGGG TTCCGTCCCG TTCAAGCTTG 1980
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 55 GGTCTACGCT GCTTCAGGTG CACGAGAACA ACATCCCGGG AGAGTACCTG GGTCTGTGTC 2220
 TCGCCAGGA TCCGACCTG GCGCAGAACG GCACCGTATC CTACTCTATC CTGCGCTGCG 2280
 ACATCGCGCA GGTGTCTATC TACACCTATG TGTCTGTGAA TCCACGAAAC GGGGCCATCT 2340
 ACGCCCTGCG CTCTTTAAC TTGAGCAGA CCAAGGCTTT TGAGTTCAAG GTGCTGTGTA 2400
 AGGACTCGGG GCGCGCGCGC CACTTGGAGA GCAACGCCAC GGTGAGGGTG ACAGTGTAG 2460
 60 ACGTGAATGA CAACGCGCCA GTGATCTGTC TCCCACTGCT GCAGAACGAC ACCGCGGAGC 2520
 TGCAGGTGCC GCGCAACGCT GGCTGGGCT ATCTGGTGAG CACTGTGCGC GCCCTAGACA 2580
 GCGACTTCCG CGAGAGCGGG CGTCTCACT ACAGATCGT GAGCGGCAAC GACGACACC 2640
 TGTTTGAGAT CGACCGCTCC AGCGCGGAGA TCCGCAOGCT GCACCTTTTC TGGGAGGAG 2700
 TGACGCCCTG GGTGAGCTG GTGGTGAAG TGAACGACCA CGCAAGCCT ACCCTGTCCG 2760
 65 CAGTGGCCAA GCTCATCATC CGCTCGTGA GCGATCCCT TCCGAGGGG GTACCAAGGG 2820
 TGAATGGCGA GCAGCACCAC TGGGACATGT CGCTCCGCT CATCGTACT CTGAGCACTA 2880
 TCTCATCAT CTTCTAGCG GGCATGATCA CCATGCGGT CAAGTGCAAG CGCGAGAACA 2940
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 70 GCAAGGGCAA GAAGAAGAG ATCAACAAA ATGATATCAT GCTGGTGCAG AGCGAAGTGG 3060
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 CCATGTACTT CGACTACAG ACCCGCTGC CCTCAGCTC GCGCGGTG GAGGTGATGT 3180
 ATCTCAAAAC GGCCTCAAC AACCTGACTG TCCTCAGGG GCACGCGGGC TGCCACACCA 3240
 GCTTCACCGG ACAAGGACT AATGCAAGCG AGACCCCTGC CACTCGGATG TCCATAATT 3300
 75 AGACAGACAA TTTTCCGCA GAGCCCAATT ACATGGGAG CAGGCGAGCAG TTTGTTCAAA 3360
 GTATTTCACT AGCTCCAGT TTAAGGACCC AGAAGAGCC AGCCTGAGAG ACAGTGGGCA 3420
 CGGGGACAGT GATCAGGCTG ACAGTGACCA AGACCTAAC AAAGGCTCTC GCTGTGACAT 3480
 GTCTGTAGG GAGGCACTCA AGATGAAGAC TACTTCACT AAAAGCCAA CACTTGAACA 3540
 AGAACAGAA GAGTGTGTTA ATTGCACAGA TGAATGCCGA GTGCTGTGTC ATTCTGACAG 3600
 GTGCTGGATG CCACAGTCC CTGACGCCAA TCAGGCTGAA AATGCAGATT ACOCACAAA 3660
 80 TCTCTTTGTA CCTACAGTTG AAGCTAATGT TGAGACTGAG ACTTACGAAA CTGTGAATCC 3720
 CACTGGGAAA AAGACTTTT GTACATTGG AAAAGACAG CGAGAGCACA CTATTCTCAT 3780
 TGCCAACTGT AACCTTATT TAAAGGCCAA ACGTGCCTG AGCCCTCTCC TCCAAAGAGT 3840
 CCGCTCAGTA TCAAGCAGCC CAACCAAGGC GTGCATCGAG CTTTGACCT CAACAAAAGG 3900
 CTCCCTGGAT GGTGTGAAG CAAACACAGG AGCCCTGGCT GAAGCAAGCA CTCAGTACTT 3960
 GCCACTGAC AGTCAATATC TGTCACCTAG TAAGCAACCA AGAGACCTC CTTCTATGGC 4020

5 TTCCGATCAG ATGGCAAGGG TCTTTGCAGA TGTGCATTCC AGAGCCAGCC GGGATTCCAG 4080
 TGAGATGGGT GCTGTCTCTG AGCAGCTTGA CCACCCCAAC AGGGATCTGG GCAGAGAGTC 4140
 TGTGGATGCA GAGGAAGTTG TGAGAGAAAT TGATAAGCTT TTGCAAGACT GCGGGGAAAA 4200
 CGACCTGTG GCTGTGAGAA AGTGAAAAAA GAAAAAAAAG AAGGCATTGG CATTTTCTTG 4260
 TCTCTTCTGT TGATTTAAAA ATGATCCCTC CTGGTGATAA CCCATTTTAC AGGGATGAAG 4320
 AAAGACCAAT GCTGCTTTAA GGCTTTTAGT GAACATCTGA AGTGCCCAAC AGTATGTTCT 4380
 TTCCACTGCT GATTTCCTTT TCAGAGATAA CAATGGTTTC GTTTTGACCA AACTTGTATT 4440
 AGGACAGAAT TAATGATGCT TAAAGAGAAA AGAAAAAAG AGAGAGAGAA AAGGAGAGAT 4500
 GAAAAAGGAG GATGAGGAGA AGAATTACCT TTTGACAAATC TGTAGGAAAG GTATGCAGTG 4560
 10 TGAGAACTGA AGTATTTCTG ATCACTCTCA GACTGTCCTC CGTGATTAT GCTGACTTAA 4620
 CTGTTTACCT ATAAACCCCA TACAAAGCAG GGTCAATAAT TGTGATCTGT GGTGGATTTC 4680
 TAGCAGTCAT CACAGGCTTC TACTGAAAGT CCTGAAAAGA CCTGCAAGTA GTCCAAGCTA 4740
 CACCAACAT TAACACATAT TTGTGTAATA CATTCTGTA TAAAGTTACC TGACACACAT 4800
 15 ATAAACACAA GGAACATTCC ATATCATTAG TCGAAAACAA AAACAAAAAA AAAACCTTTG 4860
 GTCATTTGTA AGACATCTCA TGTCAATAA AAGTTAAATG TAAAAAGATA CAGTCCATT 4920
 TGTCTGCAC ACACGTAGAC TAATTCACGT CAAAAAAA AAAAAA 4960

Seq ID NO: C67 DNA Sequence

Nucleic Acid Accession #: NM_005601.2

Coding sequence: 101..598

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1 11 21 31 41 51
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 TCTTCTCTCT CCAGGACCCA GAAGCCCTGA GCTTATCCCT ATGGAGCTCT GCGGTCCCT 120
 GGCCCTGCTG GGGGGCTCCC TGGGCTGTAT GTTCTGCTGT ATTGCTTTGA GCACCGATT 180
 CTGGTTTGAG GCTGTGGGTC CCACCCACTC AGCTCACTCG GGCCTCTGGC CAACAGGGCA 240
 TGGGACATC ATATCAGGCT ACATCCACGT GACGACAGCC TTCAGCATTA TGGCTGTTCT 300
 GTGGGCCCTG GTGTCCTGTA GCTTCTCTGT CCTGTCTGTC TTCCCTCTAC TGTTCCTCCC 360
 AGGCCACGGC CGCTTGTGCT CAACCACGCG AGCCTTTGCT GCAGCCATCT CCATGTGTGT 420
 GGCCATGGCG GTGTACACCA GCGAGCGGTG GGACCGCTT CCACACCCCT AGATCCAGAC 480
 CTCTTCTTCC TGGTCTTCT ACCTGGGCTG GGTCTCAGCT ATCTCTTTCG TCTGTACAGG 540
 TGCCCTGAGC CTGGGTGCTC ACTGTGGCGG TCCCGTCTCT GGCTATGAAA CCTTGTGAGC 600
 AGAAGGCAAG AGCGGCAAGA TGAGTTTGA GCGTTGTATT CCAAGGCTCT CATCTGGAGC 660
 CTGGGAAAG TCTGTCTCTA CATTGCCCCC CCTTCCAGC CCTTCCCCAG CCGCTCTCT 720
 TGTTCCTTCA TTCAATCAAC AAAATTGGC TGAAAAAAA AAAAAAAA AAAAAAAA 780
 AAA 783

Seq ID NO: C68 DNA Sequence

Nucleic Acid Accession #: NM_006433.2

Coding sequence: 129..566

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1 11 21 31 41 51
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 AAAGATTAAG CTGACGGCTC CTGCCCCATA AAACAGGGTG TGAAAGGCAT CTCAGCGGCT 120
 GCGCCACCAT GGCTACCTGG GCGCTCCTGC TCCTTGACAG CATGCTCTCG GGCAACCCAG 180
 GTCTGTGCTT CTCTGCTCTG AGCCCTGAGT ACTACGACCT GGCAAGAGCC CACTGCGGTG 240
 ATGAGGAGAA ATCCTGCCCC TGCCCTGGCC AGGAGGGGCC CCAGGGTGAC CTGTGTGACCA 300
 AAACACAGGA GCTGGGCCGT GACTACAGGA CCTGTCTGAC GATAGTCCAA AAACCTGAAGA 360
 AGATGTGTGA TAAGCCCAAC CAGAGAAAGT TTTCCAATGC TGCGACCCGG GTGTGTAGGA 420
 CGGGGAGGTC ACGATGGCGC GACGTCTGCA GAAATTTCT GAGGAGGTAT CAGTCTAGAG 480
 TTACCCAGGG CCTGTGCGCC GGAGAAACTG CCCAGCAGAT CTGTGAGGAC CTCAGGTTGT 540
 GTATACCTTC TACAGGTCCC CTCTGAGCCC TCTCACCTTG TCCTGTGGAA GAAGCACAGG 600
 CTCTGTCTCT CAGATCCCGG GAACCTCAGC AACCTCTGCC GGCTCCTCGC TTCTCTGATC 660
 CAGAAATCCAC TCTCCAGTCT CCGTCCCCTG ACTCCCTCTG CTGTCTCTCC CTCTCAGAG 720
 AATAAAGTGT CAAGCAAG 738

Seq ID NO: C69 DNA Sequence

Nucleic Acid Accession #: NM_002985.2

Coding sequence: 69..344

65
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1 11 21 31 41 51
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 GCGCTCCTGC ATCTGCTCTC CCATATTCCT CGGACACCAC ACCCTGCTGC TTTGCTTACA 180
 TTGCCCGGCC ACTGCCCGGT GCCCACATCA AGGAGTATTT CTACACCAAT GGCAAGTGCT 240
 CCAACCCAGC AGTCTGCTTT GTCAACCCGAA AGAACCCGCA AGTGTGTGCC AACCCAGAGA 300
 AGAAATGGGT TCGGGAGTAC ATCAACTCTT TGAGATGAG CTAGGATGGA GAGTCTTTGA 360
 ACCTGAACCT ACACAAATTT GCGTGTCTCT GCTTGTCTCT GTCTAGCTT GGGAGGCTTC 420
 CCTCACTAT CCTACCCAC CGCTCTCTTG AAGGCCCCAG ATTCTACCA ACAGCAGCAG 480
 TTACAAAAAC CTTCCCCAGG CTGGAGGTGG TGGCTCACGC CTGTAATCCC AGCACTTTGG 540
 GAGGCCAAGG TGGGTGGATC ACTTGAGGTC AGGAGTTGGA GACCAGCCTG GCCAACATGA 600
 TGAAACCCCA TCTCTACTAA AAATACAAAA AATTAGCCGG GCGTGTGAGC GGGCGCCTGT 660
 AGTCCAGCT ACTCGGAGG CTGAGGCAGG AGAATGGGT GAACCCGGGA GGGGAGCTT 720
 GCAGTGAGCC GAGATGCGCG CACTGCACCT CAGCCTGGGC GACAGAGCGA GACTCCGTCT 780
 CAAAAA AAAA AAAA AAAA AATTAGCCGG GCGTGTGAGC GGGCGCCTGT 840
 AATCCAGCT ACTCGGAGG CTAAGGCAGG AAAATTGTTT GAACCCAGGA GGTGGAGGCT 900
 GCAGTGAGCT GAGATTGTGC CACTTCACTC CAGCCTGGGT GACAAAGTGA GACTCCGTCA 960
 CAACAACAC AACAAAAAGC TTCCCAACT AAAGCTAGA AGAGCTCTG AGGCGCTGCT 1020
 TTGTCAAAAG GAAGTCTCTA GGTCTGAGC TCTGGCTTTG CCTTGGCTTT GCCAGGGCTC 1080

TGTGACCAGS AAGGAAGTCA GCATGCCCTCT AGAGGCAAGG AGGGGAGGAA CACTGCACTC 1140
TTAAGCTTCC GCCCTCTCAA CCCCTCAGAG GAGCTTACTG GCAACATGA AAAATCGGCT 1200
TACCATTAAA GTTCTCAATG CAACCATAAA AAAAAA 1237

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Seq ID NO: C70 DNA Sequence
Nucleic Acid Accession #: NM_022154.2
Coding sequence: 1381..1722

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1 11 21 31 41 51
AGTGTGGTTT TAGTTTTTCC TAAGAAGTGG CGTGGTTTGG GGCTTTATAT CCGGGAGGAG 60
CATATGTACG CAAATCCTGG GCGGTTTGGCA AACCCGGATC CGGGCGCTCT GCGCCCATGC 120
CGGGCCGGGC GTTTAGAGGC TACTGCCAGC CAGCGTTTCT GGAGCTGCCC GGCTGGTGCC 180
CTGGTGGCCT TTATCTCTGT CCCCCTTTGT CCTCTTTATC TCAGGCTCTC CAGGAGGCGC 240
GGGGGCCAC TCOCCTATC GCTCCCTCG GCTACGCTGC CACTCCAATG CCCCAGAGT 300
CGGAGCTGC TGTCTTTTGG AAGCGCCCG AGAACCAGGG CGGTCCCGCG CCACCTCTGA 360
CTGGAGCAG CGCCGAGCAC TGACGCTCCC GCCCTTGGGC AAGGACGCCA GTGCGCCCGC 420
GCGGTCCCT CTGCGCGGCA GCCCTGCGCG GGCCCTCAAG GGGAAAGCCA GGCAGGATG 480
GCCCCGGTC GCGCGGTGGC CGGCTCCTG TTGCTGGCGG CGCGCGGCT CCGAGGAGTG 540
GCGAGGGGC CAGGGCTAGC CTTGAGCAG GATGTCTGA GCGTGTTCGG CGCGAATCTG 600
AGCCTGTCCG CGCGCAGCT CCAGCACTTG CTGGAGCAGA TGGAGCGCG CTCGCGCTG 660
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TCCCTTCATG GCTTTTCAAA TGCTACCCAA ATAACCAGCT CCAATTTCTC TGTCATCTGT 780
CCAGCAGCT TACAGCAAT GAACCTTCAC CCAATGTAGG ATCGGCCCAA GCACAAAACA 840
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GCATCTCTCC TCGGATTGAT TTGACTTCCA CTGATAAAGA AATCTTATTT CCAAAAGATT 960
TTGACCTTTT TTGTGGGGCT GGCTATTGGG ACTCTTTTTT CAAATGCAAT TTTCCAACTT 1020
ATTCCAGAGG CATTGGGATT TGATCCCAAA GTGACAGATT ATGTAGAGAA GGCAGTTGCT 1080
GTGTTTGGTG GATTTTACCT ACTTTTCTTT TTGAAAGAA TGCTAAAGAT GTTATTAAAG 1140
ACATATGGTC AGAATGTGCA TACCACCTTT GGAATGATA ACTTTGGTCC TCAAGAAAAA 1200
ACTCATCAAC CTAAAGCATT ACCTGCCATC AATGGTGTGA CATGCTATGC AAATCCTGCT 1260
GTCACAGAAG CTAATGGACA TATCCATTTT GATAATGTCA GTGTGTATC TCTACAGGAT 1320
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ACGATTCGCT GGATGATAAC GCTCTGCGAT GCCCTCCACA ATTTTCATGA TGGCCTGGCG 1440
ATTGGGGCTT CTTGACCTTT GTCTCTCTTT CAGGGACTCA GTACTTCCAT AGCAATCCTA 1500
TGTGAGGAGT TTCCCCACGA GTTAGGAGAC TTGTGATGCC TACTCAATGC AGGGATGAGC 1560
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ATGTTCTCTT ATATTCTCTT GGCAGATATG TTTCAGAGA TGAATGATAT GCTGAGAGAA 1740
AAGGTAAGTC GAAGAAAAAC CGATTTTACC TTCTTCATGA TTCAGATGTC TGAATGTTA 1800
ACTGGATTCA CAGCCATTCT ACTCATTTACC TTGTATGTCAG GAGAAATCGA ATTGGAGTAA 1860
TAGAAAAATGG AAGATGGTGT TGTTAATAAA GGCATTTAAT AGATAAAAA ATCTCCAAAA 1920
AGGATTTTGA AGCTGATCCT ATTTAGTTAA AAAGATAATT TTGCTTTCAA CTGTAGGTCC 1980
AGAAAACTAA TTATTGGCAT CAGTCTGTGA AATAGTCCAT TATTTGTTGT TAAAAATGCT 2040
TCAAAGGTTT TTCAGTGTCA GTCTGAGATG CCTGGTATAT AGGAGCCTTT GGGAAATACT 2100
TATTTTTCAG TATTCATGTC ATATTAGATA TCACCATGAA GCAAGAGACA TGCACTCTAT 2160
AATCATGTAG ACCTCAGAC TCAGGGGAAA ATACAAGTTA TATCCTGAAA GCCTTTAAAA 2220
CTCTATGGTA GGATCAAGAA TTCAAATGGT TTCAGAGAGG TTTTATTCCA ATTAATTTGT 2280
TCTAGTGGTT TCAAGAGCAA GTACATCAAA ATGTAGAAGG TAAATGTAT GCAACACTAA 2340
TATAAATTAT TCCAGTCTTT TAAGGAGCCA AAGAAAAAAA AGATTTCTCA CAGCTTTTGT 2400
TTCTGTTTGT TATTTCAATT AGGAACTTGC AGTATTATTT TGAAACCAT TCTAAAAATA 2460
TAGGAGTTAG GAAATAAATA AAGTTTGTCT AGCCCTGCTA AGTTCAGGCT TAGAGGCTTA 2520
TCGCTAAGTN TAAACTTCAC CAGATTTCCAC GAAAGCTGG ATAGCTTTT TCTGACTTA 2580
TGTTGTGCTT GCACCCCTCA CAAATGGCAG AACAGTATGT AAAGCTGGTA ACACCTCGGT 2640
TTCAGTGCAC CATGTGTTTG CTTGTGAAG GTGAAGAATA TGTTGGTTTA GAGAAAGAAA 2700
TTGATGTAA TTTTATGCAA TTTACTTTTA AAGACAAACA TAACATTTTA GCAGAGAATA 2760
TTTTAATAAA TGCAAAACAA CAGCTGGACT GCTGTACATC AAGGACAGAT TAACCTGAAA 2820
ACATATGTTT CTTATGTGTG ATTGAGAGCC ATTCAGAAAA GACTTCCTTT GTGTTCACTT 2880
TATACTTTTC CATATGGTAT ACCCTGAAAA AAATTAGCAC ACCATGGTTA TTTTCTTACC 2940
TTTTATAAAA GACAGAGCCT GTTACTCAT TTAGAAGATA GAGAAATG GTCTAAAAAT 3000
GAACATCCTA GATTCACACT CCCAAGTCAC TTAAGGTGAT TTGATGGTGA GGAATAATGAT 3060
TGACAAAGCC CAACAATGAT CTCAGGAATT ACATTTTCCA ACAGACCAA AAATGTTTTC 3120
ATGTAGCAGC AATGAGATT TGGTGAATAT TTAATATATA TTTTAGTATG TATTTCACTT 3180
TATGACTGAC AATTAAAAA TATTGTTTGG CCAATAGTA AACCCCTTT TGAACCATG 3240
AAAAA

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Seq ID NO: C71 DNA Sequence
Nucleic Acid Accession #: NM_004184.2
Coding sequence: 188..1603

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1 11 21 31 41 51
CGAAAAAAGA GGGGAAGAGT ATTAAAGACC ATTTCTGGCT GGGCAGGGCA CTCTCAGCAG 60
CTCACTGCCC CAGCGTGACC AGTGGCCACC TCTGCACTGT CTTCCACAACT CTGGTCTTGA 120
CTCGTCTGCT GAACAAATCC TCTGACCTCA GGCCTGGCTGT GAACGTAGTT CTTGAGAGAT 180
AGCAACATG CCCAACAGTG AGCCCGCATC TCTGCTGAGG CTGTTCAACA GCATCGCCAC 240
ACAAGGGGAG CTGTAAGGT CCCTCAAAGC GGGAAATGCG TCAAGGATG AAATTGATT 300
TGCACTAAG ATGTTGGTGT CATTAAAAAT GAGCTACAAA GCTGCGCGCG GGGAGGATTA 360
CAAGGCTGAC TGTCTTCCAG GGAACCCAGC ACCTACCAAT AATCATGGCC CAGATGCCAC 420
AGAAGCTGAA GAGGATTTTG TGGACCATG GACAGTACAG ACAAGCAGTG CAAAAGGCAT 480
AGACTACGAT AAGCTCATG TTGCTTTTGG AAGTAGTAAA ATTGACAAAG ACCTAATAAA 540
CCGAATAGAG AGAGCCACCG GCCAAAGACC ACACCACTTC CTGCGCAGAG GCATCTTCTT 600

	CTCACACAGA	GATATGAATC	AGGTTCTTGA	TGCCTATGAA	AATAAGAAGC	CATTTTATCT	660
	GTACACGGGC	CGGGGCCCTT	CTTCTGAAGC	AATGCATGTA	GGTCACTCTA	TTCCATTAT	720
	TTTTCACAAAG	TGGCTCCAGG	ATGTATTTAA	CGTGCCTTGG	GTCATCCAGA	TGACGGATGA	780
5	CGAGAAGTAT	CTGTGGAAAG	ACCTGACCTT	GGACCAAGGC	TATGGGATG	CTGTGTAGAA	840
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	TACCTTTCAAC	CAAGTGAAAG	GCATTTTTCG	CTTCACTGAC	AGCGACTGCA	TTGGGAAGAT	1020
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15	GTCTTTTATG	TACCTGACCT	TCTTCTCTGA	GSACGAAGAC	AAGCTCGAGC	AGATCAGGAA	1440
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	CTTTGAAATA	TTGATGTGGG	GAGGTTTATT	GAGCACAAGA	TGTATTTTCAG	CCCATGCCCC	2100
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	CCTGGCTGTG	TCCGTGAGCG	GTGGACTTAG	CTAGGGAGAA	AGTCGAGGCA	GCAGCCCTCG	2520
	AGGCCCTCAC	AGATGTCTAG	GCAGGCCCTA	TTTCATCAGC	CAGCATGTGC	AGGCCTGGAA	2580
35	GAGCAAGGCC	AAATCTCAGG	GAAGTCTTGG	GTGATGTAT	CTGGGTCTCC	TCTGGAGCAC	2640
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Nucleic Acid Accession #: NM_004938.1
Coding sequence: 337..4632

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	GCCTCCGACA	CGGCTCCGGA	GGGACCGGGG	GAGCTCCAG	CGCGCCGGGA	CTGGAGACTG	240
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Seq ID NO: C73 DNA Sequence
 Nucleic Acid Accession #: NM_002081.1
 Coding sequence: 222..1898

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45 Seq ID NO: C74 DNA Sequence
Nucleic Acid Accession #: BC030205.1
Coding sequence: 45..878

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80 Seq ID NO: C75 DNA Sequence
Nucleic Acid Accession #: NM_001982.1
Coding sequence: 199..4227

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5	AGGTGTGAGG	TGGTGTGGG	GAACCTTGAG	ATTGTGCTCA	CGGGACACAA	TGCCGACCTC	420
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	TCTACTCTAC	CATTGCCCAA	CCTCCGCGTG	GTGCGAGGGA	CCCAGGTCTA	CGATGGGAAG	540
	TTTGCCATCT	TCGTCTGTGT	GAACATAAAC	ACCAACTCCA	GCCACGCTCT	GCGCCAGCTC	600
	CGCTTGACTC	AGCTCACCGA	GATTCTGTCA	GGGGGTGTTT	ATATTGAGAA	GAACGATAAG	660
10	CTTTGTGACA	TGGACACAAT	TGACTGGAGG	GACATCGTGA	GGGACCGAGA	TGCTGAGATA	720
	GTGGTGAAGG	ACAATGGCAG	AAGCTGTCCC	CCCTGTCTATG	AGGTTTGCAA	GGGGCGATGC	780
	TGGGGTCCGT	GATCAGAAGA	CTGCCAGACA	TTGACCAAGA	CCATCTGTGC	TCCTCAGTGT	840
	AATGGTCACT	CTTTGGGGCC	CAACCCCAAC	CAGTGTGCCC	ATGATGAGTG	TGCCGGGGGC	900
	TGCTCAGGCC	CTCAGGACAC	AGACTGCTTT	GCCTGCGGGC	ACCTCAATGA	CAGTGGAGCC	960
15	TGTGTACCTC	GCTGTCCACA	GCCTCTTGTC	TACAACAAGC	TAACCTTTCCA	GCTGGAAACC	1020
	AATCCCCACA	CCAAGTATCA	GTATGGAGGA	GTTTGTGTAG	CCAGCTGTCC	CCATAACTTT	1080
	GTGTGGATC	AAACATCCTG	TGTCAAGGCC	TGTCTCTCTG	ACAAGATGGA	AGTAGATAAA	1140
	AATGGGCTCA	AGATGTGTGA	GCCTTGTTGG	GGACTATGTC	CCAAAGCCTG	TGAGGGAACA	1200
	GGCTCTGGGA	GCCGCTTCCA	GACTGTGGAC	TCGAGCAACA	TTGATGGATT	TGTGAATGCT	1260
20	ACCAAGATCC	TGGGCAACCT	GGACTTTCTG	ATCACCGGCC	TCAATGGAGA	CCCTGGCAC	1320
	AAGATCCCTG	CCCTGGACCC	AGAGAAGCTC	AATGTCTTCC	GGACAGTACG	GGAGATCACA	1380
	GGTTACCTGA	ACATCCAGTC	CTGGCCGCC	CACATGCACA	ACCTCAGTGT	TTTTTCCAAT	1440
	TTGACAACCA	TTGGAGGCGA	AAGCCTCTAC	AACCGGGGCT	TCTCATTGTT	GATCATGAAG	1500
	AACCTGAATG	TCACATCTCT	GGGCTTCCGA	TCCCTGAAGG	AAATTAGTGC	TGGGCGTATC	1560
25	TATATAAGTG	CCAATAGGCA	GCTCTGCTAC	CACCACTCTT	TGAAGTGGAC	CAAGGTGCTT	1620
	CGGGGGCCTA	CGGAAGAGCG	ACTAGACATC	AAGCATAATC	GGCCGCGCAG	AGACTGCGTG	1680
	GCAGAGGGCA	AAGTGTGTGA	CCCACTGTGC	TCCTCTGGGG	GATGCTGGGG	CCCAGGCCCT	1740
	GGTCACTGCT	TGTCTGTGCG	AAATTATAGC	CGAGGAGGTG	TCTGTGTGAC	CCACTGCAAC	1800
	TTTCTGAATG	GGGAGGCTCG	AGAATTGGCC	CATGAGGCCG	AATGCTTCTC	CTGCCACCCG	1860
30	GAATGCCAAC	CCATGGGGGG	CACGTGCCCA	TGCAATGGCT	CGGGCTCTGA	TACTTGTGCT	1920
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	GGTGCCCAAG	GCCCAATCTA	CAAGTACCCA	GATGTTTCTA	ACTGTTTAGG	ACAAACACTG	2040
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35	ATTTTCTATG	TGCTGGGGCG	CACCTTTCTC	TACTGGCGTG	GGCGCCGGAT	TCAGATAAAA	2220
	AGGGCTATGA	GGCGATACTT	GGAAACGGGT	GAGAGCATAG	AGCCTCTGGA	CCCCAGTGAG	2280
	AAGGCTAACCA	AAGCTTTGGC	CAGAATCTTC	AAAGAGACAG	AGCTCCCTGA	GGGTGAATCA	2340
	CTGGCTCGGG	GTGCTTTTGG	AACTGTGCAC	AAAGGAGTGT	GGATCCCTGA	GGGTGAATCA	2400
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40	GCTGTGACAG	ATCATATGCT	GGCCATGGGC	AGCCTGGACC	ATGCCACAT	TGTAAGGCTG	2520
	CTGGGACTAT	GCCCAAGGTC	ATCTCTGCAG	CTTGTCACTC	AATATTGGCC	TCTGGGTCTT	2580
	CTGCTGGATC	ATGTGAGACA	ACACCGGGGG	GCATCTGGGC	CACAGCTGCT	GCTCAACTGG	2640
	GGAGTACAAA	TTGCCAAGGG	AATGTACTAC	CTTGAGGAAC	ATGGTATGGT	GCATAGAAAC	2700
	CTGCTGCCCC	GAAACGTGCT	ACTCAAGTCA	CCCAGTCAGG	TTGAGTGGC	AGATTTTGGT	2760
45	TGGGCTGACC	TGCTGCCTCC	TGATGATAAG	CAGCTGCTAT	ACAGTGGGC	CAAGACTCCA	2820
	ATTAAGTGA	TGGCCCTTGA	GAGTATCCAC	TTTGGGAAAT	ACACACACCA	GAGTGTATGT	2880
	TGGAGCTATG	GTGTGACAGT	TTGGGAGTTG	ATGACCTTCG	GGGCAGAGCC	CTATGCAAGG	2940
	CTACGATTGG	CTGAAGTACC	AGACCTGCTA	GAGAAGGGGG	AGCGGTTGGC	ACAGCCCCAG	3000
	ATCTGCACAA	TTGATGTCTA	CATGGTGATG	GTCAAGTGT	GGATGATTGA	TGAGAACATT	3060
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	GTGGAACAC	TTAATCGGCC	ACGTGGGAGC	CAGAGCCTTT	TAACTCCATC	ATCTGGATAC	3360
55	ATGCCCATGA	ACCAGGGTAA	TCTTGGGGGG	TCTTGCCAGG	AGTCTGCAGT	TTCTGGGAGC	3420
	AGTGAACGCT	GCCCCCGTCC	AGTCTCTCTA	CACCAATGCT	CACGGGGATG	CCTGGCATCA	3480
	GAGTCATCAG	AGGGGCTGTT	AACAGGCTCT	GAGGCTGAGC	TCCAGGAGAA	AGTGTCAATG	3540
	TGTAGAAGCC	GGAGCAGGAG	CCGGAGCCCA	CGGCCACGCG	GAGATAGGCG	CTACCATTC	3600
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60	GATGTCAACG	GTTATGTCTA	GCCAGATACA	CACCTCAAAG	GTACTCCCTC	CTCCCCGGAA	3720
	GGCACCCCTT	CTTCAGTGGG	TCTCAGTTCT	GTCTGGGTA	CTGAAGAAGA	AGATGAAGAT	3780
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65	ACTCCAGATG	AAGACTATGA	ATATATGAAT	CGGCAACGAG	ATGGAGGTGG	TCCTGGGGGT	4020
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70	CCCAAGGCTA	ATGCCAGAG	AACGTAACCT	CTGCTCCCTG	TGGCACTCAG	GGAGCATTTA	4260
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	CACCTCTGGA	GATATGAAGG	ATTACTCTCC	ATATCCCTTC	CTCTCAGGCT	CTTGACTACT	4560
75	TGGAAGTGGG	CTCTTATGTG	TGCCTTTGTT	TCCCATCAGA	CTGTCAAGAA	GAGGAAAGGG	4620
	AGGAAACCTA	GCAGAGGAAA	GTGTAATTTT	GGTTTATGAC	TCTTAACCCC	CTAGAAAGAG	4680
	AGAAGCTTAA	AATCTGTGAA	GAAAGAGGTT	AGGAGTAGAT	ATTGATTACT	ATCATAATTC	4740
	AGCACTTAAC	TATGAGCCAG	GCATCATACT	AACTTCACCC	TACATTATCT	CACCTAGTCC	4800
	TTTATCATCC	TTAAACAAT	TCTGTGACAT	ACATATTATC	TCATTTTACA	CAAAGGGAAG	4860
80	TCGGGCATGG	TGGCTCATGC	CTGTAATCTC	AGCACTTTGG	GAGGCTGAGG	CAGAAGGATT	4920
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Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

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   A G C C C C T G G C   T C C C T C T G T T   G A T C C C G G C C   C C T G C T C C A G   G C C T A C T G T   G C A A C T G C T G   120
   C T G T C A C T G C   T G C T T C T G A T   G C C T G T C C A T   C C C C A G A G G T   T G C C C G G A T   G C A G G A G G A T   180
   T C C C C C T T G G   G A G G A G G C T C   T T C T G G G A A   G A T G A C C C A C   T G G G C G A G G A   G G A T C T G C C C   240
10 A G T G A A G A G G   A T T C A C C C A G   A G A G G A G G A T   C C A C C G G A G   A G G A G G A T C T   A C C T G G A G A G   300
   G A G G A T C T A C   C T G G A G A G G A   G G A T C T A C C T   G A A G T T A A G C   C T A A A T C A G A   A G A A G A G G G C   360
   T C C C T G A A G T   T A G A G G A T C T   A C C T A C T G T T   G A G G C T C C T G   G A G A T C C T C A   A G A A C C C C A G   420
   A A T A A T G C C C   A C A G G G A C A A   A G A A G G G G A T   G A C C A G A G T C   A T T G G C G C T A   T G G A G G C G A C   480
   C G C C C C T G G C   C C G C G G T G T C   C C C A G C C T G C   G C G G G C C G C T   T C C A G T C C C C   G G T G G A T A T C   540
15 C G C C C C C A G C   T C G C C G C C T T   C T G C C C G G C C   C T G C G C C C C C   T G G A A C T C C T   G G G C T T C C A G   600
   C T C C C G C C G C   T C C C A G A A C T   G C G C C T G G C G   A A C A A T G G C C   A C A G T G T G C A   A C T G A C C C T G   660
   C C T C C T G C G C   T A G A G A T G G C   T C T G G G T C C C   G G G C G G G A G T   A C C G G G C T C T   G C A G C T G C A T   720
   C T G C A C T G G G   G G G C T G C A G G   T C G T C C G G G C   T C G G A G C A C A   C T G T G G A A G G   C C A C C G T T T C   780
   C C T G C C G A G A   T C C A C G T G G T   T C A C C T C A G C   A C C G C C T T T G   C C A G A G T T G A   C G A G G C C C T G   840
20 G G G C G C C C G G   G A G G C C T G G C   C G T G T T G G C C   G C C T T T C T G G   A G G A G G G C C C   G G A A G A A A A C   900
   A G T G C C T A T G   A G C A G T T G C T   G T C T C G C T T G   G A A G A A A T C G   C T G A G G A A G G   C T C A G A G A C T   960
   C A G G T C C C A G   G A C T G A C A C T   A T C T G C A C T C   C T G C C C T C T G   A C T T C A G C C G   C T A C T T C C A A   1020
   T A T G A G G G G T   C T C T G A C T A C   A C C G C C C T G T   G C C C A G G G T G   T C A T C T G A C T   T G T G T T T A A C   1080
25 C A G A C A G T G A   T G C T G A G T G C   T A A G C A G C T C   C A C A C C C T C T   C T G A C A C C C T   G T G G G A C C C T   1140
   G G T G A C T C T C   G G C T A C A G C T   G A A C T T C C G A   G C G A C G C A G C   C T T T G A A T G G   G C G A G T G A T T   1200
   G A G G C C T C C T   T C C C T G C T G G   A G T G G A C A G C   A G T C C T C G G G   C T G C T G A G C C   A G T C C A G C T G   1260
   A A T T C C T G C C   T G C T C T C T G G   T G A C A T C C T A   G C C C T G G T T T   T T G G C C T C C T   T T T T G C T G T C   1320
   A C C A G C G T C G   C G T T C C T T G T   G C A G A T G A G A   A G G C A G C A C A   G A A G G G G A A C   C A A A G G G G G T   1380
30 G T G A G C T A C C   G C C C A G C A G A   G G T A G C C G A G   A C T G G A G C C T   A G A G G C T G G A   T C T T G G A G A A   1440
   T G T G A A A G A C   C A G C C A G A G G   C A T C T G A G G G   G A G A C C G G T A   A C T G T C C T G T   C C T G C T C A T T   1500
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Seq ID NO: C77 DNA Sequence

Nucleic Acid Accession #: NM_004207.1
Coding sequence: 63..1460

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   C C A T G G A G G G   G G C C G T G G T G   G A C G A G G G C C   C C A C A G G C G T   C A A G G C C C C T   G A C G G C G G C T   120
   G G G G C T G G G C   C G T G C T C T T C   G G C T G T T C G   T C A T C A C T G G   C T T C T C T A C   G C C T T C C C C A   180
   A G G C C G T C A G   T G T C T T C T T C   A A G G A G C T C A   T A C A G A G A T T   T G G A T C G G C   T A C A G C G A C A   240
   C A G C C T G G A T   C T C C T C C A T C   C T G C T G C C A   T G C T C T A C G G   G A C A G G T C C G   C T C T G C A G T G   300
45 T G T G C G T G A A   C C G C T T T G G C   T G C G G C C C G   T C A T G C T T G T   G G G G G G T C T C   T T T G C G T C G C   360
   T G G C A T G G T   G G C T G C G T C C   T T T T G C G G A   G C A T C A T C C A   G G T C T A C C T C   A C C A C T G G G G   420
   T C A T C A C G G G   G T T G G G T T T G   G C A C T C A A C T   T C C A G C C C T C   G C T C A T C A T G   C T G A A C C G C T   480
   A C T T C A G C A A   G C G G C G C C C C   A T G G C C A A C G   G G C T G G C G G C   A G C A G G T A G C   C C T G T C T T C C   540
   T G T G T G C C C T   G A G C C C G C T G   G G G C A G C T G C   T G C A G G A C C G   C T A C G G C T G G   C G G G G C G G C T   600
50 T C C T C A T C C T   G G G C G G C C T G   C T G C T C A A C T   G C T G C G T G T G   T G C C G C A C T C   A T G A G G C C C C   660
   T G G T G G T C A C   G G C C C A G C C G   G G C T C G G G G C   G C C G C G A C C C   C T C C G G C G C   C T G C T A G A C C   720
   T G A G G T C T T T   C C G G G A C C G C   G G C T T T G T G C   T T T A C G C G T   G G C C G C C T C G   G T C A T G G T G C   780
   T G G G G C T C T T   C G T C C C G C C C   G T G T T G T G G   T G A G C T A C G C   C A A G G A C C T G   G G C G T G C C C G   840
   A C A C C A A G G C   C G C C T T C C T G   C T C A C C A T C C   T G G G C T T C A T   T G A C A T C T T C   G C G C G G C C G G   900
55 C C G G G G G C T T   C G T G G C G G G G   C T T G G G A A G G   T G C G G C C C T A   C T C C G T C T A C   C T C T T C A G C T   960
   T C T C C A T G T T   C T T C A A C G G C   C T C G C G A C C   T G G C G G G C T C   T A C G G C G G G C   G A C T A C G G G   1020
   G C C T C G T G G T   C T T C T G A T C   T T C T T T G G C A   T C T C T A C G G   C A T G T G G G G   G C C C T G C A G T   1080
   T G A G G T G C T   C A T G G C C A C C   A C A A G T T C T C   C A G T C C A T T   G G C C T G G T G C   G G C G T G C C C G   1140
   T G C T G A T G A   G G C G G T G G C C   G T G C T C G T C G   G G C C C C C T T C   G G G A G G C A A A   C T C C T G G A T G   1200
60 C G A C C C A C G T   C T A C A T G T A C   G T G T T C A T C C   T G G C G G G G G C   C G A G G T G C T C   A C C T C C T C C C   1260
   T G A T T T T G C T   G C T G G G C A A C   T T C T T C T G C A   T T A G G A A G A A   G C C C A A A G A G   C C A C A G C C T G   1320
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65 A A G C C G G C A A   C G C T T G C T A T   T T A T T T T A C A   A A C T G G A C T G   G C T C A G G C A G   G G C C A C G G C T   1560
   G G G C T C C A G C   T G C C G G C C C A   G G G A T C G T C   G C C C G A T C A G   T G T T T T G A G G   G G G A A G G T G G   1620
   C G G G T G G G A   A C C G T G T C A T   T C C A G A G T G G   A T C T G C G G T G   A A G C C A A G C C   G C A A G G T T A C   1680
   A A G G C A T C C T   C A C C A G G G G C   C C G C C T G C T   G C T C C A G G T   G G C C T G G G G C   C A C T G C T A T G   1740
   C T C A A G G A C C   T G A A A C C C A   T G C T T C G A G A   C A A C G T G A C T   T T A A T G G G A G   G G T G G G T G G G   1800
70 C C G C A G A C A G   G C T G G C A G G G   C A G G T G C T G C   G T G G G G C C C T   C T C A G C C C G   T C C T A C C C T G   1860
   G G C T C A C A T G   G G G C C T G T G C   C C A C C C C T C T   T G A G T G T C T T   G G G A C A G C T   C T T T C C A C C C   1920
   C T G G A A G A T G   G A A A T A A A C C   T G C G T G T G G G   T G G A G T G T T C   T C G T G C G A A   T T C A A A A A G C   1980
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Seq ID NO: C78 DNA Sequence

Nucleic Acid Accession #: NM_000358.1
Coding sequence: 48..2099

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   G C C C A A C G T   G T G T G C T G T G   C A G A A G G T T A   T T G G C A C T A A   T A G G A A G T A C   T T C A C C A A C T   240

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 AGTCTGATGT GTCCACAGCC ATTGACCTTT TCAGACAAGC CGGCTCGGC AATCATCTCT 1260
 CTGGAAAGTA GCGGTGACCC CTCTGGCTC CCCTGAATTC TGTATTCAA GATGGAACCC 1320
 20 CTCCAAITGA TGCCCAATC AGGAATTTGC TTGGAACCA CATAATTAAA GACCACTGG 1380
 CCTCTAAGTA TCTGTACCAT GGACAGACCC TGGAACTCT GGGCGGCAA AAAGTGAGAG 1440
 TTTTGTGTTA TGTGAATAGC CTCTGCATTG AGAACAGCTG CATCGCGGCC CACGACAAGA 1500
 GGGGGAGSTA CGGACCCCTG TTCACGATGG ACCGGGTGGG GACCCCCCA ATGGGGACTG 1560
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 25 CAGGACTGAG GAGACCCCTC AACCGGAAG GAGTCTACAC AGTCTTTGG CCCACAATG 1680
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 TTGCCAACAT CCTGAAATAC CACATTGGTG ATGAAATCCT GGTAGCGGA GGCATCGGG 1800
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 TGGTGAATGT CAACAGGAG CCTGTGCGG AGCCTGACAT CATGGCCACA ATGGCGCTGG 1920
 30 TCCATGTGAT CACCAATGTT CTGCAGCTC CAGCCAACAG ACCTCAGGAA AGAGGGGATG 1980
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 TTGAAGCACT ACAGGAGGAA TGCAACACGG CAGCTCTCCG CCAATTTCTC TCAGATTTCC 2160
 ACAGAGACTG TTTGAATGTT TTCAAAACCA AGTATCACAC TTTAATGTAC ATGGGCGGCA 2220
 35 CCATAATGAG ATGTGAGCCT TGTGCATGTG GGGGAGGAGG GAGAGAGATG TACTTTTAA 2280
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 CTATGGGAAA GTCTCGGCAC AGTTTTGTGA AAGCCCTTGC ACAGCTGGAG AAATGGCATC 2520
 40 ATTATGAGCT AGAGTTGAA ATGTTCTGTC AAATGTGTCT CACATCTACA CGTGGCTTGG 2580
 AGGCTTTTAT GGGGCCCTGT CCAGGTAGAA AAGAAATGGT ATGTAGAGCT TAGATTTCCC 2640
 TATTGTGACA GAGCCATGGT GTGTTGTGTA TAATAAAACC AAGAAACAT A 2691

45 Seq ID NO: C79 DNA Sequence
 Nucleic Acid Accession #: NM_006536.2
 Coding sequence: 109..2940

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 AGCATTTGAG GTCCCTATTG CAACCTGAAG TTGTGACTC TCCTGGTTCG CTTAAGTTCA 180
 GAACCTCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC 240
 55 ATTGCATTTA ATCCTCAGGT ACCTGAGAAAT CAGAACTTCA TCTCAACAT TAAGGAAATG 300
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 ATAAAGATTT TAATACCTGC CACATGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA 420
 TCATATGAAA AGGCAATGT CATAGTGACT GACTGGTATG GGGCACATGG AGATGATCCA 480
 TACACCCATC AATACAGAGG GTGTGAAAAA GAGGGAAAAAT ACATTCATTT CACACCTAAT 540
 60 TTCTTACTGA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCCGAGT GTTGTCCAT 600
 GAATGGGCCC ACCTCCGTTG GGTGTGTTT GATGAGTATA ACAATGACAA ACCTTTCTAC 660
 ATAAATGGGC AAAATCAAAAT TAAAGTGACA AGGTGTTTAT CTGACATCAC AGGCATTTTT 720
 GTGTGTGAAA AAGGTCCTTG CCCCCAAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA 780
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 65 AGTTTATCTT CTGTGGTTGA AITTTGTAAT GCAAGTACCC ACAACCAAGA AGCACCAAAC 900
 CTACAGAAC AGATGTGCAG CCTCAGAGT GCATGGGATG TAATCACAGA CTCTGCTGAC 960
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 GTACAGGCTG GTGACAAAGT GGTCTGTTA GTCTGGATG TGTCCAGCAA GATGGCAGAG 1140
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 75 CTGGGTTCTT CCCTCAGCCC AAATCTGGAG GAATTATCAC GTCTTACAG AGGTTTAAAG 1560
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 80 GGACGAAAT ACTACACAAA TAATTTTATC ACCAATCTAA CTTTTCGGAC AGCTAGTCTT 1860
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 GCCACTGTGG AAGCCTTTGT GGAAGAGAG AGCCTCCATT TTCTCATCC TGTGATGATT 2040
 TATGCCAATG TGAAACAGGG ATTTTATCCC ATTCCTAATG CCACTGTGAC TGCCACAGTT 2100
 GAGCCAGAGA CTGAGATACC TGTTACGCTG AGACTCCTTG ATGATGGAGC AGGTGCTGAT

GTTATAAAAA ATGATGGAAT TTAAGTGAAG TATTTTCTCT CCTTGTGCTC AAATGGTAGA 2160
 TATAGCTTGA AAGTGCATGT CAATCACTCT CCCAGCATAA GCACCCCCAGC CCACTCTATT 2220
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 AGCTCAGGAG GCTCCTTTTC AGTGTCTGGA GTTCCAGCTG GCCCCACCC TGATGTGTTT 2400
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 GCAATACGAG CAATGGATAG GAACTCCTTA CAGTCTGCTG TATCTAACAT TGCCCAAGCG 2760
 CCTCTGTTTA TTCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2820
 GGAGTTTAA CAGCAATGGG TTTGATAGGA ATCATTGTCC TTATTATAGT TGTGACACAT 2880
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 ATAAATATCC AAAGTGTCTT CCTTCTTAGA TATAAGACCC ATGGCCTTCG ACTACAAAAA 3000
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 TTTACATGAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAATGCAAG CTCTTACCT 3420
 CTTGCTATTT TGTATATAT ATTTAGATG ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480
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 TTTATGACAA AGGTCTATTG AATTATTATG TATGTAAGTT TCTACTCCCA TCAAGCAGC 3600
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Seq ID NO: C80 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1413

1 11 21 31 41 51
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 AAGGAAAAAA TCCAGAAAAA GCAGCACTTC TTGGGTCTGA AAGTGACCGG GCAACTGGAC 240
 ACATCTACCC TGGAGATGAT GCAAGCAGCT CGATGTGGAG TCCCGATGT CCATCAITTC 300
 40 AGGGAATGTC CAGGGGGGCC CGTATGGAGG AAACATTATA TCACCTACAG AATCAATAAT 360
 TACACACCTG ACATGAACCG TGAGGATGTT GACTAAGCAA TCCGAAAGC TTTCCAAGTA 420
 TGGAGTAATG TTACCCCTTT GAAATTCAGC AAGATTAAAC CAGGCATGGC TGACATTTTG 480
 GTGGTTTITG CCGGTGGAGC TCATGGAGAC TTCCATGCTT TTGATGGCAA AGGTGGAATC 540
 45 CTAGCCCATG CTTTGGGACC TGGATCTGGC ATTGGAGGGG ATGCACATTT CGATGAGGAC 600
 GAATTCTGGA CTACACATTC AGGAGGCACA AACTGTGTCC TCACTGCTGT TCACGAGATT 660
 GGCCATTCTT TAGGTCTTGG CCATTCTAGT GATCCAAAGG CGTAATGTT CCCACCTTAC 720
 AAATATGTTG ACATCAACAC ATTTGGCTCT TCTGCTGATG ACATACGTGG CATTCACTCC 780
 CTGTATGGAG ACCCAAAGAA GAACCAACGC TTGCCAAATC CTGCAATTC AGAACAGCTC 840
 50 CTCTGTGACC CCAATTTGAG TTTTGTGCT GTCACTACCG TGGGAAATAA GATCTTTTTC 900
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 ATTTCTTCTT TATGGCCAAC CTTGCCATCT GGCATTGAAG CTGCTTATGA AATTGAAGCC 1020
 AGAAATCAAG TTTTCTTTT TAAAGATGAC AAATACTGGT TAATTAGCAA TTTAAGACCA 1080
 GAGCCAAATT ATCCCAAGAG CATACATTCT TTTGGTTTTC CTAACCTTGT GAAAAAATTT 1140
 55 GATGCAAGCTG TTTTAAACCC ACGTTTITAT AGGACCTACT TCTTTGTAGA TAAACAGTAT 1200
 TGGAGGTATG ATGAAAGGAG ACAGATGATG GACCTGGTT ATCCCAACT GATTACCAAG 1260
 AACTTCCAAG GAATCGGGCC TAAATTGAT GCAGTCTTCT ACTTAAAAA CAAATACTAC 1320
 TATTCTTCTC AAGGATCTAA CCAATTGAA TATGACTTCC TACTCCAAAG TATCACCAAA 1380
 60 AACTGAAAA GCAATAGCTG GTTGGTTGT TGA 1413

Seq ID NO: C81 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1413

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 70 AAGGAAAAAA TCCAGAAAAA GCAGCACTTC TTGGGTCTGA AAGTGACCGG GCAACTGGAC 240
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 TACACACCTG ACATGAACCG TGAGGATGTT GACTAAGCAA TCCGAAAGC TTTCCAAGTA 420
 TGGAGTAATG TTACCCCTTT GAAATTCAGC AAGATTAAAC CAGGCATGGC TGACATTTTG 480
 75 GTGGTTTITG CCGGTGGAGC TCATGGAGAC TTCCATGCTT TTGATGGCAA AGGTGGAATC 540
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 GAATTCTGGA CTACACATTC AGGAGGCACA AACTGTGTCC TCACTGCTGT TCACGCCATT 660
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 AAATATGTTG ACATCAACAC ATTTGGCTCT TCTGCTGATG ACATACGTGG CATTCACTCC 780
 80 CTGTATGGAG ACCCAAAGAA GAACCAACGC TTGCCAAATC CTGCAATTC AGAACAGCTC 840
 CTCTGTGACC CCAATTTGAG TTTTGTGCT GTCACTACCG TGGGAAATAA GATCTTTTTC 900
 TTCAAAGACA GGTCTTCTG GCTGAAGGTT TCTGAGAGAC CAAGACCAAG TGTAAITTA 960
 ATTTCTTCTT TATGGCCAAC CTTGCCATCT GGCATTGAAG CTGCTTATGA AATTGAAGCC 1020
 AGAAATCAAG TTTTCTTTT TAAAGATGAC AAATACTGGT TAATTAGCAA TTTAAGACCA 1080
 GAGCCAAATT ATCCCAAGAG CATACATTCT TTTGGTTTTC CTAACCTTGT GAAAAAATTT 1140

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 GATGCAGCTG TTTTAAACCC ACGTTTTAT AGGACCTACT TCTTTGTAGA TAACCAGTAT 1200
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 AACTTCCAAG GAATCGGGCC TAAATTTGAT GCAGTCTCT ACTCTAAAAA CAAATACTAC 1320
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 AACTGAAAA GCAATAGCTG GTTGGTGT TGA 1413

Seq ID NO: C82 DNA Sequence
 Nucleic Acid Accession #: NM_006952.1
 Coding sequence: 11..793

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 ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAAAGATG ACATCTATGG 180
 GGCTGCCCTG ATCGGCATAT TTGTGGGCAT CTGCCTCTTC TGCTGTCTG TTCTAGGCAT 240
 TGTAGGCATC ATGAAGTCCA GCAGGAAAAT TCTTCTGGCG TATTTCAATC TGATGTTTAT 300
 AGTATATGCC TTTGAAGTGG CATCTTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360
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 TGAGAAATAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
 AGAACCTCTC AACCTGGAGG CTGTAAACT AGGCGTGCTT GGTTTTATC ACAATCAGGG 660
 CTGCTATGAA CTGATCTCTG GTCCAAATGAA CCGACACGCC TGGGGGGTGG CCTGGTTTGG 720
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30
 Seq ID NO: C83 DNA Sequence
 Nucleic Acid Accession #: NM_001793.2
 Coding sequence: 71..2560

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 1 11 21 31 41 51
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 CTGGCTGACG TGGCGGCGCT CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC 180
 CTGGGAGGCG GGAGGGCGCG AGCAGGAGCC CGGCCAGGCG CTGGGGAAGG TATTCATGGG 240
 CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
 TGGCGAGACA GTCCAGGAAA GAAGGTCAC GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
 ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
 TGAATAATGG AAGGGTCCCT TCCCCAGAG ACTGAATCAG CTCAAGTCTA ATAAAGATAG 480
 AGACACCAAG ATTTTCTACA CAGCTGCTT TGTGTGAAT AAGCCACTGG ACCGGGAGGA 540
 CTTCGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
 GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTGAGAG AATGGTGCCT CAGTGAGGGA 660
 CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
 GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTTACCA GGTACTTCTG TGATGCAAGT 780
 GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT 840
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 CATCCAGGCC ACAGACATGG ATGGGGACGG CTCACCCACC ACGGCACTGG CAGTAGTGGA 1020
 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
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 TTTTGAGGCC AAAAACAGC ACACCTGTA CGTTGAAGTG ACCAACGAGG CCCCCTTTGT 1320
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 GACTTGGAG CTGTGAGGA AGTGGCGGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
 ACGTTAGAGT GGTGTCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTGTACTTC 2760
 AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCTCAG AGGCCAAGTT TCCAGAGGCC 2820
 TCTTACCTGC CGTAAATGTC TCAACCTGT GTCTGGGCC TGGGCTGTCT GTGACTGACC 2880
 TACAGTGGAC TTCTCTCTG GAATGGAAAC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940
 TTTTATTAAT GCTATCTTCA AAACGTTAGA GAAAGTCTT CAAAGTGA GCCCAGAGCT 3000
 GCTGGGCCCA CTGGCCGTCC TGCAATTTCT GTTTCAGAC CCAATGCTT CCAATCGGA 3060

TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTTGCC CCTTATTTTT TATTTTCCCT 3120
 GTTGGCTTGC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180
 TAAAGAAACT TTTCACGAA AAAAA 3205

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Seq ID NO: C84 DNA Sequence
 Nucleic Acid Accession #: NM_005629.1
 Coding sequence: 639..2546

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 CGCGCGCGCG CACCGCCACC GGAGTCGCGG GCGAGCGCG CAGCCTTCGC GGGCCCCGCG 180
 CGCGCGCGCG GCGCGCGCGC ACAGGCCCTT GCTCGGCGCG TCGTTTGCAG ACCGCGCGCG 240
 CGGATGTGCG CCGCGCGCGG TTAGGATGAG TCTCGGCTCG GCGAGGAGCG CGCGCGAGCG 300
 GCGCGCGCGG GAGCGCGCGG CAGGAGCCTC GGGAGCGCG CCGCGCGCG CCGCGCGCG 360
 GCGCGCGCGG GCGCGCGCGG GCGCGCGCG CACACATGAG ATTCTTCAG 420
 CTCACCTTCA AGTGCTTCGT GGAAGCTTTC TGAAGTGCAG CCGCGCGCG CCGCGCGCG 480
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 ACGGCATCAT TAGCGGTGTC GCGAGCGAGA AGAAGGCGCG CCTCATCGCG CCGCGCGCG 720
 ACGGCGCGCG GCGGAGGCGG GAGCGCGCG TGGGCGTGGG GACACCGCGG GCGCGCGTGG 780
 CCGTGTGCGG GCGCGCGCGT TGGAGCGCG AGATGGACTT CATCATGTGC TCGTGGGCTG 840
 25 TCGCGGTGGG CTGCGGCAAC GTGTGGCGCT TCCCTTACCT GTGCTACAAG AACGCGCGAG 900
 GTGTGTCTCT TATTCCTTAC GTCTGTATCG CCTCGTGTGG AGGAATCCCG ATTTCTTCT 960
 TAGAGATCTC GCTGGGCGAG TTCTATGAAG CCGGCGAGCAT CAATGTCTGG AACATCTGT 1020
 CCTGTCTCAA AGGCGTGGGG TACGCTTCCA TGGTGTATGT CTCTTACTCG AACACCTACT 1080
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 30 CCGTGGCGCG ATGTGGCGAC ACCTGGAACA CTCCGAGCTG CGTGGAGATC TTCGCGCATG 1200
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 35 CCAAGTGGT CTGTGTGTG CTGCTGTGTC GTGAGTGTCT GCTGCTTGGC GCGCTGGATG 1500
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Seq ID NO: C85 DNA Sequence
 Nucleic Acid Accession #: NM_006516.1
 Coding sequence: 180..1658

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Seq ID NO: C86 DNA Sequence
 Nucleic Acid Accession #: XM_035292.2
 Coding sequence: 53..1576

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Seq ID NO: C87 DNA Sequence
 Nucleic Acid Accession #: NM_005268.1

Coding sequence: 168..989

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Seq ID NO: C88 DNA Sequence
Nucleic Acid Accession #: NM_005130
Coding sequence: 98..802

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Seq ID NO: C89 DNA Sequence
Nucleic Acid Accession #: BC022542
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 Coding sequence: 20..2143

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Seq ID NO: C99 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 501..4514

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Seq ID NO: C102 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..4480

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	CAATCTCCTA	TCAATATTGA	TGAAGATCTT	ACACAAGTAA	ATGTGAATCT	TAAGAAACTT	240
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Seq ID NO: C107 DNA Sequence
Nucleic Acid Accession #: NM_021101
Coding sequence: 221..856

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Seq ID NO: C108 DNA Sequence
Nucleic Acid Accession #: AF508964.1
Coding sequence: 98..1531

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80 Seq ID NO: C110 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
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	AACAAGGAAT	CTGCGCGCCA	GAGAGTCCCG	GGAGCGCGCG	CGGTGCGTGC	CCGGCGCGCC	660
	GGGCCATGCA	GCGACGGCGG	CGCGGAGCT	CCGAGCAGCG	GTAGCGCCCC	CCTGTAAAGC	720
	GGTTGCTGAT	GCCGGGGCCA	CTGTGAACCC	TGCCGCTGCG	CGGAACACTC	TTGCTCCCGG	780
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	ATGAGCCCGC	CATGGCGCGG	CTCTGGGGCT	TCTGCTGGCT	GGTTGTGGGC	TTCTGGAGGG	1020
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20	CTTCTCTCG	CATGCTGGCA	TTTCCGAGAT	TGGAGCCTAA	CAGTGTAGAT	CCTGAGAACA	1140
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	AAGCTTATGT	GCGACTGAGA	AATCTGACAA	TTGTGGATTG	TGGATTAATA	TTTGTGGCTC	1260
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25	ATCCATTAC	ATGCTCCTGT	GACATTATGT	GGATCAAGAC	TCTCCAAGAG	GCTAAATCCA	1440
	GTCCAGACAC	TCAGGATTTG	TACTGCCTGA	ATGAAGCAG	CAAGAATATT	CCCTGGCAA	1500
	ACCTGACAGT	ACCCAAATTG	GGTTTGGCAT	CTGCAAACT	GGCCGCACCT	AACCTCACTG	1560
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	AAGGCAACCC	CAACCCAGCG	CTTCAGTGGT	TCTATAACGG	GGCAATATTG	AATGAGTCCA	1920
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70	ATGAAGACCT	TTACAGAAAT	CCTATGGATT	GCAGCATTTT	ACTTGGCTAC	TTTATACCCA	4140
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75	GAAGAGAGGA	TGAATTTCAA	GCTGTGAGCC	AGGCAGGAGC	TCAGTATGGC	AAAGGTTCTT	4440
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Nucleic Acid Accession #: NM_130830.1
Coding sequence: 1..1746

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35 Seq ID NO: C112 DNA Sequence
Nucleic Acid Accession #: NM_002658.1
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Seq ID NO: C113 DNA Sequence
Nucleic Acid Accession #: XM_087254.1
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	GCACCAAGCA	TGGCATGAAT	GTGCTGGGCA	TGCTCTTCTT	CTCTGCCACC	ATGGGCACTC	840
	TGCTGGGCGG	CATGGGTGAC	AGCGGGGCC	CCCTGGTCTG	CTTCTGCCAC	TGCTCATATG	900
	AGTCGGTCTAT	GAAGATCGTG	GCGGTGGCTG	TGTGGTATTT	CCCTTCCGCG	ATTGTGTTCC	960
80	TCATTGCGGG	TAAGATCTTG	GAGATGGAGC	ACCCAGGGC	CGTCGGCAAG	AAGCTGGGCT	1020
	TCTACTCATG	CACCGTGGTG	TGCGGGCTGG	TGCTCCACGG	GCTCTTATAT	CTGCCCTGTC	1080
	TCTACTTCTT	CATCAACCAAG	AAGAATCCCA	TGCTCTTCAT	CCGGGCAATC	CTGCAAGGCTC	1140
	TGCTCATGCG	GCTGGCCACC	TCCTCCAGCT	CAGCCACACT	GCCCATCACC	TTCAAGTGCC	1200
	TGCTGGAGAA	CAACCAATC	GACCGCGCA	TCGCTCGCTT	CGTCTGCCCC	GTGGGTGCCA	1260
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25 Seq ID NO: C118 DNA Sequence
 Nucleic Acid Accession #: NM_005689
 Coding sequence: 278..2806

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 80 TCATCTGTGT CTTGGGGTAT GGTGCTAGCT ATGGTAAGGG AAAGGACCT TTCCGAAAAA 2940
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Seq ID NO: C119 DNA Sequence
 Nucleic Acid Accession #: NM_000676
 Coding sequence: 333..1331


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      GTCCCGGCCA CCAGCGCCCC AGCCCGGAGG CTCAGAAGCG GCAGGCGGAG GCGCGGTCCG 240
      GCGGCTATGG CCATGCCCCG GGGGTCTCAC GCGGCTGCC CTGCGCCGCG GCGCCTTCGG 300
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      CTGCGGCCGA CGTGCGCGTG GGGCTCTTCG CCATCCCTTT TGCCATCACC ATCAGCCTGG 540
      GCTTCTGCAC TGACTCTTAC GGCTGCCTCT TCCTGCGCTG CTTCGTGCTG GTGCTCACGC 600
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      CGCTCAGGTA TAAAGTTTG GTACGCGGGA CCGAGCAAG AGGGGTCAAT GCTGTCTCT 720
      GGGTCCCTGC CTTTGGCATC GGATTGACTC CATTCCTGGG GTGGAACAGT AAAGACAGTG 780
      CCACCAACAA CTCACAGAA CCCTGGGATG GAACCAAGAA TGAAGCTGC TGCCTTGTGA 840
      AGTGTCTCTT TGAGAAATGG GTCCCCATGA GCTACATGGT ATATTCAAT TTCTTTGGGT 900
      GTGTTCTGCC CCCACTGCTT ATAATGTGGT TGATCTACAT TAAGATCTTC CTGGTGGCCT 960
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      TGCATGCTGT TAAGTGTGTC ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT 1140
      GGGCAATGAA TATGGCCATT CTCTGTCTAC ATGCCAATTC AGTTGTCAAT CCCATTGTCT 1200
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      AGGCTCCAAG GATTGACAAA TATATTTATG ATCTATTTCG CTGCTTTTAC TGTGTGGATT 1560
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      ATGGTGAAGG ATTACTGAAA CTATTTTACT GTGAAACAGT GTGAACATAT ATAATGCAAA 1680
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35 Seq ID NO: C120 DNA Sequence
Nucleic Acid Accession #: NM_052932
Coding sequence: 217..786

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      GAGCCCAAGG GCGTCCCGCA TCCTGCCCTC GGAACAATGG GACTCGGCGC GCGAGGTGCT 240
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Seq ID NO: C121 DNA Sequence

Nucleic Acid Accession #: NM_004195

Coding sequence: 1..726

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Seq ID NO: C122 DNA Sequence

Nucleic Acid Accession #: AK091896.1

Coding sequence: 28..1572

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Seq ID NO: C123 DNA Sequence

Nucleic Acid Accession #: NM_002203.2

Coding sequence: 43..3588

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5	CAGTTTGGGT	ATGCAGTGCA	GCAGTTTATA	AATCCAAAG	GCAACTGGTT	ACTGGTTGGT	240
	TCACCTGGGA	GTGGCTTTCC	TGAGAACCGA	ATGGGAGATG	TGTATAAATG	TCCTGTTGAC	300
	CTATCCACTG	CCACATGTGA	AAACTAAAT	TTGCAAACTT	CAACAAGCAT	TCCAAATGTT	360
	ACTGAGATGA	AAACCAACAT	GAGCCTCGGC	TTGATCCTCA	CCAGGAACAT	GGGAACGTGA	420
	GGTTTCTCTA	CATGTGGTCC	TCTGTGGGCA	CAGCAATGTG	GGAATCAGTA	TTACACAAAG	480
10	GGTGTGTGTT	CTGACATCAG	TCTGTATTCT	CAGCTCTCAG	CCAGCTTCTC	ACCTGCAACT	540
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	CTTATATTTC	CTGCTACACC	CTGGATCACT	GCTGGTCAAA	ATATAACCAT	GATGGGCAGA	2580
15	AATTTTGATG	TAATTGACAA	CTTAATCATT	TCACATGAAT	TAAAAGGAAA	CATAAATGTC	2640
	TCGAACTATT	TGTGGGCGAG	TTACTGCGGG	TTTTTAGCCC	CCAGTTTAAA	GAGTTCAAAA	2700
	GTGCGCAGCA	ATGTCAGTGT	GAAGCTGAGA	GTACAAGACA	CCTACTTGGA	TTGTGGGAACC	2760
	CTGCAATATC	GCGAGGACCC	CAGATTCAAG	GGGTATCGGG	TGGAATCCGA	GGTGGACACA	2820
	GAACGTGAAG	TGAAAATTCA	AAAAGAAAAT	GACAACCTCA	ATATTTCCAA	AAAAGACATT	2880
20	GAAATTAATC	TCTTCCATGG	GGAAAATGGG	CAATTAATTT	GCAGTTTGA	AAATATTACT	2940
	AGAAATCAAG	ATCTTACCAC	CATCCCTTTC	AAAATTAAG	GCATCAAGAC	TGCAAGCACC	3000
	ATTGCCAACT	CTTCTAAGAA	AGTTCCGGTC	AAAGCTGGAA	ACCTGGAGCT	CTACGTCGAG	3060
	CAGGAGTACA	TCTCTTCCAC	ATGGTATTTT	CTGATTGTGC	TCCCTGCTCT	GCTAGTGATT	3120
	GTCAATTTTG	CGGCCGTGGG	GGTGACCAGG	CACAAATCGA	AGGAGCTGAG	TCGCAACACG	3180
25	AGTCACCAAC	TAGAATTGCT	GGAAAGCGAG	CTCCGSAAG	AGTACGTGA	CGGCTTTGCT	3240
	GAGCTGCAGA	TGGATAAATT	GGATGTGGTT	GATAGTTTTC	GAACTGTGCC	CTTCCCTGAC	3300
	TACAAACATT	TTGCTCTGAG	AACTTTCTTC	CCTGAGTCAG	GTGGCTTCAC	CCACATCTTC	3360
	ACTGAAGATA	TGCATAACAG	AGACGCCAAC	GACAAGAATG	AAAGTCTCAC	AGCTTTGGAT	3420
	GCCCTAATCT	GTAATAAAAG	CTTTCTTGTT	ACTGTCATCC	ACACCCCTGA	AAAGCAGAAG	3480
30	AACTTTTCTG	TGAAGGACAG	GTGTCGTGTT	GCCTCTCTCC	TAACCATTGC	ACTGCAAAAC	3540
	AAGCTGGTCT	AGCTGACCAG	CATCCTAGAG	GTGCTGACCA	GGGACTTGAT	GGAACAGTGT	3600
	AGTAACATGC	AGCCGAAACT	CATGCTGAGA	CGCAAGGAGT	CGGTCTGCGA	AAAACCTCCTC	3660
	ACAAACTGGA	TGTCGTCTCG	CTTTCTGGGA	TTTCTCCGGG	AGACTGTCCG	AGAGCCCTTC	3720
	TATTTGCTCG	TGACGACTCT	GAACAGAAA	ATTAACAAGG	GTCCCGTGGG	TGTAATCACT	3780
35	TGCAAGAGCCC	TGTACACACT	TAATGAAGAC	TGGCTGTGTT	GGCAGGTTCC	GGAATTCAGT	3840
	ACTGTGGCAT	TAAACGTCTG	CTTTGAAAAA	ATCCCGGAAA	ACGAGAGTGC	AGATGTCTGT	3900
	CGGAATATTT	CAGTCAATGT	TCTCGACTGT	GACACCATTT	GCCAAGCCAA	AGAAAAGATT	3960
	TTCCAGCAT	TCTTAAGCAA	AAATGGCTCT	CCTTATGGAC	TTCACTTAA	TGAAATTTGGT	4020
	CTTGAGCTTC	AAATGGGCAC	ACGACAGAAA	GAACCTCTGG	ACATCGACAG	TTCTCTCCGTG	4080
40	ATTTCTTGAAG	ATGGAATCAC	CAAGCTAAAC	ACCATTTGCC	ACTATGAGAT	ATCAAAATGGA	4140
	TCCACTATAA	AAGTCTTTAA	GAAGATAGCA	AATTTTACTT	CAGATGTGGA	GTACTCGGAT	4200
	GACCACTGCC	ATTGATTTTT	ACCAGATTCC	GAAGCATTC	AAGATGTGCA	AGGAAAGAGA	4260
	CATCGAGGGA	AGCACAGTTT	CAAAGTAAAA	GAATGTATC	TGACAAAGCT	GCTGTCCAGC	4320
	AAGGTGGCAA	TTCAATCTGT	GCTTGA AAAA	CTTTTGTAGAA	GCATTTGGAG	TTTACCCAAC	4380
45	AGCAGAGCTC	CATTGTCTAT	AAAATACTTT	TTTGACTTTT	TGGACGCCCA	GGCTGAAAAC	4440
	AAAAAAATCA	CAGATCCTGA	CGTCGTACAT	ATTTGAAAAA	CAACAGGCTC	TCCTCTTCGC	4500
	TTCTGGGTAA	ACATCTCTGA	GAACCTCTAG	TTTGTCTTTG	ACATTAGAAA	GACACCACT	4560
	ATAGACGCGT	GTTTGTCACT	GATTGCCAG	GCATTCATGG	ATGCATTTTC	TCTCACAGAG	4620
	CAGCAACTAG	GGAAAGGAAG	ACCAACTAAT	AAGCTTCTCT	ATGCCAAGGA	TATCCCAACC	4680
50	TACAAGAAAG	AAGTAAAACT	TTATTACAAA	GCAATCAGGG	ATTTGCCCTC	ATTGTCTATC	4740
	TCAGAAATGG	AAGATTTTTT	AACTCAGGAA	TCTAAGAAAC	ATGAAATGA	ATTTAATGAA	4800
	GAAGTGGGCT	TGACAGAAAT	TTACAATATC	ATCGTAAAT	ATTTTGTATG	GATTCTAAAT	4860
	AAACTAGAAA	GAGAACGAGG	GCTGGAAGAA	GCTCAGAAAC	AACTCTTGCA	TGTAAAGTCT	4920
	TTATTTGATG	AAAAGAAAGAA	ATGCAAGTGG	ATGTAAGCAC	TCTGGGGCCT	GGCTTAAATCT	4980
55	GGCAAAAGTT	TTGACAGCAC	TTGGGAGCAA	AATGGCTGCT	TGAGCTACTC	TGTGTCTGTTA	5040
	ATTGTGTGTT	TGCACATAGG	TTCCACTTTG	GGCACTGTCT	TTTAAAGAGA	CCAAGGCACA	5100
	TGCACAGCTT	TTAGAAAGCA	A				5121

Seq ID NO: C128 DNA Sequence

Nucleic Acid Accession #: NM_002185.1

Coding sequence: 23..1402

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	AGAACTGGAT	GACTACTCAT	TCTCATGCTA	TAGCCAGTGT	GAAGTGAATG	GATCGCAGCA	180
	TTCACTGACC	TGTGCTTTTG	AGGACCCAGA	TGTCAACACC	ACCAATCTGG	AATTITGAAT	240
	ATGTGGGGCC	CTGTGGGAGG	TAAAGTGCCT	GAATTTCAAG	AAACTACAAG	AGATATATTT	300
70	CATCGAGACA	AAGAAATCTT	TACTGATTGG	AAAGAGCAAT	ATATGTGTGA	AGGTTGGAGA	360
	AAAGAGTCTA	ACCTGC AAAA	AAATAGACCT	AACCACTATA	GTAAACCTG	AGGCTCCTTT	420
	TGACCTGAGT	GTCATCTATC	GGGAAGGAGC	CAATGACTTT	GTGGTGACAT	TTAATACATC	480
	ACACTTGCAA	AAGAAGTATG	TAAAAGTTTT	AATGCATGAT	GTAGCTTACC	GCCAGGAAAA	540
	GGATGAAAAC	AAATGGACGC	ATGTGAATTT	ATCCAGCACA	AAGCTGACAC	TCCTGCAGAG	600
	AAAGCTCCAA	CCGCGAGCAA	TGTATGAGAT	TAAAGTTGGA	TCCATCCCTG	ATCACTATTT	660
75	TAAAGGCTTC	TGGAGTGAAT	GGAGTCCAGG	TTATTAATCT	AGAACTCCAG	AGATCAATAA	720
	TAGCTCAGGG	GAGATGATC	CTATCTTACT	AACCATCAGC	ATTTTGAATT	TTTTCTCTGT	780
	CGCTCTGTTG	GTCATCTTGG	CCTGTGTGTT	ATGGAAAAAA	AGGATTAAAG	CTATGATATG	840
	GCCAGTCTCT	CCCGATCATA	AGAAGACTCT	GGAACTCTTT	TGTAAGAAAC	CAAGAAAAAA	900
80	TTTAAATGTG	AGTTTCAATC	CTGAAAGTTT	CCTGGAATGC	CAGATTCAAT	GGGTGGATGA	960
	CATTCAAGCT	AGAGATGAAG	TGGAAAGTTT	TCTGCAAGAT	ACGTTTCTCT	AGCAACTAGA	1020
	AGAATCTGAG	AAGCAGAGGC	TTGGAGGGGA	TGTGCAGAGC	CCCAACTGCC	CATCTGAGGA	1080
	TGTAGTGGTC	ACTCCAGAAA	GCTTTGGAAG	AGATTCAATC	CTCACATGCC	TGGCTGGGAA	1140
	TGTCAAGTGA	TGTGACGCCC	CTATTCTCTC	CTCTTCCAGG	TCCCTAGACT	GCAGGGAGAG	1200
	TGGCAAGAAAT	GGGCTCATG	TGTACCAGGA	CCTCTGCTTT	AGCCTTGGGA	CTACAAACAG	1260

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5 CACGCTGCC CCTCCATTTT CTCTCCAATC TGGAACTCTG ACATTGAACC CAGTTGCTCA 1320
 GGGTCAGCCC ATTCTTACTT CCCTGGGATC AAATCAAGAA GAAGCATATG TCACCATGTC 1380
 CAGCTTCTAC CAAAACCACT GAAGTGTAA AAACCCAGAC TGAACCTTACC GTGAGCGACA 1440
 AAGATGATTT AAAAGGGGAG TCTAGAGTTC CTAGTCTCCC TCACAGCACA GAGAAGACAA 1500
 AATTAGCAAA ACCCCACTAC ACAGTCTGCA AGATTCTGAA ACATTGCTTT GACCCTCTT 1560
 CTTAGTTCA GTGGCACTCA ACATGATCA AGAGCATCCT GCTTCTACCA TGTGGATTG 1620
 GTCACAAGGT TTAAGGTGAC CCAATGATTC AGCTATTT 1658

10 Seq ID NO: C129 DNA Sequence
 Nucleic Acid Accession #: NM_002722.1
 Coding sequence: 15..302

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 ACCCAGGGGA CAATGCCACA CCAGAGCAGA TGGCCAGTA TGCACTGAT CTCCGTAGAT 180
 ACATCAACAT GCTGACCAGG CCTAGGTATG GGAAGAGACA CAAAGAGGAC ACGCTGGCT 240
 TCTCGAGTG GGGGTCCCG CATGCTGCTG TCCCAGGGA GCTCAGCCG CTGGACTTAT 300
 AATGCCACT TCTGTCTCT ACGACTCCAT GAGCAGCGCC AGCCAGCTC TCCCTCTG 360
 ACCCTTGGCT CTGGCCAAAG CTGTCTCCT GCTCCACAC AGGCTCAATA AAGCAAGTCA 420
 AAGCC 425

25 Seq ID NO: C130 DNA Sequence
 Nucleic Acid Accession #: NM_032545.1
 Coding sequence: 47..718

30 1 11 21 31 41 51
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 CTATCAAGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGGTTG CCACTCAGAA 180
 GCACCGACAG TCACCGCTCA ACTGGACCTC CAGTCATTTC GGAGAGGTGA CTGGAGCGC 240
 CGAGGGCTGG GGGCCGAGG AGCCGCTCCC TACTCCCGG GCTTTCGGAG AGGGTGCCTG 300
 CGCGCGCGG CGCTGCTGCA GGAACGGCGG TACCTGCGTG CTGGGCGCTG TCTGCTGTG 360
 CCGCGCCAC TTCACCGGCC GCTACTGGA GCATGACCAG AGGCGCAGT AATCGGGCG 420
 CCTGAGCTGC CTCCCTCTCC AGACGCTGA CCGCTGTGAC CGAAGAGCT TCTCGGGC 480
 CCTGAGCTGC CTCCCTCTCC AGACGCTGA CCGCTGTGAC CGAAGAGCT TCTCGGGC 540
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 ACTCTCTCAC CGCTCTGCG GCCCGGATG GCGCGCGCAC CCTCGGTCCC TGGTCCCTTC 660
 CGTCTCTCAG CGGGAGCGCG GCCCTGCGG AAGGCGGGA CTGGGCTATC GCCTTTAATT 720
 TTCTATGTTG TAAATAATAG ATGTGTTAG TTACCGTAA GCTGAAGCAC TGGGTGAATA 780
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 AAAAAA 846

45 Seq ID NO: C131 DNA Sequence
 Nucleic Acid Accession #: NM_006533.1
 Coding sequence: 72..467

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 TCTCGGACC TGGTGTGAGG GGTGCTCTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG 180
 CGGACAGGGA GTGCAGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGCCC 240
 CCGACTGCGG ATTCCTGACC ATTCACCGGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA 300
 AGGGCGGTGG GCGGCTCTTC TGGGGAGGCA GCGTTCAGGG AGATTACTAT GGAGACTGCG 360
 CTGCTCGCTT GGGCTATTTC CCCAGTAGCA TTGTCCGAGA GGACCAAGCC CTGAAACCTG 420
 GCAAAGTGA TGTGAAGACA GACAAATGGG ATTTCTACTG CCAGTGAGCT CAGCTTACCG 480
 CTGGCCCTGC CGTTTCCCTT CCTTGGGTTT ATGCAAATAC AATCAGCCCA GTGCAAAC 538

65 Seq ID NO: C132 DNA Sequence
 Nucleic Acid Accession #: AB064272
 Coding sequence: 1..708

70 1 11 21 31 41 51
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 AAAACCAACA GAACCCACAG AAAGCCTACG CTATACTCAG AGAAGACCAT ATGCACCAAA 120
 GGGAAAAACA CACCACTCCC AGAAAAGCCT ACAGAAAACC TGGGGAAAC CACTGACCC 180
 ACTGAGACCA TAAAGGCCCC AGTAAAGTCC ACAGAAAACC CAGAAAAAAC AGCAGCAGTC 240
 ACAAGACCTA TAAACCTTTC AGTCAAGGTC ACAGGAGACA AATCTCTCAC TACTACCTCT 300
 TTCTACTTAA ATAAACTGAG AGTTACTCAT CAGGTGCCCA CTGGTTCTTT CACCTCATT 360
 ACATCTAGAA CGAAGCTGAG TTCTATCACA TCAGAAAGCCA CAGGAAACGA GAGCAATCCA 420
 TACCTCAATA AAGATGGCTC ACAGAAAGGT ATCCAGCTG GACAGATGGG AGAGAATGAT 480
 TCATTCCTCG CATGGGCCAT AGTTATTGTG GTCCCTGGTG CTGTGATTCT CCTCCTGGT 540
 TTCTTGGGCC TGATCTTCTT GGTCTCTTAT ATGATGCGGA CAGCGCGCAC ACTAACCCAG 600
 AACACCCAGT ACAATGATGC AGAGGATGAG GGTGGGCCCA ATTCTTACCC GGTCTACCTG 660
 ATGAGGAGC AGAATCTTGG CATGGGCCAG ATCCCTTCCC CACGGTGA 708

80 Seq ID NO: C133 DNA Sequence
 Nucleic Acid Accession #: NM_080870.1
 Coding sequence: 3..710


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   CCACTGAGAC CATAAAAGCC CCAGTAAAGT CCACAGAAAA CCCAGAAAAA ACAGCAGCAG 240
   TCACAAGAC  TATAAAACCT TCAGTCAAGG TCACAGGAGA CAAATCTCTC ACTACTACCT 300
   CTTCTCATCT AAATAAAACT GAAGTTACTC ATCAGGTGCC CACTGGTTCT TTCAOCCCTCA 360
10  TTACATCTAG AACGAAGCTG AGTTCTATCA CATCAGAGC CACAGGAAC GAGAGCCATC 420
   CATACCTCAA TAAAGATGGC TCACAGAAAG GTATCCAGC TGGACAGATG GGAGAGAATG 480
   ATTCAATGCC TGCATGGGCC ATAGTTATTG TGGTCTGGT GGCTGTGATT CTCTCTCTGG 540
   TGTTCTCTGG CCTGATCTTC TTGGTCTCCT ATATGATGCG GACAOCOCG ACACTAACCC 600
   AGAACACCCA GTACAATGAT GCAGAGGATG AGGGTGGCCC CAATTCCTAC CCGTCTTACC 660
15  TGATGGAGCA GCAGAATCTT GGCATGGGCC AGATCCCTTC CCCAOGGTGA TCTTGAGTGA 720
   GGCGCCAGCC CCTGGCTCTT CCATGCTCTG CCCCTTTCCT GGTGAGGAA CCGGACTCAC 780
   AATTTCTATT TCCGGGAATC CAGGAAGGGC AGAGAATACT GACGGTTACC AGTATTAACC 840
   CTTTCATCTG TCTTGAACCT GGTGGGGGAA TGAGGTGATA AGCAAGGAGG GTGTAAAGTT 900
   AGGGGACAAA AAGAAAGAA TGAATAATAC GAGCAGACAT TCTCTGTAGA AGGTAATGGT 960
20  CTGAGAATGA AAAGGTGTTT GATGGACATG TTGTGGGGGC ACCAATGCAG AACACTGCAC 1020
   TGAGTCTCAA AGGAAGGACA GGAGCCTTAT AGGCAATGCC CCAGACTGAC TTGTGAGTGG 1080
   GGTTTATGCC GAAAGGGAGG GACTGAGGGC AGAGTCTCTG GGTTCAGGA CAGCATTATG 1140
   TTAATTCATC TCACTATTAC TTAAGAGTTT GTGTGTAAC AGGCTCATCT CTGAGTCTCT 1200
   AGGACCTTGG CCCCACCCCC CATTTTTTTA ATGAAAAAAA AAAACAAAAA AAACGGATCC 1260
25  AAGAAGAAAA GAGAAATTTAT TTCTTCTCTC ACTCTCTCCA TGCCCTGGAG AAAAAAAGT 1320
   CCAGAAGAAA TCATAAATAT CTCTCATCTA CATGGTTGCT TCCTCTTCTC CCCAATCCC 1380
   TTAGTTTATC TAAATGTCTA CAGTGGAGCG CCTGTTGGTT TGGCTGTCTG GGTGTGGGT 1440
   GGACACCCGA GGAGGGGATT TTAATTTGGC CAGCAGTCTC ACCCACTGAT CTCCACCCCA 1500
   GACCTTCCCT GATTGGTGTG TCAGCATTTA TTTCTCTGTC TCTTCCACCA AAAGCCAGCT 1560
30  GTAGCTTTAT CTGTAAAAG TTACCCATCT TCTCTACTGT CCCCATTCTC TCTCTCTCCA 1620
   CCTTCACCCC AGATTCAAGT TTTCTCTCTT GTAGGCATTT CATCTGTGTG TGTTTCTGAG 1680
   ATTTCTCTCT TCTCTCTCTA TGGCCATTTC ACCTTATTAC TGATTGGGTA GAGGGGGAAA 1740
   AGGAGAATGA TGATGATAGT TTCTTCTGT CTATTGACCT TTTTATAAT AAAGTATAAC 1800
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Seq ID NO: C134 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..10674

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45  GGGGCCCCCG TGAGTATCCC CGCGCGCGCC GCTCCTGGCG ACGAAGCGGC GGGGAGCAGA 180
   GTGGAGGGCG TGCGCCAGCG GTTCCGGCGA CGCGTGCGGC TGCTGCGGGA GCTCAGCGAG 240
   CGCTTGGAGC TTGTCTTCTC GGTGGATGAT TCGTCCAGCG TGGGCGAAGT CAACTTCCGC 300
   AGCGAGCTCA TGTTCGTCCG CAAGCTGCTG TCCGACTTCC CCGTGGTGCC CACGGCCACG 360
   CGCGTGGCCA TCGTGACCTT CTGTCCAAG AACTAGTGG TGCGCGCGGT CGATTACATC 420
   TCCACCCGCG GCGCGCGCCA GCACAAGTGC GCGCTGCTCC TCCAAGAGAT CCGTGCCATC 480
   TCTTACCGAG GTGGCGGCAC CTACACCAAG GCGCGCTTCC AGCAAGCGCG GCAAAATCTT 540
   CTTCATGCTA GAGAAAACTC AACAAAAAGT GTATTTCTCA TCACTGATGG ATATTCCAAT 600
   GGGGAGACCT CTAGACCAAT TGCAGCGTCA CTGCGAGATT CAGGAGTGA GATCTTCACT 660
   TTTGCGATAT GGCAGGGGAA CATTCGAGAG CTGAATGACA TGGCTTCCAC CCCAAGGAG 720
   GAGCACTGAT ACCTGCTACA CAGTTTGAAG GAATTTGAGG CTTTAGCTCG CCGGGCATTG 780
   CATGAAGATC TACCTTCTGG GAGTTTATT CAAGATGATA TGGTCCACTG CTCATATCTT 840
   TGTGATGAAG GCAAGGACTG CTGTGACCGA ATGGGAAGCT GCAATGTGG GACACACACA 900
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60  ACAGCTTGCC CATCGGGGAC ATACAAACCT GAAGGCTCAC CAGGAGGAAT CAGCAGTTGC 1020
   ATTCAATGTC CTGATGAAAA TCACACCTCT CCACCTGGAA GCACATCCCC TGAAGACTGT 1080
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   CTGAAGCCTC CGAAAAATGG TTACTTTATC CAAAACACTT GCAACAACTA CTTCAATGCA 1200
   GCGTGTGGGG TCCGATGTCA CCTGGATTG GATCTTGTGG GAAGCAGCAT CATCTTATGT 1260
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65  CTCCGCCAGC CGAAACATGG CCACATCAGC TGTCTACAA GGGAAATGTT ATATAAGACA 1380
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70  ATGCTGAGAT GTACCACTTC TGGAAAAATG AATGTCGAG TTCAGGCAGC TGTGTGTAAA 1680
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   CAAGATTCTG CCAATGTTAC CTGGCAGATT CCAACAGCTA AAGACAACT TGGTGAAGAG 1800
   GTGTCACTCC ACGTTTATCC AGCTTTCACC CCACCTTACC TTTTCCCAAT TGGAGATGTT 1860
   GCTATCGTAT ACACGCAAC TGACCTATCC GGCACACAG CCAGCTGCTT TTTCCATATC 1920
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   GTCTCGGAGA AGGTACATGC CGCAAGCTGG GATGAGCCTC AGTCTCAGA CAACTCAGGG 2040
   GCTGAATTGG TCAATTCCAG AAGTCATACA CAAGGAGACC TTTTCCCTCA AGGGGAGACT 2100
   ATAGTACAGT ATACAGCCAC TGACCCCTCA GGCATAACA GGACATGTGA TATCCATATT 2160
80  GTCATAAAGG GTTCTCCCTG TGAATTTCCA TTCACACCTG TAAATGGGGA TTTTATATGC 2220
   ACTCGAGATA ATACTGGAGT CAACTGTACA TTAACCTGCT TGGAGGGCTA TGATTTCACA 2280
   GAAGGGTCTA CTGACAGTA TTATTGTGCT TATGAAGATG GCGTCTGGAA ACCAACATAT 2340
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	TACGATGACT	TCCTGGACAC	TGTGCAAGAA	ACAGCCACAA	GCATCGGCAA	TGCCAAGTCC	2700
	TCACGGATTA	AAAGAAATGC	CCCATATCT	GACTATAAAA	TTAAGTTAAT	TTTTAACATC	2760
5	ACAGCTAGTG	TGCCATTACC	CGATGAAAGA	AATGATACCC	TTGAATGGGA	AAATCAGCAA	2820
	CGACTCCTTC	AGACATTGGA	AACTATCACA	AATAAATCGA	AAAGGACTCT	CAACAAAGAC	2880
	CCCATGTATT	CCTTTCAGCT	TGCATCAGAA	ATACTTATAG	CCGACAGCAA	TTCATTAGAA	2940
	ACAAAAAAGG	CTTCCCCCTT	CTGCAGACCA	GGCTCAGTGC	TGAGAGGGCG	TATGTGTGTC	3000
	AATTGCCCTT	TGGGAACCTA	TTATAATCTG	GAACATTTC	CCTGTGAAAG	CTGCCGGATC	3060
10	GGATCCTATC	AAGATGAAGA	AGGGCAACTT	GAGTGCAAGC	TTTGCCTCTC	TGGGATGTAC	3120
	ACGGAATATA	TCCATCAAG	AAACATCTCT	GATTGTAAAG	CTCAGTGTAA	ACAAGGCACC	3180
	TACTCATACA	GTGSACTTGA	GACTTGTGAA	TCGTGTCCAC	TGGGCACCTA	TCAGCCAAAA	3240
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	GTGAACATT	TCGCATGTGG	AGTTCTCTGT	CCAGAAGGAA	AATTCTGCG	TTCTGGGTGA	3360
15	ATGCCCTGTC	ACCCATGTCC	TCGTGACTAT	TACCAACCTA	ATGCAGGGAA	GGCTTCTG	3420
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	TCAACTTCAG	TTCTGAATAT	TACTATTTTC	GGTGATTG	GGCATCTGGA	GTGTGTTAAAT	3540
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	CTAGTTGGGG	AATTCATTGG	TGAGTGCCCA	TCAGGTTACA	CAGGTGAGCG	GTGTGAAGAA	3780
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	GCTGGCTATC	GTTCACATG	TGTGAAAGGA	TTTGTAGGCC	TGCATGTGAA	AACAGAAAGT	3900
	AATGAATGCC	AGTCAAAACC	ATGCTTAAAT	AATGCAGTCT	GTGAAGACCA	GGTGTGGGGA	3960
25	TTCTTTGGCA	AATGCCCAAC	TGGATTTTTG	GGTACCCGAT	GTGGAAGGAA	CGTGTGATG	4020
	TGCTCTAGTC	AGCCATGCAA	AAATGGAGCT	ACCTGTAAAG	ACGGTGCCAA	TAGCTTCAGA	4080
	TGCCCTGTGT	CAGCTGGCTT	CACAGGATCA	CAGTGTGAAT	TGAACATCAA	TGAATGTGAG	4140
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 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..390

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Seq ID NO: C137 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1761

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Seq ID NO: C138 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..2310

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25 Seq ID NO: C139 DNA Sequence
 Nucleic Acid Accession #: NM_004616.2
 Coding sequence: 180..893

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 45 TCTTGGCAAA AAATTTGATT ATAGTTATTG GAATATCATT TGGACTGGCA GTTATTGAGA 840
 TACTGGGTTT GGTGTTTCTT ATGGTCTGTG ATTGCCAGAT CGGGAACAAA TGAATCTGTG 900
 GATGCATCAA CCTATCGTCA GTCAAAACCC TTTAAATAGT TGCTTTGGCT TTGTAAATTT 960
 AAATATGTAA GTGCTATATA AGTCAGGAGC AGCTGTCTTT TTAATAATGC TCGGCTAGCT 1020
 AGACCACAGA TATCTCTTAG ACATATTGAA CACATTTAAG ATTTGAGGGA TATAAGGGA 1080
 50 AATGATATGA ATGTGTATTT TTACTCAAAA TAAAGTAAC TGTTTACGTT AAAAAAATA 1140
 AAAAAAATA AAAAAAATA 1159

55 Seq ID NO: C140 DNA Sequence
 Nucleic Acid Accession #: NM_004617.2
 Coding sequence: 232..840

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 ATTGAATTGG AGACAATTAC AAGGACTCTC TGGCCAAAAA CCTTGAAGA GGCCCGTGA 180
 AGGAGGCGAGT GAGGAGCTTT TGATTGCTGA CCTGTGCTGT ACCACCCAG AATGTGCACT 240
 GGGGGCTGTG CCAGATGCTT GGGGGGAGCC CTCATTCCCC TTGCTTTTTT TGGCTTCTGT 300
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 65 CAAGAGATCT GGTTTTTCCG AGGAATATTA GGAAGCGGTG TCTTGATGAT CTTCCCTGCG 420
 CTGGTGTCTT TGGGCTTGAA GAACAATGAC TGCTGTGGGT GCTGCGGCAA CGAGGGCTGT 480
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 70 AACAGTGCC GAGAGCCTCT CAATGTGGTT CCTTGAATC TGACCCCTCT CTCCATCCTG 720
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 75 AGGCAGTTAT TCTTCTTTC CAACAGCTT TGCTCGAGTT AGAATTTTGT TATTTTCAA 1020
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 TGAAGTTTT ACATAATCA AAGGAAGAAA GCACATTTAA AATGAGAAAC TAAGACCAAT 1260
 80 TTTCTTTTTT AAGAGGAAAA AGAATGATTG ATGTATCCTA AGTATTGTTA TTTGTTGTCT 1320
 TTTTGTCTGT CCTGCTTGA GTTGTCTGTG ACTGATCTTT TGAGGCTGTG ATCATGGCTA 1380
 GGGTCTTTTT ATGTATGTTA AATTAATAAC TGAATTCAGA GGTAACTG 1428

Seq ID NO: C141 DNA Sequence
 Nucleic Acid Accession #: NM_002381.2

Coding sequence: 64..1524

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GAGACCCGAG GTCCCGGGGG CAGCCCTGGA CGCCGCCCTT CTCCTGGCGC TCCCGACGGC 240
GCGCCCGCTT CCGGGACCCG CGAGCCCTGG CGCGCCCGCG GTGCAGGTGT TTGCAAGAGC 300
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ACCAAGTGGA AAACCTTTGT CTCGCGGATA ATCGACACTC TGGCATTGG GCCAGCCGAC 420
ACGCGGTGG CAGTGGTGAA CTATGCTAGC ACTGTGAAGA TCGAGTTCCA ACTCCAGGCC 480
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GCTCGAGAGC CCTCTCTTAA CATCCCTAAG GTGGCCATCA TTGTACAGA TGGGAGGCC 660
CAGGACCCAG TGAATGAAGT GCGCGCTCGG GCCCAAGCAT CTGGTATTGA GCTCTATGCT 720
GTGGCGTGG ACCGGGCGAG CATGGCGTCC CTCAGATGA TGGCCAGTGA GCCCTAGAG 780
GAGCATGTTT TCTACGTGGA GACCTATGGG GTCAATTGAG AACTTTCCTC TAGATTCCAG 840
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ATCAGTGATG GGAAGGCAAA GCACCACTGT GAGTGTAGCC AAGGATACAC CTGGAATGCC 960
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AATGAAGACA GGAACCTTGT TTCAGTCAA GATAAATGTG CTTTGGGTAC CCATGGGTGT 1140
CAGCACATTT GTGTGAATGA CAGAACAGGG TCCCATCATT GTGAATGCTA TGAGGCTAC 1200
ACTCTGAATG CAGATAAAAA AACATGTTCA GTCCGTGACA AGTGTGCCCT AGGCTCTCAT 1260
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TCGTATCTTC AAGACTGAA CACTAAACTT GATGACATT TGGAGAAGTT GAAAATAAAT 1500
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AATTCTTTTG GCTTTGAAAC TTGCAACTTT GAGAACAAAA CAGTCCCTTA AATTTTGCAC 2460
TGCTCAATTC TGTTTTTGTG TTGCATTGTC TTTAATATAA TAAAGTTAT TACCTTTACA 2520
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Seq ID NO: C142 DNA Sequence
Nucleic Acid Accession #: NM_016639.1
Coding sequence: 40..429

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GAGCAAGCGC CAGGACCGC CCCCTGCTCC CGCGGACGCT CCTGGAGCGC GGACCTGGAC 180
AAGTGCAATG ACTGCGGCTG TTGCAAGGCG CGACCGCACA GCGACTTCTG CCTGGGCTGC 240
GCTGCAGCAG CTCCTGCCCC CTTCGCGCTG CTTTGGCCCA TCCTTGGGGG CGCTCTGAGC 300
CTGACCTTCG TGCTGGGGCT GCTTCTGGG TTTTGGTCT GGAGACGATG CCGCAGGAGA 360
GAGAAGTTCA CCACCCCAT AGAGGAGACC GCGGAGAGG GCTGCCAGC TGTGGGCTG 420
ATCCAGTGAC AATGTGCCCC CTGCCAGCG GGGCTGGCCC ACTCATCATT CATTATCCA 480
TTCTAGAGCC AGTCTCTGCC TCCAGAGCG CGCGGGAGCC AAGCTCCTCC AACCACAAGG 540
GGGGTGGGG GCGGTGAATC AACTCTGAGG CTTGGGCCCA GGGTTCAGGG GAACCTTCCA 600
AGGTGCTGCG TGCCCTGCC TCTGGCTCCA GAACAGAAAG GGAGCCTCAC GCTGGCTCAC 660
ACAAACAGC TGACACTGAC TAAGGAACGT CAGCATTTGC ACAGGGGAGG GGGGTGCCCT 720
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TCACTCAGAT GTCTGAAAT TCCACCAAG GGTCAACCT GGGGGGTAG GGACCTATT 840
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CCCAAGCGG GGAGGAGATA TTTATTTTGG GGAGGTTTGG GAGGGGAGG AGAATTATT 960
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Seq ID NO: C143 DNA Sequence
Nucleic Acid Accession #: NM_001819
Coding sequence: 113..2146

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AACGCTGCTT CTCAGCCTCC TGGGAGCCGT GGGGCTGGCG GCTGTCAATT CCATGCCAGT 180
GGATAACAGG AACCACAATG AAGGAATGCT GACTCGCTGC ATCATTGAGG TCCTCTCAA 240
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GGCAGGAGCC CCAGGGGAGG AGGACATCCA AGGCCAACA AAGCAGACA CAGAGAAATG 480
GGCAGAGGGA GGCAGGACACA GCGAGAGCG AGCGGATGAG CCCCAGTGA GCCTCTATCC 540
CTCCGACAGC CAAGTCTCTG AAGAAGTGAA GACACGCCAT TCTGAGAAGA GCCAGAGAGA 600
GGATGAGGAG GAGGAGGAGG GAGAGAACTA TCAAAAAGGG GAGCGAGGGG AAGATAGCAG 660
TGAAGAGAAA CACCTTGAAG AGCCAGGAGA GACACAAAC GCTTTCTCA ATGAAAGAAA 720
GCAGGCTTCA GCTATAAAAA AAGAGGAGTT AGTGCCAGA TCGGAAACAC ATGCTGCCGG 780
GCATTCTCAG GAGAAGACAC ATAGCCGAGA GAAGAGTAGC CAGGAGAGTG GAGAGGAGGC 840
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TGAGGAAGAG GAGGAAGATG CCACCTCTGA GGTGGACAAA CGACGACGA GCGCCAGACA 960
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TGACAAATTT CTGAGGGGTG AGGAGGAAAA TGAGCTGACC TTGAACGAGA AGAATTTCTT 1800
CCCAGAAATC AACTATGACT GGTGGGAGAA AAAGCCCTTC TCTGAGGATG TGAAGTGGGG 1860
GTATGAGAAG AGAACTCTCG CCAGGGTCCC CAAGCTGGAC CTGAAAAGGC AATATGACAG 1920
GGTGCCCAAC CTGGACCAAG TCCTTCACTA CAGGAAGAG TCAGCTGAGT TTCCAGACTT 1980
CTATGATTCT GAGGAGCCGG TGAGCACCCA CCAGGAGGCA GAAATGAAA AGGACAGGGC 2040
TGACCAGACA GTCTGACAG AGGACGAGAA AAAAGAACTC GAAAACTTGG CTGCAATGGA 2100
TTTGAATCTA CAGAAAGATG CTGAGAAATT CAGCCAAAGG GGCTGACTGT CATTTGAGCG 2160
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ACCATTTATA TACCAAGGG CAGAAAGTAG AACTTACTAT TCATTAAATG TTTGACACAA 2280
TTGGAATTGT CTTTAATTTC TGTGAGATG CTATTGAAAA TGTGAATTGC ATGACTTTGA 2340
GCATATTCTT TTCTGCAAAA TAGACATATT AACATGCTTA TGACAAATGAC TGTGCTACTG 2400
TCTTTGAAAA AATGTTGTG TCAGTTGGAA ATAATAAAG ATTCACTGA GACC 2454
  
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Seq ID NO: C144 DNA Sequence
 Nucleic Acid Accession #: XM_093082.1
 Coding sequence: 93..1988

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AGCCCAACTG TGTATTACAG ACATTGAGGT GGTACCGGTG CCTATCTCT TCTGCTTCTT 180
GTGGGGCTCT AGCAGCTGTT CTTAGCACCA GTCAGTGGCT CACTGAAGTG GAATTTAGTG 240
AGACAAAAC GGAAGCTTCA GCTTTGAAAT TGCTCTATGG AGGCTTAAAA GATCCAAAT 300
GCAAAATTAC GAAGCTCAAC TTGCAGTTTT CTATTCTGT AACCGCTGCA AAACCTCCAG 360
TTGGAATGGT TGGAAATGT TCTGTTTCT CGGGATCATT GGTGCAATCT CATTTGGCT 420
ACTGTCAGGA CAGTTCTTTC AAATGTGATC TTTGTAAGCT GCTCTGGCCT TCCACCAGAG 480
TTGCTGTGTC AAAGGATTGT GGGAGTCCTA AGTCCCTCCT ATCAGAAGGG CTGAACTGGG 540
CAGGAAGACT TGAGGCAGTG GAGGAGGTTT TGGGGTTGGG GGTGCTTGTA CAGCCCGGTG 600
ACCCAGCATC TCAGGGTGGG GGGCATTTGT AAAACTATGG GTCTTTTAGA GACTTGTGTG 660
ACTTAGAAGT CAGGCGAGAA CCAAGCCTGA GAAAAGGTGG TATGGATCTC CAGAGACCCA 720
CCCTACAAGT TGTCTCTCTT TGCAAAATCT TCTCCCTCAA ACTATTCTC TTTATTGCAT 780
TGCTTAATTC TCCTGTGTAG GTTAGTGTGG TGCAAGTGAC CATCCAGAC GGTTCCTGTA 840
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GAGAACAGCT TTCCATCCAG TGGTCTTCT TCCATAAGAA GAGAGTGGAG CCAATTTCTT 960
CTCCTTGGGA GGAGGGGAGG TGGCCAGATG TTGAGGCTGT GAAGGGCACT CTTGATGGAC 1020
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TCGAGCTGGA GCTGGAGCCA GAAACGAGT CGGAATTGGA GCCAGAGCCA GAGCCAGAGC 1920
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Seq ID NO: C145 DNA Sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..1242

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CTCATCTGCA	TCTACACCAC	CACCTGTGCC	TCCCAGAGAC	AGCTTTCCAT	CCAGTGGTCT	180
TTCTTCCATA	AGAAGGAGAT	GGAGCCAATT	TCTTCTCCTT	GGGAGGAGGG	GAAGTGGCCA	240
GATGTTGAGG	CTGTGAAGGG	CACCTCTGAT	GGACAGCAGG	CTGAATCCCA	GATTTACTTT	300
TCTCAAGGTG	GACAAGCTGT	AGCCATCGGG	CAATTTAAAG	ATCGAATTAC	AGGGTCCAAC	360
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ATCTGCGATG	TTAAACAACCC	CCCAGACTTT	CTCGGCCAAA	ACCAAGGCAT	CCTCAACGTC	480
AGTGTGTTAG	TGAACACCTTC	TAAGCCCCTT	TGTAGCGTTC	AAGGAAGACC	AGAAACTGGC	540
CACACTATTT	CCCTTTCCCTG	TCTCTCTGCG	CTTGGAACAC	CTTCCCCTGT	GTACTACTGG	600
CATAAAGTTG	AGGGAAGAGA	CATCGTGCCA	GTGAAAGAAA	ACTTCAACCC	AACCACCGGG	660
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TGCTTCGCAA	GGAATAAGGC	AAAAGCAAAG	GCAAAAGAAA	GAAATTTCTA	GACCATCGCG	900
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GACGCTACCC	AACTAGAAAT	AACTCTACCA	TCTTCCATTC	ATGAGACTGG	CCCTGATACC	1020
ATCCAGAAAC	CAGACTATGA	GCCAAAGCCT	ACTCAGGAGC	CTGCCCCAGA	GCCTGCCCCA	1080
GGATCAGAGC	CTATGGCAGT	GCCTGACCTT	GACATCGAGC	TGGAGCTGGA	GCCAGAAACG	1140
CAGTCGGAAT	TGAGGCCAGA	GCCAGAGCCA	GAGCCAGAGT	CAGAGCCTGG	GGTTGTAGTT	1200
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Seq ID NO: C146 DNA Sequence
 Nucleic Acid Accession #: NM_003020.1
 Coding sequence: 29..664

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CCCTGACCCG	GTCTCAGAAG	CAGATATCCA	GAGGCTGCTT	CATGGTGTTA	TGAGGCAATT	180
GGGCATTGCC	AGSCCCCGAG	TGGAATATCC	AGCTCACCAG	GCCATGAATC	TTGTGGGCCC	240
CCAGAGCATT	GAAGGTGGAG	CTCATGAAGG	ACTTCAGCAT	TTGGGTCCCT	TTGGCAACAT	300
CCCCAACATC	GTGGCAGAGT	TGACTGGAGA	CAACATTCCT	AAGGACTTTA	GTGAGGATCA	360
GGGGTACCCA	GACCCCTCAA	ATCCCTGTCC	TGTTGGAAAA	ACAGATGATG	GATGTCTAGA	420
AAACACCCCT	GACACTGCAG	AGTTTCAGTG	AGAGTTCAG	TTGCACCAGC	ATCTCTTTGA	480
TCCGGAACAT	GACTATCCAG	GCTTGGGCAA	GTGGAACAAG	AACTCTCTTT	ACGAGAAGAT	540
GAAGGGAGGA	GAGAGACGAA	AGCGGAGGAG	TGTCAATCCA	TATCTACAAG	GACAGAGACT	600
GGATAATGTT	GTTCGAAAGA	AGTCTGTCCC	CCATTTTICA	GATGAGGATA	AGGATCCAGA	660
GTAAGAGAGAA	GATGCTAGAC	GAAACCCAC	ATTACCTGTT	AGGCCTCAGC	ATGGCTTATG	720
TGCACGTGTA	AATGGAGTCC	CTGTGAATGA	CAGCATGTTT	CTTACATAGA	TAATTATGGA	780
TACAAAGCAG	CTGTATGTAG	ATAGTGTATT	GTCTTCACAC	CGATGATTCT	GCTTTTGTCT	840
AAATTAGAAT	AAGAGCTTTT	TTGTTTCTTG	GGTTTTTAAA	ATGTGAATCT	GCAATGATCA	900
TAATAATTAA	AATGTGAATG	TCAACAATAA	AAAGCAAGAC	TATGAAAGGC	TCAGATTTC	960
TGCAGTTTAA	AATGGTGTCT	GAGGTTGTAC	TATTTTGGCC	AAGTCTGTAG	AAAGCTGTCA	1020
TTTGATGTGA	TTATGTAGT	TCATCCAGCC	CTTGGGCATT	GTTATACACC	AGTAAAGAAG	1080
GCTGTACTCA	AGAGGAGGAG	CTGACACATT	TCACTTGGCT	GCGTCTTAAT	AAACATGAAT	1140
GCAAGCATTG	GC					1152

Seq ID NO: C147 DNA Sequence
 Nucleic Acid Accession #: NM_024021.2
 Coding sequence: 144..806

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ATTGAGGCAC	CTTTTCTGCT	GCCATGACAA	CCATGCAAGG	AATGGAACAG	GCCATGCCAG	180
GGGCTGGCCC	TGGTGTGCC	CAGCTGGGAA	ACATGGCTGT	CATACATTCA	CATCTGTGGA	240
AAGGATTGCA	AGAGAAGTTC	TTGAAGGGAG	AAACCAAGT	CCTTGGGGTT	GTGAGATTC	300
TGACTGGCCT	GATGAGCCTT	AGCATGGGAA	TAACAATGAT	GTGATGGCA	TCTAATACTT	360
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GTACCCCTGG	TGGGGTTGTG	TTAATTCGTC	CATCACATTC	TCACATGGCA	GAACAGCAT	780
CTCCACACCC	ACTTAATGAG	GTTTGAAGCC	ACCAAAAGAT	CAACAGACAA	ATGCTCCAGA	840
AATCTATGCT	GACTGTGACA	CAAGAGCCTC	ACATGAGAAA	TTACCAATAT	CCAATCTGGA	900
TACTGATAGA	CTGTGTGATA	TTATTATTAT	ATGTAATCCA	ATTATGAATC	GTGTGTGTAT	960
AGAGAGATAA	TAAATTCAAA	ATTATGTTCT	CATTTTTTTC	CCTGGAACCT	AATAACTCAT	1020
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 Coding sequence: 92..1945

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TAATTTTCCA TAAGCTATT TGGTTTAGTG CAAAGTATAA AATTATATT GGGGGGGAAT 660
80 AAGATTATAT GGACTTCTT GCAAGCAACA AGCTATTTT TAAAAAACT ATTTAACATT 720
CTTTGTGTTA TATGTTTGT TCTCCTAAAT TGTGTAAATT GCATTATAAA ATAAGAAAAA 780
CATTAAATAG ACAAATATT 799

Seq ID NO: C157 DNA Sequence
Nucleic Acid Accession #: NM_013271.1

Coding sequence: 27..809

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1      11      21      31      41      51
5      |      |      |      |      |
      TCCGGAGCCA GGCTCGCTGG GGCAGCATGS CGGGTGGCC GCTGCTCTGG GGGCGCGGG 60
      CCGGGGGGCT CGGCCTTTTG GTGCTGCTGC TGCTCGGCTT GTTTCGGCCG CCCCCCGCGC 120
      TCTGCGCGCG GCGGTAAAG GAACCCCGCG GCCTAAGCGC AGCGTCTCGC CCCTTGGCTG 180
      AGACTGGCGC TCCTGGCGCG TTCCGGCGGT CAGTGCCCGC AGGTGAGCGC GCGGGGGCGG 240
      TGCAGGAGCT GGC CGCGGGCG CTGGCGCATC TGCTGGAGGC CGAACGTCAG GAGCGGGCGC 300
      GGGCCGAGGC GCAGGAGGCT GAGGATCAGC AGGCGCGCGT CCTGGCGCAG CTGCTGGCGG 360
      TCTGGGGCGC CCGCGCAAC TCTGATCCGG CTCTGGGCGT GGAACGACGAC CCGGACGCGC 420
      CTGCAGCGCA GCTCGCTCGC GCTCTGCTCC GCGCCCGCCT TGACCTTGCC GCCTAGCAG 480
      CCCAGCTTGT CCGCGCGCCC GTCCCGCGCG CGGCGCTCCG ACCCGGCCCC CCGTCTACG 540
      ACGACGGCCC CGCGGGCCCC GATGCTGAGG AGGCAGGCGA CGAGACACCC GACGTGGACC 600
      CGAGACTGTG GAGGTACTTG CTGGGACGGA TTCTTGGGG AAGCGCGGAC TCGAGGGGG 660
      TGGCAGCCCC GCGCGCGCTC CGCGGTGCGC CGAACCGA TGTTGGGCTCT GAGCTGCCCC 720
      CTGAGGGCGT GCTGGGGGGC CTGCTGCGTG TGAACGCTT AGAGACCCCG GCGCCCGAGG 780
      TGCTGCACTG CGGCTCTTG CCACCTGAG CACTGCCCGG ATCCCGTGCA CCTGGGACC 840
      CAGAAGTGCC CCGGCTATCC CGCCACGAG ACTTCTCCCC GCGACGACGT CCAGAGCAAC 900
      TTACCCCGGC CAGCCAGCCC TCTCACCGA GGATCCCTAC CCGCTGGCCC ACAATAACAT 960
      GATCTGAGC
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Seq ID NO: C158 DNA Sequence

Nucleic Acid Accession #: NM_002245.2

Coding sequence: 183..1193

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1      11      21      31      41      51
30     |      |      |      |      |
      GGGCAGGAAG ACGGCGCTGC CCGGAGGAGC GGGGCGGGCG GCGCGCGCGG GGAGCGGGCG 60
      GCGGGCGGGA GCCAGGCCCG GCGGGGGGCG GGGGCGGGCG GGCCAGAAGA GCGGGCGGCG 120
      CGCGCTCCGG CGGCTCTGCG CGGTTGGCCT TGGCTTTGGC TTGTCGGCGC GCGGTGGAGA 180
      AGATGCTGGT GTCCCTGGCG GGCAGCTCGT GCGTGGCGCT GGTGGAGCGG CACCGCTCGG 240
      CCTGGTGCTT CGGCTTCCTG GTGCTGGGCT ACTTGCTCTA CCTGCTCTTC GGCGCAGTGG 300
      TCTTCTCTCT GGTGAGCTG CCTATGAGG ACCTGCTGCG CCAGGAGCTG CGCAGCTGGA 360
      AGCGACGCTT CTGAGGAGG CACGAGTGCC TGTCTGAGCA CGAGCTGGAG CAGTTCCTGG 420
      GCGGGTGCTT GAGGCGCAGC AACTACGCGC TGTGCGTGCT CAGCAACGCC TCGGGCAACT 480
      GGAACCTGGG CTTCACTCCG GCGCTCTTCT TCGCCAGCAC CGTCTCTTCC ACCACAGGTT 540
      ATGCCACAC CCGTCCCTTG TCAGATGGAG GTAAGGCCTT CTGCATCATC TACTCCGTCA 600
      TTGGCATTCC CTTACCCCTC CTGTTCCTGA CGGCTGTGGT CCAGCGCATC ACCGTGCACG 660
      TCACCCGAG GCGGCTCCTC TACTTCCACA TCGCTGGGG CTCTCCAG CAGGTGGTGG 720
      CCATGTCCTA TGCGGTGCTC CTGGGTTTGG TCACTGTGTC CTGCTTCTTC TTCTATCCCG 780
      CGGCTGCTCT CTCAGTCTG GAGGATGACT GGAACCTCTT GGAATCCTTT TATTTTGT 840
      TTATTTCCCT GAGCACCATT GGCCTGGGG ATTATGTGCC TGGGGAAGGC TACAATCAAA 900
      AATTGAGAGA GCTCTATAAG ATTGGGATCA CGTGTACCT GCTACTTGGC CTATTATGCA 960
      TGTGTGAGT TCTGGAAACC TTCTGTGAAC TCCATGAGCT GAAAAAATTC AGAAAAATGT 1020
      TCTATGTGAA GAGGACCAAG GACGAGGATC AGGTGCACAT CATAGAGCAT GACCAACTGT 1080
      CCTCTGCTCT GATCACAGC CAGGCAGCTG GCATGAAAGA GGACCAAGAG CAAATGAGC 1140
      CTTTGTGGGC CACCCAGTCA TCTGCCCTGG TGGATGGCCC TGCAAAACCTAT TGAGCGTAGG 1200
      ATTGTGTGCA TTATGCTAGA GCACCCAGGT CAGGGTGCAA GGAAGAGGCT TAAGTATGTT 1260
      CATTTTATC AGAATGCAAA AGCGAAAAAT ATGTCACTTT AAGAAATAGC TACTGTTTGC 1320
      AATGCTTAT TAAAAACAA CAAAAAAGA CACATGGAAC AAGAAGCTG TGACCCCGAGC 1380
      AGGATGCTA ATATGTGAGG AATGAGATG TCCACCTAAA ATTCAATATG GACAAAATTA 1440
      TCTCGACCTT ACATAGGAGG AGAATACTTG AAGCAGTATG CTGCTGTGGT TAGAAGCAGA 1500
      TTTTATACTT TTAACCTGAA ACTTTGGGGT TTGCATTAG ATCATTTAGC TGATGCTTAA 1560
      ATAGCAAAAT TTATATTAG AAGCAAAAAA AAAAAAGCAT GAGATGTGTT TTATAATAG 1620
      GTTATGTGT ACTGTTTTC ATGTACCCAC CCAAAATGAT TATTTTGGGA GAATCTAAGT 1680
      CAAACTCACT ATTATAATG CATAGGTAAC CATTAACTAT GTACATATAA AGTATAAATA 1740
      TGTTTATAT CTGTACATAT GGTTTAGGTC ACCAGATCCT AGTGTAGTTC TGAAACTAAG 1800
      ACTATAGATA TTTTGTTCCT TTTGATTTCT CTTTATACTA AAGAATCCAG AGTTGCTACA 1860
      ATAAAAAAG GGAATAATAA AACTTGAGAG TGAATAACCA T 1901
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Seq ID NO: C159 DNA Sequence

Nucleic Acid Accession #: NM_005472.1

Coding sequence: 93..404

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1      11      21      31      41      51
65     |      |      |      |      |
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      CCGAGTCTTC CCCCACCTCA ATCCCTGTTG CTATGGAGAC TACCAATGGA ACGGAGACCT 120
      GGTATGAGAG CCTGCTAGCC GTGCTGAAGG CTCTAAATGC CACTCTTCAC AGCAATTGCG 180
      TCTGCGGCGC AGGCGCCAGG CTGGGGCCAG ACAACCAAGC TGAAGAGAGG CCGGCCAGCG 240
      TACCTGGCGC TGTGACAAAC TCCTACATGT ACATTCTCTT TGTCTATGTT CTATTTGCTG 300
      TAACGTGGG CAGCCTCATC CTGGGATACA CCGCTCCCGC CAAAGTGGAC AAGCGTAGTG 360
      ACCCCTATCA TGTGTATATC AAGAACCGTG TGTCTATGAT CTAACACGAG AGGGCTGGGA 420
      CGGTGGAAGA CCAAGACACC TGGGGATTGC GTCTGGGGCC TCCAGAACTC TGCTGTGGAC 480
      TGATCAGGT CT
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Seq ID NO: C160 DNA Sequence

Nucleic Acid Accession #: NM_005245.1

Coding sequence: 187..13959

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1      11      21      31      41      51
80     |      |      |      |      |
      CTGGGCGGCC GGGCGCGGGG AGAGGGCGCG GGAGCGGCTC GTGCGGCAGG TACCATGCGG 60
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	ACGCGCGAGC	CCGCGGAGGC	CCCAGCAGGC	CCGTCCCTGC	TCGGGGGGCGC	GCTGAGACGG	120
	CGGATGAGCT	CCACGAGAGC	GCCGTGCGCA	CTTCGGGGCA	ACTTTGCGAT	TCCCGACAGT	180
	TAAGCAATGG	GGAGACATTT	GGCTTTGCTC	CTGCTTCTGC	TCCTTCTCTT	CCAACTTTT	240
5	GGAGACAGTG	ATGGCAGCCA	ACGACTTGAA	CAGACTCCTC	TGCAGTTTAC	ACACCTCGAG	300
	TACCACTGTA	CCGTGACGGA	GAACCTTGCA	GCTAAGACTT	ATGTGGGGCA	TCCTGTCAAG	360
	ATGGGTGTTT	ACATTACACA	TCCAGCGTGG	GAAGTAAGGT	ACAAAAATGT	TTCCGAGAGC	420
	AGTGAAACCG	TGTTCAAAGC	TGAAGAGTAC	ATTCTCGGAG	ACTTTTGCTT	TCTAAGAATA	480
	AGGACCAAAG	GAGGAAATAC	AGCTATTCTT	AATAGAGAAG	TGAAGGATCA	CTACACATTG	540
10	ATAGTGAAG	CACTTGAAAA	AAATACTAAT	GTGGAGGCGC	GAACAAAGGT	CAGGGTGCAG	600
	GTGCTGTAAG	CAACTGACTT	GAGACCGTTA	TTCTCACCCA	CCTCATACAG	CGTTTCTTTA	660
	CCTGAAAAAC	CAGCTATAAG	GACCAAGTATC	GCAAGAGTCA	GCGCCACGGA	TGCAGACATA	720
	GGAAACAAAC	GGAATTTTTA	CTACAGTTT	AAAGATCGAA	CAGATATGTT	TGCTATTAC	780
	CCAACCAAGT	GTGTGATAGT	GTTAACTGGT	AGACTTGATT	ACCTAGAGAC	CAAGCTCTAT	840
	GAGATGGAAA	TCCTCGCTGC	GGACCGTGGC	ATGAAGTTGT	ATGGGAGCAG	TGGCATCAGC	900
15	AGCATGGCGA	CAACTCCGGT	GCACATCGAA	CAGGCCAATG	AATGTGCTCC	GGTGATAACA	960
	GCAGTGACAT	TGTCACCATC	AGAAGCTGGC	AGGGACCCAG	CATATGCAAT	TGTGACAGTG	1020
	GATGATCTCG	TACAGGGTGC	CAATGGTGAC	ATAGCATCTT	TAAGCATCGT	GGCAGGTGAC	1080
	CTTCTCCAGC	AGTTTAGAAC	AGTGAGGTCC	TTTCCAGGGA	GTAAGGAGTA	TAAAGTCAAA	1140
	GCCATCGGGT	ACATTGATTG	GGACAGTCAT	CCTTTCGGCT	ACAACTCTAC	ACTACAGGCT	1200
20	AAAGATAAAG	CAACTCCGGC	CCAGTTCTCT	TCTGTAAAG	TCAATCAGTG	GACTTCTCCA	1260
	CAGTTCAAAG	CCGGGCCAGT	CAAGTTTGAA	AAGGATGTTT	ACAGAGCAGA	AATAAGTGAA	1320
	TTTGCTCCTC	CCAAACACCC	TGTGTCATG	GTAAGGCCA	TTCTGCTT	TTCCCATTTG	1380
	AGGTATGTTT	TTAAAGGAC	ACCTGGAAAA	GCTAAATTCA	GTTTAAATTA	CAACACTGGT	1440
25	CTCATTTCTA	TTTATAGAAC	AGTTAAAGAA	CAGCAGGCGC	CCCATTTTGA	ACTTGAAGTA	1500
	ACAACAAGTG	ACAGAAAGCG	GTCCACCAAG	GTCTGGTGA	AAGTCTTAGG	TGCAATATGC	1560
	AATCCCCCTG	AATTTACCCA	GACACGCTAC	AAAGCTGCTT	TTGATGAGAA	CGTGCCCAT	1620
	GGTACTACTC	TACGAGCCT	GAGTGCCGTA	GACCTGATG	AGGGTGAGAA	TGGGTACGTG	1680
	ACATACAGTA	TGCAAAATTT	AAATCATGTG	CCGTTTCCGA	TTGACCATTT	CAGTGGTGCC	1740
30	GTGAGTAGCT	CAGAAAACTT	GGACTACGAA	CTGATGCTTC	GGGTTTATAC	TCTGAGGATT	1800
	CGTGTGACTG	ACTGGGGCTT	GCCGTACCGC	CGGGAAGTCG	AAGTCTTAGG	TACAAATAGC	1860
	CTCAATAACT	TGAATGACAA	CACACCTTTG	TTTGAGAAAA	TAAATTTGTA	AGGGACAAAT	1920
	CCCAAGATC	TAGGCGTGGG	AGAGCAATA	ACCACTGTTT	CTGCTATTGA	TGCAGATGAA	1980
	CTTCAGTTGG	TACAGTATCA	GATTGAAGCT	GGAAATGAAC	TGGATTGTTT	TAGTTTAAAC	2040
35	CCCAACTCGG	GGGTATTGTC	ATTAAAGCGA	TCGTAATGG	ATGGCTTAGG	TGCAAGGGTG	2100
	TCCTTCCACA	CTCTGAGAA	CACAGCTACA	GATGGAGAAA	ATTTTGCCAC	ACCAATTATAT	2160
	ATCAACATAA	CAGTGGCTGC	CAGTCACAG	CTGGTAAACT	TGCAGTGTGA	AGAGACTGGT	2220
	GTGTCCAAAA	TGCTGGCAGA	GAAGCTCCTG	CAGGCAATA	AATTACACAA	CCAGGGAGAG	2280
	GTGGAGGATA	TTTTCTTCGA	TTCTCCTCT	GTCAATGCTC	ACATACCGCA	GTTTAGAAGC	2340
40	ACTCTTCCGA	CTGTATTCA	GTTAAAGGAA	AACAGCCTG	TGGGTTCAG	TGTAATTTTC	2400
	ATGAATCCA	CTGACCTTGA	CATGGCTTC	AATGGAAAA	TGGTCTATGC	TGTTCTGGA	2460
	GGAAATGAGG	ATAGTTGCTT	CATGATTGAT	ATGGAAACAG	GAATGCTGAA	AATTTTATCT	2520
	CCCTTTGAC	GTGAACACAC	AGACAAATAC	ACCTGAATA	TTACCTGCTA	TGACCTTGGG	2580
	ATACCCACAG	AGGCTGCTG	CGCTCTTCTA	CATGTCGTGG	TTGTCGATGC	CAATGATAAT	2640
45	CCACCGAGT	TTTTACAGGA	GAGCTATTTT	GTGGAAGTGA	GTGAAGACAA	GGAGGTACAT	2700
	AGTGAAATCA	TCCAGGTTGA	AGCCACAGAT	AAAGACCTGG	GGCCCAACCG	ACACGTGACG	2760
	TACTCAATTC	TTACAGACAC	AGACACATTT	TCAATTGACA	GCGTGACGGG	TGTTGTTAAC	2820
	ATCGCACCGC	CTCTGATCG	AGAGCTGCAG	CATGAGCACT	CCTTAAAGAT	TGAGGCCAGG	2880
	GACCAAGCCA	GAGAAGAGCC	TCAGCTGTTC	TCCACTGTGC	TTGTGAAGAT	ATCACTAGAA	2940
50	GATGTTAATG	ACAACCCACC	TACATTATTT	CCACTTAATT	ATCGTGTAAG	AGTCCGAGAG	3000
	GATCTTCCAG	AAGGAACCGT	CATCATGTGG	TTAGAAGCCC	ACGATCCTGA	TTTAGGTCAG	3060
	TCTGTGTCAG	TGAGATACAG	CCTTCTGGAC	CAOAGAGAG	GAAACTTCGA	TGTGGATAAA	3120
	CTCAGTGGAG	CAGTTAGGAT	CGTCCAGCAG	TTGGACTTTG	AGAAGAAGCA	AGTGATAAAT	3180
	CTCACTGTGA	GGGCCAAAGA	CAAGGGAAG	CCAGTTTCTC	TGCTTCTTAC	TTGCTATGTT	3240
55	GAAGTTGAGG	TGTTTATGTT	GAATGAGAAC	CTGCACCCAC	CCGTGTTTTC	CAGCTTTTGT	3300
	GAAAAGGGGA	CAGTGAAAGA	AGATGCACCT	GTTGGTTTCA	TGTAATGATC	GGTGTGCGCT	3360
	CATGATGAGG	ACGCCGGAAG	AGATGGGGAG	ATCOGATACT	CCATTAGAGA	TGGCTCTGGC	3420
	GTGAGTGTG	TCAAAATAGG	TGAAGAGACA	GGTGTCTAG	AGACGTCAGA	TCGACTGGAC	3480
	CGTGAATCGA	CCTCCCATTA	TTGGCTAACA	GCTTTTGCAA	CCGATCAGGG	TGTCGTGCCT	3540
60	CTTTCATCGT	TCATAGAGAT	CTACATAGAG	GTGAGGATG	TCAATGACAA	TGCACACAG	3600
	ACATCAGAGC	CTGTTTATTA	CCCAGAAATC	ATGGAAAAAT	CTCCTAAGAA	TGTATCTGTG	3660
	GTCCAGATCG	AGGCATTGTA	TCCAGATTG	AGCTCTAATG	ACAAGCTCAT	GTACAAAATT	3720
	ACAAAGTGAA	ATCCACAAGG	ATTCTTTTCA	ATACATCTTA	AAACAGGTCT	CATCACAATC	3780
	ACGTCAAGGA	AGCTAGACCG	AGAACAGCAA	GATGAACACA	TATTAGAGGT	TACTGTGACA	3840
65	GACATGGGTA	GTCCCCCCAA	ATCAACCAAT	GCAAGAGTCA	TTGTGAAAAAT	CCTTGATGAA	3900
	AATGACAACA	AACCTCAGTT	TCTGCAAAAG	TTCTACAAAA	TCAGACTCCC	TGAGCGGGAA	3960
	AAGCCAGACC	GAGAAAGAAA	TGCCAGACCG	GAGCGCTCT	ATCGCGTCA	AGCCACCGAC	4020
	AAGGATGAGG	GCCCCAATGC	AGAAATCTCC	TACAGCATCG	AAGACGGGAA	TGAGCATGGC	4080
	AAATTTTCTA	TGCAACCGAA	AACGTGAGTG	GTTTGTGCTA	AGAGGTTTTC	AGCAGCTGGA	4140
70	GAATATGATA	TTCTTTCAAT	TAAGGCAGTT	GACAAATGGT	GCCCTCAAAA	GTCACTCAAC	4200
	ACCAGACTCC	ATATTGAAATG	GATCTCCAAG	CCCAACAGT	CCCTGGAGCC	CATTTCATTT	4260
	GAAGAATCAT	TTTTTACCTT	TACTGTGATG	GAAAGTGACC	CCGTGCTCTA	CATGATTGGA	4320
	GTAATATCTG	TGGAGCCTCC	CTTTGGTTTG	ACATCACTGG	TGGCAACTAC	4380	
	GACAGTCACT	TCGATGTGGA	CAAGGGAATC	GGAACCATCA	TTGTTGCCAA	ACCTCTTGAT	4440
75	GCAGAACAGA	AGTCAAACTA	CAACCTCACA	GTGAGGCTCA	CAGATGGAAC	CACCACTATC	4500
	CTCACTCAGG	TATTCACTAA	AGTAATAGAC	ACAAATGACC	ATCGTCTCTA	GTTTTCTACA	4560
	TCAAAGTATG	AAGTTGTTAT	TCCTGAAGAT	ACAGGCGCAG	AAACAGAAAT	TTTGCAAAATC	4620
	AGTGCTGTGG	TCAGGATGGA	GAAAAACAAA	CTAATCTACA	CTCTGCAGAG	CAGTAGAGAT	4680
	CCACTGAGTC	TCAAGAAATT	TGCTCTTGAT	CTGCAACCG	GCTCTCTCTA	TACTTCTGAG	4740
80	AAACTGATC	ATGAAGCTGT	TTCAACAGCA	CACCTCAAGG	TCAATGTTACG	AGATCAAGAT	4800
	GTGCGCTGTA	AACGCAACTT	TGCAAGGATT	GTGGTCAATG	TCAGCGACAC	GAATGACCCAC	4860
	GCCCGCTGGT	TCACCGCTTC	CTCCTACAAA	GGCGGGGTTT	ATGAATCGGC	AGCCGTTGGC	4920
	TCAGTGTGTG	TGAGGCTGAC	GGCTCTGGAC	AAGGACAAAG	GGAAAAATGC	TGAAGTGCTG	4980
	TACTCGATCG	AGTCAGGAAA	TATTGGAAAT	ATTGGAAATT	CTTTTATGAT	TGATCCTGTC	5040
	TTGGGCTCTA	TTAAACTGTC	CAAAGAATTA	GATCGAAGTA	ACCAAGCGGA	GTATGATTTA	5100

	ATGGTAAAG	CTACAGATAA	GGGCAGTCCA	CCAATGAGTG	AAATAACTTC	TGTGCGTATC	5160
	TTTGTACAAA	TTGCTACAAA	CGCCTCTCCG	AAGTTTACAT	CAAAAGAAATA	TTCTGTGGAA	5220
	CTTAGTGAAA	CTGTACAGCAT	TGGGAGTTTC	GTGGGATGG	TTACAGCCCA	TAGTCAATCA	5280
5	TCAGTGGTGT	ATGAAATAAA	AGATGGAAAT	ACAGGTGATG	CTTTTGATAT	TAATCCACAT	5340
	TCTGGAACTA	TCATCACTCA	GAAAGCCCTG	GACTTTGAAA	CTTTGCCCAT	TTACACATTG	5400
	ATAATACAAG	GAACATAACAT	GGCTGGTTTG	TCCACTAATA	CAACGGTTCT	AGTTCACCTG	5460
	CAGGATGAGA	ATGACRAOCG	GCCAGTTTTT	ATGCAGGCAG	AATATACAGG	ACTCATTAGT	5520
	GAATCAGCCT	CAATTAACAG	CGTGGTCCTA	ACAGACAGGA	ATGTCCCACT	GGTGATTGGA	5580
10	GCAGCTGATG	CTGATAAAGA	CTCAAAATGCT	TTGCTTGTAT	ATCACATTGT	TGAACCATCT	5640
	GTACACAACT	ATTTTGTCTAT	TGATTCTAGC	ACTGGTGCTA	TTCATACAGT	ACTAAGTCTG	5700
	GACTATGAAG	AAACAAGTAT	TTTTCACTTT	ACCGTCCAAG	TGCATGACAT	GGGAACCCCA	5760
	CGTTTATTG	CTTGATATGC	AGCGAATGTA	ACAGTACATG	TAATTGACAT	TAATGACTGC	5820
	CCCCCTGTGT	TTGCCAAGCC	ATTATATGAA	GCATCTCTTT	TGTTACCAAC	ATACAAAGGA	5880
15	GTAAAGGTCA	TCACAGTAAA	TGCTACAGAT	GCTGATTCAA	GTGCATTCTC	ACAGTTGATT	5940
	TACTCCAACT	CCGAAGGCAA	CATCGGGGAG	AAGTTTCTA	TGGACTACAA	GACTGGTGCT	6000
	CTCACTGTCC	AAAACAACAC	TCAGTTAAGA	AGCGCTACG	AGCTAACCGT	TAGAGCTTCC	6060
	GATGGCAAGT	TTGCCGCGCT	TACCTCTGTC	AAAATTAATG	TGAAAGAAAG	CAAGGAAAGT	6120
	CACCTAAAGT	TTACCCAGGA	TGTCTACTCT	GCCTAGTGA	AAGAGAATTTC	CACCGAGGCC	6180
20	GAAACATTAG	CTGTCAATTAC	TGCTATTGGG	AGTCCAATCA	ATGAGCCTTT	GTTTTATCAC	6240
	ATCCTCAACC	CAGATCGCAG	ATTTAAATAA	AGCGCACTT	CAGGGGTCTT	GTCAACCACT	6300
	GGCAGCGCCT	TCGATCGTGA	GCAGCAGGAG	GCCTTTGATG	TGGTTGTAGA	AGTGATAGAG	6360
	GAACATGAAT	CTTCTGAGT	GGCCACGTT	GTCTGAAAGG	TCAATTGTGA	AGACCAAAAT	6420
	GATAATGCGC	CGGTGTTTGT	CAACCTTCCC	TACTACGCCG	TGTTAAAGT	GGACACTGAG	6480
25	GTGGGCCATG	TCATTCTGCTA	TGTCAGTGCT	GTAGACAGAG	ACAGTGGCAG	AAACGGGGAA	6540
	GTGCATTACT	CCGTAAGGAA	ACATCATGAA	CACTTTCAAA	TTGACCCCTT	GGGTGAAATT	6600
	TCACCTAGAAA	AGCAATTTGA	GCCTGACACC	TTAAATAAAG	AATATCTTGT	TACAGTGGTT	6660
	GCATAAGATG	GGGGAAGCCC	GGCCTTTTCA	GGGAAGTTA	TGTTCCGAT	CACGTGTCATG	6720
	AATAAGCCCA	TGCCGTGTTT	TGAAAAACCT	TTCTACAGTG	CAGAGATTGC	AGAGAGCATC	6780
30	CAGGTGCACA	GGCCTGTGGT	CCACGTGCAG	GCTAACAGCC	CGGAAGGCCCT	GAAAGTGTTT	6840
	TACAGCATCA	CAGACGGAGA	CCCTTTACAG	CAGTTCACTA	TTAACTTCAA	TACTGGAGTT	6900
	ATCAATGTCA	TAGCTCTCTT	GGACTTTGAG	GGCCACCCGG	CATATAAGCT	GAGCATAACG	6960
	GCACCTAGAT	CCTTGACCGG	CGCTCATGCT	GAAGTATTG	TGGACATCAT	AGTAGACGAC	7020
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35	TCTGTAAATG	GAACGTCTGT	TGTTCAAGTT	AGAGCCACCG	ATTCTGATTC	AGAACCAAAAT	7140
	AGAGGAATCT	CATACACAGAT	GTTTGGGAAT	CACAGCAAGA	GTCAATGATCA	TTTTCATGTA	7200
	GACAGCAGCA	CTGGCCTCAT	CTCACTACTC	AGAACCCTGG	ATTACGAGCA	GTCCCGGCAG	7260
	CACACGATTT	TTGTGAGGGC	AGTTGATGGT	GGTATGCCCA	CGCTGAGCAG	TGATGTGATT	7320
	GTACCGGTGG	ACGTTACCGA	CCTCAATGGT	AATCCACCAC	TCTTTGAACA	ACAGATTAT	7380
40	GAAGCCAGAA	TTAGCGAGCA	CGCCCTCAT	GGGCATTTCG	TGACCTGTGT	AAAAGCCTAT	7440
	GATGCAGACA	GTTAGCAGAT	AGACAAAGTT	CAGTATTCCA	TTCTGTCTGG	CAATGATCAT	7500
	AAACATTTTG	TCATTGACAG	TGCAACAGGG	ATTATCAACC	TCTCAAACTC	GCACCGGCAC	7560
	GGCCTGAAGT	CATTTTACAG	TCTTAACTCG	TCAGTGTCTG	ATGGAGTTTT	TAGAAGTTCC	7620
	ACCCAGGTTC	ATGTAAGTGT	AATTGGAGGC	AATTGTCACA	GTCTCTGCTT	CCTTCAGAAC	7680
45	GAATATGAAG	TGGAAGTATG	TGAAAACGCT	CCCTACATA	CCCTGGTGAT	GGAGGTGAAA	7740
	ACTACGGATG	GGGATTTCTGG	TATTTATGGT	CAGTTACTTT	ACCATATTTT	AAATGACTTT	7800
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	CGAGAAACCC	CGGCGGAGAA	AGTGATCTCA	GTCCGTTTAA	TGGCTAAGGA	TGCTGGAGGA	7920
	AAAGTTGCTT	TCTGCACCGT	GAATGTCAAT	CTTACAGATG	ACAATGACAA	TGCACCCAAA	7980
50	TTTTCAGCAA	CCAAATACGA	AGTGAATATC	GGGTCCAGTG	CTGCTAAAGG	GACTTCAAGT	8040
	GTAAAGTCTG	CGATGAGGCG	CGATGAGGCG	TCCAATGCCG	ACATCAACCTA	TGCCAATTGA	8100
	GCAGACTCTG	AAAGGTGAAA	AGAGAATTTG	GAAATTAACA	AACTGTCCGG	CGTAATCACT	8160
	ACAAAGGAGA	GGCTCATTTG	CTTGGAAAT	GAATCTCTCA	CTTTCTTTGT	TAGAGCTGTG	8220
	GATAATGGGT	CTCCATCAAA	AGAATCTGTT	GTTCTGTGCT	ATGTTAAAT	CCTTCCACCG	8280
55	GAAATGCAAG	TTCCAAATTT	TTCAAGAACT	TTCTATACCT	TTACAGTGTG	AGAGGACGTT	8340
	CCTGTTGGAA	CAGAGATAGA	TCTCATCCGA	GCAGAACATA	GTGGGACTGT	TCTTTACAGC	8400
	CTGGTCAAG	GGAAATCTCC	AGAAAGCAAT	AGGGATGAGT	CCTTTGTGAT	TGACAGACAG	8460
	AGCGGAGAC	TGAAGTTGGA	GAAGAGTCTT	GATCATGAGA	CAACTAAGTG	GTATCAGTTT	8520
	TCCATACTGG	CCAGGTGAC	TCAAGATGAC	CATGAGATGG	TGGCTTCTGT	AGATGTTAGT	8580
60	ATCCAAGTGA	AAGATGCAAA	TGACACAGC	CGGTCCTTTG	AATCTAGTCC	ATATGAGGCA	8640
	TTCAATTTTG	AAAACCTGCC	AGGGGGAGT	AGAGTAATTC	AGATCAGGCG	ATCTGATGCT	8700
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	ATTGAATCCT	TTGCCATTAA	CATGGAAACA	GGCTGGATTA	CAACTTTAAA	GGAACTTGAC	8820
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Seq ID NO: C163 DNA Sequence
Nucleic Acid Accession #: NM_000958
Coding sequence: 389..1855

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Nucleic Acid Accession #: NM_002659.1
Coding sequence: 427..1434

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Seq ID NO: C165 DNA Sequence
Nucleic Acid Accession #: AK027843.1
Coding sequence: 193..1731

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 Nucleic Acid Accession #: NM_000574.1
 Coding sequence: 66..1211

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Seq ID NO: C168 DNA Sequence
 Nucleic Acid Accession #: NM_003667.2
 Coding sequence: 49..2772

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30 Seq ID NO: C169 DNA Sequence
 Nucleic Acid Accession #: NM_003506.1
 Coding sequence: 259..2379

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 ATGGCCTACA ACATGACGTT TTTCCCTAAT CTGATGGGTC ATTATGACCA GAGTATTTGC 420
 GGGGTGGAAA TGGAGCAATT TCTTCTCTC GCAAATCTGG AATGTTCAAC AAACATTGAA 480
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 GTAACTTTTG ATCCACACAC AGAATTCTCT GGTCTCAGA AGAAAAACA ACAAGTCCAA 720
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5 TGTGATTTTT ATAGTCTCGT TTTAGGAATT TCACAGATCT AAATTATGTA ACTGAAATAA 3060
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Seq ID NO: C170 DNA Sequence
 Nucleic Acid Accession #: NM_000582
 Coding sequence: 88_990

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GGCATCACCT	GTGCCATACC	AGTTAAACAG	GCTGATTCTG	GAGTTTCTGA	GGAAAAAGCAG	180
CTTTACAACA	AATACCCAGA	TGCTGTGGCC	ACATGGCTAA	ACCGTGACCC	ATCTCAGAAG	240
CAGAATCTCC	TAGCCCCACA	GACCTTTCCA	AGTAAGTCCA	ACGAAAGCCA	TGACCCACATG	300
GATGATATGG	ATGATGAAGA	TGATGATGAC	CATGTGGACA	GCCAGGACTC	CATTGACTCG	360
AAAGACTCTG	ATGATGTAGA	TGACACTGAT	GATTCTCACC	AGTCTGATGA	GTCTCACCAT	420
TTCTGATGAAT	CTGATGAATC	GGTCACTGAT	TTTCCACGGG	ACCTGCCAGC	AACCGAAGTT	480
TTCACTCCAG	TGTGCCACAC	AGTAGACACA	TATGATGGCC	GAGGTGATAG	TGTGTTTAT	540
GGACTGAGGT	CAAAATCTAA	GAACTTTCCG	AGACCTGACA	TCCAGTACCC	TGATGTCTACA	600
GACGAGGACA	TCACCTCACA	CATGGAAAGC	GAGGAGTTGA	ATGGTGCATA	CAAGGCCATC	660
CCCGTTGCC	AGGACCTGAA	CGCGCTTCT	GATTGGGACA	GCCGTGGGAA	GGACAGTTAT	720
GAAACGAGTC	AGCTGGATGA	CCAGAGTGCT	GAAACCCACA	GCCACAAGCA	GTCCAGATTA	780
TATAAGCGGA	AAGCCAAATGA	TGAGAGCAAT	GAGCAITCCG	ATGTGATTGA	TAGTCAGGAA	840
CTTTCCAAAG	TCAGCCGTGA	ATTCACAGC	CATGAATTTT	ACAGCCATGA	AGATATGCTG	900
GTGTAGAGCC	CCAAAGTAA	GGAAGAAGAT	AAACACCTGA	AATTTGCTAT	TTCTCATGAA	960
TTAGATAGTG	CATCTTCTGA	GGTCAATTAA	AAGGAGAAAA	AATACAATTT	CTCACTTTGC	1020
ATTAGTCAAA	AAGAAAAAAT	GCTTTATAGC	AAAATGAAG	AGAACATGAA	ATGCTTCTTT	1080
CTCAGTTTAT	TGTTGAATG	TGTATCTATT	TGAGTCTGGA	AATAACTAAT	GTGTTTGATA	1140
ATTAGTTTAG	TTGTGGCTT	CATGGAAACT	CCCTGTAAAC	TAAAGCTTC	AGGGTTATGT	1200
CTATGTTTAT	TCTATAGAAG	AAATGCAAA	TATCACTGTA	TTTTAATATT	TGTTATTTCT	1260
TCATGATATG	AAATTTATGT	AGAAGCAAAC	AAAATACTTT	TACCCACTTA	AAAAGAGAAT	1320
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TATCTTTTGT	TGTTGTGAAT	AAATCTTTTA	TCTTGAATGT	AATAAGAAAT	TGGTGGTCTC	1440
AATGCTTAT	TTGTTTCCC	ACGGTTGTCC	AGCAATTAAT	AAAACATAAC	CTTTTCTACT	1500
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Seq ID NO: C171 DNA Sequence
 Nucleic Acid Accession #: NM_002821
 Coding sequence: 150..3362

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CCTCAGCTCC	TTTTCTGTAG	CCCGCCGCGA	TGGGAGCTGC	CGCGGGATCC	CCGGCCAGAC	180
CCCGCGGGT	GCCTCTGCTC	AGCGTCTGCG	TGCTCGCGCT	GCTGGGGGCT	ACCCAGACAG	240
CCATTGTCTT	CATCAAGCAG	CGGTCTCTCC	AGGATGCAC	GCAGGGGGCG	CGGGCGCTGC	300
TTGCTGTGTA	GTTTGAAGGT	CCGGGCCCGG	TACATGTGTA	CTGGCTGCTC	GATGGGGCCC	360
CTGTCCAGGA	CACCGAGCGG	CGTTTCGCC	AGGGCAGCAG	CCTGAGCTTT	GCAGCTGTGG	420
ACCGGCTGCA	GGACTCTGGC	ACCTTCCAGT	GTGTGGCTCG	GGATGATGTC	ACTGGAGAAG	480
AAGCCCGCAG	TGCCAAGGCC	TCCTTCAACA	TCAATGGAT	TGAGGCAGGT	CCTGTGCTCC	540
TGAAGCATCC	AGCCTCGGAA	GCTGAGATCC	AGCCACAGAC	CCAGGTTCACA	CTTCGTGCTC	600
ACATTGATGG	GCACCTCTCG	CCCACTTACC	AATGGTTCCG	AGATGGGACC	CCCTTTCTCG	660
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GCAGCCAGAA	CTTCACTTGT	AGCATGTGCT	ATGAAAGCTT	TGCCAGGGTG	GTGCTGGCAC	840
CCAGGAGCT	GGTAGTAGCG	AGGTATGAGG	AGGCCATGTT	CCATTGCCAG	TTCTCAGCCC	900
AGCCACCCCG	GAGCCTGCTG	TGGCTCTTTG	AGGATGAGAC	TCCCATCACT	AACCGCAGTC	960
GCCGCCACCA	CCTCCGACAG	GCCACAGTGT	TTGCCAAGCG	GTCTCTGCTG	CTGACCCAGG	1020
TCCGGCCAGC	CAATGCAAGG	ATCTACCGCT	GCATTGGCCA	GGGCGCAGAG	GGCCCAACCA	1080
TCATCTCTGA	AGCCACACTT	CACCTAGCAG	AGATTGAAGA	CATGCCGCTA	TTTGAGCCAC	1140
GGGTGTTTAC	AGCTGGCAGC	GAGGAGCGTG	TGACCTGCTC	TCCCCCAAG	GGTCTGCCAG	1200
AGCCAGCGGT	GTGGTGGGAG	CACGCGGGAG	TCCGGCTGCC	CACCCATGGC	AGGGTCTACC	1260
AGAAGGGCCA	CGAGCTGGTG	TTGGCCAATA	TTGCTGAAG	TGATGCTGGT	GTCTACACCT	1320
GCCAGCGGCG	CAACTGGGCT	GGTCAGCGGA	GACAGGATGT	CAACATCACT	GTGGCCACTG	1380
TGCCCTCTGT	GCTGAAGAAG	CCCCAAGACA	GCCAGCTGGA	GGAGGGCAAA	CCCGGCTACT	1440
TGGATTGCTT	GACCCAGGCC	ACACCAAAAC	CTACAGTTGT	CTGGTACAGA	AACCAATGTC	1500
TCATCTCAGA	GACTCAAGCG	TTGAGGTCTT	TCAAGAATGG	GACCTTGCGC	ATCAACAGCG	1560
TGAGGGGTGA	TGATGGGACA	TGGTACCGTT	GTATGAGCAG	CACCCAGGCC	GGCAGCATCG	1620
AGGCGCAAGC	CCGTGTCCAA	GTGCTGGAAA	AGCTCAAGTT	CACACCACCA	CCCCAGCCAC	1680
AGCAGTGCAT	GGAGTTTGAC	AAGGAGGCCA	CGGTGCCCTG	TTGAGCCACA	GGCCGAGAGA	1740
AGCCCACTAT	TAAAGTGGAA	CGGGCAGATG	GGAGCAGCCT	CCAGAGATGG	GTGACAGACA	1800
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TTATCACCTT	CAAAAGTGAA	CCAGAGCGTA	CGACTGTGTA	CCAGGGCCAC	ACAGCCCTAC	1980
TGCAGTGGGA	GGCCAGGGGG	GACCCCAAGC	CGCTGATTCA	GTGGAAGGCG	AAGGACCGCA	2040
TGCTTGAGCC	CACCAAGCTG	GGACCCAGGA	TGCACATCTT	CCAGAATGGC	TCCCTGTGTA	2100
TCCATGAAGT	GGCCCTCTAG	GACTCAGGCC	GCTACACCTG	CATTGCAAGC	AACAGCTGCA	2160
ACATCTAGAA	CACGAGGCCG	CCCTCTATG	TGTTGGACAA	GCCTGTGCGG	GAGGAGTCGG	2220
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	GAGGGCCTTT	GCAGAACGGG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
	GCTTGGGCTC	CGCCCCCGCG	GCCACCAACA	AACGCCACAG	CACAAGTGAT	AAGATGCACI	2520
	TCCCACGGTC	TAGCCTGCGG	CCCATCACCA	CGCTGGGGAA	GAGTGAGTTT	GGGGAGGTGT	2580
	TCCTGCGAAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAGA	GACCCTGGTA	CTTGTGAAGA	2640
	GCCTGCAGAC	GAAGGATGAG	CAGCAGCAGC	TGSACTTCCG	GAGGGAGTTG	GAGATGTTTG	2700
	GGAAGCTGAA	CCAGGCCAAC	GTGGTGCGGC	TCCTGGGGCT	GTGCGGGAG	GCTGAGCCCC	2760
	ACTACATGGT	GCTGGAATAT	GTGGATCTGG	GAGACCTCAA	GCAGTTCCTG	AGGATTTCOA	2820
10	AGAGCAAGGA	TGAAAAATTG	AAGTCACAGC	CCCTCAGCAC	CAAGCAGAAG	GTGGCCCTAT	2880
	GCACCAGAGT	AGCCCTGGGC	ATGGAGCACC	TGTCCAACAA	CGCTTTGTG	CATAAGGACT	2940
	TGGCTGCGCG	TAACTGCCTG	GTCACTGCC	AGAGACAAGT	GAAGGTGTCT	GCCCTGGGCC	3000
	TCAGCAAGGA	TGTGTACAAC	AGTGAGTACT	ACCACCTCCG	CCAGGCTCGG	GTGCGCGTGC	3060
	GCTGGATGTC	CCCCGAGGCC	ATCCTGGAGG	GTGACTTCTC	TACCAAGTCT	GATGTCTGGG	3120
	CCTTGGTGT	GTGATGTGGG	GAAGTGTTTA	CACATGGAGA	GATGCCCAT	GCTGGGCAGG	3180
15	CAGATGATGA	AGTACTGGCA	GATTTCGAGG	CTGGGAAGGC	TAGACTTCCT	CAGCCCGAGG	3240
	GCTGCCCTTC	CAAACTCTAT	CGGCTGATGC	AGCGCTGCTG	GGCCCTCAGC	CCCAAGGACC	3300
	GGCCCTCCTT	CAGTGAGATT	GCCAGCGCCC	TGGGAGACAG	CACCGTGGAC	AGCAAGCCGT	3360
	GAGGAGGGAG	CCCCCTCAGG	ATGGCCTGGG	CAGGGGAGGA	CATCTCTAGA	GGGAAGCTCA	3420
	CAGCATATAG	GGCAAGATCC	CTGTCTCTCT	GGGCCCTGAG	GTGCCCTAGT	GCAACAGGCA	3480
20	TTGCTGAGGT	CTGAGCAGGG	CCTGGCCTTT	CCTCCTCTTC	CTCACCTCA	TCCTTTGGGA	3540
	GGCTGACTTG	GACCCAAACT	GGGCGACTAG	GGCTTTGAGC	TGGGCAGTTT	CCCCTGCCAC	3600
	CTCTTCTCT	ATCAGGGACA	GTGTGGGTGC	CACAGGTAAC	CCCAATTTCT	GGCCTTCAAC	3660
	TTCTCCCTT	GACCGGGTCC	AACTCTGCCA	CTCATCTGCC	AACTTTGCCT	GGGGAGGGCT	3720
	AGGCTTGGGA	TGAGCTGGGT	TTGTGGGGAG	TTCTTAATA	TTCTCAAGTT	GCTGGGCACAC	3780
25	AGGGTTAATG	AGTCTCTTGC	CCACTGGTCC	ACTTGGGGGT	CTAGACCAGG	ATTATAGAGG	3840
	ACACAGCAAG	TGAGTCTCTC	CCACTCTGGG	CTTGTGCACA	CTGACCCAGA	CCCAAGTCTT	3900
	CCCCACCTTT	CTCTCTCTTC	CTCATCTTAA	GTGCCCTGCA	GATGAAGGAG	TTTTCAGGAG	3960
	CTTTTGACAC	TATATAAACG	GCCCTTTTTC	TATGCAACAC	GGCGGGCTTT	TATATGTAAT	4020
	TGCAAGCTGG	GCTGGGTGGG	CATGGGAGGT	AGGGGTGGGC	CCTGGAGATG	AGGAGGGTGG	4080
30	GCCATCTTTA	CCCCACACTT	TTATGTGTGT	CGTTTCTTGT	TTGTTTGTIT	TTTTTGTITT	4140
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Seq ID NO: C172 DNA Sequence

Nucleic Acid Accession #: NM_002309.2

Coding sequence: 65..673

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	TGGGGCGGGG	AGCCCCCTCC	CCATCACCCT	TGTCAAGCCG	ACCTGTGCCA	TACGCCACCC	180
	ATGTACAAAC	AACTCATGCA	ACCAGATCAG	GAGCCAACTG	GCACAGCTCA	ATGGCAGTGC	240
	CAATGCCCTC	TTTATTCTCT	ATTACACAGC	CCAGGGGGAG	CCGTTCCCA	ACAACCTGGA	300
	CAAGCTATGT	GGCCCCAAGC	TGACGGACTT	CCCGCCCTTC	CAAGCCCAAG	GCACGGAGAA	360
45	GGCCAAAGCT	GTGGAGCTGT	ACCGCATAGT	CGTGTACCTT	GGCACCTCCC	TGGGCAACAT	420
	CACCCGGGAC	CAGAAGATCC	TCAACCCCTG	TGCCCTCAGC	CTCCACAGCA	AGCTCAACGC	480
	CACCGCCGAC	ATCCTCGGAG	GCCTCCTTAG	CAACGTGCTG	TGCCCGCTGT	GCAGCAAGTA	540
	CCAGCTGGGC	CATGTGGAGG	TGACCTACGG	CCCTGACACC	TGGGGTAAAG	ATGTCTTCCA	600
	GAAGAAGAAG	CTGGCTGTCT	AACTCCTGGG	GAAGTATAAG	CAGATCATCG	CCGTGTTGGC	660
50	CCAGGCCTTC	TAGCAGGAGG	TCTTGAAGTG	TGCTGTGAAC	CGAGGGATCT	CAGGAGTTGG	720
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	GGGGGCTGCT	GGCAGACCCC	GAGGGTGCC	GGCCAGTCCA	CTCCACTCTG	GGCTGGGCTG	840
	TGATGAAGCT	GAGCAGAGTG	GAAACTTCCA	TAGGGAGGGA	GCTAGAAGAA	GGTGGCCCTT	900
	CCTCTGGGAG	ATTGTGGACT	GGGGAGCGTG	GGCTGACTT	CTGCCTCTAC	TTGTCCCTTT	960
55	GGCCCCCTGC	TCACTTTGTG	CAGTGAACAA	ACTACACAG	TCATCTACAA	GAGCCCTGAC	1020
	CACAGGTGGA	GACAGCAGGG	CCCAGGGGAG	TGGACCAAGC	CCCAGCAAT	TATCACCATC	1080
	TGTGCTTTTG	GTGCCCCCTTA	GSTTGGGACT	TAGGTGGGCC	AGAGGGGCTA	GGATCCCAAA	1140
	GGACTCCTTG	TCCCTTAGAA	GTTTGATGAG	TGGAAGATAG	AGAGGGGCTT	CTGGGATGGA	1200
	AGGCTGTCTT	CTTTTGAAGA	TGATCAGAGA	ACTTGGGCAT	AGGAACAATC	TGGCAGAAGT	1260
60	TTCCAGAAGG	AGGTCACTTG	GCATTACGGC	TCTTGGGGAG	GCAGAGAAGC	CACCTTCAGG	1320
	CCTGGGAAGG	AAGACACTGG	GAGGAGGAGA	GGCCTGGAAA	GCTTTGGTAG	GTTCCTCGTT	1380
	CTCTTCCCCG	TGATCTTCCC	TGCAGCCTGG	GATGGCCAGG	GTCTGATGGC	TGGACCTGCA	1440
	GCAGGGGTTT	GTGGAGGTGG	TGAGGGCAGG	GGCAGGTTCG	TAACTCAGGT	GCAGAGGTTT	1500
	TGAGGGACCC	AGGCTCTTCC	TCTGGGTAAA	GGTCTGTAAG	AAGGGGCTGG	GGTAGCTCAG	1560
65	AGTAGCAGCT	CACATCTGAG	GCCCTGGGAG	GTCTTGTGAG	GTCAACACAG	GGTACTTGAG	1620
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	TCTCAGGGAA	CCCTGAGCTC	CAAGCGTGCT	GTGCGTCTGA	CCTGGCATGA	TTTCTATTTA	1740
	TTATGATATC	CTATTATAT	TAACTTATTG	GTGCTTTCAG	TGGCCAAAGT	AATTCCTCTT	1800
	TCCCTGTGTC	CTACTCAACA	AAATATGATG	ATGGCTCCCG	ACACAAGCGC	CAGGGCCAGG	1860
70	GCTTAGCAGG	GGCTGGTCTG	GAAATCGACA	ATGTTACAAG	TGGAATAAGC	TTACGGGTGA	1920
	AGCTCAGAGA	AGGGTCGGAT	CTGAGAGAAT	GGGGAGGCTT	GAGTGGGAGT	GGGGGGCCTT	1980
	GCTCCACCCC	CATCCCTTAC	TGTGACTTGC	TTTAGCGTGT	CAGGGTCCAG	CGTCAGGGG	2040
	CTGGGCCAAT	TTGTGGAGAG	GCGGGTGCC	TTTCTGTCTT	GCTTCCAGGG	GGCTGGTTCA	2100
	CACGTGCTT	GGGGGCCCCA	GCATGTGTT	GTGAGGCGCA	CTGTTCTTGG	CAGATATTGT	2160
75	GCCCCCTGGA	GCAGTGGGCA	AGACAGTCTT	TGTGGGCCAC	CCCTGCTCTT	TTTCTGTGTC	2220
	CCCATGTCTG	CTCTGAAATA	GCGCCCTGGA	ACAACCTGTC	CCCTGCACCC	AGCATGCTCC	2280
	GACACAGCAG	GGAGCTCCT	CCTGTGGCCC	GGACAACCAT	AGACGGTGGC	GGGGGCTGG	2340
	CTGGGCCAGA	CCCCAGGAAG	GTGGGGTAGA	CTGGGGGAT	CAGCTGCCCA	TTGCTCCCAA	2400
	GAGGAGGAGA	GGGAGGCTGC	AGACGCTTGG	GACTCAGACC	AGGAAGCTGT	GGGGCTCTCT	2460
80	GCTCCACCCC	CATCCCACTC	CCACCCATGT	CTGGGCTCCC	AGGCAGGGAA	CCCGATCTCT	2520
	TCCTTTGTGC	TGGGGCCAGG	CGAGTGGAGA	AACGCCCTCC	AGTCTGAGAG	CAGGGGAGGG	2580
	AAGGAGGACG	CAGAGTTGGG	GCAGCTGCTC	AGAGCAGTGT	TCTGGCTTCT	TCTCAAAACC	2640
	TGAGCGGGCT	GCGGCGCTCC	AAGTTCCTCC	GACAAGATGA	TGGTACTAAT	TATGTAAGTT	2700
	TTCACTCACT	TTGACCTTTT	CCCTGTGCT	CTCTAAGCAC	TTTACCTGGA	TGGCGGCTGG	2760

5	GCAGTGTGCA	GGCAGGTCCT	GAGGCTTGGG	GTTGGGGTGG	AGGGTGGGGC	COGGAAGTTG	2820
	CCATCTGTCC	ATCCCAACAG	CAAGACGAGG	ATGTGGCTGT	TGAGATGTGG	GCCCACTCA	2880
	CCCTGTGTCA	GGATGCAGGG	ACTGCTTCT	CCTTCCTGCT	TCATCCGGCT	TAGCTTGGGG	2940
	CTGGCTGCAT	TCGCCAGGA	TGGGCTTGA	GAAAGACAAA	CTTGTCTGGA	AACCAGAGTT	3000
	GCTGATTCCA	CCCGGGGGGC	COGGCTGACT	CGCCATCAC	CTCATCTCCC	TGTGGACTTG	3060
	GGAGCTCTGT	GCCAGGCCCA	CCTTGCAGCC	CTGGCTCTGA	GTCGCTCTCC	CACCCAGCCT	3120
	GGACTTGGCC	CCATGGGACC	CATCCTCAGT	GCTCCCTCCA	GATCCCGTCC	GGCAGCTTGG	3180
	CGTCCACCTT	GCACAGCATC	ACTGAATCAC	AGAGCCTTTG	CGTGAAACAG	CTCTGCCAGG	3240
10	COGGGAGCTG	GGTTTCTCTT	CCCTTTTAT	CTGCTGGTGT	GGACCAACAG	TGGGCTTGGC	3300
	CGGAGGAGAA	GAGAGTTTAC	CAAGAGAGAT	GTCTCCGGGC	CCTTATTAT	TATTTAAACA	3360
	TTTTTTTAAA	AAGCACTGCT	AGTTTACTTG	TCTCTCCTCC	CCATCGTCCC	CATCGTCTCC	3420
	CTTGTCCCTG	ACTTGGGGCA	CTTCCACCTT	GACCCAGCCA	GTCCAGCTCT	GCCTTGGCGG	3480
	CTCTCCAGAG	TAGACATAGT	GTGTGGGGTT	GGAGCTCTGG	CACCCGGGGA	GGTAGCATTT	3540
15	CCCTGCAGAT	GGTACAGATG	TTCTTGCCCT	AGAGTCATCT	CTAGTTCCCC	ACCTCAATCC	3600
	CGGCATCCAG	CCTTCAGTCC	CGCCACGCTG	CTAGCTCCGT	GGGCCCAACG	TGGGCTTGA	3660
	GAGGTTTCCC	TCCTTCTCTT	CCACTGAAAA	GCACATGGCC	TGGGTGACA	AATTCTCTTT	3720
	TGATGAATGT	ACCTTGTGGG	GATGTTTCAT	ACTGACAGAT	TATTTTATT	TATTCAATGT	3780
	CATATTTAAA	ATATTTATTT	TTTATACCAA	ATGAATCACT	TTTTTTTTTA	AGAAAAAAA	3840
20	GAGAAATGAA	TAAAGAACTC	ACTCTTCG				3868

Seq ID NO: C173 DNA Sequence
Nucleic Acid Accession #: XM_097508
Coding sequence: 44..2788

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	GACACTTGTT	TGTCACTGT	CAATAATCAT	CTCTGCCCGG	GACCTCAGCA	TGAACAACT	120
30	CACAGAGGCT	CAGCTGGCC	TCTTCCACCA	CCTGCGCTTC	TTGGAGGAGC	TGCGTCTCTC	180
	TGGGAACCAT	CTCTCACACA	TCCACAGGAC	AGCATTCTCT	GGTCTCTACA	GCCTGAAAT	240
	CCTGATGCTG	CAGAACAATC	AGCTGGGAGG	AATCCCGGCA	GAGGCGCTGT	GGGAGCTGCC	300
	GAGCTTGCAG	TGCTTGGGCC	TAGATGCCAA	CCTCATCTCC	CTGCTCCCGG	AGAGGAGCTT	360
	TGAGGGGCTG	TCCTCCCTCC	GCCACCTCTG	GCTGGAGGAC	AATGCACTCA	CGGAGATCCC	420
	TGTCAAGGCT	CAACAACAAC	TCCTTGGCCT	GCAGGCCATG	ACCCTGGCCC	TCAACCGCAT	480
35	CAGCCACATC	CCGACTACCG	CGTTCCAGAA	TCTCACCAGC	CTTGTGGTGC	TGCATTTGCA	540
	TAACAACCGC	ATCCAGCATC	TGGGAGCCCA	CAGCTTCGAG	GGGCTGCACA	ATCTGGAGAC	600
	ACTAGACCTG	AATTATAACA	AGCTGCAGGA	GTTCCTCTGT	GCCATCCGGA	CCCTGGGCAG	660
	ACTGCAGGAA	CTGGGGTTCC	ATAACAACAA	CATCAAGGCC	ATCCCAAGAA	AGGCCTTCAT	720
40	GGGGAACCTT	CTGCTACAGA	CGATACACTT	TTATGATAAC	CCAATCCAGT	TTGTGGGAG	780
	ATCGGCATTC	CAGTACCTGC	CTAAACTCCA	CACACTATCT	CTGAATGGTG	CCATGGACAT	840
	CCAGAGTTT	CCAGATCTCA	AAGGCACCAC	CAGCTTGGAG	ATCCTGACCC	TGACCCGCGC	900
	AGGCATCCGG	CTGCTCCCAT	CGGGGATGTG	CCAACAGCTG	CCCAGGCTCC	GAGTCTCGGA	960
	ACTGTCTCAC	AATCAAAATG	AGGAGCTGCC	CAGCCTGCAC	AGGTGTGAGA	AATTGGAGGA	1020
45	AATCGGCCCT	CAACAACAAC	GCATCTGGGA	AATTGGAGCT	GACACCTTCA	GCCAGCTGAG	1080
	CTCCCTGCAA	GCCTTGGATC	TTAGCTGGAA	CGCCATCCGG	TCCATCCACC	CCGAGGCTTT	1140
	CTCCACCTCT	CATCTCCCTG	TCAAGCTGGA	CCTGACAGAC	AACCACTGGA	CCCACTGCCC	1200
	CTCGCTGGGA	TATGGGGGCT	TGATGCATCT	GAAGCTCAAA	GGGAACCTTG	CTCTCTCCCA	1260
	GGCCTTCTCC	AAGGACAGTT	TCCCAAAACT	GAGGATCCCT	GAGGTGCCCT	ATGCCTACCA	1320
50	GTGCTGCCCC	TATGGGATGT	GTGCCAGCTT	CTTCAAGGCC	TCTGGGCGAG	GGGAGGCTGA	1380
	AGACCTTCAC	CTTGATGATG	AGGAGTCTTC	AAAAAGGCCC	CTGGGCTTCC	TTGCCAGACA	1440
	AGCAGAGAAC	CACATATGAC	AGGACCTGGA	TGAGCTCCAG	CTGGAGATGG	AGGACTCAAA	1500
	GCCACACCCC	AGTGTCCAGT	GTAGCCCTAC	TCCAGGCCCT	TTCAAGCCCT	CTGAGTACCT	1560
	CTTTGAAAGC	TGGGGCATCC	GCCTGGCCGT	GTGGGCCATC	GTGTGCTCT	CCGTGCTCTG	1620
	CAATGGACTG	GTGCTGCTGA	CGTGTGTCG	TGGGGGCCCT	GTCCCTCTGC	CCCGGTCAA	1680
55	GTTTGTGTTA	GGTGGGATG	CAGGCGCCAA	CACCTTGACT	GGCATTTCCT	GTGGCTTCT	1740
	AGCCTCAGTC	GATGCCCTGA	CCTTTGGTCA	GTCTCTGAG	TAGGAGGCC	GCTGGGAGAC	1800
	GGGGCTAGGC	TGCCGGGGCA	CTGGCTTCT	GGCAGTACTT	GGTTCGGAGG	CATGGGTGCT	1860
	GCTGTCTACT	CTGGCCGAG	TGCAGTGAG	CGTCTCCGTC	TCCTGTGTCC	GGGCTATGG	1920
	GAAGTCCCCC	TCCTTGGGCA	CGTTTGGAGC	AGGGGTCTTA	GGCTGCCTGG	CATGGCAGG	1980
60	GCTGGCCGCC	GGCTGCCGCC	TGGCCTCAGT	GGGAGAAATAC	GGGGCTTCCC	CACCTGCTCT	2040
	GGCTACGCG	CCACCTGAGG	GTCCAGCCAGC	AGCCCTGGGC	TTCAACGCTG	CCCTGGTGAT	2100
	GATGAACCTG	TTCTGTTTCC	TGCTGCTGGC	CGGTGCTTAC	ATCAAACTGT	ACTGTGACCT	2160
	GGCGGGGGGC	GACTTTGAGG	CGGTGTGGGA	CTGGGCCATG	GTGAGGCAAG	TGGCCTGGCT	2220
	CATCTTGGCA	GAGGGGCTCC	TCTACTGTCC	CGTGGCCTTC	CTCAGCTTTG	CCTCCATGCT	2280
65	GGGCTCTCTT	CCTGTACAGC	CCGAGGCCGT	CAAGTCTGTC	CTGCTGGTGG	TGCTGCCCT	2340
	GGCTGCTTGC	CTCAACCCAC	TGCTGTACTT	GCTCTTCAAC	CCCACTTCCC	GGGATGACCT	2400
	TGCGGGGCTT	CGGCCCGCG	CAGGGGACTC	AGGGCCCTTA	GCCTATGCTG	CGGCCGSGGA	2460
	GCTGGAGGAG	AGCTCCTGTG	ATTCTACCCA	GGCCCTGGTA	GCCTTCTCTG	ATGTGGATCT	2520
70	CATTCTGGAA	GCTTCTGAAG	CTGGGGGCC	CCCTGGGCTG	GAGACCTATG	GCTTCCCTTC	2580
	AGTGACCTCT	ATCTCCTGTC	AGCAGCCAGG	GGCCCCCAGG	CTGGAGGGCA	GCCATTGTGT	2640
	AGAGCCAGAG	GGGAACCACT	TTGGGAACCC	CCAAACCTCC	ATGGATGGAG	AACTGTGCTG	2700
	GAGGGCAGAG	GGATCTACGC	CAGCAGGTGG	AGGCTTGTCA	GGGGGTGGCG	GCTTTAGGCC	2760
	CTCTGGCTTG	GCCTTTGCTT	CACACGTGTA	AATATCCCTC	CCCACTTCTT	TCTTCCCTTC	2820
75	TCTTCCCTTT	CTCTCTCTCC	CCTGGGTGAA	TGATGGCTGC	TTCTAAACAA	AATACAACCA	2880
	AAACTCAGCA	GTGTGATCTA	TAGCAGGATG	GCCCAGTCCC	TGGCTCCACT	GATCACCTCT	2940
	CTCCTGTGAC	CATCACCAAC	GGGTGCTCTT	TGGCCTGGCT	TTCCCTTGGC	CTTCTCAGC	3000
	TTCACTTGA	TACTGGGGCT	CTTCTTGTTC	ATGTCTGAAG	CTGTGGACCA	GAGACCTGGA	3060
	CTTTGTCTG	CTTAAGGGGA	ATGAGGGGAG	TAAAGACAGT	GAAGGGGTGG	AGGGTTGATC	3120
80	AGGGCAGAGT	GGACAGGGAG	ACCTCACAGA	GAAAGGCTTG	GAAGGTGATT	TCCCGTGTGA	3180
	CTCATGATA	GGATACAAAA	TGTGTTCCAT	GTACCAATTA	TCTTGACATA	TGCCATGCAT	3240
	AAGACTTCC	TATTAATAA	AGCTTTGGAA	GAG			3273

Seq ID NO: C174 DNA Sequence
Nucleic Acid Accession #: NM_130849

Coding sequence: 101..2044

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   GGAGCTGGGG CTGCTTCTGG CTGTGCTGGT GGTGACGGCG ACGGCGTCCC CGCTGCTGG 180
   CTGTCTGAGC CTGCTCACTT CTGGCCAGGG CGCTCTGAT CAGAGGGCTC TGGGCGGCCT 240
   GTTAAATACG CTGGCGGACC GTGTGCATCG CACCAACGGG CCGTGTGGAA AGTGCTGTGC 300
10  TGTGGAGGAG GCCCTGGGCC TGGGCGAGCC TGAGGGGTCA GGGCTGCCCC CGGGCCGGGT 360
   CCTGGAGGCC AGGTACGTCG CCGGCTCAG TGGCGCGGCC GTCTGTACC TCAGCAACCC 420
   CGAGGGCACC TGTGAGGACA CTGGGGCTGG CCTCTGGGCC TCTCATGCAG ACCACCTCCT 480
   GGCCTGTCTC GAGAGCCCCA AGGCCCTGAC CCGGGGCTGG AGCTGGCTGC TGCAGAGGAT 540
   GCAGGCCCGG GCTGCCGGCC AGACCCCAAA GACGGCTGCG GTAGATATCC CTCAGCTGCT 600
15  GGAGGAGGCG GTGGGGGCGG GGGCTCCGGG CAGTGTCTGC GGGCTCTGGT CTGCCCTGCT 660
   GGACCATGTC AGGAGCGGGT CTTGCTTCCA CGCTTGGCG AGCCCTCAGT ACTTCGTGGA 720
   CTTTGTGTTC CAGCAGCACA GCAGCGAGGT CCCTATGACG CTGGCCGAGC TGTCAAGCTT 780
   GATGCAAGCG CTGGGGGTGG GCAGGGAGGC CCACAGTGAC CACAGTCATC GGCACAGGGG 840
   AGCCAGCAGC CCGGACCTCG TGCCCTCAT CAGCTCCAGC AACAGCTCCA GTGTGTGGGA 900
20  CACGGTATGC CTGAGTGCCA GGGACGTGAT GGCTGCATAT GGACTGTGGG AACAGGCTGG 960
   GGTGACCCCG GAGGCTCTGG CCCAATGAG CCCTTGGCTG CTCACACAGC AGCTGAGTGG 1020
   AGCCTGCACT TCCAGTCCA GGGCCCGCTG CCAGGACCGA CTCAGCCAGT CAGAGAGGTA 1080
   TCTGTACGGC TCCTTGGCCA CGTGTCTAT CTGCTCTGCG GCGGTCTTTG GCCTCCTGCT 1140
   GCTGACCTGC ACTGGCTGCA GGGGGGTGCG CCACTACATC CTGCAGACCT TCCTGAGCCT 1200
25  GGCACTGGGT GCACCTCACT GGAAGCTGTG CCTGCATCTG ACCCCCAAGG TGCTGGGGCT 1260
   GCATACACAC AGGCAAGAGG GCCTCAGCCC ACAGCCACCC TGGGCGCTCC TGGCTATGCT 1320
   GGCCTGGCTC CAGGCTCTCT TCCTGTGTGA GAACCTCTTC AATCTCTGCG TGCCAGGGA 1380
   CCGGAGGAGC CTGGAGGAGC GGCCTTGGCG CCACAGCAGC CATAGCCACG GGGGCCACAG 1440
   CCAAGTGTG TCCTGTCAGC TGCCACCCAG CGAGCTCCGG CAGCCCAAGC CCCCCACGA 1500
30  GGGCTCCCGG GCAGACCTGG TGGCGGAGGA GAGCCCGGAG CTGCTGAACC CTGAGCCAG 1560
   GAGACTGAGC CCAGAGTTGA GGCTACTGCC CTATATGATC ACTCTGGGCG ACGCCGTGCA 1620
   CAACCTCGCC GACGGGCTGG CCGTGGGCGC CGCCTTGGCG TCCTCTGGA AGACCGGGCT 1680
   GGCACCTCG CTGCGCTGT TCTGCCACGA GTTGCCACAC GAGCTGGGGG ACTTCGCGCG 1740
   CTTGCTGAC GCGGGGCTGT CCGTGCAGCA AGCACTGCTG CTGAACCTGG OCTCGCGCT 1800
35  CACGGCTTCT GCTGGTCTCT ACGTGGCACT CGCGTTGGA GTGAGGAGG AGAGCGAGGC 1860
   CTGATCCTG GCATGAGCCA CCGGCTGTT CCTTACGTA GCACTCTGCG ACATGCTCCC 1920
   GGCGATGTTA AAGTACGGG ACCCGGGGCC CTGGCTCCTC TTCCTGCTGC ACAAGTGGG 1980
   CCTGCTGGGC GGTGAGACCG TCCTGCTGCT GCTGTCCCTG TACAGGAGAT ACATCACCTT 2040
   CTGATACCTT GCCCTAGTCC CCCACCTTTC ACTTAAGATC CCACCTCA CAACTTACA 2100
40  GCCAGAAAC CAGAGGCCCC TATAGAGGCC CAGTCCCAA CTCCAGTAAA GACACTCTTG 2160
   TCCTTGGAAA AAAAAAAAAA AAAAAAAAAA AA 2192
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Seq ID NO: C175 DNA Sequence

Nucleic Acid Accession #: NM_018971

Coding sequence: 1..1128

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   AAGCTGGCCA CGCTCAGCCT GCTGCTGTGC GTGAGCCTAG CGGGCAACGT GCTGTTCGCG 120
   CTGCTGATCG TGGCGGAGCG CAGCCTGCAC CGGCCCGCT ACTACCTGCT GCTCGACCTG 180
   TGCTTGGCGG ACGGGCTGCG CGGCTCGGCC TGCTCCCGG CCGTCACTGCT GCGGGCGCG 240
   CGTGGCGGCG CCGCGCGGCG GGGCGCGCG GGGCGGCTGG GCTGCAAGCT GCTCGCTTTC 300
   CTGGCGCGCG TCTTCTGCTT CCAAGCGGCC TTCTGCTGCG TGGGCGTGGG GGTCAACCGC 360
55  TACCTGGCCA TGGCGACCA CCGCTTCTAT GCAGAGCGCG TGGCGGCTGG GCGGTGCGCC 420
   GGCATGCTGG TGTGCGCGCG CTGGCGGCTG GCGCTGGCGG CGGCTTTCCT GCCAGTGTCT 480
   GACGGCGGTG GCGACGACGA GGAAGCGCGG TGCGCCTGAG AGCAGCGGCC CGACGGCGCC 540
   CCGCGCGCGC TGGGCTTCTT GCTGCTGCTG GCGTGGTGG TGGGCGCCAC GCACCTGCTC 600
   TACCTCGGCC TGCTCTTCTT CATCCAGCAC CGCGCGCAAG TGGCGGCCCG GCGCTGCTG 660
60  CCGCGCGTCA GCCACGACTG GACCTTCCAC GGGCGGGGCG CCACCGGCCA GCGCGCGGCC 720
   AACTGGAAGC CGGCTTTCG CCGCGGGCCC ACGCGCGCGG CGCTTGTGGG CATCGGCCC 780
   GCAGGGCGCG GCGCGGCGCG GCGCGGCTTC CTGCTGCTGG AAGAATTCAA GACGGAGAAG 840
   AGGCTGTGCA AGATGTTCTA GCGCGTCAAG CTGCTCTTCC TGCTCCTCTG GGGGCCCTAC 900
   GTGTTGGCCA GCTACCTGCG GGTCTGTGCG CGGCGCGCGG CCGTCCCGCA GGCCTACCTG 960
65  ACGGCTTCGG TGTGGCTGAC CTTGCGGAG GCGGCGATCA ACCCGTTCGT GTGCTTCTTC 1020
   TTCAACAGGG AGCTGAGGGA CTGCTTCAGG GCGCAATTCC CTGCTGCCA GAGCCCGCG 1080
   ACCACCCAGG GACCCATCC CTGCGACCTG AAAGGCATTG GTTTATGA 1128
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Seq ID NO: C176 DNA Sequence

Nucleic Acid Accession #: NM_005631

Coding sequence: 290..2653

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   CCGTTCGCGG CCTCGCAGC CCAACATGCG CCGCGGGTTC CAAAGTTTGC GAAGTTGGGC 120
   GCGGAGGGGC GCGGGCGCGC GGAGGCTCGG GGGGGGCGCG GCGCCGAGTT CTCTGGGCGC 180
   ACAGGTGCGC TGAGCGCGCT CCGCGGCGCG CGAGGTGCTG CGTGTGGCGG GGGGGCTCG 240
   AGGAGCAGGC GGGGGCGCGG GGGCTTTTGC TGAGTTGGCG GGGTTGGCCA TGGCGGCTGC 300
80  CGGCCAGCGC CGGGGGCGCG AGCTCCCGCT CTGGGGCTG CTGCTGTGCG TGCTGCTGGG 360
   GGACCCGCGC CGGGGGCGCG CCTCGAGCGG GAACGCGACC GGGCTTGGGC CTCGGAGCGC 420
   GCGCGGAGGC GCGAGGAGGA GCGCGGCGGT GACTGGCCCT CCGCGCGCGC TGAGCCACTG 480
   CCGCGGGGCT GCGCCCTGCG AGCCGCTGCG CTACAACTG TGCTTGGGCT CCGTGTCTGC 540
   CTACGGGGCC ACCTCCACAC TGCTGGCGCG AGACTCGGAC TCCAGGAGG AAGCGCAGG 600
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	CAAGCTCGTG	CTCTGGTGGG	GCCTCCGGAA	TGCCCCCGGC	TGCTGGGCAG	TGATCCAGCC	660
	CCTGCTGTGT	GCCGTATACA	TGCCCAAGTG	TGAGAAATGAC	CGGGTGGAGC	TGCCAGCCG	720
	TACCTCTGCG	CAGGCCACCC	GAGGCCCTTG	TGCCATGCTG	GAGAGGGAGC	GGGGCTGGCC	780
	TGACTTCTGT	CGCTGCACCT	CTGACCGCTT	CCCTGAAGGC	TGCAACGAATG	AGGTGCAGAA	840
5	CATCAAGTTC	AACAGTTTCA	GCCAGTGCBA	AGTGCCCTTG	GTTCGACAGC	ACAAACCCAA	900
	GAGCTGGTAC	GAGGAGCTGG	AGGGCTGCGG	CATCCAGTGC	CAGAAACCCG	TCTTCACAGA	960
	GGCTGAGCAC	CAGGACATGC	ACAGCTACAT	CGCGCCCTTC	GGGGCCGTCA	CGGGCCCTCG	1020
	CACGCTCTTC	ACCCTGGCCA	CATTGCTGGC	TGACTGGGCG	AACCTGAATC	GCTACCCCTG	1080
	TGTTATTCTC	TTCTACGTCA	ATGCGTGCTT	CTTTGTGGGC	AGCATTGGCT	GGCTGGCCCA	1140
10	GTTCATGGAT	GGTGCCCGCC	GAGAGATCGT	CTGCCGTGCA	GATGGCACCA	TGAGGCTTGG	1200
	GGAGCCCAAC	TCCAATGAGA	CTCTGTCTTG	GTCTCATCAT	TTTGTGATCG	TGTACTACGC	1260
	CCTGATGGCT	AGTGTGGTTT	GGTTTGTGGT	CCTCACTAT	GCCTGGCACA	CTTCTTTCAA	1320
	AGCCCTGGGC	ACCACTTACC	AGCCTCTCTC	GGGCAAGACC	TCCTACTTCC	ACCTGCTCAC	1380
	CTGGTCACTC	CCCTTTGTCC	TCACTGTGGC	AATCCTTGCT	GTGGCGCAGG	TGGATGGGGA	1440
15	CTCTGTGAGT	GGCATTTGTT	TTGTGGGCTA	CAAGAACTAC	CGATACCTTG	CGGGCTTCGT	1500
	GCTGGCCCAAC	ATCGGCTGGG	TGCTCATCGT	GGGAGGCTAC	TTCTCTATCC	GAGGAGTCA	1560
	GACTCTGTTC	TCCATCAAGA	GCAACCAACC	CGGCTGCTG	AGTGAGAAGG	CTGCCAGCAA	1620
	GATCAACGAG	ACCATGCTGC	GCCTGGGCAT	TTTTGGCTTC	CTGGCCCTTG	GCTTTGTGCT	1680
	CATTACCTTC	AGCTGCCACT	TCTACGACTT	CTTCAACCAG	GCTGAGTGGG	AGCGCAGCTT	1740
20	CCGGGACTAT	GTGCTATGTC	AGGCCAATGT	GACCATCGGG	CTGCCCAACA	AGCAGCCCAT	1800
	CCCTGACTGT	GAGATCAAGA	ATCGCCCGAG	CCTTCTGGTG	GAGAAGATCA	ACCTGTTTGC	1860
	CATGTTGGTA	ACTGGCATCG	CCATGAGCAC	CTGGGTCTGG	ACCAAGGCCA	CGCTGCTCAT	1920
	CTGGAGGGCT	ATCTGTGTCA	GGTTGACTGG	GCAGAGTGAC	GATGAGCCAA	AGCGGATCAA	1980
	GAAGAGCAAG	ACGATTTGCC	AGGCCCTTCT	TAAGCGGCAC	GAGCTCCTGC	AGAACCCAGG	2040
25	CCAGGAGCTG	TCCTTCAGCA	TGCACACTGT	GTCCCAAGAC	GGGCCCCTGG	CGGGCTTGGC	2100
	CTTTGACCTC	AATGAGCCCT	CAGCTGATGT	CTCCTCTGCC	TGGGCCCAAG	ATGTACCCAA	2160
	GATGGTGGCT	CGGAGAGGAG	CCATACTGCC	CCAGGATATT	TCTGTCAACC	CTGTGGCAAC	2220
	TCCAGTGCCC	CCAGAGGAAC	AAGCCAACTT	GTGGCTGGTT	GAGGCAGAGA	TCTCCCCAGA	2280
	GCTGCAGAA	CGCCTGGGCC	GGAAGAAGAA	GAGGAGGAAG	AGGAAGAAGG	AGGTGTGCC	2340
30	GCTGGGCGCG	CCCCCTGAGC	TTACCCCTGC	TGCCCTTGCC	CCCAGTACCA	TTCTCTGACT	2400
	GCCTCAGCTG	CCCCGGCAGA	AATGCCTGGT	GGCTGCAGGT	GCCTGGGGAG	CTGGGGACTC	2460
	TTGCCAGCAG	GGAGCGTGGA	CCCTGGTCTC	CAACCCATTC	TGCCCAGAGC	CCAGTCCCCC	2520
	TCAGGATCCA	TTTCTGCCCA	GTGCACCGGC	CCCCGTGGCA	TGGGCTCATG	GCCGCGGACA	2580
	GGGCTTGGGG	CCTATTCACT	CCCGCACCAA	CCTGATGGAC	ACAGAACTCA	TGGATGCAGA	2640
35	CTCGGACTTC	TGAGCCTGCA	GAGCAGGACC	TGGGACAGGA	AAGAGAGGAA	CCAATACCTT	2700
	CAAGGCTCTT	CTTCTCACC	GAGCATGCTT	CCCTAGGATC	CGTCTTCCA	GAGAACCTGT	2760
	GGGCTGACCT	CCCTCCGAGG	AGAGTTCTGG	ATGTCCTGGT	CAAGCAGACA	GGACTGTGGG	2820
	AAAGAGCCTA	ACATCTCCAT	GGGGAGGCTT	CACCCAGGGG	ACAGGGCCCT	GGAGCTCAGG	2880
	GTCTTGTGTT	CTGCCCTGCC	AGCTGCAGCC	TGGTTGGCAG	CATCTGCTCC	ATCGGGCAG	2940
40	GGGATATGTA	GAGCTTGTGG	TGGGGCAGGA	ACGGTGGAGG	CAGAGGTGAC	AGTTCCACAG	3000
	GTGGGCTTTG	GTGGCCAGGG	AGGCAGCCTA	GCCTATGTCT	GGCAGATGAG	GGCTGGCTGC	3060
	CGTTTCTGCG	CTGTAGGGGT	GCCCTTCTCT	GGCAGTCTCA	GTCCAAAGT	GTGACTGTGG	3120
	TCATTAGTCC	TTTGTCTAAG	TAGGGCCAGG	GCACCGTATT	CCTCTCCAG	GTGTTTGTGG	3180
	GGCTGGAAGG	ACCTGCTCCC	ACAGGGGCCA	TGTCTCTCT	TAATAGTGG	CACCTACCCA	3240
45	AACCCATCTT	TGTTTCTCCT	ATATCCTCCT	TCTCTGTGTC	CATTTCAGTT	CAGTTTCAAG	3300
	GGTGCCAAAC	TCTTTGCGTT	TCTTTTGTGT	TGATGAGGAC	CCAGAGCTGC	TGCACACACT	3360
	CACCTCTAAC	CCCTCCCTCT	CGCTGCTGGG	CCCATCTCC	ACAGGAGAGA	CTGGTTGGGC	3420
	TCTAGGGCCT	CAGTCTGGAG	TGGGATAGGA	GCAGTGAATG	ACAAAGCCTC	TGAAAGATGC	3480
	ATCATCTCTT	CCTCACACCC	ATTTAGTGGG	GGATGGGTCC	TCTAGACTTG	AGGGGCTACC	3540
50	CTGGGAAGCT	CTGGTAGCTT	CAGCCAGGCA	AGAAAGCTTC	CTTCAACCTG	CATAGCCGGT	3600
	GGGTGAGGAG	ATTCACCACT	TCATAGCCTT	CCAAACATGT	TCCCAAGGCC	CCACTTTCAA	3660
	GAATCAGACA	GCAGGAAGCC	ATAGATGCTG	GCTGGGTTCC	AGGTTATGGG	GAGAAGAAAT	3720
	ACAGTCAATA	AAAGGTTTTT	GTATAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	3780
55	A						3781

Seq ID NO: C177 DNA Sequence
Nucleic Acid Accession #: AK094595
Coding sequence: 1..2853

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	TCAGCGCCAG	CAGAGCCGCT	GCCCTACTTC	CTGCAGGAGC	CACAGGAAGC	CTACATTGTG	180
65	AAGAACAAGC	CTGTGGAGCT	CGCTGCGCG	GCCTTCCCG	CCACACAGAT	CTACTTCAAG	240
	TGCAACGGCG	AGTGGGTGAG	CCAGAACGAC	CACGTCAAC	AGGAAGGCT	GGATGAGGCC	300
	ACCCTGGGGG	CGCGGGGCGG	CCTGGGGGTG	CGGAGGTG	AGATCGAGGT	TGCGGGCAG	360
	CAGGTGGAGG	AGCTCTTTGG	GCTGGAGGAT	TACTGGTGCC	AGTGGTGGC	CTGGAGCTCC	420
	GCGGGCACCA	CCAAGAGTGG	CCGAGCCTAC	GTCCGCTATG	CCTACCTGGC	CAAGAACTTC	480
70	GATCAGGAGC	CTCTGGGCAA	GGAGGTGCCC	CTGGACCATG	AGGTTCTCCT	GCAGTGGCGC	540
	CGCGCGGAGG	GGGTGCTGCT	GGCGGAGGTG	GAATGGCTCA	AGAATGAGGA	TGTATCGGAC	600
	CCACCCAGG	ACACCAACTT	CTGTCTCACC	ATCGACCA	ACCTCATCAT	CGGCCAGGCC	660
	CGCTGTGCG	ACACTGCCAA	CTATACCTGC	GTGGCCAGAA	ACATCGTGGC	CAAAAGCGCG	720
	AGCACCACTG	CCACCGTCA	CGTCTAGCTG	AATGGGGCT	GGTCCAGCTG	GGCAGAGTGG	780
75	TCACCTGCT	CCAAACGCTG	TGGCGGAGGC	TGGCAGAAAG	GCACCGGAGC	CTGCACCAAC	840
	CCCGCTCCAC	TCAAACGAGG	GGCCTTCTGC	GAGGGCCAGG	CATTCCAGAA	GACCGCTGCG	900
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 Nucleic Acid Accession #: NM_004625
 Coding sequence: 310..1359

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Seq ID NO: C179 DNA Sequence OBR3
 Nucleic Acid Accession #: NM_003786
 Coding sequence: 71..4654

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Seq ID NO: C180 DNA Sequence

Nucleic Acid Accession #: NM_004626
Coding sequence: 124...1188

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Seq ID NO: C181 DNA Sequence
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GCGCGCGCG GCGCTCCCTC TACAGCGACG TCAGCACTGG CTTGAGGTTG CGGTGCGGCA 2040
80 CCGCGAGCTC CTTGTCTTAT CCAAGCAGA TGCCATTGTC CAGGTCTGA GCGAGGGGA 2100
GGGGCGCGCC AGGAGGGGTG GAGAGGGGG CGAGGAGACC CAAGTGCAGC GAAGGGACAC 2160
TTGATGGGCT GAGGTTCCCA CCGCTTCACT GTGTTGATTG CTATTAGCAT GATAATGAAC 2220
TCTTAATGGT ATCCATTAGC TGGGACTTAA ATGACTCACT TAGAACAAAG TACCTGGCAT 2280
TGAAGCCTTC CAGACCCAGC CCCTTTTCTT CATTGATGT GCGGGAGGCT CTTCCGCCA 2340

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5 CGCGTTAATT TCTGTTGGCT GAGGAGGGTG GACTCTGCGG CGTTTCCAGA ACCCGAGATT 2400
 TGGAGCCCTC CCGGCTGCA CTGGCTGGG TTGTCAGTCA GATACACAGA TTTCACCTGG 2460
 GAGAACTCTT TTTCTCCCT CGACTCTTCC TACGTAAACT CCCACCCCTG ACTTACCCTG 2520
 GAGGAGGGGT GACCGCCACC TGATGGGATT GCACGGTTTG GGTATTCTTA ATGACCCAGC 2580
 AAATGCGCTTA AGTAAACAAA CAAGAAATGT CTAAATTATA CACCCACAGT AAATACGGGT 2640
 TTCTTACATT AGAGGATGTA TTTATATAAT TATTGTTAA ATTGTAAAAA AAAAAAGTGT 2700
 AAAATATGTA TATATCCAAA GATATAGTGT GTACATTTTT TTGTAAAAAG TTTAGAGGCT 2760
 TAACCCCTGTA AGAACAGATA TAAGTATTCT ATTTTGTCAG TAAATGACT TTGTATAAAT 2820
 10 GATTTAACCA TTGCCCTCTC CCGCGCTCTT TCTGAGCTGT CACCTTTAAA GTGCTTGCTA 2880
 AGGACGATG GGGAAAATGG ACATTTTCTG GCTTGTCATT CTGTACACTG ACCTTAGGCA 2940
 TGGAGAAAAAT TACTTGTATA ACTCTAGTTC TTAAGTGTGT AGCCAAGTAA ATATCATTGT 3000
 TGAACGTAAA TCAAAATGTA GTTTTGTGAC CTTCGCCAAA GACCGTGTGT TTCATGGGAG 3060
 CTCCTTTCTG ATCCATGGAT AACAACTCTC ACTTTAGTGG ATGTAAATGG AACCTCTGCA 3120
 15 AGGCAGTAAT TCCCTTAGG CCTTGTATT TATCCTGCAT GGTATCACTA AAGGTTTCAA 3180
 AACCTGAAA AAAAA 3195

Seq ID NO: C182 DNA Sequence
 Nucleic Acid Accession #: XM_050625
 Coding sequence: 222..1109

20 1 11 21 31 41 51
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 CCGGGTGGGA GCGCCCGGGA GCTGCGCGCG GGCTTGCGAGC GCCTGCGCCG CGCTGTCTCTC 60
 CCGGTGTCCC GCTTCTCCGC GCCCAGCCG CCGGCTGCCA GCTTTTGGGG GCCCCGAGTC 120
 25 GCACCCAAGG AAGAGAGCGG GCCCGGGACA AGCTCGAACT CCGGCCGCGT GCGCCCTGCC 180
 CGGCTCGGCT CCGTCTGCCC CCTCGGGGTC GCGCGCCAC GATGCTGCAG GCGCCTGGCT 240
 CGCTGCTGCT GCTCTTCTCT GCTCTGCACT GCTGCGCTGG CTGCGCGCGC GGGCTCTTCC 300
 TCTTTGGCCA GCCCGACTTC TCCTACAAAG GCAGCAATTG CAAGCCCATC CTGCGCAACC 360
 30 TGCAAGCTGG GAACGGCATC GAATACCAAG ACATGCGGCT GCCCAACCTG CTGGGCCAAG 420
 AGACCAATGA GAGGGTGTCT GAGCAGGCGG GCGCTTGGAT CCGCTGTGCT ATGAAGCAGT 480
 GCCACCGGGA CACCAAGAGT TTCTGTGCTC CGCTCTTGCG CCGCTGTGCT CTGATGACC 540
 TAGACGAGAC CATCCAGCCA TGCCACTGCG TCTGCGTGCA GGTGAAGGAC CGCTGCGCCC 600
 CGGTCATGTC CGCCTTGGGC TTCCCTGGGC CCGACATGCT TGAGTGCGAG CGTTTCCCCC 660
 35 AGGACAACGA CCTTTGCATC CCGCTCGCTA GCAGCGACCA CCTCTGCCA GCCACGAGG 720
 AAGCTCCAAA GGTATGTGAA GCGTGCAAAA ATAAAAATGA TGATGACAAAC GACATAATGG 780
 AAGCGCTTTG TAAAAATGAT TTGCACTGA AAATAAAAGT GAAGGAGATA ACCTACATCA 840
 ACGAGATAC CAAAATCATC CTGGAGACCA AGAGCAAGAC CATTTACAAAG CTGAACCGTG 900
 TGTCCGAAGG GGAAGCTGAG AAATCGGTGC TGTGGCTCAA AGACAGCTTG CAGTGCACTT 960
 40 GTGAGGAGAT GAACGACATC AACCGCGCCT ATCTGCTCAT GGGACAGAAA CAGGGTGGGG 1020
 AGCTGGTGTG CACCTCGGTG AAGCGGTGGC AGAAGGGGCA GAGAGAGTTC AAGCGCATCT 1080
 CCGCAGCATC CCGCAAGCTG CAGTGCTAGT CCGGCATCC TGATGGCTCC CAGGCGCTG 1140
 CTCCAGAGCA CGGCTGACCA TTTCTGCTCC GGGATCTCAG CTCCCGTTCC CCAAGCACAC 1200
 TCCTAGTGTG TCAGGCTCTA GCCTGGGCGG CTTCGCCCTG CTTTGTGCAC GTTTGTATCC 1260
 45 CCAGCATTTT CTGAGTTATA AGGCCACAGG AGTGGATAGC TGTTTTCCAC TAAAGGAAAA 1320
 GCCCACCAGA ATCTGTAGA AATATTCAA CTAATAAAAT CATGAATATT TTTATGAAGT 1380
 TT 1382

Seq ID NO: C183 DNA Sequence
 Nucleic Acid Accession #: NM_001306.1
 Coding sequence: 199..861

50 1 11 21 31 41 51
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 GCGGCGCGCG TCGGTGAGTC AGTCCGTCCG TCGTTCGTCT CGTGGGGCGG CCGCAGCTCC 120
 55 GCGCAGGCCG AGCGGCCCGG GCCCTCGTCT TCCCGCACC CGAGCCACC CGGTGGAGCG 180
 GGCCTTGGCG CCGCAGCCAT GTCCATGGGC CTGGAGATCA CGGCGACCGC GCTGGCGGTG 240
 CTGGGCTGGC TGGGCACCAT CGTGTGCTGC GCGTGGCCCA TGTGGCGCGT GTCGGCTTTC 300
 60 ATCGGCAACA ACATCATCAC GTGCGAGAAC ATCTGGGAGG GCCTGTGGAT GAACTGGGTG 360
 GTGCGAGACA CCGGCGAGAT GCAGTGCAAG GTGTAGAGCT CGCTGTGGC ACTGCCACAG 420
 GACCTTCAGG CGGCGCGGCG CCTCATGCTG GTGGCCATCC TGCTGGCCCG CTTCGGGCTG 480
 CTAGTGGCGC TGGTGGGCGC CCAGTGCACC AACTGGGTGC AGGACGACAC GGCCAAGGCC 540
 AAGATCACCA TCGTGGCAGG CGTGTCTGTC CTCTCGCGCG CCTGTCTCAC CCTCGTGGCG 600
 65 GTGTCTGGGT CGGCCAACAC CATTATCCGG GACTTCTACA ACCCCGTGGT GCGCCGAGCG 660
 CAGAAAGCGG AGATGGGCGG GGGCCTGTAC GTGGGCTGGG CGGCCGCGCG GCTGCGAGCTG 720
 CTGGGGGGCG CGCTGCTCTG CTGCTCTGTT CCGCCACGCG AGAAGAAAGTA CACGGCCACC 780
 AAGGTCTGCT ACTCCGCGCC GCGCTCCACC GCGCCGGGAG CCAGCTCGGG CACAGGCTAC 840
 GACCGCAAGG ACTAGCTCTA AGGAGACAGC GCAGGGAGAC CCCACCAACA CCACCAACAC 900
 70 CAACACCAAG ACCACCAAG CGAGCTGGAG CGGCAACAG GCCATCCAGC GTGCAGCCTT 960
 GCCTCGGAGG CCAGCCACC CCCAGAGGCC AGGAAGCCCG CGGCTGGAGC TGGGGCAGCT 1020
 TCCCGAGCAG CCAAGGCTTT GCGGGCCGGG CAGTGCAGCT CGGGGCCAGG GGACCAACCT 1080
 GCATGGAGTG TGAACCTTCA CCTTCTGGA GCAAGGGGCC TGGGTGACCG CCAATACCTG 1140
 ACCACCCCGT CGAGCCCATC CGGGCCGCTG CCCCCTATGT GCGCTGGGCA GGGACCGGCA 1200
 75 GCGCTGGAGG GGGCACTTGA TATTTTCAA TAAAAAGCTC TCGTTTACG 1250

Seq ID NO: C184 DNA Sequence
 Nucleic Acid Accession #: NM_012449.1
 Coding sequence: 66..1085

80 1 11 21 31 41 51
 | | | | | |
 CCGAGACTCA CGGTCAAGCT AAGGCGAAGA GTGGGTGGCT GAAGCCATAC TATTTTATAG 60
 AATTAATGGA AAGCAGAAAA GACATCAAAA ACCAAGAAGA ACTTTGGAAA ATGAAGCCTA 120
 GGAGAAATTT AGAAGAAGAC GATTATTGTC ATAAGGACAC GGGAGAGACC AGCATGCTAA 180

5 AAAGACCTGT GCTTTTGCAT TTGCACCAA CAGCCCATGC TGATGAATTT GACTGCCCTT 240
 CAGAACCTTA GCACACACAG GAACCTTTTC CACAGTGGCA CTTGCCAATT AAAATAGCTG 300
 CTATTATAGC ATCTCTGACT TTCTTTTACA CTCTCTGAG GGAAGTAATT CACCCTTTAG 360
 CAACCTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTCAATCAAC AAAGTCTTGC 420
 CAATGGTTTC CATCACTCTC TTGGCATTGG TTTACCTGCC AGGTGTGATA GCAGCAATTG 480
 TCCAACCTTA TAATGGAAAC AAGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT 540
 TAACAAGAAA GCAGTTTGGG CTCTCTCAGT TCTTTTTTGC TGTAAGTGCAT GCAATTTATA 600
 GTCTGTCTTA CCCAATGAGG CGATCTTACA GATACAAGTT GCTAAACTGG GCAATCAAC 660
 AGGTCCAACA AATAAAGAA GATGCCTGGA TTGAGCATGA TGTTTGGAGA ATGGAGATT 720
 10 ATGTGTCTCT GGAATTTGTT GGATTGGCAA TACTGGCTCT GTTGGCTGTG ACATCTATTTC 780
 CATCTGTGAG TGACTCTTTG ACATGGAGAG AATTTCACTA TATTCAAGAGC AAGCTAGGAA 840
 TTGTTTCCCT TCTACTGGGC ACAATACACG CATGTATTTT TGCTTGGAAAT AAGTGGATAG 900
 ATATAAACA ATTGTATGAG TATACACCTC CAACCTTTAT GATAGCTGTT TTCTTCCAA 960
 15 TTGTGTCTCT GATATTATAA AGCATACTAT TCCTGCCATG CTTGAGGAAG AAGATACTGA 1020
 AGATTAGACA TGTTTGGGAA GACGTACCA AATTAACAA AACTGAGATA TGTTCCAGT 1080
 TGTAAGAATA CTGTTTACAC ACATTTTGT TCAATATTGA TATATTTTAT CACCAACATT 1140
 TCAAGTTTGT ATTTGTAAAT AAAATGATTA TTCAAGGAAA AAAAAAATA AAAAA 1195

Seq ID NO: C185 DNA Sequence
 Nucleic Acid Accession #: NM_001775.1
 Coding sequence: 70..972

25 1 11 21 31 41 51
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 CTAAGACTCT CTTGCTGCTC AGCCTCCTGC CGGCTCTATC TTCGCCACGC CAACCCCGCC 60
 TGGAGCCCTA TGGCCCAACTG CGAGTTTCAG CGGTGTCTCG GGGACAAACC CTGCTGCCGG 120
 CTCTCTAGGA GAGCCCAACT CTGTCTTTGG GTCAAGTATCC TGGTCTGTAT CCTCGCTGG 180
 GTGCTCGCGG TGTCCTCTCC GAGGTGGGCG CAGACGTGGA GCGGTCCGGG CACCACCAAG 240
 CGCTTTCCCG AGACCGTCTC GCGCGATGCG GTCAAGTACA CTGAAATTTA TCCTGAGATG 300
 30 AGACATGTAG ACTGCCAAG TGTATGGGAT GCTTTCAAG GTGCATTTAT TTCAAAACAT 360
 CCTTGCACCA TTAAGTGAAG AGACTATCAG CCACTAATGA AGTTGGGAAC TCAGACCGTA 420
 CCTTGCACCA AGATTCTTCT TGGAGCAGA ATAAAGATC TGGCCCATCA GTTCACACAG 480
 GTCCACCGGG ACATGTTTAC CCTGGAGGAC ACGCTGCTAG GCTACCTTGC TGATGACCTC 540
 ACATGTGTG GTGAATTCAA CACTTCCAAA ATAACTATC AATCTTCCCG AGACTGGAGA 600
 35 AAGGACTGCA GCACCAACCC TGTTCAGTA TTCTGGAATA CGGTTTCCCG CAGGTTTGCA 660
 GAAGCTGCTT GTGATGTGTT CCAATGTGAT CTCAATGGAT CCCGCAAGTA AATCTTTGAC 720
 AAAAAACAGA CTTTTGGGAG TGTGGAAGTC CATAATTTGC AACCAGAGAA GGTTCAGACA 780
 CTAGAGGCCT GGGTGATACA TGGTGAAGA GAAGATTCCA GAGACTTATG CCAGGATCCC 840
 ACCATAAAG AGCTGGAATC GATTATAAGC AAAAGGAATA TTCAATTTTC CTGCAAGAAT 900
 40 ATCTACAGAC CTGACAAAGT TCTTCAGTGT GTGAAAAATC CTGAGGATTC ATCTTGACCA 960
 TCTGAGATCT GAGCCAGTCC CTGTGGTTGT TTTAGCTCCT TGACTCCTTG TGTTTATGT 1020
 CATCATACAT GACTCAGCAT ACCTGTGTTG GCAGAGCTGA AGATTTTGGA GGTCTCTCA 1080
 CAATAAGGTC AATGCCAGAG ACGGAAGCCT TTTTCCCAA AGTCTTAAA TAACCTATAT 1140
 CATCAGCATA CCTTTATTGT GATCTATCAA TAGTCAAGAA AAATTATTGT ATRAGATTAG 1200
 45 AATGAAATTT GTATGTTAAG TTACTTCTT TAG 1233

Seq ID NO: C186 DNA Sequence
 Nucleic Acid Accession #: XM_120513.2
 Coding sequence: 1..2208

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 TACGCTTTCG GAGCTTTTAT GTTCCGATG AGCTCAGAGG CCGGATGCT CGGGGAAAGC 120
 55 AGGACCCCAA AGCCCCGTAA ACACCGCGCG ACCACCGGG CCAAGATCTT CAAGAGGTTT 180
 TTTTCAAGAG GATCGGAGAG CAATTCCCGA TTGGTGAAG AACTTGTCTGT AATACACAG 240
 TACTCTGACG ACCCCGCCCC AACGACTAGC CCCTCCTCTG TGCAACCCCG AGAGTTTGGG 300
 GTCATGCAGG GGGCGCCACG AGCTCGTTTC GGAAGCCGGA CCCCGCCCGC AGCCGACGAA 360
 GCCTCGAGTC CACATCTGGG CATTGGGAG GCAGCCTGTC AATCAGGAGC TCGGGCGGCA 420
 60 GCGCCCGCGG CGGGGGCTCG GCGATGCCAG CCTCAGCGAC AGCGCGCGCG GCGCGCGGCC 480
 ACGGCACAGA CACACACCTT CCCACACGCG CACACCGGG CAGACCCGCG GGCAGGCGG 540
 CGGAGGCACC CTCGAGCCCC GCGCCCGCGC GGGGAGGGGA CGTGCTCCGA GGGACCGGCC 600
 CCGAGGCGCC GATGAGGAGA AGAGATGCAG CCGGAGAGG AGGGGCCCCG GTTCCCAAA 660
 65 ATCTACAGC AGCGCAGCCC CTACAGCGTC CTCAAGACGT TCCCCAGCAA GAGACCGCGG 720
 CTGGCCAAAG GCTACGAGCG ACCCAACCTG GTGGAGCTGC GCGACGCGCA CTTGAGGACT 780
 CCGGCGCCCG CCGCGCCCGC GTCCCCCGCC GCCTCCTCGT GCTCTTCTGT GCGCGCTGTC 840
 GTCAAGACTCG GGGCTCTCTC GCGTCCGCCA CGCGGTGGAT TTGCGGCGCG GGGAAACCATC 900
 CCGCCCTCTC TTCTGCCCCC GGGAGTCGCA GGCACCTCTG TCCACCGGCC CAGCTGTGTG 960
 70 TCCCGCCAT CCCCTCGTCC CGTCCGTGG CACGCTGCGG CGCGCGGGG AGGGACCTCA 1020
 CATACACATA TGTGGAGGTC CCAATCCACA CTTCAGGAT CTGACACCAT GGTCTCTGTC 1080
 TTTGGATTGA TGGCTCAGAG AAGATGGCAG CATAGATCTT TAAAGCAGTT TGAGTGGGGA 1140
 ATTCTTGGAT CTGGGGTAC TTGGCCATGT GGACAGGATT GGCTGGAGAA GAGGGGTGAG 1200
 GTGGCGGTCC TGCTGCCAAG GTCTGAGGGT AATACTGCTC CTAGAAGAG TCGAATGATC 1260
 75 TTGATGCTCT TTGCCAGCA GTGCAAGTGA GTTCTTAGCC TCTTAAATTG TGGAGGAAAA 1320
 CTCCTGAGCT CCAACCAATC TCAGTCCATG ATTTCTTGGG TAAAGCAGGA AGGCTCAAGT 1380
 TACAAGAAA GACAGGAGCA CTGTACATT GGGAAAGGGG TCCACAGTCA GACCTCAGAC 1440
 AATGTAGACA TAGAGATGCA GTATATGCAA AGGAAACAC AAACCTCTGC CTTTTTGAGG 1500
 GTTTTCACTG ACTCTCTACA AAATTACCTG CTCTCGGAA GCTTTTCAAC TCCAAACCCC 1560
 80 TCGTACGCA GTGAATATGG CCATCTGGCC GACGTGATC CTCTGTCAAC CTCTCTGTG 1620
 CATACATTAG AAAATATTTT ACTTGATTCC ACAGCTTCCC TGTGTAAATC TAGGCATCTA 1680
 TCCAGAGAGC CCCCAAGTCA GAGTGATTTT CCAATCCTT TGCAGCAGGC CTTGGCTGGG 1740
 GGTGCTTCAA GACCATTTTC AGGGGACAG CAAAGCATCG CTTACAGGAT GAACTCTGAA 1800
 CTTGAGGATG GCATCCGAG CCGCTGCCCT TTGAGTTGTG AGGCCTTGA AATGGATTG 1860
 ACCTCCTTGG GAAGCAAGCA GCTGTGAAC AACTATCTG TCTACATAAC GAGCAACAG 1920

TGGGATGAGG CTGTAAATTC TTCAAAGAAA GATGGGAGAC GGCTCCTTCG ATACCTCATC 1980
 AGATTTGTTT TCACAACCGA TGAGCTTAAG TACTCATGCG GCCTTGGGAA AAGGAAAAGG 2040
 TCAGTGCAGT CAGGAGAGAC AGGTCCCGAA AGACGCCCTC TGATCCAGT TAAAGTAAAC 2100
 TGCTCCGAG GTACTGCTATC CTTCGGCTCA GTGTACCAT CTGTATCTC ATTTACOCGC 2160
 ATTGGCTGTG GCTCTCCCCG TACAAGTGT TACGCTTCTG TATTTTGA 2208

Seq ID NO: C187 DNA Sequence
 Nucleic Acid Accession #: AB037745.1
 Coding sequence: 26..1744

10

1	11	21	31	41	51	
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CTCAGACAT	GACTTCATG	TTCTCACTC	GGTGTGCCA	GGATTTAGAC	CTCCGCACTC	180
GGTGATGGC	GACACAGAG	ATAAAGAGT	GGCCAGAAT	ACATTTGCT	TTGAGACCTC	240
CTGTTCTGT	AACCTGTAG	TCTACTTCAT	GGTGGGTGT	AATCTTAGA	CCAACACTCC	300
TTGTGAGAG	TGGAAAGGT	CCAAAGGCA	ACAGTCTAT	ACCTACATCA	TTGAGGAGAA	360
CATACCAAG	AGCTTCACCT	GGGCTTCCA	GAGGACCACT	TTTCATGAG	CAAGCAGGAA	420
GTACACCAAT	GAGCTTGCCA	AGATCTACTC	CATCAATGT	ACCAATGTTA	TGAATGGCGT	480
GGCTCCTAC	TGCCGTCCT	GTGCCCTAGA	AGCTCTGAT	GTGGGCTCCT	CCTGCACCTC	540
TTGTCTGCT	GGTTACTATA	TTGACCGAGA	TTCAAGAAAC	TGCCACTCCT	GCCCCCTAA	600
CACAATTCTG	AAGGCCACC	AGCCTTATG	TGTCCAGGCC	TGTGTGCCCT	GTGGTCCAGG	660
GACCAAGAAC	AACAAGATCC	ACTCTCTGT	CTACAATGAT	TGCACCTTCT	CAOGCAACAC	720
TCCAACCAGG	ACTTTCACAT	ACAACCTCTC	CGCTTTGGCA	AACACCGTCA	CTCTTGCTGG	780
AGGGCCAAAG	TTCACTTCCA	AAGGGTTGAA	ATACTTCCAT	CACCTTACCC	TCAGTCTCTG	840
TGGAAACCG	TGTCTGTGT	CACCGACAAT	GTCACTGACC	TCCGGATTCC		900
TGAGGGTGAG	TCAGGGTCT	CCAAATCTAT	CACAGCCTAC	GTCTGCCAGG	CAGTCATCAT	960
CCCCCAGAG	GTGACAGAG	ACAAGGCCGG	GGTTTCTCTA	CAGCCTGTCA	GCTTGTCTGA	1020
TCGACTTATT	GGGGTGACAA	CAGATATGAC	TCTGGATGGA	ATCACCTCCC	CAGCTGAACT	1080
TTTCCACCTG	GAGTCTCTGG	GAATACCGGA	CGTGATCTTC	TTTTATAGGT	CCAATGATGT	1140
GACCCAGTCC	TGCAGTCTG	GGAGATCAAC	CACCATCCGC	GTCAAGTGCA	GTCCACAGAA	1200
AACGTCTCCT	GGAAATTTGC	TGCTGCCAGG	AACGTGTCTA	GATGGGACCT	GTGATGGCTG	1260
CAACTTCCAC	TTCTCTGTGG	AGAGCGCGGC	TGCTTGCCCG	CTCTGCTCAG	TGGCTGACTA	1320
CCATGCTATC	GTGAGCAGCT	GTGTGGCTGG	GATCCAGAAG	ACTACTTACG	TGTGGCGAGA	1380
ACCCAAGCTA	TGCTCTGGTG	GCAATTTCTC	GCCTGAGCAG	AGAGTCACCA	TCGCAAAAC	1440
CATAGATTTT	TGGCTGAAAG	TGGGCATCTC	TGCAGGCCAC	TGTACTGCCA	TCTGTCTCAC	1500
CGTCTTGACC	TGCTACTTTT	GGAAAAAGAA	TCAAAAACTA	GAGTACAAGT	ACTCCAAGCT	1560
GGTGATGAAT	GCTACTCTCA	AGGACTGTGA	CCTGCCAGCA	GCTGACAGCT	GCGCATCAT	1620
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GATCAAAATCA	TTTACCTCCA	AGCAGCCAGC	TCTGTCCACC	ATCTCTCTTT	CAGAGGACTC	1740
CTGATGATT	TGACTCAGTG	CGCTGGAAGA	CATCCTCAGG	AGGCCAGGAC	ATGACACCTG	1800
GAGAGGCCACT	GCCTGCCCTCA	CCTGCCCTCT	CACCTTGCA	AGCAGCTTGG	CAAGCCTCGG	1860
GCGATTTGGG	TGCCAGCATC	CTGCAACACC	CACCTGTGGA	AATCTCTTCA	TGTGGCGCTT	1920
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CCTCAAACT	GCCAAATATA	CCCACTCTTT	GTTTGTAAAT	TATGCCCTTG	CTTGATATCT	2040
GTTTCCCAAA	ATGGCCCATC	CGCCAGAGCC	ATAGCTTGGT	CTGCTCATAA	TTCTTATAGC	2100
TTTGAATGA	AAATATTCTT	ATCTTCTTAA	GTATAGAAAC	TATTTCTCT	GTCTCTAAC	2160
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GATCCATTTC	CCCTGGATAA	CCAGCTCAAA	GGGAGTGAAA	ATGGTAGTCT	GAGGCGAAGG	2340
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TCAGCCTGT	AATCCAGCA	CTTTGGGAGG	CCGAGGCCGG	CAGATCATGA	GGTGGGAGA	2460
TTGAGACCAT	CCTGGCTAAC	ACGGTGAAGC	CCCGTCTCTA	CTGAAATAC	AAAAAATTAG	2520
CCGGCGGTG	TGGCGGTGTC	CTGTGGTCCC	AGCTACTCGG	GAGGCTGAGG	CGGGAATA	2580
GGGTGGGCT	GGAAAGGGGA	GCTTGCAGTG	AGCGAGATC	GCGCACTGTC	ACTCCATCCA	2640
GCCTGGGTGA	CAGAGTGAGA	CTCTGCCTCA	AAAAAAGAAA	AAAAAAGAAA	AAGCAAAAG	2700
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CCATCTCAGC	CTCTCAAGTA	GCTGGGACTA	CGAGTGTGCA	CCACAGGCT	CACATAATTT	2880
TGTGTTTTTT	GTAGACACGG	GGTTTCACCG	TGTTGCCACG	GCTGCTCTCC	AACTCTCTGG	2940
CTCAAGTGAT	CTGTCCGCTT	CGGCCTCCCA	AACTGCTGGG	ATTACAGGCA	TAAGCCACTG	3000
CACCTAGCCT	TTTATTTGTT	TTTTAAACCA	CGTAGCTCAT	TGCTTCTCT	TAAGTAAATG	3060
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GACATAGCAA	ACCTGTGAG	TGAGGAAAT	TCCCATCTCT	TGAGTGCCCC	CGTCTAGAA	3300
GTTTGGGCCA	TATTATGAA	CAGGGGTCTC	TTATTGAA	AGAGCAAG	GAGGCCAAGA	3360
TTTTAATGGG	GCACTTTAGG	GGATACAGCC	CACATGGGCA	TGGGCTGAG	GTGGCGTGA	3420
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AAAAGGAAT	GAATCCCGAG	CCCATACGCC	AGCACCAGAA	TCAACCAAGT	CTTCAAGGAA	3540
GGAAAGCTAG	GAGAGTTTAA	CAAGATTTTC	ACTGGGCCCA	GCACTGGTGG	TCACACCTGT	3600
AATCCCAAGG	CAGAATGGTG	GCTTGAAGTC	AGGAGTTCAA	GACCAAGCTG	GGCAACACAG	3660
TGAGACCCCTG	TCTCTAAAAA	ATTTAAAAAT	AAACAAGGTG	TTCAACCAAG	TGGGATACCT	3720
CTCACTATTA	AGCCCCATATC	TTTCTCTTTT	TTTCACTTTC	AATTGCTTTG	TGTGATAAAA	3780
AACTAAAGAG	ACTTCTGGTC	CAATTCTGG	CAACATCCCT	TCTGAAAGGT	GAGTAGAGTG	3840
GGTGTCTTCT	ATGCCCATTT	TCCCAATT	TACACAACT	ATTATCAATG	AACTTTTAA	3900
TACCTAGAAT	GGGTAAACCC	AGAGCAAGAC	TTTAAATTAC	CTTCTCTTT	CTTCTACTGG	3960
CAGTTCTGCC	TCCATCACTA	TCAGGCTAGG	GTGACCTTCC	CTTGGTCAAG	CCCCAATTGC	4020
CCATGATTTC	TGCCCTTGCC	CTTCTCCAG	TGACCAATTG	GTGACCAGAT	GGTAGATATA	4080
GAAAGGGGAT	GGCAATTGCA	AGTGACTAGT	CTGCCACAAA	ATGCTCATCT	GATTAGCCAC	4140
TGCTGCCCTG	GCAATGGCTT	TGTAAGAGTC	AATGAGAACT	AGAGCCAGGC	TGTGGTCCCT	4200
GGCCATCAAC	AGTGTGGGTG	ACGCGAGGGA	GTCCCTTTGG	TTTAAATAAT	CCAGTTTCTC	4260
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5 TGTGGAAGT TCCCCAGTG TGGATGCAGA TACGCAGCTC CTGAGCTCCA GCCTAAAGTC 4380
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 CAAAGGCCAC AGACAGCCCT TAGACTATTC CGGAAACAGT AGGAAAAATT ACATATGTCT 4500
 10 TAGACTTCTT TATTCTGACT CCACTGATT TTAGCATAAT ACTTTAAGGA GCTACTTTTT 4560
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 ACAGCTTTAT TGAGATATAA TTCACATATT ATACAATTCA CCTTTAAAC ATACGATTCA 4740
 ATGGTTTTCA GCAAACTCAC AGAGTTGTCC GCCCACTTGA GAGCAAAAC ATGTTCAATT 4800
 15 TTCTTTTCTT TTTTTTTTTT GAGACAGAGT CAGCTTTGTC GCCCAGGCTG GAGTGCAGTG 4860
 CCATGATCTT GGCTCACTGC AGCCTCCCCA TCCTGGGTTT AAGTGATCTT TCTGCTTCAG 4920
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Seq ID NO: C188 DNA Sequence

Nucleic Acid Accession #: NM_014324.1

Coding sequence: 89..1237

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Nucleic Acid Accession #: XM_091332.1

Coding sequence: 1..1401

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Seq ID NO: C190 DNA Sequence
 Nucleic Acid Accession #: XM_054869.2
 Coding sequence: 26..2902

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Seq ID NO: C191 DNA Sequence
 Nucleic Acid Accession #: NM_000793.2
 Coding sequence: 401..1222

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	160	GTGAGAAATG	ACGCGTGCAT	ATGCTACACA	TATGTGCTTC	TCAGTTGCAG	AAAAATGACT	6300
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Seq ID NO: C192 DNA Sequence
Nucleic Acid Accession #: NM_006549.2
Coding sequence: 824..2590

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	AGGCCAAGGC	GGGTGAGATCA	CGAGGTCAAG	AATTCAAGAT	TAGCCTGGAC	AACATGGTGA	240
	AACCCCATCT	CTACGAAAAA	TACAAAAATT	AGCCCAAGTAT	GGTGGCCGGC	GCCTGTAAATC	300
	CCAGCTACTC	GGGAGACTGA	GGCAGAGAAC	TGCTTGAACC	TGGGAGGCAG	AGGTTGCAGT	360
	GATCCGAGAT	CGCGTCACTG	CACCTCAGCG	TGGGCGACAG	AGCGAGACTC	CGTTTCAGAA	420
50	AAGAAAAAAA	AAAAAATAAA	AAAAAGGGAG	TCCGGGTGGA	GCTCTCATTT	GCTCGTTGCA	480
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	ACCCAGTTAA	CTAGAGGGCT	TTGAACCTTT	TATTAACCTG	GAGGTTGACT	CTCCTGTCAA	600
	CTCGATTCCC	TTTTTGGCTGT	TTGGCAGGGT	CAGTGAGACA	TCCCTTGGGT	CGCTCGACCC	660
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55	TTATCCAGCT	GGGGGATCCA	ACGCACACTT	AAGGCTCCAG	CAAAGTGGCT	CGCTGCGCGG	780
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65	GGAGTCTCAC	CACGTCTCCA	TCAOGBGTAT	GCAGGACTGT	GTGCAGCTGA	ATCAGTATAC	1320
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	CAAGATCGCT	GACTTTGGTG	TGAGCAATGA	ATTCAAGGGC	AGTGACCGGC	TCTCTCCCAA	1860
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	CCTGGAATTT	CCAGACCCAG	CCGACATAGC	TGAGGACTTG	AAGGACCTGA	TCACCCGTAT	2100
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Seq ID NO: C193 DNA Sequence
 Nucleic Acid Accession #: NM_018646
 Coding sequence: 217..2394

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CTCCTTCTAG CTGCAAAAGA TAATGATGTC CAGGCCCTGA ACAAGTTGCT CAAGTATGAG 420
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Seq ID NO: C194 DNA Sequence

Nucleic Acid Accession #: NM_021910.1

Coding sequence: 260..601

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Seq ID NO: C195 DNA Sequence

Nucleic Acid Accession #: NM_005971.2

Coding sequence: 176..439

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1304

Seq ID NO: C196 DNA Sequence
Nucleic Acid Accession #: NM_004961.2
Coding sequence: 55..1575

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30	GAAGCTTTTG	TGTGCCAGAT	TGTCAACACT	GAGGGAAGTG	ATGGAGAGGA	GCGCCCGTCT	1320
	TGCTCAGCCC	AGCAGCCCCC	TAGCCCAAGT	AGCCCTGAGG	GTCCCCGCG	CCTCTGTCTC	1380
	ANGCTGGCCT	GCTGTGAGTG	GTGCAAGCGT	TTTAAAGAGT	ACTTCTGCAT	GGTCCCGGAT	1440
	TGTGAGGCCA	GTACCTGGCA	GCAGGGCCCG	CTCTGCATCC	ATGTCTACCG	CCTGGATAAC	1500
	TACTCGAGAG	TTGTTTCTCC	AGTGACTTTC	TTCTCTCTCA	ATGTGCTCTA	CTGGCTTGTT	1560
35	TGCCTTAACT	TGTAGGTACC	AGCTGGTACC	CTGTGGGGCA	ACCTCTCCAG	TTCCCCAGGA	1620
	GGTCCAAAGC	CCTTCCCAAG	GGAGTTGGGG	GAAAGCAGCA	GCAGCAGCAG	GAGCGACTAG	1680
	AGTTTTTCTT	GCCCATTCCT	CCAAACAGAA	GCTTGCAGAG	GGTTGTCTTT	TGCTGCCCTT	1740
	CTCCCTTACC	TGGCCCATTC	ACTGAGTCTT	CTCAGCAGAC	CATTTCAAAT	TATTAATAAA	1800
	TGGGCCACCT	CCCTCTTCTT	CAAGGAGCAT	CGGTGATGCT	CAGTGTTCAA	AACCCAGGCC	1860
40	ACTTAGTGAT	CAGCTCCCTA	AAACCATGCG	TAAGTACAGG	CGGATTAGCT	ATCTTCCAAC	1920
	AATGCTGACC	ACCAGACAAT	TACTGCAATT	TTCCAGAGCC	CCACTATTGC	CTTGTAGTGG	1980
	CTTTGGGCCC	AGTTCTGGCC	TCAGCCTCAA	AGTGCACCGA	CTAGTGTGCT	GCCTATACCT	2040
	GGCACCTCAT	TAAGATGCTG	GGCAGCAGTA	TAACAGGAGG	AAGAGATCCC	TCTCCTTTGG	2100
	TCAGATTATT	ATGTTCTCAG	TTCTCTCTCC	CTGCTACCCC	TTTCTCTGCA	GATAGATAGA	2160
45	CACCTGGCATT	ATCCCTTTAG	GAAGAGGGGG	GGGCAGCAG	AGAGCCTATT	TGGGACAGCA	2220
	TTCTCTCTCT	TCTGCTGCTG	TGACATCTCC	CTCTCTCTGC	TGGCTCCATC	TTTGTCTGTC	2280
	ACTACCAATT	CAATGCCCTT	CATCCAATGG	GTATCTAATT	TTGTGTGTGA	TTATAGTAAC	2340
	TACTCCCTGC	TTTATATGCC	ACCCTCTTCC	TTCTCTTTGA	CCCCTGTGAC	TCTTCTGTGA	2400
	ACTTTCCGAG	TGACTTCCCC	TAGCCCTGAC	CCAGGCACTA	GGCCTTGGTG	ACTTCTCTGG	2460
50	GCCAAGAAAC	TAAAGAAACT	CGGCTTTGCA	ACAGGCATTA	CTCGCCATTG	ATTGGTGCCC	2520
	ACCCAGGGCA	CACGTGCGGA	GTTCTATCAC	TTGCTTGACC	CCTGGACCCA	TAAACCAATC	2580
	CACGTGTATA	CCCGGGGCAC	TCTAACCATC	ACAATCAATC	AATCAAATTC	CCCTAAATTT	2640
	GTATGCACT	GGAACTTTGG	CAAGCACTT	TTGACAGATT	GTGCTGATTT	GGAGCTTCAT	2700
	GATAGCCTTG	TGACATCTTT	AGGGCAGGAT	TCTTATCCCC	ATTTTGAGCA	TGAAACCCCT	2760
55	GAGTCACAGA	TTTCTGTGGG	ACTGTGGATC	TCACTGGAAG	CTATCCAAGA	GCCCACTGTC	2820
	ACCTTCTAGA	CCACATGATA	GGGCTAGACA	GCTCAGTTCA	CCATGATTCT	CTTCTGTGAC	2880
	CTCTGCTGGC	ACACAGGTGG	CAAGGCCCGA	AATGGCGAAC	TCTCTTTAGC	TCAATTTCTG	2940
	GGCCTGAGGT	GCTCAGACTG	CCCCCAAGAT	CAAACTCTCT	CTGGCTGTAG	TAAACCAAGT	3000
	GAATGAATTT	GGACATGCCC	CAATGCTTCT	ATATGCTAAG	TGAAATCTGT	GTCTGTAAAT	3060
60	TGTTGGGGGG	TGGATAGGGT	GGGGTCTCCA	TCTACTTTTT	GTCAACATCA	TCTGAAATGG	3120
	GGAAATATGT	AAATAAATAT	ATCAGCAAAG	CAAAAAGAAA	AAAAAATA		3168

65

Seq ID NO: C197 DNA Sequence
Nucleic Acid Accession #: NM_021984.1
Coding sequence: 572..1753

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70	TCCAAAGTTC	TTCCAGTCCT	CCTAGGCATC	TTATTGATCC	TCCAGTCGAG	AACATGTATA	120
	CAGAGAAGTG	CTCAAATCAT	AAGTGTACAG	CTGATGAGTT	GTCAAAAAAT	GACCAAGCCG	180
	GTGTAAGAGAA	AGCCAAATCA	AGGACCCGAA	TGTGAGCAGG	ACCTCAGAA	CCCTTTTGT	240
	CAGTCCCTCC	CAGCAAGAGC	AGCAGTATCC	GGACTTCTAA	CACCATCGGG	TGAGGGGACC	300
	TCAGACTGAA	TCAAAGAAATG	AAGCCTCTTC	CGTGATGTTT	GTCTATGGCC	CCGAGCCCA	360
75	GCCTCTGGAA	AATCAGCTCC	TCTCTGAGGA	AACAAAGTCA	ACTGAGACTG	AGACTGGGAG	420
	CAGAGTTGGC	AAACTGCCAG	AAGCCTCTCG	CATCCTGAAC	ACTATCCTGA	GTAAATTATGA	480
	CCACAAACTG	CGCCCTGGCA	TTGGAGAGAA	GCCCACTGTG	GTCACTGTGT	AGATCTCTGT	540
	CAACAGCCTT	GGTCTCTCT	CTATCTTAGA	CATGGAATAC	ACCATGACA	TCACTCTCTC	600
	CCAGACTTGG	TACGACGAAC	GCTCTGTGTA	CAAGACACCC	TTTGTGCTCT	TTGTTCTGAA	660
80	TGGCAATGTG	GTGAGCCAGC	TATGGATCCC	GGACACCTTT	TTTGGGAATT	CTAAGAGGAC	720
	CCAAGAGCAT	GAGATCAACA	TGCCCAACCA	GATGGTCCCG	ATCTACAAGG	ATGGCAAGGT	780
	TTTGTACACA	ATTAGGATGA	CCATTGATGC	CGGATGCTCA	CTCCACATGC	TCAGATTTCC	840
	AATGGAATCT	CACCTCTGCC	CTCTATCTTT	CTCTAGCTTT	TCTTATCTCT	AGAATGAGAT	900
	GATCTACAGA	TGGGAAATTT	TCAAGCTTGA	AATCAATGAG	AAGAATCTCT	GGAGCTCTTT	960

5	CCAGTTGGAT	TTTACAGGAG	TGAGCAACAA	AAC TGAAATA	ATCACAAACC	CAGTTGGTGA	1020
	CTTCATGGTC	ATGACGATT	TCTCAATGT	GAGCAGGCGG	TTTGGCTATG	TTGCCCTTCA	1080
	AAACTATGTC	CCTTCTCCG	TGACCAAGAT	GCTCTCCTGG	GTTCCTTTT	GGATCAAGAC	1140
	AGAGTCTGCT	CCAGCCCGGA	CCTCTCTAGG	GATCACTCT	GTTCGACCA	TGACCAAGTT	1200
	GGGCAOCTTT	TCTGTAAAGA	ATTTCOOCOG	TGCTCTCTAT	ATCACAGCCT	TGGATTCTTA	1260
	TATCGCCATC	TGCTTCTGCT	TCTGCTTCTG	CGCTCTGTTG	GAGTTTGTCT	TGCTCAACTT	1320
	CTTGATCTAC	AACCAAGACAA	AAGCCCATGC	TTCTCCTAAA	CTCCGCCATC	CTCGTATCAA	1380
	TAGCCGTGCC	CATGCCCGTA	CCOCTGCAAG	TTCCCGAGCC	TGTGCCCGCC	AACATCAGGA	1440
10	AGCTTTTGTG	TGCCAGATTG	TCACCACTGA	GGGAAGTGAT	GGAGAGGAGC	GCCCGTCTTG	1500
	CTCAGCCAG	CAGCCCCCTA	GCCAGGTAG	CCCTGAGGGT	CCCCGAGCC	TCTGTCCAA	1560
	GCTGGCTG	TGTGAGTGGT	GCAAGCGTTT	TAAGAAGTAC	TTCTGCATGG	TCCCGATTG	1620
	TGAGGGCAGT	ACCTGGCAGC	AGGCCCGCCT	CTGCATCCAT	GTCTACCGCC	TGGATAACTA	1680
	CTGAGAGTT	GTTCCTCCAG	TGACTTCTT	CTTCTCAAT	GTGCTCTACT	GGCTTGTGTT	1740
15	CCTTAACCTG	TAGGTACAG	CTGGTACCCT	GTGGGGCAAC	CTCTCCAGTT	CCCCAGGAGG	1800
	TCCAAGCCCC	TGCGCAAGGG	AGTTGGGGGA	AAGCAGCAGC	AGCAGCAGGA	GCGACTAGAG	1860
	TTTTTCTG	CCCATTCCCC	AAACAGAAAGC	TTGCAGAGGG	TTTGTCTTTG	CTGCCCTCT	1920
	CCCTACCTG	GCCCATTCAC	TGAGTTTCT	CAGCAGACCA	TTTCAAAATTA	TTAAATAAATG	1980
	GGCCACCTCC	CTCTTCTTCA	AGGAGCATCC	GTGATGCTCA	GTGTTCAAAA	CCACAGCCAC	2040
20	TTAGTGATCA	GCTCCCTAAA	ACCATGCCTA	AGTACAGGCG	GATTAGCTAT	CTTCCAACAA	2100
	TGCTGACCAC	CAGACAATTA	CTGCATTTT	CCAGAAGCCC	ACTATTGCCT	TTGCAGTGCT	2160
	TTCCGCCAG	TTCTGGCCTC	AGCCTCAAAG	TGCACCGACT	AGTTGCTTGC	CTATACCTGG	2220
	CACCTCATTA	ACCTGGCTGGG	CAGCAGTATA	ACAGGAGGAA	GAGATCCCTC	TCCTTGTGTC	2280
	AGATTATTAT	GTTCCTCAGTT	CTCTCTCCCT	GCTACCCCTT	TCTCTGCAGA	TAGATAGACA	2340
25	CTGGCAGATT	CCCTTAGGA	AGAGGGGGGG	GCAGCAAGAG	AGCCTATTG	GGACAGCATT	2400
	CCTCTCTCTC	TGCTGCTGTG	ACATCTCCCT	CTCCTGCTG	GCTCCATCTT	TGCTCTGCAC	2460
	TACCAATTCA	ATGCCCTTCA	TCCAATGGGT	ATCTATTTT	GTGTGTGATT	ATAGTAACATA	2520
	CTCCCTCTG	TATATGCCAC	CCTCTTCCCT	CTCTTGACC	CCTGTGACTC	TTTCTGTAA	2580
	TTTCCAGTG	ACCTCCCCTA	GCCCTGACCC	AGGCACTAGG	CCTTGTGAC	TTCTGGGGC	2640
30	CAAGAACTA	AGGAAACTCG	GCTTGCAC	AGGCATTACT	CGCCATTGAT	TGGTGCCAC	2700
	CCAGGGCACA	CTGTGGAGT	TCTATCACTT	GCTTGACCCC	TGGACCCATA	AACAGTCCA	2760
	CTGTATATACC	CGGGGCACTC	TAACCATCAC	AATCAATCAA	TCAAATTTCC	TTAAATTTGT	2820
	ATGGCACTGG	AACCTTGGCA	AAGCACTTTT	GACAAGTTGT	GTCTGATTGG	AGCTTCATGA	2880
	TAGCCTTGTG	ACATCTTAG	GSCAGGATTC	TTATCCCAT	TTTGCAAGAT	AAAACCTGTA	2940
35	GTCCAGATT	TCTGTGGGAC	TGTGGATCTC	ACTGGAAGCT	ATCCAAGAGC	CCACTGTCTC	3000
	CTTCTAGACC	ACATGATAGG	GCTAGACAGC	TCAGTTTACC	ATGATTCTCT	TCTGTCACT	3060
	CTGTGGGAC	ACCACTGGCA	AGGCCAGAA	TGGCGACCTC	TCTTTAGCTC	AAATTTCTGG	3120
	CCTGAGGTGC	TCAGACTGCC	CCCAAGATCA	AATCTCTCCT	GGCTGTAGTA	ACCCAGTGA	3180
	ATGAATTTGG	ACATGCCCCA	ATGCTTCTAT	ATGCTAAGTG	AAATCTGTGT	CTGTAATTTG	3240
40	TTGGGGGTG	GATAGGGTGG	GCTCTCCATC	TACTTTTTGT	CACCATCATC	TGAAATGGGG	3300
	AAATATGTAA	ATAAATATAT	CAGCAAAGC				3329

Seq ID NO: C198 DNA Sequence
Nucleic Acid Accession #: NM_021987.1
Coding sequence: 572..1657

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	CAGAGAAGTG	CTCAAAATCAT	AAGTGTACAG	CTGATGAGTT	GTCAAAAAT	GACCAACAGC	180
	GTGTAAGAAA	AGGCAAAATCA	AGGACCCGAA	TGTGAGCAGG	ACCTCAGAA	CCCCCTTTGT	240
	CACCTGCTCC	CAGCAAAAGCG	AGCACTATCC	GGACTTCTAA	CACCATCCGG	TGAGGGGACC	300
	TCAGACTGAA	TCAAGAAATG	AAGCCTCTTC	CGGTGATGTT	GTCTATGGCC	CCAGCCCCCA	360
55	GCCCTGGA	AATCAGCTCC	TCTCTGAGGA	AACAAAGTCA	ACTGAGACTG	AGACTGGGAG	420
	CAGAGTTGGC	AAACTGCCAG	AAGCCTCTCG	CATCCTGAAC	ACTATCCTGA	GTAATTATGA	480
	CCACAAACTG	CGCCCTGGCA	TTGGAGAGAA	GCCCACTGTG	GTCACTGTTG	AGATCTCCGT	540
	CAACAGCCTT	GGTCCCTCTC	CTATCCTAGA	CATGGAATAC	ACCATTGACA	TCATCTTCTC	600
	CCAGACCTGG	AATTTCTAAGA	GGACCCACGA	GCATGAGATC	ACCATGCCCC	ACCAGATGGT	660
60	CCGATCTAC	AAGGATGGCA	AGGTGTTGTA	CACAATTAGG	ATGACCATTG	ATGCCGAGTG	720
	CTCACTCCAC	ATGCTCAGAT	TTCCAATGGA	TTCTCACTCT	TGCCCTCTAT	CTTTCTCTAG	780
	CTTTTCTTAT	CCTGAGAATG	AGATGATCTA	CAAGTGGGAA	AATTTCAAGC	TTGAAATCAA	840
	TGAGAAGAAC	TCCTGGAAGC	TCTTCCAGTT	TGATTTTACA	GGAGTGAGCA	ACAAAACCTGA	900
	AATAATCACA	ACCCAGTGTG	GTGACTTCAT	GGTCATGAGC	ATTTTCTTCA	ATGTGAGCAG	960
65	GCGGTTTGGC	TATGTTGCGT	TTCAAACATA	TGTCCCTTCT	TCCGTGACCA	CGATGCTCTC	1020
	CTGGGTTTCC	TTTTGGATCA	AGACAGAGTC	TGCTCCAGCC	CGGACCTCTC	TAGGGATCAC	1080
	CTCTGTCTG	ACCATGACCA	CGTTGGGCAC	CTTTTCTCGT	AAGAAATTCC	CGCGTGTCTC	1140
	CTATATCACA	GCCTTGGATT	TCTATATCGC	CATCTGCTTC	GTCTTCTGCT	TCTGTGCTCT	1200
	GTGAGGATT	GCTGTGCTCA	ACTTCTGAT	CTACAACAG	ACAAAAGCCC	ATGCTTCTCC	1260
70	TAAACTCCGC	CATCCTCGTA	TCAATAGCCG	TGCCCATGCC	CGTACCCGTG	CACGTTCCCG	1320
	AGCCTGTGCC	CGCCAAACATC	AGGAAGCTTT	TGTGTGCCAG	ATTGTACCCA	CTGAGGGAAG	1380
	TGATGGAGAG	GAGCGCCCGT	CTTGCTCAGC	CCAGCAGCCC	CCTAGCCAG	GTAGCCCTGA	1440
	GGGTCCCGCG	AGCCTCTGCT	CCAAGCTGGC	CTGCTGTGAG	TGGTGCAAGC	GTTTTAAGAA	1500
	GTACTTCTGC	ATGCTCCCGG	ATTGTGAGGG	CAGTAOCTGG	CAGCAGGGCC	GCCTCTGCTAT	1560
75	CCATGCTAC	CGCCTGGATA	ACTACTCGAG	AGTTGTTTTT	CCAGTGACTT	TCTTCTCTT	1620
	CAATGTGCTC	TACTGGCTTG	TTTGGCTTAA	CTTGTAGSTA	CCAGCTGTA	CCCTGTGGGG	1680
	CAACCTCTCC	AGTTCCCGAG	GAGGTCCAAG	CCCCCTGCCA	AGGGAGTTGG	GGGAAAGCAG	1740
	CAGCAGCAGC	AGGAGGAGCT	AGAGTTTTTC	CTGCCCCATT	CCCCAAACAG	AAGCTTGCAG	1800
	AGGGTTTGTG	TTTGTGCCCC	CTCTCCCCCTA	CCTGGCCCCAT	TCACTGAGTT	TTCTCAGCAG	1860
80	ACCATTTCAA	ATTATTAAATA	AATGGGCCAC	CTCCCTCTTC	TTCAAGGAGC	ATCCGTGATG	1920
	CTCAGTGTTC	AAAACCAACAG	CCACTTAGTG	ATCAGCTCCC	TAAAACCATG	CCTAAGTACA	1980
	GGCGGATTAG	CTATCTTCCA	ACAAATGCTGA	CCACAGACA	ATTACTGCAT	TTTTCCAGAA	2040
	GGCCACTATT	GCCTTTGCAG	TGCTTTCCGG	CCAGTTCTGG	CCTCAGCCCTC	AAAGTGCACC	2100
	GACTAGTTGC	TTGCCATATC	CTGGCACCTC	ATTAAGATGC	TGGGACAGCA	TATAACAGGA	2160
	GGAAGAGATC	CCTCTCCTTT	GCTCAGATTA	TTATGTTCTC	AGTTCTCTCT	CCTGCTTACC	2220

	CCTTTCTCTG	CAGATAGATA	GACACTGGCA	TTATCCCTTT	AGGAAGAGGG	GGGGGACGA	2280
	AGAGAGCCTA	TTTGGGACAG	CATTCTCTCT	TCTCTGCTGC	TGTGACATCT	CCCTCTCCTT	2340
	GCTGGCTCCA	TCTTTGCTCT	GCATACCAA	TTCAATGCC	TTCAATCCAAT	GGGTATCTAT	2400
5	TTTTGTGTGT	GATTATAGTA	ACTACTCCCT	GCCTTATATG	CCACCTCTCT	CCTTCTCTTT	2460
	GACCCCTGTG	ACTCTTCTCT	TAACCTTCCC	AGTGACTTCC	CCTAGCCCTG	ACCAGGCACT	2520
	AGGCCTTGGT	GACTTCTCTG	GGCCAAGAAA	CTAAGGAAAC	TCGGCTTTGC	AACAGGCATT	2580
	ACTCGCCATT	GATTGGTGCC	CACCCAGGGC	ACACTGTCCG	AGTTCATATC	CTTGCTTGAC	2640
	CCCTGGACCC	ATAAACCACT	CCACTGTTAT	ACCCGGGGCA	CTCTAACCAT	CACAATCAAT	2700
10	CAATCAAAIT	CCCTTAAAIT	TGTATGGCAC	TGGAACCTTG	GCAAAGCACT	TTTGACAAGT	2760
	TGTGTCTGAT	TGGAGCTTCA	TGATAGCCTT	GTGACATCTT	TAGGGCAGGA	TTCTTATCCC	2820
	CATTTTGTCAG	ATGAAAACCC	TGAGTCACAG	ATTTCTGTGG	GACTGTGGAT	CTCACTGGAA	2880
	GCTATCCCAAG	AGCCCACTGT	CACCTTCTAG	ACCACATGAT	AGGGCTAGAC	AGCTCAGTTC	2940
	ACCATGATTC	TCTTCTGTCA	CCTCTGCTGG	CACACCAAGT	GCAAGGCCCA	GAATGGCGAC	3000
15	CTCTCTTTAG	CTCAATTTCT	GGGCTGAGG	TGCTCAGACT	GCCTCCCAAG	TCAATCTCT	3060
	CCTGGCTGTA	GTAACCCAGT	GGAAATGAAT	TGGACATGCC	CCAATGCTTC	TATATGCTAA	3120
	GTGAAATCTG	TGTCTGTAAT	TTGTTGGGGG	GTGGATAGGG	TGGGCTCTCC	ATCTACTTTT	3180
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20	Seq ID NO: C199 DNA Sequence						
	Nucleic Acid Accession #: NM_021990.1						
	Coding sequence: 1309..2490						
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	TCCAAAGTTC	TTCCAGTCCT	CCTAGGCATC	TTATTGATCC	TCCAGTCGAG	AACATGTATA	120
	CAGAGAAGTG	CTCAAAATCAT	AAGTGTACAG	CTGATGAGTT	GTCAAAAAAT	GACCAAGCGG	180
	GTGTAAGAAA	AGCCAAATCA	AGGACCCGAA	TGTGAGCAGG	ACCTCAGAAAG	CCCCCTTTGT	240
30	CACCTGCTCC	CAGCAAAAGG	AGCACTATCC	GGACTTCTAA	CACCATCGGT	GAGTTTCATA	300
	CCTTGGCAGA	TGGCCTTTAA	CATTTTTGTT	TAATTCAATT	ATCTTACTA	ATCTTCTTCT	360
	TTTTCTTGGC	TGTGGTGCAT	GGCTGTGGAG	CTCAGGCTGG	ACTCCGTGTT	GGCAGCCAGT	420
	TCCTGGATGG	CTGTCTGTGG	GTGGAGGACT	CCTGCCCTTC	CTGTCTTAGAC	ACCCACAAGG	480
	GCTGCTCTTT	AGCCTCCTTC	CCTTCATCCC	CTTCCCCTGC	CCCCAGTGCA	ACGAGTATTA	540
35	CACAAACCAAC	AAAACCGCAA	AATATTCCCA	CAATTTTCTG	GTCCCTCTGT	GGAGAGGCCG	600
	CTCTGGCTTT	TCCCTCTAGC	CCTGGCCCTC	TGCCCTCTCC	TCACTCCTGG	TTGGTGTCTG	660
	TCAGGCTGAC	TAGAGGCCAA	GGCGACCAAC	ACTAGGCAAA	CGCGGCCAGC	GCTCAGACAT	720
	AAATGCCCTC	TTCAATTTCAC	GTGTAACATT	CTTTTAAAT	CTAGGCTCTG	GTTTTGTGTA	780
	TTTTTTCTTA	AATAAAGAG	TGATCATAAA	AGAGGGACAG	CATAGAAAGT	CCCCAAAGAG	840
40	CAGCAAGAGT	TTAAAGAAAT	TCACAAGCCT	AATCTGTAC	TGCTCTTATA	TTTGCTATTA	900
	CCAGTCACAA	TTAACTAGG	TTTTGTGTG	AAAACCTGTT	TTGGTTTGCT	TCGTCCCCAA	960
	GAGGCACAGT	CTGGGGCCCC	TACAGAGTGC	AGGGCAGAGC	TTCAATTTTC	GTTTGAATGT	1020
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	TATGGCCCCC	AGCCCCAGCC	TCTGAAAAAT	CAGCTCCTCT	CTGAGGAAAC	AAAGTCAACT	1140
45	GAGACTGAGA	CTGGGAGCAG	AGTTGGCAAA	CTGCCAGAAG	CCTCTCGCAT	CTGAACACT	1200
	ATCTTGAGTA	ATTATGACCA	CAAACTGCCG	CCTGGCATTG	GAGAGAAGCC	CAGTGTGGTC	1260
	ACTGTTGAGA	TCTCCGTCAA	CAGCCTTGGT	CCTCTCTCTA	TCCTAGACAT	GGAATACACC	1320
	ATTGACATCA	TCTTCTCCCA	GACCTGGTAC	GACGAACGCC	TCTGTTACAA	CGACACCTTT	1380
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50	AGGAATTCTA	AGAGGACCCA	CGAGCATGAG	ATCACCATGC	CCAACAGAT	GGTCCGATC	1500
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55	ACAAACCCAC	AGTCTGACTT	CATGGTCAATG	ACGATTTTCT	TCAATGTGAG	CAGGCGGTTT	1800
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	ACAGCCCTGG	ATTTCTATAT	CGCCATCTGC	TTGCTCTTCT	GCTTCTGCGC	TCTGTTGGAG	2040
60	TTTGTGTGTC	TCAACTTCCCT	GATCTACAAC	CAGACAAAAG	CCCATGCTCT	TCCTAAATCT	2100
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	GCCCGCCAAC	ATCAGGAAGC	TTTTGTGTGC	CAGATTGTCA	CCACTGAGGG	AAGTGATGGA	2220
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	CGCAGCTCT	GCTCCAAGCT	GGCTGTCTGT	GAGTGGTGCA	AGOGTTTATA	GAAGTACTTC	2340
65	TGCATGGTCC	CCGATTGTGA	GGGCAGTACC	TGGCAGCAGG	GCGCCTCTG	CATCCATGTC	2400
	TACCGCTGGG	ATACTACTCT	GAGAGTTGTT	TTCCCACTGA	CTTCTCTCTT	CTTCAATGTC	2460
	CTCTACTGGC	TTGTTTGCCT	TAACTTGTAG	GTACCAGCTG	GTACCCTGTG	GGGCAACCTC	2520
	TCCAGTTCCC	CAGGAGGTCC	AAGCCCTCTG	CCAAGGGAGT	TGGGGGAAAG	CAGCAGCAGC	2580
	AGCAGGAGCG	ACTAGAGTTT	TTCCCTGCCC	ATTCCCCAAA	CAGAAGCTTG	CAGAGGGTTT	2640
70	GTCTTTGCTG	CCCTCTTCCC	CTACCTGGCC	CATTCACTGA	GTTTTCTCAG	CAGACCATTT	2700
	CAAAATTATA	ATAAATGGGC	CACCTCCCTC	TTCTTCAAGG	AGCATCCGTG	ATGCTCAGTG	2760
	TTCAAAACCA	CAGCCACTTA	GTGATCAGCT	COCTAAAACC	ATGCCTAAGT	ACAGGCGGAT	2820
	TAGCTATCTT	CCAACAATGC	TGACCAACAG	ACAATTACTG	CATTTTTCCT	GAAGCCCACT	2880
	ATTGCGCTTG	CAGTGTCTTC	GGCCAGTTTC	TGGCCTCAGC	CTCAAGTGC	ACGACTAGT	2940
75	TGCTTGTGCT	TACCTGGCAC	CTCAATTAAGA	TGCTGGGCAG	CAGTATAACA	GGAGGAAGAG	3000
	ATCCCTCTCC	TTTGGTCAGA	TTAATTATGT	CTCAGTTCTC	TCTCCCTGCT	ACCCCTTTCT	3060
	CTGCAGATAG	ATAGACACTG	GCAATTATCCC	TTTAGGAAGA	GGGGGGGGCA	GCAAGAGAGC	3120
	CTATTTGGGA	CAGCATTCCT	CTCTCTCTGC	TGCTGTGACA	TCTCCCTCTC	CTTGCTGGCT	3180
	CCATCTTTGG	TCTGCACTAC	CAATTCAATG	CCCTTCATCC	AATGGGTATC	TATTTTGTG	3240
80	TGTGATATA	GTAACACTCT	CCTGCTTTAT	ATGCCACCTC	CTTCCCTCTC	TTTGACCCCT	3300
	GTGACTCTTT	CTGTAACTTT	CCAGTGACT	TCCCTTAGCC	CTGACCAGGC	ACTAGGCCCT	3360
	GGTGACTTCT	TGGGGCCAA	AAACTAAGGA	AACCTGGCTT	TGCACAGGC	ATTACTGGCC	3420
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	CCCATAAACC	AGTCACACTGT	TATACCGGGG	GCACTCTAAC	CATCACAATC	AATCAATCAA	3540
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Seq ID NO: C200 DNA Sequence
Nucleic Acid Accession #: NM_021819.1
Coding sequence: 39..1619

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CTCCTCTACG CAGCTTTAGG TACAAGCTCA GCTTCAAAGG CCAAGGCTG GCATTGCTGTC 180
GGGCTGGAAT ACCCTCTGCG AGCCATCATG GAGACGCCAT CCTGGGCTCG GAGGAAGTGC 240
GGCTGAGGCC ATCCATGAGG AACCGGAGTG GCGCGGTGTG GAGCAGGGCC TCTGTCCCTC 300
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Seq ID NO: C201 DNA Sequence
Nucleic Acid Accession #: XM_117036.1
Coding sequence: 25..495

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GGCCCGTGGG GGTCTTCTCG ACCACACAGG TGCCCGAGGG AGGCAGGGCA GGGCCCGGTG 240
GGACCCAGCC CCGAAACGCA GGGTGTGCCC CACGTTTGA GCGCGCTCG CGTGTCTGGT 300
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TGTACCGGCC ACAGCGGGCG CACGTGCGT GGTCTGTGTT CTGGAAGAG TCCGAACAG 420
GCAGCCCCCG AGACAGGGAG GGGCCACGCG GTGCCAGGG GAAGTGGGGA TGGGAATGAG 480
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CGGAACCTGT CACGTTCACT GGTGAACCTG GTGGGAGTGG AATCCATCTC AACAGAGCTG 600
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Seq ID NO: C202 DNA Sequence
Nucleic Acid Accession #: XM_167803.2
Coding sequence: 1162..1488

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GGTCTCTTCC CAACCAAGCC CACCCAGGC ACATTAGCGA CCAGGCTTGG GCTTCCCCAG 540
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TGGGCCGAGG GCGGGGTAGG CTAGCACGGG AGGTAAGGGT GGTATGGGAT GGGGCGGGGG 660
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5 AGCCTTGCC ACCATCCCAG GACTTTGGGC AAGTCACCCG CACTCCCTGG GCCTCGGTTT 780
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Seq ID NO: C203 DNA Sequence
 Nucleic Acid Accession #: NM_024780.1
 Coding sequence: 31..1023

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 25 ACCCTCATTG GCCAGGACAT CTACCGGCTC CTTCTGATGG ATTTTGTGTT CTCTTTAGTC 240
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 50 CCCTGTGAG GTGTGTATCA TGACCATCAA AGTCTACGT CAAGCTAGCT TTGCAGTGGC 1680
 AGTACCGTAG CCAATGAGAT TTATCCGAGA CGCGATTATT GCTAATTGGA AATTTTCCCA 1740
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Seq ID NO: C204 Protein Sequence
 Protein Accession #: Eos sequence

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 CAGTGAGAAA GAAGGCTTGC AGGAGGCAGG AGATGCTGTC CGATGACCAC GTGAATGAAA 240
 TCATCTACA GGTGTGAAT GTTTCCTCTG GGGTCCAAAG CCACCCATCC TCAAATCAGA 300
 TTTTTCAGA AAAGGTGCTG CTAGACTCAA GCATCAACAT GGTTTTGTCA ATATCTGACA 360
 65 TTGATGTGAT AGACTCTCAG ACAGTCAGCA AAAGGAATGA CCAAAGGGT AACCAAGTGC 420
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 TGGGCATAGA CACTCCTGGT TCTTCACATG AAACGTGTTCA AGGACAGAAG TTAATCGCAT 540
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 AGATCAATTG AGGCAAGTTT GGAACCAAGC TCCTCTCTTA TTTCAACTTT CTGAGATGGC 840
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 75 GTTATTTTAG GGACACAGTG ATGTACTATG GCTTTTACAC CAATTCACCC ATCCAGCAG 1020
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Seq ID NO: C205 DNA Sequence
Nucleic Acid Accession #: NM_002250.1
Coding sequence: 397..1680

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Seq ID NO: C206 DNA Sequence
Nucleic Acid Accession #: NM_025257.1
Coding sequence: 1..2139

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Seq ID NO: C207 DNA Sequence
 Nucleic Acid Accession #: NM_016180.1
 Coding sequence: 26..1618

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Seq ID NO: C208 DNA Sequence
 Nucleic Acid Accession #: NM_003273.1
 Coding sequence: 255..2024

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Seq ID NO: C209 DNA Sequence
Nucleic Acid Accession #: NM_015720.1
Coding sequence: 21..1838

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Seq ID NO: C210 DNA Sequence
Nucleic Acid Accession #: NM_001197.3
Coding sequence: 61..543

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Seq ID NO: C211 DNA Sequence
 Nucleic Acid Accession #: AF272357
 Coding sequence: 83..1060

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Seq ID NO: C212 DNA Sequence
 Nucleic Acid Accession #: NM_004445.1
 Coding sequence: 799..3819

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Seq ID NO: C213 DNA Sequence
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 Nucleic Acid Accession #: NM_002151.1
 Coding sequence: 246..1499

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	GTGTGGACGA	GGGGAGGCTG	CCCCACACCC	AGAGGCTGCT	GGAGGTCACT	TCCGTGTGTG	660
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	ACCAAGGGGG	CTATCTTCCC	TTTCGGGACC	CCAACAGCGA	GGAGAACAGC	AACGATATTG	1020
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25	CACCTCTCTG	ACCCCACTGT	AAATATTGTT	CTGCTGTCTG	GGACTCTCTG	CTAGGTGCCC	1740
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Nucleic Acid Accession #: AB037745.1
Coding sequence: 26..1744

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	GGTGATGGCA	GACACAGAGA	ATAAAGAGGT	GGCCAGAATC	ACATTGTGCT	TTGAGACCTT	240
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	TGTGGAGACG	TGGAAGGTTT	CCAAAGGCAA	ACAGTCTCTAT	ACCTACATCA	TTGAGGAGAA	360
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	CACCTACGCT	TTTATTTGTT	TTTTAAACCA	CGTAGCTCAT	TGCCTTCTCT	TAAGTAAATG	3060
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Nucleic Acid Accession #: NM_004864.1
Coding sequence: 26-952

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Nucleic Acid Accession #: NM_052858.1
Coding sequence: 54..1259

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25 Seq ID NO: C434 DNA Sequence
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 Coding sequence: 261..2861

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 CCTCGGCTG GGATTTTCA GCTGGAAATA TAGAAAATAT CTAGCCCAAA GCCTTCATTT 3120
 TAAGACTGG GGAAGGTGAG CCCCAGAT GGGAAAGAAC CACACAGCTA AGGGAGGGCC 3180
 TGGGAGGCC CACCTAGGCC CTTGTGCCA CACCAATTG CCTCAACAAC CGGCCCCAGA 3240
 GTGCCCGGC ACTCTGAGG TAGCTTCTGG AAATGGGGAC AAGTCCCTC GAAGGAAAG 3300

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AAATGACTAG AGTAGAATGA CAGCTAGCAG ATCTCTTCCC TCCTGCTCCC AGCGCACACA 3360
AAACCCGCCCT CCCCTTGGTG TTGGCGGTCC CTGTGGCCTT CACTTGTGTC ACTACCTGTC 3420
AGCCGAGCCT GGGTGCACAG TAGCTGCAAC TCCCCATTGG TGCTACCTGG CTCTCTGTGC 3480
TCTGCAGCTC TACAGGTGAG GCCCAGCAGA GGGAGTAGGG CTGCGCATGT TTCTGGTGAG 3540
CCAAATTGGC TGATCTTGGG TGCTGAACA GCTATTGGGT CCACCCAGT CCCTTTCAGC 3600
TGCTGCTTAA TGCCCTGCTC TCTCCCTGGC CCACCTTATA GAGAGCCCAA AGAGCTCCTG 3660
TAAGAGGGAG AACTCTATCT GTGGTTTATA ATCTTGACAG AGGCACCAGA GTCTCCCTGG 3720
GTCTTGTGAT GAACACTATT TATCCCCCTT CTGCCCCCAA CCACAAACTC TTCTCTTCAA 3780
AGAGGGCCTG CCTGGCTCCC TCCACCCAACT GCACCCCATG AGACTCGGTC CAAGAGTCCA 3840
TTCCCCAGT GGGAGCCAAC TGTCAGGGAG GTCTTTCCCA CCAACATCTC TTCAGCTGCT 3900
GGGAGGTGAC CATAGGGCTC TGCTTTTAAA GATATGGCTG CTTCAAAGGC CAGAGTCACA 3960
GGAAGGACTT CTTCCAGGGA GATTAGTGGT GATGAGAGAG AGAGTTAAAA TGACCTCATG 4020
TCCTTCTGT CCACGGTTT GTTGAGTTT CACTCTTCTA ATGCAAGGGT CTCACACTGT 4080
GAACCACTTA GGATGTGATC ACTTTCAGGT GGCCAGGAAT GTTGAATGTC TTGGCTCAG 4140
TTCATTAAAA AAAGATATCT ATTTGAAAGT TCTCAGAGT GTACATATGT TTCACAGTAC 4200
AGGATCTGTA CATAAAAGTT TCTTCTCTAA ACCATTCAAC AAGAGCCAAT ATCTAGCAT 4260
TTTCTTGGTA GCACAAATTT TCTTATTGCT TAGAAAAATG TCCTCCTTGT TATTTCTGTT 4320
TGTAAGACTT AAGTGAGTTA GGTCTTTAAG GAAAGCAACG CTCCTCTGAA ATGCTTGTCT 4380
TTTTTCTGT GCGGAATATG CTGGTCTTT TTGGGAGATT AGATGTATAG AGTGTATTGA 4440
TGTAACATT TCTGTAGGC ATCACCATGA ACAAGATAT ATTTCTATT TATTTATTAT 4500
ATGTGCATT CAAGAAGTCA CTGTCAGAGA AATAAAGAAT TGTCTTAAAT GTCATGATTG 4560
GAGATGTCCT TTGCATTGCT TGAAGGGGT GTACCTAGAG CCAAGGAAAT TGGCTCTGGT 4620
TTGAAAAAT TTTGCTGTTA TTATAGTAAA CATACAAAGG ATGTCAAAAA AAAAAAATAA 4680
AAAAAATAA AAAAAAATAA AA 4702

Seq ID NO: C217 Protein Sequence
Protein Accession #: NP_005805.1

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1 11 21 31 41 51
| | | | |
MVGKMPVLV TLCAVRVIVD AISVETPDQV LRASQGSVLT LPCTYHTSTS SREGLIQWDK 60
LLLTHTERVV IWPPSNKNYI HGELYKNRVS ISNNAEQSDA SITIDQLTMA DNGTYECSVS 120
LMSDLBGNK SRVRLVLVLP PSKPECGLEG ETIIGNNIQL TCQSKBGSPT PQYSWKRYNI 180
LNQBPPLAQF ASGQFVSLKN ISTDTSGYII CTSSNEEGTQ FCNITVAVRV PSMNVALYVG 240
IAGVVAALI IIGIIYCCC CRGKDDNTED KEDARPNREA YBEPPEQLRE LSREREEDDD 300
YRQBEQRSTG RESPDHLQD 319

Seq ID NO: C218 Protein Sequence
Protein Accession #: Eos sequence

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1 11 21 31 41 51
| | | | |
MGSRTFESPL HAVQLRWGPR RRPPLLPLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF 60
GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCF WGASPTQCTP IEFDSKGSRL 120
LESSLSSESG EEPVYKSLQ WPGATVRAHG SSILACAPLY SWRTEKEPLS DFGVTCYLSL 180
DNFTRILEYA PCRSDFSWAA GQGYCQGGFS AEPTKTGRVV LGGPGSYFWQ GQILSATQEQ 240
IAESYYPYL INLVGQQLQT RQASSIYDSS YLGSVAVGE FSGDDTDFV AGVPKGNLTY 300
GVVTILNGSD IRSLNPFSGE QMASYFGYAV AATDVNGDGL DDLVVGAPLL MDRTPDGRPQ 360
EVGRVYVYLQ HPAGIEPTPT LTLTGHEDEFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET 420
QQGVVVFVFG GPGGLGSKPS QVLQPLMAAS HTPDFFGSAL RGRDRLDGNG YPDILVGSFG 480
VDKAVVYRGR PIVSASASLT IFFAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI 540
GFTVELQDW QXQKGGVRRR LPLASRQATL TQTLILQNGA REDCREMKIY LRNESEFRDK 600
LSPHIALNLF SLDPQAPVDS HGLRPALHYQ SKSRIEDKAQ ILLDOGEDNI CVPDILQLEVF 660
GBQNHVYLDG KNALNLTFRA QNVGEGGAYE AELRVTAPE AEYSGLVRHP GNFSSLSCDY 720
FAVNQSRLLV CDLGNFMKAG ASLWGGRLFT VPHLRDTKKT IQDFQILSK NLNNSQSDVV 780
SPRLSVEAQA QVTILNGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSI 840
SQGVLESCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPGSLHGH QKREAPSR 900
SASSGPQLK CPEAECFLRL CELGPLHQEE SQSLQLHFRV WAKTFLQREH QPFSLQCEAV 960
YKALKMPYRI LPRQLFOKER QVATAVQWTK AEGSYGVPLW IILAILFLGL LLLGLLIYIL 1020
YKLGPFKRLS PYGTAMEKAQ LKPPATSDA 1049

Seq ID NO: C219 Protein Sequence
Protein Accession #: NP_002412.1

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1 11 21 31 41 51
| | | | |
MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDRQ VEKRRNSGPV 60
VEKLKQMGEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTTRYEN 120
YTPDLPRADV DHAIEKAPQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
LAHAFQPGPG IQGDAHFDED ERWTNNFREY NLHRVAABAL GHSGLSLSHST DIGALMYPSP 240
TFSGDVQLAQ DDDIGIQAIY GRSQNFVQPI GPQTPKACDS KLTPTDAITTI RGEVMPFKDR 300
PYMRTNPFYP EVELNFISVP WPQLPNGLEA AYEFADRDEV RPFKGNKYMA VQGGNVLEGY 360
PKDIYSSGPF PRTVKHIDAA LSEENTGKTY FFWANKYWRY DEYKRSNDPG YPKMLAHDFF 420
GIGHKVDVAF MKDGFYFPFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN 469

Seq ID NO: C220 Protein Sequence
Protein Accession #: Eos sequence

80

1 11 21 31 41 51
| | | | |
MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDRQ VEKRRNSGPV 60
VEKLKQMGEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTTRYEN 120
YTPDLPRADV DHAIEKAPQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
LAHAFQPGPG IQGDAHFDED ERWTNNFREY NLHRVAABAL GHSGLSLSHST DIGALMYPSP 240

TFSGDVQLAQ DDIDGIIQAIY GRSQNFVQPI GPQTPKACDS KLTFDAITTI RGEVMPFKDR 300
FYMRTNPFYP EVELNFISVF WPQLPNGLEA AYEFADRDEV RFPKGNKYNA VQGQNVLHGY 360
PKDIYSSGFG PRVVKHIDAA LSEENTGKTY FVANKYWRY DEYKRSMDPG YPKMIAHDFP 420
GIGHKVDVAF MKDGFYFFFH GTRQYKFPDK TKRILTLQKA NSWFNCRKN 469

Seq ID NO: C221 Protein Sequence
Protein Accession #: NP_055146.1

1 11 21 31 41 51
MVRKPVVSTI SKGGYLQGNV NGRLPISLGNK EPPGQEKVQL KRKVTLLRGV SIIIGTIIGA 60
GIFISPKGVL QNTGSGVMSL TIWTVCGVLS LFGALSYAEL GTTIKSGGH YTYILEVFGP 120
LPAFVRVWVE LLIIRPAATA VISLAFGRYI LEPPFIQCEI PELAIKLITA VGITVVMVLN 180
SMSVSWSARI QIFLTFCKLT AILIIIVPGV MQLIKGQTON FKDAFSGRDS SITRLPLAFY 240
YGMAYAYAGW YLNFVTEEEV NFEKTIPLAI CISMAITIGV YVLTNAVYFT TINAEELLS 300
NAVAVTFSEF LLGNFSLAVP IFVALSCFGS MNGGVFAVSR LFYVASREGH LPEILSMIHV 360
RKHTEPLPAVI VLHPLTMI ML FSGDLSLLN FLSFARWLFI GLAVAGLIYL RYKCPDMHRP 420
FKVPLFIPAL FSTCLFMVA LSLYSDPFST GIGFVITLTG VPAYYLFIIW DKICPRWFRIM 480
SEKITRITLQI ILEVVPEDK L 501

Seq ID NO: C222 Protein Sequence
Protein Accession #: NP_003237.1

1 11 21 31 41 51
MGLAWGLGV FLHMVCGTNR IPESGGDNV FDIPELTGAA RKGSRRRLVK GPDPSSPAFR 60
IEDANLIPPV PDDKFDQDLD AVRAEKGFLL LASLRQMKKT RGTLLALERK DHSQGVFSV 120
SNGKAGTLDL SLTVQKQHV VSVREALLAT GQWKSITLFV QEDRAQLYID CEKMEAEILD 180
VPIQSVPFTRD LASIARLRIA KGGVNDNFQ VLNQVRVFG TTPEDILRNK GCSSTSLLV 240
TLDNNVWGS SPAIRTYIG HKTDLQAIC GISCELSM VLBLRLRTI VTTLQDSIRK 300
VTEENKELAN ELRRPLCYH NGVQYRNNEE WTVDSCTECH CQNSVTICK VSCPIMPASN 360
ATVPDECCP RCWPSDSADD GWSFSEWTS CSTSCGNGIQ QGRSCDSLN NRCEGSSVQT 420
RTCHIQECHK RPKQDGGWGH WSPWSSCSVT CGDGVITRI LCNSPSPQMN GKPCBGEARE 480
TKACKDACP INGGWGFWSF WDICSVTCG GVQKRSRLCN NPAPQFGGKD CVGDVTENQI 540
CNKQDCPIDG CLSNPCFAGV KCTSYPDGWS KCGACPPGYS GNGIQCTDVD ECKEVPDACE 600
NHNGEHRCEH TDPGYNCLPC PPRFTGSPQF QGQVEHATAN KQVCKPRNPC TDGTHDCNKN 660
AKCNYLGHYS DPMYRCECKP GYAGNGIICG EDTDLGWP NNLVCVANAT YHCKDNCNPN 720
LPNSGGQEDYD KDGIGDACDD DDDNDKIIPD RDNCFPHYNP AQYDYDRDDV GDRCDNCPYN 780
HNPDAQDTON NGEADACAD IDGDGILNER DNCQYVYNVD QRTDMDGVG DQCDNCPLEH 840
NPDQLSDSD RIGDTCDNQ DIEDDGHQNN LONCPYVFNQ NQADHDKDGK GDACDHDHDDN 900
DGIPDDKDCN RLVPNPQKD SDGDRGDAC KDDFDHDSVP DIDDICPENV DISETDFRRP 960
QMIPLDFKGT SQNDPNWVVR HQGKELVQTV NCDPGLAVGY DEFNAVDFSG TPFINTERDD 1020
DYAGFVPGYQ SSSRFYVVMW KQVTQSYWDT NPTAQGYSG LSVKVVNSTT GPGEHLRNAL 1080
WHTGNTPGQV RTLNHDPRHI GWKDFATYRW RLSHRPKTGF IRVVMYEGKK IMADSGPIYD 1140
KTYAGGRLLGL FVFSQEMVFP SLDKYECRDP 1170

Seq ID NO: C223 Protein Sequence
Protein Accession #: NP_002183.1

1 11 21 31 41 51
MPLLNLGRFL LASCWIIIVRS SPTPGSEHGS AAPDCPSCAL AALPKDVNS QPEMVEAVKK 60
HILNMLHLKK RPDVTQPFVK AALLNAIRKL HVGKVGENG YVEIEDDIGRR AEMNELMEQT 120
SEIITPABSG TARKTLHFELI SKEGSDLSV EAEVWLFLK VPKANRTRK VTIRLFQQOK 180
HPQGLDGTGE EAEVGLKGE RSELLLSEKV VDARKSTWHV FVVSIIQRL LDQKSSLDV 240
RIACEQCES GASLVLLGKK KKKKEEGEOK KKGGEKGAG ADEEKEQSHR PFLMLQARQS 300
EDHFRHRRRR GLECDGKVINI CCKQFFVSF KDIGWNDWII APSGYHANYC EGECPSHIAG 360
TSGSSLSFHS TVINHYMRG HSPFANLKSC CVPTKLRPMS MLYYDDQNI IKKDIQNMIV 420
EEGCS 426

Seq ID NO: C224 Protein Sequence
Protein Accession #: NP_000086.1

1 11 21 31 41 51
MVPDTACVLL LTLAALGASG QGQSPLGSDL GPQMLRELQE TNAALQDVVD WLRQQVREIT 60
FLKNTVMEDC ACGMQQSVRT GLPSVRPLLH CAPGFCPPGV ACIQTESGGR GPCPCAGFTG 120
NGSHCTDVNE CNAHPCFPV RCINTSPGFR CSACPPGYSG PTHQGVGLAF AKANKQVCTD 180
INECETQHN CVFNSVCINT RGSFQCGPCQ PGFVGDAQSG CQGAQRFCP DGSPSECHH 240
ADCVLERDGS RSCVCRVGA GNGILCGRDT DLDGFPDEKL RCPKPCQCRKD NCVTVFNSGQ 300
EDVDRDGIGD ACDPDADGDG VFNEKDNCP VERNPDQRNTD EDKMGDACDN CRSQKNDQK 360
DTDQDGRDA CDDIDGDRI RNQADNCFRV FNSDQKSDG DGIGDACDNC POKSNPDQAD 420
VDHDFVGDAC DSDQDQGDG HQDSRDNCP VFNSAQDSD HDGQGDACDD DDDNDGVFDS 480
RDNCLRVNP QGEDADRDGV GDVCQDDFDA DKVVDKIDVC PENAEVTLTD FRAFQTVVLD 540
PEGDAQIDPN WVLNQGREGI VQTMNSDPGL AVGYTAFNGV DFEGTYHVNT VTDDDYAGFI 600
FGYQSSSFY VVMWQMEQT YHQAHPFRAY AEPGIQLKAV KSSTGPGEQ L RNALWHTGDT 660
ESQVRLWKD PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDITMRGG 720
RLGVPCFSQS NIIMANLRYR CNDTIPEDYE THQLRQA 757

Seq ID NO: C225 Protein Sequence
Protein Accession #: NP_612464

1 11 21 31 41 51

MRPQGPAAASP QRLRGLLLLL LLQLPAPSSA SEIPKKGKKA QLRQREVVDL YNGMCLQGPA 60
 GVPGRDGSFG ANGIPGTPGI PGRDGFKEGK GECLESFEE SWTPNYKQCS NSSLNYGIDL 120
 GKIAECTPTK MRSNSALRLV FSGSLRLKCR NACCQRWYPT FNGAECSGPL PIEAIYYLDQ 180
 GSPENNSTIN IERTSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIIEE 240
 LFK 243

Seq ID NO: C226 Protein Sequence
 Protein Accession #: NP_003216.1

1 11 21 31 41 51
 MATMENKVIC ALVLVSLMAL GTLARAQTET CTVAERERQN CGFPFGVTPSQ CANKGCCPDD 60
 TVRGVPWCFY PNTIDVPPEE ECEP 84

Seq ID NO: C227 Protein Sequence
 Protein Accession #: NP_056234.1

1 11 21 31 41 51
 MPKRAHWGAL SVVILLLNHG PRVALACPHP CACYVPSEVH CTFRSLASVP AGIARHVERI 60
 NLGFSNIQAL SETSPAGLTK LELLMHNGNE IPSIPDQALR DLSSLQVFKF SYNKLRVITG 120
 QTLQGLSNLM RLHIDHNKIE FIHPQAPNGL TSLRLHLLEG NLLHQLHPST FSTPTFLDYP 180
 RLSTIRHLYL AENMVRLTPA SMLRNMPLE NLYLQGNPMT CDCEMRWFLE WDAKSRGILK 240
 CKDKAYEGG QLCAMCFSPK KLYKHEIHKL KDMTCLKPSI ESPLRQNRSR SIEEEQEQEE 300
 DGGSQLILEK FQLPQWSISL NMTDEHGMV NLVCDIKKPM DVYKIHNLQT DFPDIDINAT 360
 VALDFECPMT RENYKLMKL IAYYSEVPVK LHREMLSKD PRVSYQYQD ADEEALYITG 420
 VRAQLIAEPE WVMQPSIDIQ LNRRQSTAKK VLLSYTYQYS QTISTKDTQK ARGSRVWVIE 480
 PSGAVQQRDT VLEGGPQLCS CNVKASESPS IFWVLPDGS I LKAPMDPDFS KFSILSSGWL 540
 RIKSMEPSDS GLYQCLAQVR DEMDRMVYRV LVQSPSTQPA EKDTVTIGIK PGESVTLPCN 600
 ALAIPFAHLS WILFNRRIN DLANTSHVYM LPNGTLLSIPK VQVSDSGYR CVAVNQGGAD 660
 HPTVGTITVK KSGSLPSKRG RRPKAKALSR VREDIVEDEG GSGMGDEENT SRRLHHPKQ 720
 EVPLKTKDDA INGDKKAKRG RRKLKLWKS EKEPEINVAE GRRVFESRRR INMANKQINP 780
 ERWADILAKV RGNLKPQTE VPPLIKTTSP PSLSEVTPP PPAVSPSPAS PVQTVTSAGE 840
 SSADVPLLGE BEHVLGTISS ASMGLEHNHNV GVILVBEPTV STPLEEVVDD LSEKTEITS 900
 TEGDLKGTAA PTLISBPYEP SFTLHLLDTV YEKPTHEETA TEGWSAADVG SSPEPTSEY 960
 EPFLDAVSLA ESEPMQYFDP DLETKSQPDE DMKEDTFAH LTPTPTIWN DSSTSOLFED 1020
 STIGEPGVPG QSHLQGLTDN IHLVKSLSST QDTLLIKKGM KEMSQTLQGG NMLEGDPHS 1080
 RSSESGQBS KSTLDPDSTL GIMSSMSPVK KPAETTGTIL LDKDTTITVT TFRQKVAPSS 1140
 TMSHTPSRRR FNGRRRLRPN KFRHRHKQTP PTTFAPSETF STQPTQAPDI KISSQVBSL 1200
 VFTAWDNTV NTPKQLEMEK NAEPTSKGT RRRKHKRPNK HRYTPTSTVS RASGSKPSPS 1260
 FENKRNIVT PSSETILLPR TVSLKTEGYP DSLDYMTTR KIYSSYPKVQ ETLFVITYKT 1320
 SDGKEIKDGV ATNVDKHKSD ILVTGESITN AIPTSRSLVS TMGEFKRESS FVGFPPTPTW 1380
 NPSTAQPR LQTDIPVTS GENLTDPLLL KELEDVDFTS EPLSLLTST PPHQEEAGSS 1440
 TLLSSIKVEV ASSQASTTTL DQDHLTTVA ILLSETRPQN HTPTAARMKE PASSSPSTIL 1500
 MSLQQTITTK PALPSPRISQ ASRDSKENVP LNYVGNPETE ATPVNNBGTQ HMSGPNELST 1560
 PSSDRDAFNL STKLELEKQV FGSRSLPRGP DSQRQDGRVH ASHQLTRVPA KPILPTATVR 1620
 LPEMSTQAS RYFVTQSQR HWTNKPEITT YPSGALPENK QFTTPTLSST TIPLFLHMSK 1680
 PSIPSKFTDR RTDQFNGYSK VEGNNNIPAE RNPVKGPPSP RIPHYSNGRL PFTNTKLSF 1740
 POLGVTRRQ IPTSPAFVVR ERKVIPGSYN RIHSHSTFHL DFGPAPPLLL HTPQTGTGSPS 1800
 TNLQNIPIVS STQSSISFIT SSVQSSGSPH QSSSKFFAGG PPASKFWSLG EKPQILTKSP 1860
 QTVSVTAED TVFPCEATGK PKPFVTVTKV STGALMTPT RQRPEVLKN GTLVIRKQV 1920
 QDRGQYMDA SNLHGLDRMV VLLSVTVQQP QILASHYQDV TVYLGDTIAM ECLAGTPAP 1980
 QISWIFPDR VHQTVPVES RITLHENRTL SIKEASPSDR GVYKCVASNA AGADSLAIRL 2040
 HVALAPRIQ QEKVLSISLP PGLSIHICT AKAAPLPSVR WVLGDGTQIR PSQFLHGNLF 2100
 VFPNGTLYIR NLAPKDSGRY ECVAAANLVGS ARRTVQLNVQ RAAANARITG TSPRRTDVRY 2160
 GGTLLKDCSA SGDPNPRILW RLPSKRMIDA LPSFDSRIKV FANGTLVKS VTDKADAGYL 2220
 CVARNKQVSS VVLKVDVVM KPAKIEHKEE NDHKVFYGGD LKVDCAVATG PNPESISWLP 2280
 DGLSVNSFMQ SDDSGGRTKR YVFPNGTLY FNEVGMRBEG DYTCFAENQV GKDEMVRVK 2340
 VVTAPATIRN KTYLAVQVY GDVTVACEA KGEPMKVTV LSPTNKVIPT SSEKYQIVQD 2400
 GTLLIQKAQR SDSGNYTCLV RNSAGEDRKT VHIRVNVQPP KINGNENPIT TVREIAAGGS 2460
 RKLIDCKAEG IPTPRVLWAF PEGVVLPAFY YGNRITVHGN GSLDIRSLRK SDSVQLVOMA 2520
 RNEGGEARLI VQLTVLEPME KPIFDPISE KITAMAGHTI SLNCSAAGT TPLVWVLPN 2580
 GTDLQSGQL QRFYHKADGM LHSIGLSVD AGAYRCVARN AAGHTERLVS LKVLKPEAN 2640
 KQYENLVSI NGETLKLPT PPGAGQGRFS WTLFNGMHL GPQTLGRVSL LDNGTLTVRE 2700
 ASVFDRTGYV CRMETEGPS VTSIPVIVIA YPPRITSEPT PVIYTRPGNT VKLNCMAMGI 2760
 PKADITWELP DKSHLKAGVQ ARLYGNRFLH PQGSLTIQHA TQRDAGFYKC MAKNLGSDS 2820
 KTTYIHVF 2828

Seq ID NO: C228 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MPQTKLTRTG APADYRVILK TSQEDELQVP DDISVRVMSS QSVLWSMVD VLEKQKQVVA 60
 SRQYTVRYRE KGELARWDYK QIANREVLIE NLIPDTVEYF AVRISQGERD GKMSTSVFQR 120
 TPESAPTAP ENLNVNPNVG KPTVVAASWD ALPETEGKVK VCLLDITGLFS VSGFPQSAKS 180
 FQNTFFHTPR LSNHLEQSPS PILETLLLPW WMVCSIGNAI FSKSGPTQGE AWDLTTPKPSL 240
 SLCOQECSCQ QKDPSCLAYL IDIQTKQVKN DPQLEGSVFG PCFLFYFLTF MLDIGGFSPI 300
 MCYEDP7VSS LTGNLSKGA ASKADVQONT EDNGKPEKPE PSSPSPRAPA SQHPSVPAS 360
 PQGRNAKDL LDKNKLKILAN GGAPRKPQLR AKKAEELDLQ STEITGEEL GSREDGPMSP 420
 SDTQDQKRTL RPPSRHGHV VAPGRATAVA RMPALPRREG VDKPGFSLAT QPRPGAPPSA 480
 SASPAHAST QTSRHRPLP ASLNDNDLVD SDEDERAVGS LHPKGAFAQ RPALSPSRQS 540
 PSSVLDRSS VHPGAKPASP ARRTPHSGAA EEDSSASAPP SRLSPPEGGS SRLLTQPHL 600
 SSPLSKGGKD GEDAPATNSV APSRSTWSSS VSHLSSRTQ VSEGAASOG ESHGDDGRED 660

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GGRQAEATAQ TLRARPASGH FHLLRHKPPA ANGRSPSRFS IGRGPRLQPS SSPQSTVPSR 720
 AHPRVPSHSD SHPKLSSGIH GDEEDEKPLP ATTVNDHVPS SSRQPISRGW EDLRRSPQRG 780
 ASLHRKEPIF ENPKSTGADT HPQGYSSLA SKAQDVQQST DADTEGHSPK AQPGSTDRHA 840
 SPARPPAARS QQHPSVPRRM TPGRAPQQP PPPVATSQHH PGQSRDAGR SPSQPRLSLT 900
 QAGRPRPTSQ GRSHSSSDPY TASSRGMLPT ALQNDQEDAQ GSYDDDDSTEV EAQDVRAPAH 960
 AARAKEAAS LFKHQQVESF TGAGAGGDHR SQRGHAASPA RPSRPGGPQS RARVPSRAAF 1020
 GKSEPPSKRP LSSKSQQSVS AEDEEEDAG FFKGSKEDLL SSSVPKWPSS STPRGGKDAD 1080
 GSLAKEEREP AIALAPRGGS LAPVKRPLPP PPGSSPRASH VPSRPPPSA ATVSEFVAGTH 1140
 PWPRTYTRAP PGHFTTTPML SLRQRMHAR FRNPLSRQPA RPSYRQGVNG RPNVEGKVL 1200
 GSNKGPNQQR IINGPQGTKN VVDLDRGLVL NAEGRYLQDS HGNPLRIKLG GDGRTIVDLE 1260
 GTFVVSVDGL PLFGQGRHGT PLANAQDKPI LSLGGKPLVG LEVIKKTTHP PTTTMMQPTT 1320
 TTPLPTTTT RPTTATMQP TTTTTPLETT TPRPTTATR RTTTRRPTT VRTTTRTTT 1380
 TTPKPTTIP TCPPGTLEHR DDDGNLIMSS NGIPECYAEE DEFSGLETDT AVPTTEAYVI 1440
 YDEDEYFETS RPTTTEPST TATTPRVIPE EGAISSFPPEE EFDLAGRKRF VAPYVTYLNK 1500
 DPSAPCSLTD ALDHFQVDSL DEIIPNDLKK SLDPPQHAPR NITVVAVEGC HSFVIVDWDK 1560
 ATPGDLVTGY LVYSASYEDF IRNKFSTQAS SVTHLPFLEN KPNTRYFKV QAQNPHGYGP 1620
 ISPSVSFVTE SDNPLLVVRP PGSELGSGHS LSNMIPATRT AMDGNM 1666

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Seq ID NO: C229 Protein Sequence
 Protein Accession #: NP_003005.1

1 11 21 31 41 51
 MFLSILVALC LMLHLALGVR GAPCEAVRIP MCREMPWNIT RMPNHLHHST QENAILAIEQ 60
 YEELVDVNC AVLRFFFFCAM YAPICTLEFL HDPIKPKCKSV CQRARDDCFP LMKMYNHSWF 120
 ESLACDELAV YDRGVCSISE AIUTDLEPVD KWIDITPDMM VQERPLDVDC KRLSPDRCKC 180
 KKKVKPLATY LSKNYGYVVI AKIKAVQSRG CNEVTTVVVD KEIFKSSSPI PRTOVPLITN 240
 SSCQCCHILP HQDVLIMCYE WRSRMMLLEN CLVEKNRDL SKRSIQWEER LQEQRRTVQD 300
 KKKTAGRTSR SNPPKPKGKP PAKPASPKK NIKTRSAQKR TNPKRV 346

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Seq ID NO: C230 Protein Sequence
 Protein Accession #: NP_005931.1

1 11 21 31 41 51
 MAPAAWLRS AARALLPFML LLLLQPPPLL ARALPPDVH LHAERRGQFP WHAALPSSPA 60
 PAPATQEAAP PASSLRPPRC GVPDPDSGLS ARNRQKRFLV SGRWNEKTDL TYRILRFPWQ 120
 LVQEQVQRTM ABALKVNSDV TPLTFTVEHE GRADIMIDFA RYWHGDDLPF DGPFGILAH 180
 FFPKTHREGD VHFYDETWI IGDDQGTDL QVAHEFGHV LGLQHTTAAK ALMSAFYTFR 240
 YPLSLSDDC RGVQHLVYGP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA 300
 VSTIRGELFP FKAGFVNRIR GGQLQPGYPA LASRHWQGLP SPVDAAFEDA QGHIFWFOGA 360
 QYVVDYGEKP VLGAPAPTEL GLVRFVPHAA LVNKGPERNKI YFPRGRDYWR FHPSTRRVDS 420
 PVPFRATDWR GVPSEIDAAF QDADGAYTFL RGRLYWKFD P VKVKALEGFP RLVGPDFFGC 480
 AEPANTFL 488

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Seq ID NO: C231 Protein Sequence
 Protein Accession #: NP_076927

1 11 21 31 41 51
 MGENDPFAVE APFSFRSLFG LDDLKISFVA PDADAVAQI LSLPLKFPF IIVIGIALI 60
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVAV GQONAVLQVF 120
 TAASWKTMCV DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEQGFREHVP SIDHLLPDDK 180
 VTALHHSVIV REGCASGHVV TLQCTACGRH RGYSSRIVGG NMSLLSQWFW QASLQPPQYH 240
 LCGGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL QPVCLTNEMI QPVCLPNSEE NFFDGVKVCWT SGWGATEDGG DASEFVLNHA 360
 VPLISNKNIC HRDVGYYGIS PSMLCAGYLT GGVDSCQGDS GGPLVCQERR LWKLVGATSF 420
 GIGCAEVNKP GVYTRVTSFL DWIHEQMERD LKT 453

60
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Seq ID NO: C232 Protein Sequence
 Protein Accession #: NP_003211

1 11 21 31 41 51
 MLWKLTDNIK YEDCEDRHGD TSNGTARLPQ LGTVGQSPYT SAPPLSHTPN ADFQPPYFPP 60
 PYQPIYVQSQ DPYSHVNDPY SLNPLHAQPO PQHPGWPGQR QSQESGLLET HRGLFHLQSG 120
 LDPRRDYRRH EDLLHGHAPH SSGLDLSIH SLFPAIEVVP HVEDPGINIP DQTVIKKGFP 180
 SLSKSNSNAV SAIPINKDNL FGGVVNPNNEV FCSVPGRSL LSGTSKYKVT VAEVQRRLSP 240
 PECLNASLIG GVLRRAKSKN GGRSLREKLD KIGLMLPAGR RKAANVTLLT SLVEGEAVHL 300
 ARDPGYVCET EPPAKAVAEF LNRQHSDFNE QVTRKNMLLA TKQICKETD LLAQDRSPIG 360
 NSRPNPILP GIQSCLTFFN LISHGFGSPA VCAAVTALQN YLTEALKAMD KMYLSNNPNS 420
 HTDNNAKSSD KEEKERK 437

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80

Seq ID NO: C233 Protein Sequence
 Protein Accession #: NP_002979.1

1 11 21 31 41 51
 MKGLAAALLV LVCTMALCSC AQVGTNKELC CLVYTSWQIP QKFIVDYSET SPQCPKPGVI 60
 LITKRGRIQC ADPNKKVQK YISDLKLANA 89

Seq ID NO: C234 Protein Sequence
 Protein Accession #: NP_004054.1

1 11 21 31 41 51
 5 MILQAHLSL CLIMLYLATG YQEGKPSGP LKPMFYSIYE GQEPSQIIFQ FKANPPAVTF 60
 ELTGETDNIF VIEREGLLYY NRALDRETRS THMLQVAALD ANGIIVEGVPV PITIEVKDIN 120
 DNRPTFLQSK YEGSVRQNSR PGKPFLYVNA TDLDPPATPN GQLYYQIVIQ LPMINNVMYF 180
 QINNKTGAIS LTBEGSQELN PAKNPSYNLV ISVKDMGGQS ENSFSDTTSV DIIVTENIWK 240
 APKPVEMVEN STDHPPIKIT QVRWNPQGAQ YSLVDKEKLP RFPFSIDQEG DIIVTQPLDR 300
 10 EEKDAYVFFA VAKDEYQKPL SYPLEIHVKV KDINDNPPTC PSPVTVEVQ ENERLGNISIG 360
 TLTAHDRDEE NTANSFLNRYR IVEQTPKLFM DGLFLIQTYA GMLQAKQSL KKQDTPOYNL 420
 TIEVSDKDFK TLCPVQINVI DINDQIPIFE KSDYGNLTIA EDTNIGSTIL TIQATDADEP 480
 FTGSSKILYH IIKGSEGRLL GVDTPDHTNT GYVILKKPLD FETAAVSNIV FKAENPEPLV 540
 PGVKYNASSF AKFTLIVTDV NEAPQFSQHV FOAKVSEDVA IGTKGVNVTIA KQPEGLDISY 600
 15 SLRQDTRGWL KIDHVTGEIF SVAPLDREAG SPYRVQVAT EVGSSLSV SEPFLILMDV 660
 NDNPPRLAKD YTGLPFCPL SAPGSLIFEA TDDQHLFRG PHFTFSLGSG SLQNDWEVSK 720
 INGTHARLST RHTEPEEREY VVILIRINDGG RPPLGIVSL PVTFCSCVEG SCFRPAGHQT 780
 GIFTVGMVAG ILLTLLVIG IILAVVFIRI KKDKGKDNVE SAQASEVKPL RS 832

Seq ID NO: C235 Protein Sequence
 Protein Accession #: NP_004434.1

1 11 21 31 41 51
 25 MARARPPPPP SPPPGLLPLL PPLLLLPLLL LPAGCRALEE TMDTKWVTS ELAWTSHPES 60
 GWEEVSGYDE AMNPRTYQV CNVRESSQNN WRTGFIWRR DVQEVYVELK FTVRDCNSIP 120
 NIFGSCKETP NLFYYEADSD VASASSPFWM ENPYVKVDIT APDESFSRLD AGRVNTKVR 180
 FGPLSKAGFY LAFQDQGACM SLISVRAFYK KCASTTAGFA LPPETLTGAE PTLVIAAPT 240
 CIPNAVESVS PLKLYCNGDG EMMVPVGACT CATGHEPAK ESQCRPCPPG SYKAKQGGP 300
 30 LCPCCPNST TSPAASICTC HNNFYRADSD SADSACTTVP SPFRGVISNV NETSLILEWS 360
 EPRDLGGRDD LLYNVICKKC HGAGGASACS RCDNVEFVP RQLGLTERRV HISHLLAHT 420
 YTFEVQAVNG VSGKSLPFR YAAVNITNQ AAPSEVPTLR LHSSSGSSLT LSWAPPERPN 480
 GVILDYEMKY FKSEGIATP VTSQMSVQL DGLRFDARYV VQVRARTVAG YGQYSRPAEF 540
 ETTSEKSGSA QQEQEQLPLI VGSATAGLVF VVAVVVIIV CLRKQRHSD SEYTEKLQY 600
 IAPGMKVIID PFTYEDPNEA VREFAKEIDV SCVKIEBIVG AGEFGEVCRG RLKQFGRREV 660
 35 FVAIKTLKVG YTERQRDPL SBASIMQFD HPNIIRLEGV VTKSRPVMIL TEFMENCALD 720
 SFLRLNDGQF TVIQLVGLMR GIAAGMKYLS EMNVVHRDLA ARNILVNSNL VCKVSDFGLS 780
 RFLEDDPSDP TYTSSLGKPI PIRWTAPEAI AYRKFTSASD VWSYGVIMWE VMSYGERPYW 840
 DMSNQVINA VEDQYRLPFP MDCPTALHQL MLDCKVRDRN LRKPSQITVN TLDKLIRNAA 900
 40 SLKVIASQAS GMSQPLDRT VFDYTTPTTV GDWLDAIKMG RYKESFVSAG FASFDLVAQM 960
 TAEDLLRIGV TLAGHQKCLL SSIQDMRLQM NQTLFVQV 998

Seq ID NO: C236 Protein Sequence
 Protein Accession #: NP_001795.1

1 11 21 31 41 51
 45 MYVGVLDKD SPVYPGPARP ASLGLGPANY GPPAPPPAPP QYPDFSSYSH VEPAPAPPTA 60
 WGAPFPAPKD DWAAAYGPGP AAPAASPASL AFGPPDFDSP VPAPPGPGPG LLAQPLGGPG 120
 50 TPSSPGAQRP TPYENMRSSV AAGGGGGSGK TRTKDKYRVV YTDHQRLELE KBPHYSRYIT 180
 IRRKSELAAN LGLTERQVKI WFOHRRAKER KVNKKQQQQ QPPQPPMAHD ITATPAGPSL 240
 GGLCPSTSL LATSSPMVK EEFLE 265

Seq ID NO: C237 Protein Sequence
 Protein Accession #: NP_068813.1

1 11 21 31 41 51
 55 MGSDRARKGG GGPKDFGAGL KYNSRHEKVN GLEEGVEFLP VNNVIKKVEKH GPGRWVVLAA 60
 VLIIGLLVLL GIGFLVWHIQ YRDVRVQKVF NGYMRITNEN FVDAYENSNR TEFVSLASKV 120
 60 KDALKLLYSV VPFLGPYHKQ SAVTAFSEGS VIAYYWEFS IPQHLVEEAE RVMAEERVVM 180
 LPFRARSLKS FVVTSVVAFP TDSKTVQRTQ DNSCSFGLHA RGVELMRFTT PGFPDSPYPA 240
 HARQWALRG DADSVLSLTF RSFDLASCDE RGSDLVTYVN TSLPMEPHAL VQLCGTYPPS 300
 YNLTFHSSQN VLLITLITNT ERRHPQFEAT FPQLPRMSSC GRLRKAQQT FNSFYYPGHY 360
 65 PPNIDCTWNI EVFNNQHVKV RFKFFYLLEP GVPAGTCPKD YVEINGEKYC GERSQFVVT 420
 NSNKITVRPH SDQSYTDGTF LAEYLSYDSS DPCPGQFTCR TGCIRKELR CDGWADCTDH 480
 SDELNCSCDA GHQFTCKNKF CKPLFWVCDN VNDCCNSDE QGSCCPAQTF RCSNGKCLSK 540
 SQCCNGKDDC GQGSDEASCP KVNVTCTKH TYRCLNGLCL SKGNPECDGK EDCSDGSEK 600
 DDCDGLRSTP RQARVVGTD ADEGEWPMQV SLHALQQGH ICGASLISPNW LVSAHCKYID 660
 70 DRGFRYSOPT QMTAFGLHLD QSQRAPGVQ ERRLKRIISH PFFNDFTFDY DIALLELEKP 720
 ABYSSMVRPI CLFDASHVFP AGKAIWVGW GHTQYGGTGA LILQKGEIRV INQTTCEMLL 780
 PQQITPRMMC VGFLSGGVDS CQGDGSGPLS SVEADGRIFQ AGVVSWDGC AQRNKPGVYT 840
 RLPLFRDWIK ENTGV 855

75 Seq ID NO: C238 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 80 MPPFLLEAV CVPLFSRVPP SLPLQEVHVS KBTIGKISAA SKMMWCSAAV DIMFLDGSN 60
 SVKGSGPERS KHPAITVCDG LDISPERVRV GAFQPSSTPH LEPLDSPST QQEVKARIK 120
 MVFKGARTET ELALKYLLER GLPGGRNASV PQILIVTDG KSQGDVALPS RQLKERGVTV 180
 FAVGVFRPRM EELHALASEP RGQHVLLAQ VEDATNGLFS TLSSAICSS ATPDCRVEAH 240
 PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCPCPCD 300
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEK RVDLLFLDS SAQTTLDGFL 360

5 RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT 420
 LTGSALRQAA ERGFGSATRT QDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVS 480
 EAVRAELEEI TGSFVKHVMVY SDPQDLFNQI PELQGLKCSR QRPQCRTQAL DLVFMILTSA 540
 SVGPNFAQM QSFVRSCALQ FEVNPDTVQV GLVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
 APYLGGVCSA GTALLHIYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQLRNNGI 660
 SVLVVGVGPFV LSEGLRRLAG PRDSLHVAA YADLRYHQDV LIEWLCEAK QPVNLCKPSP 720
 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR FLRRP 755

10 Seq ID NO: C239 Protein Sequence
 Protein Accession #: Eos sequence

15 1 11 21 31 41 51
 MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
 SVGKGSFERS KHFALTVCDD LDISPVRV V GAFQSSSTPH LEFPLDSFST QOEVKARIKR 120
 MVFKGGRRTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSGQDVALPS KQLKRGVTV 180
 PAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLPS TLSSSAICSS ATPDCRVEAH 240
 PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCPCPCD 300
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
 20 RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT 420
 LTGSALRQAA ERGFGSATRT QDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVS 480
 EAVRAELEEI TGSFVKHVMVY SDPQDLFNQI PELQGLKCSR QRPQCRTQAL DLVFMILTSA 540
 SVGPNFAQM QSFVRSCALQ FEVNPDTVQV GLVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
 APYLGGVCSA GTALLHIYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQLRNNGI 660
 25 SVLVVGVGPFV LSEGLRRLAG PRDSLHVAA YADLRYHQDV LIEWLCEAK QPVNLCKPSP 720
 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSSCVCSV QGWILETFLR HMAFVQEGSS 780
 RTPPSNYREG LGTEMVPTFW NVCAPGP 807

30 Seq ID NO: C240 Protein Sequence
 Protein Accession #: XP_097386.1

35 1 11 21 31 41 51
 MPKSEPLGCL SPASRAPGSA AATGAWLPAA SGGPGPLGPP CTCPPRSIGR GRAGSRAGSS 60
 PSGCVCVSGI LRVVSVGDPA SRRWVDLSN SEDLSLLTP MIVGTGGVGG GWARGWVPAQ 120
 EKEVAEGSGH AGRGNRRRLQ RVYGARSWIL GRKPCQLRL PASGGFVQPP PCPSPATACR 180
 WGFKFGVAFW GAAQHPFLCR LGGGRVPSA TRTLDGF 217

40 Seq ID NO: C241 Protein Sequence
 Protein Accession #: CAC03433

45 1 11 21 31 41 51
 MLSTDTFTFA SWELVVVRVDH PNEEQQKQVT LRVSGDLHVG GVMLKLVEQI NISQDWSDF 60
 LWWEQKHCWL LKTHWTLDKY GVQADAKLLP TPQHKMLRLR LFNLMVRLR VFSFVVFKA 120
 VSDICKILNI RRSBELSLK PSQDYFKKK KKKKNNKEPI IEDILNLESS PTAGSSVSP 180
 GLYSKTMTPY YDPINGTPAS STMTWFSOSP LQEQNCSTLA FSQPPQSFEA LADMYQPSRL 240
 VDKAKLAGW LDSSRSLEMQ GIQDEDEQLL RFKYYSFFDL NPKYDAVRIN QLYBQARWAI 300
 LLEEDICTEE ENLIFPAALQY HISKLSLSAE TQDPAGESEV DEIEAALSNI EVTLGGKAD 360
 50 SLLEEDITDIP KLADNLKLF PKKLLPKAFK QYWFIPKDT S IAYFKNKELE QGEPLKLN 420
 RGCEVVPDVN VAGRFKGIKL LIPVADGME MYLRCDHENQ YAQWMAACML ASKGTMTADS 480
 SYQPEVLNII SFLRMKNRNS ASQVASSLEN MDNPECFVS PRCAKKHKS QLAARILEAH 540
 QNVAQMLPVE AKLRFIQAWQ SLPEFGLTY LVRPKGSKD DILGVSYNRL IKIDAATGIP 600
 55 VITWRTNIK QNWNWETRQ VVIEFDQNVF TAFTCLSDAC KIVHEYIGGY IFLSTRSKDQ 660
 NETLDEDLFH KLTGGQD 677

60 Seq ID NO: C242 DNA Sequence
 Nucleic Acid Accession #: NM_005170
 Coding sequence: 337..918

65 1 11 21 31 41 51
 GGGCGTGAGA AAGGCGACGG CGGCGGCGCG GAGGAGGGTT ATCTATACAT TAAAAACCA 60
 GCGCGCTCGG CGCGCGCTGC GGAGACCTGG GAGAGTCCGG CCGCACGCGG GGGACACGAG 120
 CGTCCCACGC TCCTGGCGCG GTACGCGCTG CCACACTAG GCTCTCTATC CCGGGCTCC 180
 AGACGACCTA GGACGCGTGC CTTGGGAGT TGCGTGGCGG GCGCGTGCCA GAAGCCCCCT 240
 TGGGGCGCCA CAGTTTTCCT CGTGGCTCC GGTCTCTCTG CTGACCTCTT CTTGGCGCGC 300
 GCGGGAACCT GGACGCGGCG GGTGGATGCA GGCGGATGG ACGGCGGCAC ACTGCCAGG 360
 70 TCGCGGCCCC CTGCGCCCC CTGCTCTGTC GGCTGCGCTG CCGGCGGAG ACCGCGCTCC 420
 CCGGACTGT TGCTCTGCG CCGGCGGCG CGACCGGCGA CGCGAGAGC CGGAGGCGGC 480
 GCAGCGGCGG TAGCGCGCG CAATGAGCGG GAGCGCAACC GCGTGAAGCT GGTGAACCTG 540
 GGCTTCCAGG CGCTGCGGCA GCACTGCGCG CACGCGCGCG CCAGCAAGAA GCTGAGCAAG 600
 GTGGAGACGC TGGCTCAGC GTGGAGTAC ATCGCGCGCG TGCGAGCGCT GCTGGCGGAG 660
 75 CACGAGCGCG TGCGCAACGC GCTGGCGGGA GGGCTGAGGC CGCAGGCGGT GCGGCGGTCT 720
 GCGCGCGCGG GCGCGCGCAG GACCAACCGG GTGCGCGCTT CGCCCTCCCG CGCTTCTCTG 780
 TCCCGCGGCC CCGGGGCGAG CTGCGAGCCC GGCTCCCGCG GTTCCGCTTA CTCGTCCGAC 840
 GACAGCGGCT GCGAAGGCGC GCTGAGTCTT CGCGAGCGCG AGCTACTCGA CTTCTCCAGC 900
 80 TGGTTAGGGG GCTACTGAGC GCCCTCGACC TA 932

Seq ID NO: C243 Protein Sequence
 Protein Accession #: NP_060233.1

1 11 21 31 41 51

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MSGGHQLQLA	ALMFWLLMAT	LQAGFGRTGL	VLA AA VESER	SAEQKAVIRV	IPLMDPTGK	60
LNLTLGVFA	GVAEITPAEG	KIAMQSHPLYL	CNADDDNLE	PGFISIVKLE	SPRRAPRPLC	120
SLASKARMAG	ERGA SAVLEF	ITEDRAAAEQ	LQOPLGLTWP	VVLIWGNDAE	KLMEFVYKIQ	180
KAHVRIELKE	PPANFDYDVW	ILMTVVGTIF	VIIASVLR	RCRPHSRPD	PLQORTAWAI	240
SQLATRRYQA	SCRQARGSWP	DSGSSCSSAP	VCAICLEEPS	BQELRVISC	LHEFHRNCVD	300
PWLHQHRTCP	LCVFNITEGD	SFSQSLGPSR	SYQSPGRRLLH	LIRQHPGHAH	YHLPAAYLLO	360
PSRSAVARPP	RPQFPLPSQE	PGMGPRIHRF	PRAAHPRAPG	BQRLLAGAQH	PYAQGWGMSH	420
LQSTSQHFAA	CPVPLRRARP	PDSSGSGBSY	CTERSGYLAD	GPASDSSSGP	CHGSSSDSVV	480
NCTDISLQGV	HGSSSTFCSS	LSSDFDPLVY	CSPKGDPRV	DMQPSVTSRP	RSLDSVVFTG	540
ETQVSSVHY	HRHRHHYK	RFQWHRKPG	PETGVQSRP	PIPRTPQPE	PSPDQQVTG	600
SNSAAPSGRL	SNPQCFRALP	EPAPGPVDAS	SICPSTSSLF	NLQKSSLSAR	HPQRKRGGP	660
SEPTPGSRPQ	DATVHPACQI	FPHYTPSVAY	PWSPEAHPLI	CGPPGLDKRL	LPETPGPCYS	720
NSQFVWLCLT	PRQPLEPHFP	GEGPSEWSSD	TAEGRPCYP	HCQVLSAQPG	SEBELCELCE	780
QAV						783

Seq ID NO: C244 DNA Sequence
Nucleic Acid Accession #: NM_004289
Coding sequence: 493..1695

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1	11	21	31	41	51	
GCGGCGGCT	CGTCCACCGG	AGGAGCCGGC	GCCAGCGTGG	ACGGCGGCAG	CCAGGCTGTG	60
CAGGGGGGGG	GCGGGGACCC	CGGAGCGGCT	CGGAGTGGCC	CCTTGGACGC	CGGGGAAGAG	120
GAGAAGGCAC	CCGCGGAACC	GACGCGCTCAG	GTGCCGACG	CTGGCGGATG	TGCGAGCGAG	180
GAGAATGGGG	TACTAAGAGA	AAAGCACGAA	GCTGTGGATC	ATAGTTCCCA	GCATGAGGAA	240
AATGAAGAAA	GGGTGTGAGC	CCAGAAGGAG	AACTCACTTC	AGCAGAATGA	TGATGATGAA	300
AACAAATAG	CAGAGAAACC	TGACTGGGAG	GCAGAAAAGA	CCACTGAATC	TAGAAATGAG	360
AGACACTGTA	ATGGGACAGA	TACTTCTTTC	TCTCTGGAAG	ACTTAITCCA	GTTCCTTTCA	420
TCACAGCCTG	AAAATTCACT	GGAGGGCATC	TCATTGGGAG	ATATTCTCT	TCCAGGCAGT	480
ATCAGTGATG	GCATGAATTC	TTGAGCACAT	TATCATGTAA	ACTTCAGCCA	GGCTATAAGT	540
CAGGATGTGA	ATCTTCTATG	GGCCATCTTG	CTTTGTCCCA	ACAATACATT	TAGAAGAGAT	600
CCACAGCAAA	GGACTTCACA	GTCAACAAG	CCATTCTGCG	AGTTAAATTC	TCATACCACC	660
AATCCTGAGC	AAACCCCTTC	TGGAACATA	TTGACAGGAT	TTCTTTCAAC	GGTTGACAA	720
CATATGAGGA	ATCTAACAA	CCAAGACCTA	CTGTATGACC	TTGACATAAA	TATATTGTAT	780
GAGATAAACT	TAATGTCAAT	GGCCACAGAA	GACAACTTTG	ATCCAAATCG	TGTTTCTCAG	840
CTTTTGTATG	AACCAAGATC	TGATTCTGGC	CTTTCTTTAG	ATTCAAGTCA	CAATAATACC	900
TCGTGTATCA	AGTCTAATTC	CTCTCACTCT	GTGTGTGATG	AAGGTGCTAT	AGGTTATTGC	960
ACTGACCATG	AATCTAGTTC	CCATCATGAC	TTAGAAGGTG	CTGTAGGTGG	CTACTACCCA	1020
GAACCCAGTA	AGCTTTGTCA	CTTGGATCAA	AGTGATTCCTG	ATTTCCATGG	AGATCTTACA	1080
TTTCAACAGT	TATTTTCATA	CCACACTTAC	CACITACAGC	CAACTGCACC	AGAATCTACT	1140
TCTGAACCTT	TTCCGTGGCC	TGGGAAGTCA	CAGAAGATAA	GGAGTAGATA	CCTTGAAGAC	1200
ACAGATAGAA	ACTTGAGCCG	TGATGAACAG	CGTGCTAAAG	CTTTGCATAT	CCCTTTTCT	1260
GTAGATGAAA	TTGTCCGCAT	GCGTGTGTAT	TCTTTCAATA	GCATGTTAAG	TAGATATTAT	1320
CTGACAGACC	TACAACTCTC	ACTTATCCGT	GACATCAGAC	GAAGAGGGAA	AAATAAAGTT	1380
GCTGCGCAGA	ACTGTCTGTA	ACGCAAAATG	GACATAATTT	TGAATTTAGA	AGATGATGTA	1440
TGTAACTTGC	AAGCAAGAAA	GGAAACTCTT	AAGAGAGAGC	AAGCAATG	TAACAAAGCT	1500
ATTAACTATA	TGAACAGAAA	ACTGCATGAC	CTTTATCATG	ATATTTTATG	TAGATTAAGA	1560
GATGACCAAT	GTAAGCCAGT	CAATCCCAAC	CACATGCTC	TCCAGTGTAC	CCATGATGGA	1620
AGTATCTTGA	TAGTACCCAA	AGAACTGGTG	GCCTCAGGCC	ACAAAAGGAA	AACCCAAAAG	1680
GGAAAGAGAA	AGTGAGAGAA	AACTGAAGAT	GGACTCTATT	ATGTGAAGTA	GTAATGTTCA	1740
GAAACTCTTG	ATTTGGATCA	GAAACCAATG	AAACTGCTTC	ATGAATTTGA	TCTTTAAGTA	1800
CTGCTACTTG	ATAACTCAG	TTAAGCTGT	TTTGAAGCTT	ACATGGACAA	ATGTTTAGGA	1860
CTTCAAGATC	ACACTTGTGG	GCAATCTGGG	GGAGCCACAA	CTTTTCATGA	AGTGCAATGT	1920
ATACAAAATT	CATAGTTATG	TCCAAAGAA	AGGTTAACAT	GAACCCCAAG	TAAGACTTTC	1980
CATCTTGCGA	GCCATCTCTT	TTAAGAGTAA	GTTGGTTACT	TCAAAAAGAG	CAACACTGCG	2040
GGATCAAAAT	ATTTTAAGAG	GTATTTCAGT	TTTAAATGCA	AAATAGCCTT	ATTTTCATTT	2100
AGTTTGTATG	CACATAGTGT	AGCTTTTCAA	ACACTATTTT	AATCTTTATA	TTTAACTTAT	2160
AAATTTTGCT	TTCT					2174

Seq ID NO: C245 Protein Sequence
Protein Accession #: NP_004433

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1	11	21	31	41	51	
MALRLGAAL	LLLPLLAAVE	ETLMDSTTAT	AELGWMVHPP	SGWEEVSGYD	ENMNTIRTYQ	60
VGNVPESQON	NWLRTKPIRR	RGARIRHVEM	KFSVRDCSSI	FSVPGSCKET	FNLYYYEADF	120
DSATKTFPNW	MENPHVKVDOT	IAADESFSQV	DLGGRVMKIN	TEVRSFGPVS	RSGFYLAPOD	180
YGGCMSLIIV	RVFYRKCPRI	IQNGAIFQET	LSGAESTSLV	AARGSCIANA	BEVDVPIKLY	240
CNGDGEWLVP	IGRCMKAGF	BAVENGTVCR	GCPSTGFFKAN	QGDEACTHCP	INSRTTSEGA	300
TNCVCNRNGY	RADLDPLDMP	CTTIPSAPQA	VISSVNETSL	MLEWTPPRDS	GGREDLVYNI	360
ICKSCGSGRG	ACTRCGDNVQ	YAPRQLGLTE	FRIYISDILLA	HTQYTFBIQA	VNGVTDQSPF	420
SPQFASVNIT	TNQAAFSAVS	IMHQVSRVTD	SITLSWSQPD	QFNGVILDYE	LQYKEKELSE	480
YNATAIKSPT	NTVTVOGLKA	GAIVVPQVRA	RTVAGYGRYS	GKMYPTQMTB	AEYQTSIQEK	540
LPLIIGSSAA	GLVFLIIVVV	IAIVCNRRRG	PERADSEYTD	KLQHYTSGHM	TPGKMIYIDP	600
PTYEPNEAV	REPAKEIDIS	CVKIEQVIGA	GEFGEVCSGH	LKLPGKREIF	VAIKTLKSGY	660
TEKQRDRFLS	EASIMGQPDH	PNVHLEGVY	TKSTFVMIIT	EFMENGSLDS	FLRQNDGQPT	720
VIQLVGMRLG	LAAGMKYLLAD	MNVVHRDLAA	RNILVNSNLV	CKVSDFLSLR	FLEDDTSDPT	780
YTSALGGKIP	IRWTAPEAIQ	YRKPTSASDV	WSYGVIMWBY	MSYGERPYNW	MTNQDVINAI	840
EQDYRLPPFM	DCPSALEQLM	LDCWQKDRNH	RPRFGQIVNT	LDRMIRNPNS	LKAMAPLSSG	900
INLPLLDRTI	PDYTSFNTVD	EWLEAIKMGQ	YKESPANAGF	TSFDVVSQMM	MEDILRVGLT	960
LAGEQKILN	SIQVMRAQMN	QIQSVEV				987

Seq ID NO: C246 Protein Sequence

Protein Accession #: NP_114148.1

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1      11      21      31      41      51
5      |      |      |      |      |
MDARRVPQKD LRVKKNLKKF RYVKLISMET SSSSDSDSCDS FASDNFANTR LQSVREGCRT 60
RSQCRHSGPL RVAMKFPARS TRGATNKKAE SRQPSSENSVT DSNDSSEDES GNMFLKRAL 120
NIKQNKAMLA KLMSELESFP GSFRGRHPLP GSDSQSRRPR RRTFPGVASR RNFERRARPL 180
TRSRSRILGS LDALPMEEEE EEDKYMLVRK RKTVDGYMNE DDLPRSRRSR SSVTLPHIIR 240
PVBEITEGGV GERLQQFSKR RYITVEWALL VINAVRLLI PKQTAETQTA GAFEASSVAP 300
10     AFETVMVKRS QMLCWIRTGI ARLVEESATA VSAGSEMDGV RLGS LCI 347

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Seq ID NO: C247 Protein Sequence
Protein Accession #: NP_036577.1

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1      11      21      31      41      51
15     |      |      |      |      |
MENPSPAAL GKALCALLLA TLGAAGQPLG GESICSARAP AKYSITFTGK WSQTAPPKQY 60
PLFRPPAQWS SLLGAHSSD YSMWRKNQYV SNGLRDFAEER GEAWALMKBI EAAGEALQSV 120
HAVFSAPAVP SGTGQTSAEL EVQRRHSLVS FVVRIVPSFD WFGVDSLDL CDGDRWREQA 180
20     ALDLYPDAG TDSGTTFSSP NFATIPQDTV TEITSSSPSH PANSFYYPRL KALPPIARVT 240
LVRLRQSFPRA FIPPAFVLPVS RDNEIVDSAS VPETPLDCEV SLWSSWGLCG GHCGRLGTKS 300
RTRYVRVQPA NNGSPCPELE EBAECVPDNC V 331

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Seq ID NO: C248 Protein Sequence
Protein Accession #: NP_063947.1

```

1      11      21      31      41      51
30     |      |      |      |      |
MLQDFDSQDP LNSLDVKFLR KPRIPIIIL LSLASIIIV VLIKVILDKY 60
YFLCGQLPHF IPRKQLCDGE LDCFLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVLDSAT 120
GNWFSACFDN FTEALAEAC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
GPCLSGSLVS LHCLACGKSL KTRPVVGGEE ASVDSWPMQV SIQYDKQHC GGSILDPHNV 240
LTAACHCFKHH TDVFNKWKRA GSDKLGSFPS LAVAKIIIE FNPMPYKND IALMKLQFPL 300
TFSGTVRPIC LPFFDEELTP ATPLWIIWGW FTKQNGGKMS DILLQASVQV IDSTRCNADD 360
35     AYQGEVTEKM MCAGIPEGGV DTCQDSSGGP LMVQSDQMHV GVIGSWGYGC GGPSTPGVYT 420
KVSAYLNIWY NVWKAEAL 437

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Seq ID NO: C249 Protein Sequence
Protein Accession #: NP_003036.1

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1      11      21      31      41      51
40     |      |      |      |      |
MGCKVLLNIG QQMLRRKVVD CSREETRLSR CLNTFDLVAL GVGSTLGAGV YVLGAVARE 60
NAGPAIVISF LIAALASVLA GLCYGEFGAR VPKTGSAYLY SYVTVGELWA FITGWNILIS 120
45     YIIGTSSVAR ANSATPDELI GRPIGEFSRT HMTLNAPGVL AENPDIFAVI IILILTGLLT 180
LGVKESAMVN KIFTCINVLV LGPIMVSGFV KGSVKWQLT EEDFGNTSGR LCLNNDTKEG 240
KPGVGGFMPF GFSGVLSGAA TCFYAFVGFQ CIATTGEEVK NPQKAI PVGI VASLLICFIA 300
YFGVSAALTL MMYFPCLDNN SPLDPAFKHV GWGAKYAVA VGSICALSAS LLGSMFPMFR 360
VIVAMEDGL LFKFLANVND RTKTPILATL ASGAVAAVMA FLFDLKLVD LMSIGTLAY 420
50     SLVACVLVL RYQPEQPNLV YQMASTDEL DPADQNELAS TNDSQLGFLP EAMFSLKTI 480
LSPKNMEPSK ISGLIVNIST SLIAVLIITP CIVTVLGREA LTKGALWAVF LLAGSALLCA 540
VVTGVINRQP ESKTKLSFVK PFLPVLPILS IFVNVYLMQ LDQGTWVRA VMMLIGFIY 600
FGYGLWHEE ASLDADQART PDGNLDQCK 629

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Seq ID NO: C250 Protein Sequence
Protein Accession #: NP_002767.1

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1      11      21      31      41      51
60     |      |      |      |      |
MRAPHLHLSA ASGARALAKL LPLLMAQLWA ABAALLPQND TRLDPEAYGA PCARGSQPMQ 60
VSLFNGLSFH CAGVLVDQSW VLTAAHCGNK PLWARVGDDH LLLQGEQLR RTTRSVVHPK 120
YHQSGSPILP RRTDEHDLML LKLARPVVPG PRVRALQLPY RCAQPGDQCQ VAGWGTTAAR 180
RVKYNKGLTC SSITILSPKE CEVFPYGVVT NNMICAGLDR GQDPQSQSDG GPLVCDLTLQ 240
65     GILSWGVYPC GSAQHPAVYT QICKYMSWIN KVIRSN 276

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Seq ID NO: C251 Protein Sequence
Protein Accession #: XP_095088.3

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1      11      21      31      41      51
70     |      |      |      |      |
MTRAATAEPG RVSPASPARS TAGLPRAFLO SLRTLLDILD DWQRGCVHLR EIQSLWVEAR 60
ELPSQVLEGL SQRRGPQPGA AVRSRRGGAV PRGARAVPER CAGTETRGRG RCSGLQRLGG 120
GFRGCPADPC ARGERRHTI TSGVDCGLLK QMKELEQEKV VLLQGLEMA QGRDWYQQQL 180
75     QQVQERQRL GQSRASADFG AVGSPRLGR LLEKVEQVAR WLGEELAEAC AGRALPTSSS 240
GPPCSALTST SSPGWQQQII LMLKEQNRL TQEVTEKSER ITQLEQKSAL IKQLFEARAL 300
SQQDGLSPA GPHIEPLTRF RLPVLTWAGA LLSPHSPQLL LPLSADSGGP LHELPTWFP 360
AVLWVPSPG KRTAHARLHP HQRPAEGAWQ LGCGAEAAPE TCGTLPHFES HKTTCFDSL 420
GGPCQBEQDR SWSHLGAADF VAPAVAKVTP NREDAAGSRH GDICPLCPKG LLTFRDIAIE 480
FSLAEWQLD HAQQLYRDV MLENYRNLF LGMTVSKPD LACLEQNKEP QNKRNMMAA 540
80     KHPVTCSEFN QDLQPEQSIK DSLQKVIPT YGKCGHENLQ LKCKCKRVE CEVHKGGYND 600
LNQCLSNQTN KIPQTHKCVK VPSKFSNSNR HNARYTGKKG LKCKKYGKSF CMFSLNQHQ 660
IIHTKEKSYK CEECGKSPNH SSSGTHKRI LTGEKPYRCE ECGKAFRWPS NLTRHKRIHT 720
GEKPYACEEC GAAPRRSSTL TNHKRHTGE RPYKCEBCKG AFSVSSALIY HKRIHTGEK 780
YTCEBCKGAF NCSSTLTKTHK IIHTGEKPYT CEEGRTFNC SSTVKAHKRI HTGEKPYKE 840

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5
10
BCDKAFKMS SLAKHKIHT GEKPYKCSDS KALAKSSEVQ KVSQGDGNG IRVHKKKETO 900
GNLVRNKNEN RTGLFQIRAA VRPNRDPNMG QQEGSLTDPI QRKEPDLQN HYDHQNALED 960
QRNTGVGGLL TFRDVVIEFS LEEWQCLDHA QONLYRDVML ENYRNLVSLG IAVSKPDLIT 1020
CLEQNKKEPMN IKRNMVTKH PDLPELGIK DSLQKVIPIR YKSGHDNLQ VRTCKSMGEC 1080
EVQKGGCNEV NQCLSTTQNK IPQTHKCVKV FGKFNENRHR KTRHTGKGHF KCKYKGSFC 1140
MVSQLEHQHI IHTRENSYQC EECGKPFNCS STLSKHKRIH TGEKPYRCCE CGKAPTWSST 1200
LTKHRRIRHG EKPYTCEECG QAFPSRSTLA NHRIRHTGK PYTCEECGA FSLSSSLTYH 1260
KRIHTGEKPY TCEECGKAFN CSTLEKHKI IHTGEKPYK KECGKAFAPS STLNTHKRIH 1320
TGEKPYKCE CDAKFWSSS LANHKSMTG EKPYKCE 1357

Seq ID NO: C252 Protein Sequence
Protein Accession #: NP_114433.1

15
20
1 11 21 31 41 51
MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWPFYHKS CYGYFRKLNR WSDAELEQCS 60
YGNQAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQWQWIDG AMYLYRSWSG 120
KSMGNKHKCA EMSNNNFLT WSSNECNKRQ HFLCKYRP 158

Seq ID NO: C253 Protein Sequence
Protein Accession #: XP_051860.2

25
30
35
40
1 11 21 31 41 51
MDGVNLSTEV VYKKGQDYRF ACYDRGRACR SYRVRFLCGK FVRPKLVTI DTNVNSTILN 60
LEDNVQSWKP GDTLVIASTD YSMYQABEFQ VLPSCRSCAP QVKVAGKPMY LHIGEEIDGV 120
DMRAEVLGLS RNIIVMGEME DKCYPYRNHI CNPFDFTDP GHKIFALGFK AAHLEGTELK 180
HMQQQLVQQY PIHFLAGDV DERGGYDPPT YIRDLSEHT FSRCVTVGHS NGLLIKDVVG 240
YNSLGHCPFT EDGPFERNFT DHCLGLLVKS GTLLPSDRDS KMCKMITGDS YPGYIPKPRQ 300
DCNAVSTFWM ANPMNNLINC AAGSEETGF WPIFHHVPTG PSVGMYSPOY SEHIPLGKPY 360
NNRAHSNYRA GMIIDNGVKT TEASAKDKRP FLSIISARYS PHQDADPLFK REPATIRHPI 420
AYKNQDEGAW LRGGDVWLDG CRPADNGIGL TLASGGTFPY DDGSKQETKN SLFVGESGNV 480
GTEMMDNRIM GPQGLDHSGR TLPIGQNPFI RGIQLYDGP I NIQNTCTFRK VALEGRHTSA 540
LAFRLANAWQ SCCHNNVTGI APEDVPITR VFFGEGPWF NQLDMGDKT SVFHDVDGVS 600
SEYFGSYLTK NDNLVVRHFD CINVPDWRGA ICSGCYAQMY IQAYKTSNLR MKIINKDFPS 660
HPLYLEGALT RSTHYQQYQF VVTLLKQYTI HWDQAPARL AIWLINFNGK DWIRVGLCYP 720
RGTTFSILSD VHNRLKQTS KTGVPVRTLQ MDKVEQSYPG RSHYYWDEDS GLLPLKKAQ 780
NEREKPAFCS MKGCEKIKK ALIPKNAGVS DCTATAYPKF TERAVVDVPM PKKLFQSLK 840
TKDHFLEVM ESKQHFFHL WNDPAYIEVD GKYPSSSEDG IQVVVIDGNQ GRVVSHTSFR 900
NSILQGIPWQ LFNIVATIPD NSIVLMASKG RYVSRGPWTR VLEKLADRG LKLKEQMAFV 960
GPKGSFRPW VTLDTEDHKA KIPQVPIPV VKKKKL 996

Seq ID NO: C254 Protein Sequence
Protein Accession #: NP_055188.1

45
50
1 11 21 31 41 51
MTALSSENCN FOYQLRQTNQ PLDVNYLLFL IILGKILLNI LTLGMRRKNT CQNFMEYFCI 60
SLAFVDLILL VNISIIILYFR DFVLLSIRPT KYHICLPTQI ISFTYGLHY PVFLTACIDY 120
CLNFSKTKTL SFKQKLPYF FTVILIMISV LAYVLGDPFI YQSLKAQNAV SRHCPFYVSI 180
QSYWLSFFWM MILFVAFITC WEEVTTLVQA IRTSYMET ILYPPFSSHS SYTVRSKKIP 240
LSKLIVCFLS TWLPFVLLQV IIVLLKVQIP AYIEMNIPWL YFVNSFLIAT VYWFNCHKLN 300
LKDIGLPLDP FVNNKCCFIP LTIPLNLEIE KPISIMIC 338

Seq ID NO: C255 Protein Sequence
Protein Accession #: Eos sequence

60
65
70
75
1 11 21 31 41 51
MALVLGSLLL LGLCGNSPFG QPSSSTDAPK AMNYELPATN YETQDSHKAG PIGILFELVH 60
IFLYVVQPRD FPEDTLRKFL QKAYESKIDY DKIVYYEAGI ILCCVLGLLF IILMPLVGYF 120
FCMCRCCNKC GGEHQRQKE NGPFLKCFE ISLLVICIII SIGIFYGPAV NHQVRTRIKR 180
SRKLADSNFK DLRTLLNETP EQIKYILAQY NTKDKAPTQ LNSINSVLGG GILDRLRPNI 240
IPVLDEIKSM ATAIKETKEA LENMNSTLKS LHQQSTQLSS SLTSVITSLR SSLNDPLCLV 300
HPSSETCNSI RLSSLQLNSN PELRQLPPVD AELDNVNVVL RTDLGLVQQ GYQSLNDIPD 360
RVQRQTITVV AGIKRVLNSI GSDIDNVQTR LPIQDILSAF SVYVNNTESY IHRNLPLEE 420
YDSYMWLGLL VICSLTLTIV IFYYLGLLCG VCGYDRHATP TTRGCVSNTG GVFLMVGVGL 480
SPLFCWILMI IIVLTFVFGA NVEKLICEPY TSKELEPVL DTPYLLNEDWE YLSSGLKLPNK 540
SKMKLTFFEQV YSDCKUNRGT YGTLHLQNSP NISEHLNINE HTGSISSELE SLKVNLIPL 600
LGAAGRKNLQ DFAACGIDRM NYDSYLAQTG KSPAGVNLIS PAYDLERAN SLPPGNLRNS 660
LKRDQTIKT IQQRVLPIE QSLSTLYQSV KILQRTGNGL LERVTRILAS LDFAPQNFITN 720
NTSSVIEET KKYRTIIGY FEHYLQWIEF SISEKVASCK PVATALDTAV DVFLCSYIID 780
PLMLPWFPGI KATVFLPALP IFAVKLAKYR RRMDSDEVVD DVETIPMKQM ENGNNGYHKD 840
HVGIRHNPVM TSPSQH 856

Seq ID NO: C256 Protein Sequence
Protein Accession #: NP_149038.1

80
MKAIHLTL ALLSVNTAIN QGNSADAVTT TBTATSGPTV AAADTTETNF PETASTTANT 60
PSPPTATSPA PPIIETHSSS TIPTAPFPII STHSSSTIPI PTAADSESTI NVNLSATSDI 120
ITASSPNDGL ITWVPSETQS NNEMSPITTD NQSGGPTTGT ALLETSTLNS TGSPNQCQDD 180
PCADNSLCVK LKNTSFCLCL EGYTYSSTC KKGKVPFGKI SVTVSETFDP ESKHSMAYQD 240

5 LHSEITSLFK DVFGTSVYQG TVILTVSTSL SPRSEMRADD KFMVNTIVTI LAETTSIDNEK 300
 TVTEKINKAI RSSSSNPLNY DLTLRCDYVG CNQTADDCIN GLACDCKSDL QRPNPQSPFC 360
 VASSLKCPDA CNAHQKQCLI KKSQGAPECA CVPGYQEDAN GNCQKCAPGY SGLDCKDKPQ 420
 LILITVGTIA GIVILSMIIA LIVTARSNNK TKHIEENLI DEDFQNLKLR STGPTNLGAE 480
 GSVFPKVRIT ASRDSQMNP YSRHSSMPRP DY 512

Seq ID NO: C257 Protein Sequence
 Protein Accession #: NP_001423.1

10 1 11 21 31 41 51
 | | | | |
 MTAGRRMEML CAGRVFALLL CLGFHLLQAV LSTTVIPSCI PGESSDNCTA LVQTEDNPRV 60
 AQVSITKCSS DMNGYCLEHG CIYLVDMSON YRCCEVGYTG VRCEHFFLTV HQPLSKEYVA 120
 15 LTVILILFL TVVGSTYYF CRWYRNRSK EPKKEYERV SGDPPLPQV 169

Seq ID NO: C258 Protein Sequence
 Protein Accession #: AAC63902.1

20 1 11 21 31 41 51
 | | | | |
 MDRSKENCIS GPKVATAPVG GPKRVLVTTQ IPCONPLEVN SGQAQRVLCV SNSSQRVPLQ 60
 AQKLVSCHKP VONQKQKQLQ ATSVPHVPSR PLMNTQKSKQ PLPSAPENNP EELASKQKN 120
 EESKKRQWAL EDFEIGRPLG KGFQGNVILA REKQSKFILA LKVLFAQLE KAGVEHQLRR 180
 25 EVEIQSHLRH PNILRLYGYF HDATRVYLIL EYAPLGTVYR ELQKLSKFDE QRTATYITEL 240
 ANALSYCHSK RVIHREDIKPE NLLLSAGEL KIADFGWSVH APSRRRTTLC GTLDYLPPEM 300
 IEGRMHDEKV DLWSLGVLCY EFLVGKPPFE ANTYQETKYR ISRVEFTFPD FVTEGARDLI 360
 SRLLRKHNPSQ RPLMLREVLEH PWITANSSKP SNCQNKESAS KQS 403

30 Seq ID NO: C259 Protein Sequence
 Protein Accession #: NP_037504.1

35 1 11 21 31 41 51
 | | | | |
 MSRTAYTVGA LLLLGLTLLP AAEKKKKGSQ GAIPPPDKAQ HNDSEQTQSP QPQGSERNRGR 60
 QQGRGTAMPQ BEVLESSQEA LHVTERKYLK RDWCKTQPLK QTIHEEGCNS RTIINRFCYG 120
 QCNSEFYIPRH IRKEEGSPQS CSFCKPKKFT TMMVTLCPE LQPPTKKKRV TRVKQRCRIS 180
 IDLD 184

40 Seq ID NO: C260 Protein Sequence
 Protein Accession #: Eos sequence

45 1 11 21 31 41 51
 | | | | |
 MKVGVLMNIS PFTFTDGGGG FLGKNDGIKT KKEILVNIKK HLGPVEEYQL LLQVITYRDSK 60
 EKRDLRNLK LLKPLLLWSH GLIRIIRAKA TTDNLSLNGV LQCTCEDSYT WFPSPCLDPQ 120
 NCYLHTAGAL PSCECHLNNL SQSVNFCERT KIWGTFKINE RPTNDLLNSS SAIYSKYANG 180
 IEIQKKAYE RIQGFESQVQ TQFRNGSIVA GYEVVGSSSA SELLSAIEHV AERAKTALHK 240
 LPFLEDGSFR VFGKAQCNDI VFGFGSKDDE YTLPCSSGYR GNITAKCESS GWQVIRETCV 300
 50 LSLLEELNKN FPMIVGNATE AAVSSFFVQNL SVIIRQNPST TVGNLASVVS ILSNSSLSL 360
 ASHFVRSNST MEDVISIADN ILSASVTNW TVLLREEKYA SSRLLLETEN ISTLVPTTAL 420
 PLNFSRKPID WGIIPVNIQS LKRGYSYQIK MCPONTSIPI RGRVLIGSDQ FORSLPETTI 480
 SMASITLGNL LPSVKNNGNA VNGFVISTVI QNYSINEVFL PFSKIESNLS QPHCFWDFPS 540
 HLQWMDAGCH LVNETQDIVT CQCTHLTSFS ILMSPFVPSI IFPVVKWITY VGLGISIGSL 600
 55 ILCLIIEALF WKQIKKSQTS HTRRICMVNI ALSLLIADVN FIVGATVDTT VNPSSGVCTAA 660
 VFFTHFFYLS LFFWMLMGI LLAIRIILVF HMAQHLMA VGFCLGYGCP LIISVITIAV 720
 TQPSNTYRKR DVCMLNWSNG SKPLLAFFVP ALAIVAVNEF VVLLVLTKLV RPTVGERLSR 780
 DDKATIIIRVG KSLILITPLL GLTWGFGIGT IVDSONLAWH VIFALLWAFQ GPFILCFGIL 840
 LDSKLRQLLF NKLSSALSSWK QTEKQNSDDL SAKPKFSKPF NPLQNKGYA FSHTGDSSDN 900
 60 IMLTQFVNSE 910

Seq ID NO: C261 Protein Sequence
 Protein Accession #: NP_000575.1

65 1 11 21 31 41 51
 | | | | |
 MTSKLAVALL AAFILISAALC EGAVLPSAK ELRCQCIKY SKPFPKPKIK ELRVIESGPH 60
 CANTETIIVKL SDGRELCCLDP KENWVQRVVE KFLKRAENS 99

70 Seq ID NO: C262 Protein Sequence
 Protein Accession #: NP_005594.1

75 1 11 21 31 41 51
 | | | | |
 MSTERDSETT FDEDSQPNDE VVPYSODETE DELDDQGSAA EPQNRVNRRE AENREPFPRK 60
 ECTWQVQAND RYHQBQPHM NTKFLCIKES KYANNAIKTY KYNAPTIFIM NLPEQFKRAA 120
 NLYPLALLIL QAVPQISTLA WYTTLVPLLV VLGVTAKDL VDDVARHMD KEENRTCEV 180
 IKDGRFKVAK WKEIQVGVVI RLKKNDFVPA DILLSSSEP NSLCYVETAE LDGETNLKPK 240
 MSLEITDQYL QREDTLATFD GFIECEEPNN RLDKFTGTLP WRNTSPFLDA DKILLRGCVI 300
 80 RNTDFCHGLV IFAGADTKIM KNSGKTRPKR TKIDYLMNYM VYTIFFVVLIL LSAGLAIGHA 360
 YWEAQVGNSS WYLYDGEDDT PSYRGFLIFW GYIIVLNTMV PISLYVSVEV IRLGQSHFIN 420
 WDLQMYAEK DTPAKARTTT LNBQLGQIHY IFSDKTGTLT QNIMTFKKCC INQGIYGDHR 480
 DASQNNHKKI EQVDFSWNTY ADGKLAFVDH YLIEQIQSGK EPEVRQFFPL LAVCHTMVD 540
 RTDQQLNQQA ASPDEGALVN AARNFGPAFL ARTQNTITIS ELGTERTYNV LAILDPNDR 600
 KRMSIIVRTP EGNIKLYCKG ADTVIYERLE RMNPTKQETQ DALDIPANET LRTLCCLCYKE 660

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10

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IEEKEFTSMN KKFMAASVAS TNRDEALDKV YEEIEKDLIL LGATAIEDKL QDGVFPETISK 720
LAKADIKIWN LTGDKKETAE NIGFACELLT EDTTICYGED INSLHARME NQRNRGGVYA 780
KFAFPVQESP PPPGGRNALI ITGSMNLNELL LEKKTIRNKI LKLPFRTEE ERMRTQSKR 840
RLEAKGEQQR KNFVDLACBC SAVICCRVTP KQKAMVVDLV KRYKAITLA IGDGANDVNM 900
IKTAHIGVGI SQQEGMQAVM SSDYSFAQFR YLQRLLLVHG RWSYIRMCKP LRYFFYKNTA 960
FTLVHFWYSF FNGYSAQTAY EDWFTILYNV LYTSLPVLLM GLLDQDVSDK LSLRPPGLYI 1020
VGQRDLLENY KRFPVSVLLHG VLTSMLFFI PLGAYLQTVG QDGEAPSDYQ SPAVTIASAL 1080
VITVNFQIGL DTSYWTFFNA FSIFGSIALLY FOIMFDFHSA GIHVLFPFSAF QFTGTASNAL 1140
RQPYINLTII LTVAVCLLPV VAIRPLSMTI WPSSEDKIQK HRKRLKAEEQ WQRROQVFRR 1200
GVSTRRSAYA FSHQRGYADL ISSGRSIRKK RSLPLDAIVAD GTAEYRRTGD S 1251

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Seq ID NO: C263 Protein Sequence
Protein Accession #: XM_044533

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20
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1 11 21 31 41 51
| | | | |
MLRTAMGLRS WLAAPNGALP PRPPLILLLL LLLLQPPPP TWALSPRISL PLGSEERPFL 60
RPEAEHISNY TALLSRDGR TLYVGAREAL FALSSNLSP PGGEYQELLW GADAEKKQQC 120
SPKGDQPRD CQNYIKILLP LSGSHLFTCG TAAFSPMCTY INMENPTLAR DEKGNVLLED 180
GKGRCPFPFN FKTALVVDG ELYTGTVSSF QGNDPAISRS QSLRPTKTES SLNWLQDPAF 240
VASAIPBSL GSIQGGDDKI YPFSEBTQGE FEFENTIVS RIARICXGDE GSERVLQQRW 300
TSFLKAQLLC SRPDDGPPFN VLQDVFTLSP SPQDWRDTLP YGVFTSQMHR GTTBGSVAVC 360
FTKQDVQVVF SGLYKEVNRK TQWYTVTHP VFTPRPGACI TNSARERKIN SSLQLPDRVL 420
NPLKDHFMAD GQVRSRMLLL QPQARYQVVA VHRVPLGHT YDVLFLGTGD GRLEKAVSVG 480
PRVHIIEELQ IFSSGQPVQN LLLDTHRGLL YAAASHSGVVQ VEMANCGLYR SCGDCLLARD 540
PYCAWSGSSC KHVSLYQPQL ATRFWIQDIE GASAKDLCSA SSVVSPSPVP TGEKPCQVQ 600
PQFNTVNTLA CPLLSNLATR LWLRNGAPVN ASASCHVLPT GDLLLVGTQQ LGFQCWSLE 660
EGFQQLVASV CPFEVEDGVA DQTEGSGSVF VIISTRVSA PAGGKASWGA DRSYWKFLV 720
MCTLPVLAVL LPVLPFLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNGLGPPST 780
PLDHRGYQSL SDSPFGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS BIRDSVV 837

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Seq ID NO: C264 Protein Sequence
Protein Accession #: NP_008950.1

35
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1 11 21 31 41 51
| | | | |
MASQNRDPAI TSVAARKGA EPSGGAARGP VGKRLQQLM TLMMSGDKGI SAPPESDNLF 60
KWVGTIHGAA GTVYEDLRYK LSLFPPSGYP YNAPTVKFLT PCYHFNVDQ GNICLDILKE 120
KWSALYDVRT ILLSIQSLG EPNIDSLPNT HAABLWKNPT AFKYLQETY SKQVTSQEP 179

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Seq ID NO: C265 Protein Sequence
Protein Accession #: NP_055399.1

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50

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1 11 21 31 41 51
| | | | |
MGRGMGFLPG LLGAVWLLSS GHGSEQPPEP AAQRFCQVVS GYLDCTCDV ETIDRFNNYR 60
LFPRLQLLIE SDYFRYKVN LKRPCPFWND ISQCGRRDCA VKPCQSDEVP DGIKSASYKY 120
SEERANLIBE CBQAERLGAV DESLSEBTQK AVLQWTKHDD SSDNFCEADD IQSPBAEYVD 180
LLLNPERYTG YKGPDAWKI NVIYEENCFK POTIKRPLNP LASGQGTSEE NTFYSWLEGL 240
CVERAPRYRL ISGLHASINV HLSARYLLQE TWLEKKWGHN ITFQQRFDG ILTEGEGPRR 300
LKNLYFLYLI ELRLASKVLV PFERPDQQLF TGNKIQDEN KMLLEILHE IKSFLPHFDE 360
NSFFAGDKKE KHLKEDFRL HFRNISRIMD CVGCFKCLRW GKLTQQLGT ALKILFSEKL 420
IAMPESGSPS YEFILTRQEI VSLPNAFGRI STSVKELENF RNLLQNIH 468

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Seq ID NO: C266 Protein Sequence
Protein Accession #: NP_002879.1

60
65

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1 11 21 31 41 51
| | | | |
MQPRRQLRPA FWSGPRGRP TAPLLALLL LAPVAAPAGS GGPDDPGQPQ DAGVPRRLQ 60
QKARAALHFP NFRSGSPSAL RVLAEVQEGR AWINPKEGCK VHVVPSTERY NPESLLQEGE 120
GRLGKCSARV FFKNQKPRPT INVTCTRIE KKKRQQEDYL LYKQMKQLKN FLEIVSIPDN 180
HGHIDPSLRL IWDLAPLGSS YVMWEMTTQV SHYYLAQLTS VRQWVRKT 228

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Seq ID NO: C267 Protein Sequence
Protein Accession #: NP_005400.1

70

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1 11 21 31 41 51
| | | | |
MSVKGMAIAL AVILCATVVQ GFPMFKRGRC LCIGPGVKAV KVADIEKASI MYPNNCDKI 60
EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF 94

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Seq ID NO: C268 Protein Sequence
Protein Accession #: FGENSEH predicted

75
80

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1 11 21 31 41 51
| | | | |
MLRQVLRRLQ QSFCHRLGLC VSRHPVFFLT VPAVLITITFG LSAIINRFQPE GDLERLVAPS 60
HSLAKIERSL ASSLFPLDQS KSQLYSDLHT PGRYGRVILL SPTGDNILLQ AEGILQTHRA 120
VLEMKVNHKG YNYTFSHLCV LRNDKKCVL DDIISVLEDL RQAAVENKIT ARVQVRYFNT 180
KLKVCSPQML LPIKEAALHF LP 202

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Seq ID NO: C269 Protein Sequence
Protein Accession #: NP_002429.1

	1	11	21	31	41	51	
5	MRLPLLLVFA	SVIPGAVLLL	DTRQFLIYNE	DHKRCVDVAVS	PSAVQTAACN	QDAESQKFRW	60
	VSESQIMSVA	FKLCIGVPSK	TDWVAITLYA	CDSKSEFQKW	ECKNDTLGI	KGEDLFFNYG	120
	NRQEKINIMLY	KGSGLWSRWK	IYGTIDNLCS	RGYEAMYTLL	GNANGATCAF	PFKFNKMYA	180
	DCTSAGRSBG	WLWCGTTTDDY	DTDCLFGYCP	LKFEKSGESLW	NKDPLTSVSY	QINSKSAITW	240
	HQARKSCQQQ	NABELLSITEI	HEQTYLTGLT	SSLTSGLWIG	LNLSLFSNSGW	QWSDRSPFRY	300
10	LNLWPGSPSA	EPGKSCVSLN	PGKNAKWENL	ECVQKLGYYC	KKGNTTLNSF	VIPSESDVPT	360
	HCPSQMWPYA	GHCYKIHRE	KKIQRDALTT	CRKEGGDLTS	IHTIBELDFI	ISQLGYEPND	420
	ELWIGLANDIK	IQMYFEWSDG	TPVTFTKWLK	GEPSHENNRQ	EDCVVMKGD	GYWADRGCEW	480
	PLGYICKMKK	RSQGPETVEV	EKGCRKGWKK	HHFYCYMIGH	TLSTFAEANK	TCNNENAYLT	540
	TIEDRYEQAF	LTSFVLGRPE	KYFWTGLSDI	QTKGTFQWTI	EEBVRPTHWN	SDMPGRKPGC	600
15	VAMRTGIAGG	LWDVLKDEK	AKFVCKHWA	GVTHPPKPTT	TPEPKCPEDW	GASSRTSLCF	660
	KLYAKGKHEK	KTFWFSRDFC	RALGGLASI	NNKEEQOTIW	RLITASGSYH	KLFWLGLTYG	720
	SPSEGFTWSD	GSPVSYENWA	YGEFNYYQNV	EYCGELKGGP	TMSWINDICE	HLNNWICQIQ	780
	KGQTPKPEPT	PAPQDNPPVT	EDGWVIYKDY	QYFYSKEKET	MDNARAFCKR	NFGDLVSIQS	840
	ESEKKPLWKY	VNRNDAQSAY	FIGLLISLDK	KFAWMDGSKV	DYVSWATGEP	NFANEDENCV	900
20	TMYSNSGFWN	DINGCYPNAY	ICQRHNSIN	ATTVMPTMPS	VPSGCKEGWN	FYSNCKCFIF	960
	GMFEERKNW	QEARAKICIG	GGNLVSIQNE	KEQAFITYHM	KDSTFSAWTG	LNDVNSEHTF	1020
	LWTDGRGVHY	TNWGKGYPGG	RRSSLSYEDA	DCVVIIGGAS	NEAGKWMDDT	CDSKRGYICQ	1080
	TRSDPSLTNP	PATIQTDGTV	KYKSSYSILM	RQKFQWHEAE	TYCKLHNSLI	ASILDPSYNA	1140
	FAWLQMETSN	ERNVIALNSN	LTDNQYTWD	KWRVRYTNWA	ADEPKLKSAC	VYLDLDGYWK	1200
25	TARCKLDFPF	LCKRSDEIPA	TEPPQLPGRC	PESDHTAWIP	FHGHCYIIES	SYTRNMGQAS	1260
	LECLRMGSSL	VSTESAAESS	PLSYRVEFLK	SKTNFWIGLF	RNVGTWLMW	NNSPVSVFVN	1320
	NTGDPGGERN	DCVALHASSG	PWSNIHCSSY	KGYICKRPKI	IDAKPTHELL	TTKADTRKMD	1380
	PSKPSNVVAG	VVITIVLLIL	TGAGLAAYFF	YKRRRVHLPO	EGAFENTLYP	NSQSSPGTSD	1440
	MKDLVGNIEQ	NEHSVI					1456

30 Seq ID NO: C270 Protein Sequence
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
35	MVLLHWCLLW	LIFPLSSRTQ	KLPTRDEELF	QMQRDKAPF	HDSSVIPDGA	EISSYLPRDT	60
	PKRYFFVVEE	DNTPLSVTVT	PCDAPLEWKL	SLQELPEDRS	GEQSGDLEPL	EQKQKQIINE	120
	EGTELPSLTNP	NDVSYPISSS	SPSGLYQLDL	LSTEDTHFK	VIATITPESD	QPYPELPYDP	180
	RVDVTSLGRT	TVTLAWKPSF	TASLLKQPIQ	YCVVINKEHN	PKSLCAVEAK	LSADDAFPMMA	240
40	KPGKLDPSFF	DFAHFGFPPD	NSGKERSFQA	KPSPKLGRHV	YSRPFVDIQR	ICIGMKNIPT	300
	VSDLKPDQTY	YFDVFNVIN	SNMSTAYVGT	FARTKEEAKQ	KTVBLKDGKI	TDVFKRKGGA	360
	KFLRFAPVSS	HQKVTFPIHS	CLDAVQIQVR	RDGKLLLSQN	VBGIIQQFQLR	GRPKAKYLVR	420
	LKGNKKGASM	LKILATTRPT	KQSPFSLPED	TRIKAFDKLR	TCSSATVAVL	GTQERNKFCI	480
	YKKEVDNDYN	EDQKREBQNG	CLGPDIRKKS	EKVLCKYFHS	QNLQKAVTTE	TIKGLQPGKS	540
45	YLLDVYVIGH	GGHSHVKQSK	VVKTRKFC				568

Seq ID NO: C271 Protein Sequence
Protein Accession #: AAH34229.1

	1	11	21	31	41	51	
50	MEKVQLEFEN	QEMEKGLQEF	RSTRNKEKED	RESSEYYWKS	GKVGKLVNQS	YMMSONKGNV	60
	VKPSAGVKVL	KLLKQIQEP	VKPTVNYKMA	NSSECEKPKI	NGRVCOQCEN	KAALLVLEEC	120
	GEDYCSGCFA	NVHQKGLKLI	HRTTLLQARS	QILLFNVLDA	HQFIDVNPDP	EPKEENNSTK	180
	ETSKIQKPK	SVLLQKSSSE	VEITTMKRAQ	RTKPRKSLLC	EGSFDEEASA	QSPQEVLSQW	240
55	RTGNEDDNKK	QNLHAAVKDS	LEECEVQTNL	KINREPLNIE	LKEDILSYME	KLWLKGRRT	300
	PQEQLFKCYQ	IRSHIHMKPL	VMHSLVKMKT	MKIVMVRPK	YNTQLFYCQ		349

Seq ID NO: C272 Protein Sequence
Protein Accession #: NP_078963.1

	1	11	21	31	41	51	
60	MEKLWLKKHR	RTPQEQLFKM	LSDTFPHPE	TTGDAQCSQN	ENEDSDGEE	TKVQHTALLL	60
	PVETLNIERP	EPSLKIVELD	DTYEEFEFA	ENIVPYKVKL	ADADSQRSCA	FEDCQKNSFP	120
65	YENGHQHHRV	FDKGRDFLN	LCLRNSSTYY	KDNSKGETSN	TDFDNIVDPD	VYSSDIEKIE	180
	ESTSPERNLK	EKNIGLESNQ	KSDSDCVSLR	SKDTLLGRDL	EKAPIEEKLS	QDIKESLELS	240
	NLYKRPSFEE	SKTTKSSILL	QEIACRSKPI	TKQYQGLERF	PFDITNERLN	LLPSHRLN	300
	NSSTRITLAE	DREWIPDHS	SEYADNAIVL	GVLQGAQSPS	SSRKQKMGQ	KSQRPSTANF	360
70	PLNSVKESS	SCLSSSHPRS	RSAAAQSSSR	AASEISEIEY	IDITDQNELS	LDDTTDQHTL	420
	DNLEKELQVL	RSLADTSEKL	YSLTSEEFDP	FSSQSLNISQ	ISTDFLKTSH	VRGPCGVVEL	480
	SCSGRDTIKI	SLLSLSESST	DEBEEDFLNK	QHVITLPSK	ST		522

Seq ID NO: C273 Protein Sequence
Protein Accession #: NP_005399.1

	1	11	21	31	41	51	
75	MKVSALLCL	LIMTAAPNPQ	GLAQPDALNV	PSTCCPTPSS	KKISLQRLKS	YVITTSRCPQ	60
80	KAVIFRTKLG	KETCADPKKE	WQNYMKHLG	RKARTLKT			98

Seq ID NO: C274 Protein Sequence
Protein Accession #: BAC05158.1

	1	11	21	31	41	51
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MFLLTGGVSL	KSAEKNPDPT	WLQDKSWBEE	CRASEFPAPR	GLRQHFCEHI	YEWREIYDSK	60
EPHNAKFPAP	MDKNLNLQK	IIILRCLRPD	KITPAITNYV	TDKLGKQFVE	PPPPDLTKSY	120
LDSNCTIPLI	PVLSPGADPM	ASLLKFPANDK	SMSGNKFOAI	SLQGGQGPPIA	AKMIKAAIEE	180
GTWVCLQNC	LAVSWMPMLE	KICEDFTSET	CNSSPRLMLT	SYPSKFPVPT	ILQNGVKMTN	240
EPFTGLRLNL	LQSYLTDPVS	DPEFPKQCRG	KELLFINEYD	TIPFEAISYL	TGECNYGGRV	300
TDNDWRLLLL	TMLADFYNLY	IVENPHYKFS	PSGNYFAPPK	GTIEDYIEFI	KKLPFTQHPE	360
IPGLHENVDI	SKDLQQTCTL	PESLLLTQGG	SKQTGASGST	DQILLEITKD	ILNKLPSDFD	420
IEMALRKYPV	RYEESMNTVL	VQEMERFNNL	IITIRNTLRD	LEKAIKGVVV	MDSALEALSS	480
SLLVGKYPEI	WAKRSPSLK	PLGSYITDFL	ARLNFLQDMY	NSGKPCVFWL	SGFFFTQAFI	540
TGAMQNYARK	YTPPIDLLGY	EFEVIPSPTS	DTSPEDGVYI	HGLYLDGARN	DRESGLLAEQ	600
YPKLLFDLMP	IWIKPQTKS	RIIKSDAYVC	PLYKTSEKRG	TLSTTGHSTN	FVIAMLLKTD	660
QPTRHWIKRG	VALLCQLDD					679

Seq ID NO: C275 Protein Sequence
Protein Accession #: AAA60212.1

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1	11	21	31	41	51	
MAESHLQWML	LLLLPTLCGP	GTAAWITSSL	ACAQGPEFWC	QSLEQALQCR	ALGHCLQEVW	60
GHVGAADDLC	ECEDIVHIIL	KMAKEAIPQD	TMRKFLEQEC	NVLPLKLLMP	QCNQVLDDYF	120
PLVIDYFQNL	TDNNGICMHL	GLCKSRQPEP	EQEPGMSDPL	PKPLRDLPLD	PLLDKLVLPV	180
LPGALQARPG	PHTQDLSEQQ	FPIPLPYCWL	CRALIKRIQA	MIPKALAVA	VAQVCRVVEL	240
VAGGICQCLA	ERYSVILDT	LLGRMLPQLV	CRVLVLRCSMD	DSAGFRSPGT	EWLPRDSECH	300
LCMSVTQAG	NSSEQAIPQA	MLQACVGSWL	DREKCKQFVE	QHTPQLLTLV	PRGWDARTTC	360
QALGVCGTMS	SPLQCIHSPD	L				381

Seq ID NO: C276 Protein Sequence
Protein Accession #: NP_631911.1

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1	11	21	31	41	51	
MLGCGIPALG	LLLLLQGSAD	GNGIQGFFYP	WSCEGDIWDR	ESCGGQAAD	SPNLCLRLRC	60
CYRNGVCYHQ	RPDENVRKHH	MWALVWTCSG	LLLLSCSICL	FWWAKREDVL	HMPGFLAGPC	120
DMSKSVSLLS	KHRGTKTTPS	TGSVPVALSK	ESRDVBOGTE	GEOTEEGEET	EGEEED	177

Seq ID NO: C277 Protein Sequence
Protein Accession #: NP_473364.1

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1	11	21	31	41	51	
MKLVITIFLV	TISLCSYSAT	AFLINKVPLP	VDKLAPLPLD	NILPFMDPLK	LLKTLGISV	60
EHLVGLRKC	VNELGPEASE	AVKKLEALS	HLV			93

Seq ID NO: C278 Protein Sequence
Protein Accession #: FGENSEH predicted

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1	11	21	31	41	51	
MPLSYAYKNA	ETLAGRHTSS	WMSRGAYQRR	NTRAAGRPEE	CTDRNWHAGR	TRGINLQGLE	60
ERCSDVFGVS	FFWVVRGLAG	SGAKLQTFPT	AQEGAPTQVR	QAEALLKCRQ	SGRPRGGGAE	120
SERARDASML	SPLSAAMRNY	PTSSTIPPRR	SYSPTIEAHK	SYSCLPDMK	ISMAESGPSL	180
DSLDDLEDEG	SGSPFLVTHL	YFLGVVTTGM	BQLDFETGPN	IFDLQIYVKD	EVGVTDLQVL	240
TVQVTDVNEF	PQPGNLAEED	HLRADQPHFN	AHSHTYVRVV	ATALARHRLR	SSIGSPFLGT	300
FCVVVGMYFP	LISPPKSPRM	SANGTLFSTT	ELDFEAGHRS	FHLIVEVRDS	GGLKASTEIQ	360
VNIIVNLNDV	PRPTSPTRVY	TVLEELSPGT	IVANITAEED	DDEGFPSHLL	YSITTVSKYF	420
MINQLTGTIQ	VAQRIDRDAG	ELRQNPTISL	EVLVKDRPYG	GQENRIQITF	IVEDVNDNPA	480
TCQKFTFRSS	LHPALCSKTL	TWMDTVLDCP	HAADKDIPTV	GRFTKERGLI	GLTVPHGWGS	540
LTIMAEKKEE	QVTSYMDGSR	QRDRACVGLK	LLIKPSDLMR	LSHYHENSNG	KTCPDHSISS	600
YQVPPTTCRN	SRIQATNNED	TSSVTVTVNI	LEENDEKPIC	TPNSYFLALP	VDLKVGTNIQ	660
NFKLTCTDLD	SSPSRFRYSI	GPGNVNNHPT	FSPNAGSNVT	RLLLTSRFDY	AGGFDPKIWDY	720
KLLVYVTDNN	LMSDRKCAEA	LVETGTVTLS	IKVIPHPTTI	ITTTPRPRVT	YQVLRKNVYS	780
PSAWYVFPVI	TLGSILLGLL	LVYLVVLLAK	AIHRHCPCCK	GKNKEPLTKK	GETKTAERDV	840
VVETIQMNTI	FDGAIDPEP	EQASLELYAL	LPSCCDPSFV	TLRKVQVCGE	SEETGQCSGH	900
ITLPGKIPVD	DPRKQETGLQ	GDPEVWTLCP	AVKVVVGSPQ	AERCIRLALS	LKKYSSD	957

Seq ID NO: C279 Protein Sequence
Protein Accession #: XP_168571.1

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1	11	21	31	41	51	
MINQLTGTIQ	VAQRIDRDAG	ELRQNPTISL	EVLVKDRPYG	GQENRIQITF	IVEDVNDNPA	60
TCQKFTFRSS	VPERTAGTGL	LLDLNKFCDP	DDSEAPNNRF	NPTMPSGVGS	GSFRLQDPAG	120
SGKIVLIGDL	DYENPSNLAA	GNKYTVIIQV	QOVAPPYYKN	NVYVYILTSP	ENEFPLIPDR	180
PSYVFDVSR	RPAQHLSSGP	EEKRLLSICM	VRAVCHHGL	HIASGSPRPV	GRPIGSHFQ	240
TLPLQDWBEQ	QTSDEKERRNE	DCRERRRGGN	YPDEHYL			277

Seq ID NO: C280 Protein Sequence
Protein Accession #: NP_005257.2

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1	11	21	31	41	51	
MGDSWFLGNP	LEEVHGHSTV	VGKVWLTVLF	IFRMLVLGTA	ABSSWGDQEA	DPRCDTIQPG	60
QCNVCYDQAF	PISHIRYVWL	QIIPVSTPSL	VYMGHAMHTV	RMQEKRLRLR	AERAKEVRGS	120

GSYEYFPAEK AELSCWEEGN GRIALQGTLL NTYVCSILIR TTMEVGFIVG QYPIYGIFLT 180
 TLHVCRRSPC PHPVNCYVSR PTERNVFIVE MLAVAALSLL LSLAELYHLG WKKIRQRFVK 240
 PRQHMAKQCL SGPSVGVQVS CTPPPDFNQC LENGPGGKPF NPFSSNMASQ QNTDNLVTEQ 300
 VRGQEPTQGE GFIIQVRIGQK PEVPNGVSPG HRLPHGYHSD KRRLSKASSK ARSDDLVS 358

Seq ID NO: C281 Protein Sequence
 Protein Accession #: NP_055274.2

1 11 21 31 41 51
 10 | | | | |
 MYLSICCCFL LWAPALTLKN LNYSPVEEQG AGTVIGNIGR DARLQPLFP AERGGGGRSK 60
 SSSYRVLENS APHLLDVAD SGLLYTKQRI DRESLCRENA KCQLSLEVFA NDKEICMIKV 120
 EIQDINDNAP SFSSDQIEMD ISENAAPGTR FPLTSAHDPD AGENGLRTYL LTRDDHGLFG 180
 LDVKSRRDGT KPELVVIQKA LDREQONHHT LVLTALDGGG PPRSATVQIN VKVIDSNDNS 240
 15 PVFEAPSYLV ELPENAPLGT VVIDLNATDA DEGPNGEVLY SPSVVPDRV RELFSIDPKT 300
 GLIRVKGNDL YEENGMLRID VQARDLGNP IPAHCKVTVK LIDRNDNAPS IGFVSVRQGA 360
 LSEAAPPGTV IALVRVTD RD SGKNGQLQCR VLGGGTGGG GGLGGPGGSV PFKLEENYDN 420
 FTVVTDRLP DRETQDEYNV TIVARDGGSP PLNSTKSPAI KILDENDNPP RFTKGLYVLQ 480
 VHENNIPGEY LGSVLAQDPD LGQNGTVSYS ILPSHIGDVS IYTVSVNPT NGAIYALRSF 540
 20 NFEQTKAFEF KVLAKDSGAP AHLESNATVR VTULDVNDNA FVIVLPTLQN DTAEQLVPRN 600
 AGLGYLVSTV RALDSDFGES GRLYEIVDG NDDHLEIDP SSGEIRTLHP FWEDVTPVVE 660
 LVVKVTDHGL PTLSSAVAKLI IRSVSGSLPE GVPRVNGBQH HMDMSLPLIV TLSTISILL 720
 AAMITIAVKC KRENKEIRTY NCRIAEYSHP QLGGGKGGKK KINKNDIMLV QSEVEERNAM 780
 NVNMVSSSPS LATSMPYFDY QTRLPLSSFR SEVMYLPAS NNLTVPQCHA GCHTSFTGQG 840
 25 TNASETPATR MSIIQTDNFP AEPNMGSRQ QFVQSISVAP RLRTQKEPA 889

Seq ID NO: C282 Protein Sequence
 Protein Accession #: NP_005592.1

1 11 21 31 41 51
 30 | | | | |
 MELCRSLALL GSGSLGMLFCL IALSTDWFBE AVGPTHSAHS GLMPTGHGDI ISGYIHVTQT 60
 FSIAMAVMAL VSVSFLVLSG FPSLFPPGHG PLVSTTAAFA AAIMSVVAMA VYTSEWDQP 120
 35 PHPQIQTPFS WSPYLGWVSA ILLCTGALS LGARCGGPRP GYETL 165

Seq ID NO: C283 Protein Sequence
 Protein Accession #: NP_006424.2

1 11 21 31 41 51
 40 | | | | |
 MATWALLLLA AMLIGNPGLV FSRLSPEYYD LARAHLRDEE KSCPCLAQEG PQGDLTKTQ 60
 ELGRDYRTCL TIVQKLKKMV DKPTQSVSN AATRVCTGR SRWRDVCNRF MRRYQSRVTQ 120
 GLVAGETAQQ ICEDLRLCIP STGPL 145

Seq ID NO: C284 Protein Sequence
 Protein Accession #: NP_005594.1

1 11 21 31 41 51
 50 | | | | |
 MKVSAALAV ILIATLALCAP ASASPYSSDT TPCCPAYIAR PLPRAHIKEY FYTSGKCSNP 60
 AVVFVTRKMR QVCANPEKKV VREYINSLEM S 91

Seq ID NO: C285 Protein Sequence
 Protein Accession #: NP_071437.1

1 11 21 31 41 51
 60 | | | | |
 MAPGRAVAGL LLLAAAGLGG VAEGPGLAFS EDVLSVPGAN LSLSAAQLQH LLEQMGAASR 60
 VGVPEPGQLH FNQCLTAEI FSLHGFSSNAT QITSSKPSVI CPAVLQQLNP HPCEDRPHK 120
 TRPSHSEVWG YGFLSVTIIN LASLLGLILT PLIKKSYFPK ILTFPVGLAI GTLFSNAIFQ 180
 LIPEAPGFDP KVDSTVEKAV AVFGGFYLLF FFERMLKMLL KTYGQNGHTH FGNDNFGPQE 240
 KTHQPKALPA INGVTCYANP AVTEANGHIL FDNVSVVSLQ DGKKEPSSCT CLKGPKLSEI 300
 65 GTIAWMITLC DALHNFIDGL AIGASCTLSL LQGLSTSLAI LCBEFFPHELG DFPVILLNAGM 360
 STRQALLFNF LSACSCYVGL AFGILVGNPF APNIIPALAG GMPLYISLAD MPPEMNDMLR 420
 EKVTRGRKTF TFFMIQNAGM LTGFTAILLI TLYAGEIELE 460

Seq ID NO: C286 Protein Sequence
 Protein Accession #: NP_004175.1

1 11 21 31 41 51
 70 | | | | |
 MPNSEPASLL ELFNSTATQG ELVRSKAGN ASKDEIDSAV KMLVSLKMSY KAAAGEDYKA 60
 DCPGPNPAPT SNHGPDATGA EEDFVDFWTV QTSSARGIDY DKLIVRFSS KIDKELINRI 120
 ERATGQRPHH FLRRGIFFSH RDMNQVLDAY ENKKPPYLYT GRGPSSEAMH VGHLPPIFT 180
 KMLQDVFNVP LVIQMTDDEK YLWKDLTLDQ AYGDVENAK DIIACGFDIN KTFIFSDLDY 240
 MGSSEGFYKN VVKIQKHVTF NQVKGIFGFT DSDCIGKISF PAIQAPSPS NSFPQIFRDR 300
 80 TDIQCLIPCA IDQDPYFRMT RDVAPRIGV KPALLHSTFF PALQGAQTKM SASDPNSSIF 360
 LTDTAQIKT KVNKHAFSGG RDTIEHRQF GGCNDVDVSF MYLTFLEDD DKLBQIRKDY 420
 TSGAMLTGEL KKALIEVLQP LIAEHQARRK EVTDEIVKEF MTPRKLSDFF Q 471

Seq ID NO: C287 Protein Sequence

Protein Accession #: NP_004929.1

	1	11	21	31	41	51	
5	MTVFRQENVD	DYYDTGEEELG	SGQFAVVKKC	REKSTGLQYA	AKFIKKRRTK	SSRRGVSRED	60
	IEREVSILKE	IQHPNVITLH	EYENKTDVI	LILELVAGGE	LFDFLAEKES	LTEBEATEFL	120
	KQILNGVYYL	HSIQIAHFDL	KPENIMLLDR	NVPKPRIKII	DFGLAHKIDF	GNEPKNIFGT	180
	PEFVAPPIVN	YELGLLEADM	WSIGVITYIL	LSGASPFGLD	TKQETLANVS	AVNYEFDEY	240
10	PSNTSALAKD	FIRRLLVKDP	KKRMITQDSL	QHPWIKPKDT	QQALSRKASA	VNMEKPKKFA	300
	ARKKKQSVR	LISLCQLRSR	SFLSRSNMSV	ARSDDTLDEE	DSFVMAKIIH	AINDDNVFGL	360
	QHLGLSLSNY	DVNQPNKHGT	PPLLIAAGCG	NIQILQLLIK	RGSRIDVDOK	GGSNVYMAA	420
	RHGHVDTLKF	LSENKCPLDV	KDKSGEMALH	VAARYGHADV	AQVTCASAAQ	IPIERTKEE	480
	TPLECAAMHG	YYSVAKALCE	AGCNVNIKNR	EGETPLLTAS	ARGYHDIVEC	LAHKGADLNA	540
15	CDKDGIALH	LAVRRQCMVE	IKTLLSQGCF	VDYQDRHGNT	PLHVACKDGN	MPIVVALCEA	600
	NCNLDISNRY	GRTPLHLAAN	NGILDVVRYL	CLMGASVEAL	TTDGKTAEDL	ARSEQHERVA	660
	GLLARLRKDT	HRGLPIQQLR	PTQNLQPRIK	LKLFQHGSGG	KTTLVESLKC	GLLRSFFRRR	720
	RPRLSSTNSS	RPPFSPPLASK	PTVSVINNL	YPGCENVSVR	SRSMMPFEPGL	TKGMLEVFVA	780
	PTHHFPCSAD	DQSTKALDIQ	NAYLNGVGD	SVWEFSGNPV	YPCCYDYFAA	NDPTSIVHVV	840
20	FSLSEPYBIQ	LNVRVFWLSF	LKSLVFPVEP	IAPGGKLNKP	LQVVLVATHA	DIMNVPRPAG	900
	GEFGYDKDTS	LLKRIINRRPG	NDLHISNKL	VLDAGASGSK	DMKVLNRHLQ	EIRSQTIVSVC	960
	PPMTHLCEKI	ISTLPSWRKL	NGPNQLMSLQ	QFVYDVQDQL	NPLASEEDLR	RIAQQLHSTG	1020
	EINIMQSETV	QDVLLDPRW	LCTNVLGKLL	SVETPRALHH	YRGYTVBEDI	QRLVPDSDVE	1080
	ELLQILDAMD	ICARDLSSGT	MVDVPAIKT	DNLHRSWADE	EDEVVMVGGV	RIVPVEHLTP	1140
25	PPCGIFHKVQ	NLCRWIHQO	STEGDADIRL	WVNGCKLANR	GAELLVLLVN	HQGGIEVQRV	1200
	GLSTEKIKCC	LLLDVSCSTI	ENVMATTLPG	LLTVKHVLS	QQLRHHEHPV	MIYQPRDFFR	1260
	AQTLKETSLT	NTMGGYKESP	SSIMCPGCHD	VYSQASLGMD	THASDINLIT	RRKLSRLDLP	1320
	PDLGKDWCL	LAMNLGLPDL	VAKYNTNNGA	PKDFLPSPHL	ALLREWTTYP	ESTVGTLMASK	1380
	LRELGRDDAA	DLLLKASSVF	KINLDGNQGE	AYASSCNSGT	SYNSISSVVS	R	1431

Seq ID NO: C288 Protein Sequence
Protein Accession #: NP_002072.1

	1	11	21	31	41	51	
35	MELRARGWNL	LCAAALVAC	ARGDPASKSR	SCGEVRQIYG	AKGFSLSQVP	QAEISGEHLR	60
	ICPQGYTCCT	SEMEENLANR	SHAELETALR	DSSRVLQAML	ATQLRSFDDH	FQHLNDSEH	120
	TLQATFPFAP	GELTYQNARA	FRDLYSELRL	YRGANLHLE	ETLAEFWARL	LRLPKQLHP	180
	QLLLEDDYLD	CLGKQAEALR	PPGEAPREL	LRATRAFVAA	RSFVQGLGVA	SDVVRKVAQV	240
40	PLGPECSRVA	MKLVCARCL	GVFGARPCPD	YCRNVLLKGL	ANQADLDAEW	RNLLDSMVL	300
	TDKFWGTSGV	ESVIGSVHTW	LAEAINALQD	NRDTLTAKVI	QCGNPKVNP	QGGPEEKRR	360
	RGKLAPRERP	PSGTLEKLVS	EAKAQLRDVQ	DFWISLPGTL	CSEKMALSTA	SDDRCWNGMA	420
	RGRYLPVVMG	DGLANQINN	EVEVDITKPD	MTIRQQIMQL	KIMTNLRSA	YNGNDVDPQD	480
	ASDDGSGSGS						490

Seq ID NO: C289 Protein Sequence
Protein Accession #: AAH30205.1

	1	11	21	31	41	51	
50	MIILYLFLL	LWEDTQGNF	KDGIFHNSIW	LERAAGVYHR	BARSGKYKLT	YAEAKAVCEP	60
	EGGHLATYKQ	LEBAARKIGF	VCAAGWMARK	RVGYPIVKPG	PNCQFGKTGI	IDYIGRLNRS	120
	ERWDAYCYNP	HAKGCGVFT	DPKQIFKSPG	FPNEYEDNQI	CYWHIRLKYG	QRHLSEFLDP	180
	DLEDDPGCLA	DVVEIYDSYD	DVHGFGVRYC	GDLPDDIIS	TGNVMTLKPL	SDASVTAGGF	240
55	QIKYVAMDPV	SKSSQGNYS	TTSTGNKNFL	AGRFPSHL			277

Seq ID NO: C290 Protein Sequence
Protein Accession #: NP_001973.1

	1	11	21	31	41	51	
60	MRANDALQVL	GLLFSLARGS	EVGNSQAVCP	GTNLGLSVTG	DAENQYQTYL	KLYERCEVVM	60
	GNLEIVLTGH	NADLSFLQWI	REVTGYVILVA	MNEPSTLPLP	NLRVVRGTQV	YDGKFAIFVM	120
	LNNTNNSSHA	LRQLRLTQLT	EILSGGVYIE	KNDKLCMDT	IDWRDVRDR	DAEIVVKDNG	180
	RSCPPCHEVC	KGRCKWPGSE	DCQTLTKTIC	APQCNGHCFG	PMPNQCCHDE	CAGGCSGPD	240
65	TDCFACRHFN	DSGACVPRCP	QPLVYNKLT	QLEPNPHTKY	QYGGVCVASC	PENFVVDQTS	300
	CVRACPPDKM	EVDKNGLKMC	EPCGGLCPKA	CEGTGSGSRF	QTVDSNIDG	FNCTKILGN	360
	LDPLITGLNG	DPWHKIPALD	PEKLNVPRTV	REITGYLNIQ	SWPPHMHNFS	VFSNLTTIGG	420
	RSLYNRGFSL	LIMQNLNVT	LGFRSLKEIS	AGRIYISANR	QLCYHSLNHW	TKVLRGPTTE	480
70	RLDIKHNRP	RDCVAEGKVC	DPLCSSGGCM	GPGPGQCLSC	RNYRGGVCV	THCNFLNGEP	540
	REFAEARCF	SCHPECPQMG	GTATCNGSGS	DTCAQCAHFR	DGPHCVSSCP	HGVLAGAKPI	600
	YKYPDVQNEC	RPCHENTCQG	CKGPQLQDCL	QTLVLVIGKT	HLTMALTVIA	GLVVFMMGL	660
	GTFLYVRGRR	IQNKRAMRRY	LERGESIEPL	DPSEKANKVL	ARIPKETELR	KLKVLGSGVP	720
	GTVHGKWTIP	EGESIKIPVC	IKVIEDKSGR	QSPQAVTDEM	LAIGSLDHAI	IVRLGLCPG	780
75	SSLQLVTQYL	PLGSLLDHVR	QHRGALGPQL	LLNWCQVQIAK	GMYYLEEGHM	VHRLAARNV	840
	LLKSPSQVQV	ADPGVADLLP	PDDKQLLYSE	AKTPIKMMAL	ESIHPGKYTH	QSDVMSYQVT	900
	VWELMTFGAS	PYAGLRALAE	PDLLKGERL	AQPQICTIDV	YVMVVKCMMI	DENIRPTPKE	960
	LANEFTRMAR	IQNRYLVIKR	ESGPGIAPGP	EPHGLTNKKL	EEVELEPELD	LDDLEAED	1020
	NLATTLTGS	LSLFPVGLNR	PRGSQSLLSP	SSGYMPMNQ	NLGSSQCESA	VSGSSERCP	1080
80	PVSLHMPRPG	CLASESEGH	VTGSEALQE	KVSMCRSRSR	SRSPRPGRDS	AYHSQRHSL	1140
	TPVTPLSPPG	LEEDVNGYV	MPDTHLQGP	SSREGTLSSV	GLSSVLGTEE	EDEDEEYETM	1200
	NRNRHSPPH	PPRPSLEEL	GYEYMDVGS	LSAALGSTQS	CPLHPVPIMP	TAGTTPDEYD	1260
	EYMNRRQDGG	GPGGDYAMG	ACPASEQGYE	EMRAFQGP	QAPHVHYARL	KTLRSLEATD	1320
	SAFNDPDYWH	SRLFPKANAQ	RT				1342

Seq ID NO: C291 Protein Sequence
Protein Accession #: NP_001207.1

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5  1      11      21      31      41      51
   |      |      |      |      |      |
MAPLCPSFWL PLLIPAPAPG LTVQLLSLL LLMPVHPQRI PRMQEDSPLG GSSGSEDPL 60
GEEDLPSEED SPREEDPPGE EDLPGEEDLP GEEDLPEVKP KSEEEGSLKL EDLPTVEAPG 120
DPQEPQNNAH RDKEGDDQSH WRYGGDPPWE RVSPACAGRF QSPVDIRPQL AAFPCALRPL 180
RLIGFQLPPL PELRLRNNGH SVQLTLFPGL EMALGPGRFY RALQLHLHWG AAGRFGSEHT 240
10 VEGHRFFAEI HVVHLSTAFV RVDEALGRPG GLAVLAFLF EGPEENSAYE QLLSRLEEIA 300
EESGETQVPG LDISALLPSD PSRYFYQYEGS LTPPPCAQGV IWTVFNQIVM LSAKQLHTLS 360
DTLMGPGDSR LQLNFRATQP LAGRVIEASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF 420
GLLFAVTSVA FLVQMRRQHR RGTGKGVSYR PAEVAETGA 459

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15 Seq ID NO: C292 Protein Sequence
Protein Accession #: NP_004198.1

```

20  1      11      21      31      41      51
   |      |      |      |      |      |
MGGAVVDEGP TGVKAPDGGW GNAVLFGCFV ITGFSYAPFK AVSVFFKELI QEFGIGYSDT 60
AWISSILLAM LYGTGPLCSV CVNRFGCRPV MLVGGLPASL GMVAASPCRS IIQVYLITGV 120
ITGLGLALNP QPSLIMLNRY FSKRRPMANG LAAAGSPVFL CALSPGLQLL QDRYGNRGGF 180
LTLGGLLLNC CVCAALMRPL VVTAQPGSGP PRPSRRLDL SVFRDRGFVL YAVAASVMVL 240
GLFVPPVFFV SYAKDLGVFD TKAAPLLTIL GFIDIFARPA AGFVAGLGKV RPYSVYLFSP 300
25 SMFFNGLADL AGSTAGDYGG LUVFCIFPGI SYGMVGAQLF EVLMAIVGTH KPSAIGLVL 360
LMEAVAVLVG PPSGGKLLDA THVYMYVFIL AGAEVLTSSL ILLLAGNFFCI RKKPKPEPQE 420
VAAAEELKHL KPPADSGVDL REVEHFLKAE PEKNGEVVHT PETSV 465

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30 Seq ID NO: C293 Protein Sequence
Protein Accession #: NP_000349.1

```

35  1      11      21      31      41      51
   |      |      |      |      |      |
MALFVRLIAL ALALALGPAA TLAPAKSPFY QLVQHSRLR GROHGNVCA VQKVGITNRK 60
YFTNCKQNYQ RKICGKSTVI SYECCPGYEK VPGEKGCAPL LPLSNLYETL GVVGSTTTQL 120
YTDREKLRP EMEGPGSPFI FAPSNEAWAS LPABVLDSL VSNVIELLNA LRYHMVGRRV 180
LTDELKHGMT LTSMYQNSNI QIEHYPNGIV TVNCARLLKA DHATNGVVH LIDKVVITIT 240
NNIQQIIEIE DTFETLRAAV AASGLNTMLE GNGQYTLAP TNEAFKIPS ETLNRLIGDP 300
40 EALRDLINNH ILKSAMCAEA IVAGLSVETL EGTTLVGVCS GDMLTNGKA IISNKDILAT 360
NGVIHYIDEL LIPDSAKTLF ELAAESDVST AIDLFRQAGL GNLGSGSERL TLLAPLNSVF 420
KDGTFPIDAH TRNLLRNHII KDQLASKYLY HGQTLETLLG KKLRVFVYRN SLCIENSCLA 480
AHDKRGYGT LFTMDRVLTG PMGTVMVLK GDNRFMSLVA AIQSAGLTET LNREGVYTF 540
APTNEAFRAL PPRERSRLIG DAKELANILK YHIGDEILVS GGIGALVRLK SLQGDKLEVS 600
45 LKNNVSVNKH EPVAEPDIMA TNGVVHVITN VLQPPANRPQ ERGDELADSA LEIFKQASAF 660
SRASQSVRL APVYQKLLER MKH 683

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Seq ID NO: C294 Protein Sequence
Protein Accession #: NP_006527.1

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50  1      11      21      31      41      51
   |      |      |      |      |      |
MTQRSIAGPI CNLKFVTLV ALSSSELPFL AGVQLQDNGY NGLLIAINPQ VPENQNLIEN 60
IKEMITEASF YLFNATKRRV PFRNIKILIP ATWKANNNSK IKOESYEKAN VIVTDWYGAH 120
GDDPYTLQYR GCGKEGKYIH FTFNPLANDN LTAGYGRGRG VPVHEWAHLR WGVFDEYNDD 180
55 KPFYINGQNG IKVTRCSSDI TGIFVCEKGP CPQENCIISK LFKEGCTFIY NSTQNTATASI 240
MFMQSLSSVV EFCNASTHNQ EAPNLQNMOC SLRSAMDVIT DSADFHHSFP MNGTELPPPP 300
TFSLVQAGDK VVCLVLDVSS KMAEADRLLO LQQAAPFYLK QIVEIHTFVG IASFDSKGEI 360
RAQLHQINEN DDKRLVSYL PTTVSAKTDI SICGLKKGK EVVEKINGKA YGSMVILVTS 420
60 GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLIELSRLT GGLKFFVFDI SNSNSMIDAF 480
SRISSTGTDI FQHIQLEST GENVKPHQL KNTVTVDNTV GNDTMFLVTW QASGPPPIIL 540
FDPDGRKYIT NNFITNLTFR TASLWIPGTA KPGHWYTLN NTHSLQALK VTVTSRASNS 600
AVPPATVEAF VERDSLHFFH PVMYIANVKQ GFYPIILNATV TATVEPETGD PVTLRLLDDG 660
AGADVINKDG IYSRYFFSFA ANGRYSKVBH VNHSPSISTP AHSIPGSHAM YVPGYTANGN 720
65 IQMNAPEKSV GRNEBERKNG PSRVSSGGSF SVLGVPAGEH FDFVFPCKII DLEAVKVEEE 780
LTLSTAPAGE DFDQQAQTSY EIRMSKSLQN IQDDFNAIL VNTSKRNPQQ AGIRBIFTFS 840
PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY 900
LILKSVLTAM GLIGIICLII VVTHHTLSRK KRADEKENGIT KLL 943

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70 Seq ID NO: C295 Protein Sequence
Protein Accession #: Eos sequence

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75  1      11      21      31      41      51
   |      |      |      |      |      |
MKFLILLILL ATASGALPLN SSTSLKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60
KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHFP REMPGGPVNR KHYITYIRIN 120
YTFDMNRREDV DVAIRKAPQV WSNVTPLKFS KINTGMADIL VVPARGAHGD PHAFDGGGGI 180
LABAFPGGSG IGGDAHFDED EFWTHSCGT NLPLTAVHEI GHSGLGHSS DPKAVMFPTY 240
KQVDINTFRL SADDIRGIQS LYGDPEKQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFP 300
80 FKDRFFWLKV SERPKTSVNL ISSLMPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP 360
EPNYPKSTHS FGPFPVVKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQNM DPGYPKLITK 420
NQGGIGPKID AVFYSKNKYK YFPQGSNQFE YDFLLQRIK TLKSNWFGC 470

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Seq ID NO: C296 Protein Sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
 5 MKPLLILLQ ATASGALPLN SSTSLKQNV LFGERYLEKP YGLEINKLPV TKMKYSGNLM 60
 KEKIQEMQHF LGLKVTGQLD TSTLENQHAP RCGVPDVHFF REMPGGPFVWR KHYITYRINN 120
 YTPDMNREDV DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVFARGAGHD PHAFDQKGGI 180
 LAHAFGPQSG IGGDAHFDDE EFWTTHSGGT NLFLTAVHAI GHSGLGLGHS DPKAVMPPTY 240
 KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFP 300
 FKDRFPWLKV SERPKTSVNL ISSLMPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP 360
 10 EPNYPKSIHS FGPFNFVKKI DAAVFNPRFY RTYFFVDNQY WRVDERRQMM DPGYPKLITK 420
 NFGGIGPKID AVFYSKNKYP YFFQGSNQFE YDFLLQRIK TLKSNWFGC 470

Seq ID NO: C297 Protein Sequence
 Protein Accession #: NP_008883.1

1 11 21 31 41 51
 15 MAKDNSTVRC FQGLLIFQNV IIGCCGIALT ABCIPFVSDQ HSLYFLLEAT DNDDIYGAAW 60
 IGIFVGLCLF CLSVLGIVGI MKSSRKILLA YFILMPVYA FEVASCITAA TQRDFFTPNL 120
 20 FLKQMLERYQ NNSPPNNDQ WKNGVTKTW DRLMLQDNCC GVNQPSDNQK YTSAPRTENN 180
 DADYFMPRQC CVMNLIKPEL NLEACKLGVP GFYHNQGCYE LISGPMNRHA NGVAMFGFAI 240
 LCWTFWLLG TPFYWSRIEY 260

Seq ID NO: C298 Protein Sequence
 Protein Accession #: NP_001784.2

1 11 21 31 41 51
 30 MGLFRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGABQEPGOA LGKVFMCPCP 60
 QSPALFSTDN DDFTVRNGET VQERRSLKER NPLKIPPSKR ILRRHKRDWV VAPISVPENG 120
 KGPPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPGVFAV EKETGWLLLN KPLDREBIAK 180
 YELGHAUSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
 DEDDAIYTYN QVVAYSLSHQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 35 TDMGDGSGTT TAVAVVEILD ANDNAPMFDQ QKYEARVPEN AVGHEVQRLT VTDLDAPNSP 360
 AWRATYILING GDDGDHPTIT THPESNQIIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEFVC VYTAEDPDKE NQKISYRILR 480
 DPAGWLAMPD DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLTLD 540
 VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
 40 TVVLSLKKPL KQDTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660
 GAVLALLFL LVLALLVRKK RKIKEPLLLP EDDTRDNVYF YGEGGGGEED QDYDITQLHR 720
 GLEARPEVVL RNDVAPTIIIP TMYRPRPAN FDEIGNFIIE NLKAANTDPT APPYDTLLVF 780
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGEDED 829

Seq ID NO: C299 Protein Sequence
 Protein Accession #: NP_005620.1

1 11 21 31 41 51
 50 MAKKSANGI YSVSGDEKKG PLIAPGPDGA PAKGDPVGL GTPGGR LAVP PRETWTRQMD 60
 PIMSCVGFV GLGNWRFPY LCYKNGGGVF LIPYVLIALV GGIPFFLEI SLGQPMKAGS 120
 INVWNICPLF KGLGYASMVI VFYCNYYIM VLANGFYLV KSFTTLTPWA TCGHTWNTFD 180
 CVELFRHEDC ANASLANLTC DQLADRRSPV IEFWENKVL RSGGLEVPGA LNWEVTLCLL 240
 ACWLVVPCV WGVKSTGKI VYFATATPPY VLVVLLVRGV LLPGALDGI YLKPDPWSKL 300
 55 GSPQVWIDAG TQIFPSYAIG LGALTALQSY NRPNNCYKD AIIALALINSQ TSFFAGFVVF 360
 SLIGMAAEQ VGHISKVAES GPGLAFIAYP RAVTLMVPAP LWAALFFPM LLLGLDSQFV 420
 GVEGFIITGL DLLPASYIFR PQREISVALC CALCFVIDLS MVTGGGMVVF QLFDYYSASG 480
 TTLNQAEFV CVVAVWVGA DRFMDDIACM IGYRCPWMK WCHSFTPLV CMGIFLNVV 540
 YVEPLVYNT YVYPWNGEAM GWAPALSSML CVPLELLGCL LRAKGTMAER WQHLTQPIWG 600
 60 LHELEYRAQD ADVRLTTLT PVSESSKV VESVM 635

Seq ID NO: C300 Protein Sequence
 Protein Accession #: NP_006507.1

1 11 21 31 41 51
 65 MEPSSKKLTG RLMLAVGGAV LGSLLQFGYNT GVINAPQKVI EEPYNQTVWH RYGESILPTT 60
 LTTLSLSVA IFSVGMIGS FSVGLFVNRF GRNSMLMMN LLAFVSAVLM GFSKLKGSPE 120
 MLILGRPIIG VYCGLTTFGV PMYVGEVSPT AFRGALGTLH QIGIVVGILI AQVFGLDSIM 180
 70 GNKDLWPLLL SIIFIPALLQ CIVLPFCPS PRFLINENE ENRAXSVLKK LRGTADVTHD 240
 LQEMKEESRQ MREKRVITL ELFRSPAYRQ PILIAVVLQ SQQLSGINAV FYYSTSIFEK 300
 AGVQQPVYAT IGSIGVNTAP TVVSLFVVER AGRRTLHLIG LAGMAGCAIL MTIALALLEQ 360
 LFWMSYLSIV AIFGPFVAFB VGGPIPMFI VAELFSQGP PAALAVAGFS NWTNFIIVGM 420
 CPQYVEQLCO PYVFIIFTVL LVLFPIFTYF KVPETKGRTP DEIASGFRQG GASQSDKTPE 480
 75 ELFHLGADS QV 492

Seq ID NO: C301 Protein Sequence
 Protein Accession #: XP_035292.2

1 11 21 31 41 51
 80 MAGAGFKRRA LAAPAAEKEE EAREKMLAAK SADGSAPAGE GBGVTLQRNI TLLNGVAITV 60
 GTIIGSGIFV TPTGVLEKAG SPGLALVWA ACGVFSIVGA LCYAEGLTTI SKSGGDYAYM 120
 LEVYGSLPAP LKLWIELLII RPSSQYIVAL VFATYLLKPL PPTCFVPEEA AKLVACLVL 180
 LITAVNCYSV KAARTVQDAF AAALKLALAL IILLGFVQIG KGDVSNLDPN PSEGTCKLDV 240

5 GNIVLALYSQ LPAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300
 STEQMLSSSE VAVDFGNYHL GVMSEIIPVF VGLSCFQSVN GSLFTSSRLP FVGSREGHLP 360
 SILSMIHQPL LTPVPFSLVFT CVMTLLEYAFS KDIFSVINFF SFFNWLICAL AIIGMIWLRL 420
 RKPELERPIK VNLALPVFFI LACLFIAVS FWKTFVECGI GFTIISGLP VYFFGVWVKN 480
 KPKMLLQGIF STTVLCQRLM QVVPQET 507

Seq ID NO: C302 Protein Sequence
 Protein Accession #: NP_005259.1

10 1 11 21 31 41 51
 MNWSIFEGLL SGVNYKSTAF GRWLSLVFI FRVLVYLVTI ERVMSDDHKO FDCNTRQPGC 60
 SNVCDEFEPF VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRRHREAHG ENSGRLYLNP 120
 GKRRGGLWWT YVCSLVFKAS VDIAFLYVFH SFYPKYILPF VVKCHADPCF NIIVDCFISKP 180
 15 SEKNIFTLFM VATAAICILL NLVELIYLVS KRCHCELAAR KAQAMCTGHH PHGTTSSCKQ 240
 DDLISGDLIF LGSDSHPPLL PDRPRDHVKK TIL 273

Seq ID NO: C303 Protein Sequence
 Protein Accession #: NP_005121.1

20 1 11 21 31 41 51
 MKICSLTLLS FLILLAAQVLL VEGKKVKVNG LSKVVSSEKQ DTLGNTQIKQ KSRPGNKGKF 60
 VTKDQANCRW AATQESEGIS LKVECTQLDH EFSCVPAGNP TSCLKLWDER VYWKQVARNL 120
 25 RSQKDICRYS KTAVTRVCR KDFPSSSLKL VSSTLFGNTK PRKEKTEMSP REHIKKGKTT 180
 PSSLAVTQTM ATRAPECVED PDMANQRKTA LEFCGETWSS LCTFFLSIVQ DTSC 234

Seq ID NO: C304 Protein Sequence
 Protein Accession #: AAH22542

30 1 11 21 31 41 51
 MCSEIILRQE VLKDGFRHDL LIKVKFGESI EDLHTCRLLI RQDIPAGLYV DPEYLASLRE 60
 RNITEAVMVS ENFDIEAPNY LKSESEVLTY ARRDSQCIDC FQAFLPVHCR YHRPHSEDEG 120
 35 ASIVVNNPDL LMFCDQAGSR RMIRFRFDSF DKTIEFPILK CWAHSEVAAP CALENEDICQ 180
 WNMKMYKSVY KNVILQVVG LTVHTSLVCS VILLITILCS KKKKK 225

Seq ID NO: C305 Protein Sequence
 Protein Accession #: NP_004985.1

40 1 11 21 31 41 51
 MSLWQPLVLV LLVLGCCFAA PRQRQSTLVL FPGDLRTNLT DRQLAEVLYL RYGYTRVAEM 60
 RGESKSLGPA LLLLQKGLSL PETGELDSAT LKAMRTPRCG VPDLGRFQTF EGDLLKWHEN 120
 45 ITYWIQNYSE DLPRVIDDA FARAPALWSA VTPLTFTRVY SRDADIVIQF GVAEHGQGYF 180
 PDGKDGLLAH APFPGPGIQG DAHFDDELW SLGKGVVVPF RFGNADGAAC HFFPIFEGRS 240
 YSACTTDRGS DGLFWCSTTA NYDTDDRFGP CPSERLYTRD GNADGKPCQF PFIFQGGQYS 300
 ACTTDRGSRG YRWCAATTAY DRDKLFGFCF TRADSTVMGG NSAGELCVFP FTFLGKEYST 360
 CTSEGRGDGR LWCATTSNPD SDKKWGFCDP QGYSLFLVAA HEFGHALGLD HSSVPEALMY 420
 50 PMYRFTGEGP LHKDDVNGIR HLYGFRPEPE PRPPTTTTPQ PTAPPTVCPT GPPTVHPSER 480
 PTAGPTGPPS AGPTGPTTAG PSTATTVPIS PVDDACNVNI FDAIASIGNQ LYLFRDQKYN 540
 RFSEGRGSRP QQPFLIADKW PALPRKLDV FEEPLSKLF PFSGRQVWVY TGASVLGPRR 600
 LDKLGLGADV AQVTGALRSR RGMMLLFSGR RLWRFVKAQ MVDPRSAEVS DRMPFGVPLD 660
 55 THDVQYREK AYFCQDRFYW RVSSRSRLNQ VDQVGYVTYD ILQCPED 707

Seq ID NO: C306 Protein Sequence
 Protein Accession #: NP_000204

60 1 11 21 31 41 51
 MAGPRPSPWA RLLLAALISV SLSGTIANRC KKAPVKSCFE CVRVKDCAY CTDEMFRDRR 60
 CNTQAEKLLA GCQRESIVVM BSSFQITEET QIDTTLRRSQ MSPQGLRVRL RPEGERHFEL 120
 EVFEPLESPV DLYIIMDFSN SMSDDLNLK KMGQNLARVL SOLTSDYITG FGKFDKVSFV 180
 65 PQTDNRPEKL KEFWNSDEFP FSEKNVISLT EDVDEFRNKL QGERISGNLD APEGGFDAIL 240
 QTAVCTDIG WRPDSTHLLV FSTESAFHYE ADGANVLAI MSRNDERCHL DTTGTYYQYR 300
 TQDYPSPVTL VRLLAGHNII PIPAVTNYSY SYYEKLETFY PVSSGLVQLQE DSSNIVELLE 360
 BAFNRIRSNL DIRALDSPRG LRTEVTSKMF QKTRTGSFHI RRGVGVITYQV QLRALHVDG 420
 THVQQLPEDQ KGNILKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV 480
 70 CSEGWSGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHCVCYGEGR YEGQFCEYDN 540
 PQCPRTSGFL CNDRGRCSMG QCVCEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCECGR 600
 CHCHQSSLYT DTICEINYSI IHPGLCEDLR SCVQCQANGT GEKKGRTCEB CNFKVMKVD 660
 LKRAEIVVVR CSFRGDDDDC TYSYTMEGDG APGFNSTVLV HKKKDCPPGS FWWLIPLLLL 720
 LLEPLALLLL LCWKYCACK ACLALLPCCN RGHMVGFKED HYMLRENLMA SDHLETPMLR 780
 75 SGNLKGDRDV RWKVNNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTRER 840
 AQLRQEVEN LNEVYRQISG VHKLQQTFR QQPNAKKQD HTIVDTVLMA PRSAKPALLK 900
 LTKQVEQRA FEDLVKAPGY YTLTADQDAR GMVEFQEGVE LVDVVRVFLP RPEDDDEKQL 960
 LVEAIDVPAG TATLGRRLVN ITIIEQARD VVSFEQPEFS VSRGDQVARI PVIRRVLDGG 1020
 KSQVSYRQD GTAQGNRDIY PVEGELLFQ GEAWKELQVK LLELQEVDSL LRGRQVRRFH 1080
 80 VQLSNPKFGA HLQQPESTTI IIRDPDELDR SFTSOMLSSQ PPHGDLGAP QNPNAKAAGS 1140
 RKIHPNWLPP SGKPMGYRVK YWIQGDSSE AHLLDSKVPV VELTNLYPYC DYEMKVCAYG 1200
 AQGEGPVSSL VSCRTHQEV SEPGRALFNV VSSTVTQLSW AEPATNGEI TAYEVCYGLV 1260
 NDNRPIDGFM KKVLDNPNK RMLLIENLRE SQPYRYTVKA RENGAGWGP ERINLATQP 1320
 KRFMSIPIIP DIPIDVAGSG EDYDSFLMYS DDVLRSPSGS QRPVSDDTG CGMKFEPPLG 1380
 EELDLRRTVW RLPELIPRL SASSGRSSDA BAPTAPETTA ARAGRAAAMP RSATFPGPPGE 1440

5 HLVNGRMDFA PFGSTNSLHR MTTTSAAYG THLSFHVPHR VLSTSTLTR DYNLSLTRSEH 1500
 SHSTTLPRDY STLTSSVSHD SRLTAGVPTD PTRLVPSALG PTLRLVSNQE PRCEPLOGGY 1560
 SVEYQLLNGG BLHRLNIPNP AQTSSVVVDEL LFNHSYVPRV RAQSQDQWGR BREGVITIES 1620
 QVHPQSPLCP LFGSAPTLST PSAPGPLVFT ALSPDSLQLS WERPRRPNGD IVGYLVTCEM 1680
 AQGGGPATAF RVDGDSPEER LTVPLGSENV PYKFKVQART TEGFPEREG IITIESQDGG 1740
 FFPQLGSRAG LFQHLQSEY SSITTTHTSA TEPFLVDGLT LGAQHLEAGG SLTRHVTQEF 1800
 VSRTLTSGT LSTMDQQFF QT 1822

10 Seq ID NO: C307 Protein Sequence
 Protein Accession #: NP_076404.1

15 1 11 21 31 41 51
 | | | | |
 MGFNLTAKL PNNELHQES HNSGNRSDGP GKNTTLHNEF DTIVLFVLYL IIFVASILLN 60
 GLAVWIFPHI RNKTSPIFYL KNIVVADLIM TLTPFPRIHV DAGFGFWYFK FILCRYTSVL 120
 FYAMMTSTV FLGLISIDRY LKVVKFFGDS RMYSTFTKV LSCVWVIMA VLSLPIILT 180
 NGQPTEDNIH DCSKLKSLG VKWHTAVTV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQP 240
 ISQSSRRKKH NQSIKVVAV FFTCFLPYHL CRIPPTPSHL DRLLDESAQK ILYYCKEITL 300
 FLSACNVCLD PIYFFMCRS PSRRLLPKSN ITRSESIRS LQSVRRSEVR IYYDYTDV 358

20 Seq ID NO: C308 Protein Sequence
 Protein Accession #: NP_065840.1

25 1 11 21 31 41 51
 | | | | |
 MVWCLGLAVL ELVISQADG RGKPEVVSVV GRAEESVVLG CDLLPPAGRP PLHVIWLRP 60
 GFLLPFIQF GLYSFRIDPD YVGRVRLQKG ASLQIEGLRV EDQGWYECRV PFLDQHIFED 120
 DFANGSWVHL TVNSPPQFQE TPPAVLEVQE LEPTVLRCA RGSPILPHVTW KLRGKDLQGG 180
 QGVQVQNGT LRIIRVERGS SGVYTCQASS TEGSATHATQ LLVLGPPVIV VPKNSTVNA 240
 SQDVSLACHA EAYPANLTY S WFDNINVFH ISRLQPRVQI LVDGSLRLLA TQDDAGCYT 300
 CVPSNGLLHP PSASAYLTVL CMGVIKCPV RANPPLLEVS WTKDGKALQL DKFPGMSQGT 360
 EGSLIIALGN EDALGEYSCT PYNSLGTAGP SPVTRVLLKA PPAFIERPKE EYFQEVGREL 420
 LIPCSAQGDP PFVVSWTQVG RGLQQAQVD SNSSLILRPL TKEAHGHWEK SASNAVARVA 480
 TSTNVYVLGT SPHVVTNVS VALPKGANVS WEPGFDGGYL QRFVWYTPK AKRPDRMHED 540
 35 WSLAVPVGA AHLVPLGLP HTQYQFSVLA QNKLGSQFSS EIVLSAPEGL PTPAAGPLP 600
 PTEIPPPLSP PRGLVAVRTP RGVLLHWDPP ELVPKRLDGY VLEGRQGSQG WEVLDPVAVG 660
 TETELLVPLG IKDVLVEFRL VAPAGSFVSD PSNTANVSTS GLEVYPSRTQ LPGLLPQPV 720
 AGVVGVCFL GVAVLVLSILA GCLLNRRRAA RRRKRRLRQD PPLIFSPTGK SAAPSALGSG 780
 SPDSVAKLKL QGSPVPSLRQ SLLWGDPAQT PSPHPDPPSS RGLPLEPIC RGPDRFVMG 840
 40 PTVAAPQERS GREQAERTP AQRLARSFDC SSSSPSGAPQ PLCIEDISPV APPPAAPPSP 900
 LFGPGPLLQY LSLPFPFREM VGDWNPLEE PSFAAPPDYM DTRCRPTSSF LRSPTFPVS 960
 PRESSLPGAV GAGATAEPY TALADWTLRE RLLPGLLPAA PRGSLTSQSS GRGSASFRLP 1020
 PSTAPSAGGS YLSPAPGDT S WASGPERWP RREHVVTYSK RRNTSVDENY EWDSEFPQDM 1080
 45 ELLETLEHGL ASSRLRPEAE TELGVKTPPE GCLLNTAHTV GPEARCAALR EEFLAFRRER 1140
 DATRARLPAY RQPFVHEPQA TLL 1163

Seq ID NO: C309 Protein Sequence
 Protein Accession #:

50 1 11 21 31 41 51
 | | | | |
 MLTKPLQGP APPGTPTPPP GKKDRBAFEA EYRLGPLLKG GFGTVFVAGH RLTDRLQVAI 60
 KVIPRNRVLG WSPFLSDSVTC PLEVALLWKV GAGGGHFGVI RLLDWFETQE GFMLVLERPL 120
 PAQDLFDYIT EKGPLGSGPS RCFPGQVVA IQHCHSRGVV HRDIKIDENIL IDLRRCAGKL 180
 55 IDFGSGALLH DEPYTDFDGT RYVSPFENIS RHQYHALPAT VWSLGMILYD MCGDIPFER 240
 DQILEAELH FPAHVSPDC ALIRCLAPK PSSRPSLEBI LLDPMQTPA EDVTPQLQR 300
 RPCPGLVLA TLSLAWPGLA PNGQKSHPMA MSQG 334

60 Seq ID NO: C310 Protein Sequence
 Protein Accession #: NP_002501.1

65 1 11 21 31 41 51
 | | | | |
 MECLYYLGF LLLAARLPLD AAKRPHDVLG NERPSAYMRE HNQLNGWSSD ENDWNEKLYP 60
 VWKRGDMRWK NSWKGGRVQA VLTSDSPALV GSNITFAVNL IFPRCQKEDA NGNIVYERNC 120
 RNEAGLSADP YVYNNTAMSE DSDGNGTQ SHINVFPGDK FPHHPGWRN WNFYVVFHTL 180
 GQYFQKLGR SVRVSVNTAN VTLGPQLMEV TVYRRHGRAY VPIAQVKDQV VVTDQIPFV 240
 TMFQKNDRNS SDETFLKDLP IMPDVLHDP SHFLNYSTIN YKWSFGDNTG LPVSTNHTVN 300
 70 HTYVLNGTFS LNLTVKAAAP GPCPPPPPPP RPSKPTPSLG PAGDNPLELS RIPDENQCIN 360
 RYGHFQATIT IVEGILEVNI IQMTDVLMPV PWPESLIDF VVTCQGSIPT EVCTIISDPT 420
 CRITQNTVCS PVDVDEMCLL TVRRTFNGSG TYCVNLITGD DTSALITSTL ISVPDRDPAS 480
 PLRMANSALI SVGCIAIPVT VISLLVYKKH KEYNPIENSP GNVVRSGKLS VFLNRAKAVP 540
 PFGNQEKDPL LKQEFKGV S 560

75 Seq ID NO: C311 Protein Sequence
 Protein Accession #: Bos seq

80 1 11 21 31 41 51
 | | | | |
 MRILKFLAC IQLLCVCRLD WANGYYRQR KLVEEIGWSY TGALNQKNGW KKYPCTNSPK 60
 QSPINIDEDL TQVNVLEKLL KPGQNDKTSL ENTPIENTGK TVBINLTNDY RVSGGVSEMV 120
 FKASKITFW GKQNMSSDGS EHSLEGQKFP LEMQIYCPDA DRPSSFEAV KKGKLRALS 180
 ILFEVGTEN LDFKAIIDGV ESVSRFGQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC 240
 TDTVDWIVFK DTVSISESQL AVPCBVLTNQ QSGYVLMNDY LQNNFREQQY KFSRQVFSSY 300

	TGKEEIHAEV	CSSEPENVQA	DPENYTSLLV	TWERPRVVD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLFFE	420
	LIGTEEIIKE	EEEGKDIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
5	RSPTRGSEFS	GKGDVNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPT	VEGTASLND	540
	GSKTVLRSPH	MNLSTGAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPTITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLEM	PHYSTPAYFP	720
	TEVTPHAPT	SSRQQLVST	VNVVYSQTTQ	PVYNASNS	HESRIGLAEG	LESEKKAVIP	780
10	LVIVSALTFI	CLVLVVGILI	YWRKCFQTAH	FYLEDSTSPR	VISTPPTPIF	PISDDVGAIP	840
	IKHFPKHVAD	LHASSGFTTE	FEEVQSCTVD	LGITADSSNH	PDNKHKNRYI	NIVAYDHSRV	900
	KLAQLASKDG	KLTDVINANY	VDGYNRPKAY	IAAQGLPKST	AEDFWRMIWE	HNVEVIVMIT	960
	NLVEKGRRK	DQYNPADGSE	EYGNFLVTQK	SVQVLAYYTV	RNFTLRNTKI	KKGSQKGRPS	1020
	GRVVTQYHYT	QMPDMGVFEY	SLPVLTFVRK	AAAYAKRHAVG	FVVVHCSAGV	GRGTGYIVLD	1080
15	SMLQQIQHEG	TVINPGFLKH	IRSQRNYLVQ	TEEQYVFIHD	TLVEAILSKE	TEVLDSHIHA	1140
	YVNALLIPGP	AGKTKLEKQP	QLLSQSNIQQ	SDYSAALKQC	NREKNRTSSI	IPVERSRRVGI	1200
	SSLSGEGTDY	INASYINGGY	QSNFPIITQH	PLLETIKDFW	RMWDHNAQL	VVMIPDQGNM	1260
	AEDEFVYVWF	KDEPINCESF	KVTLMAEHKK	CLSNEEKLII	QDFILEATQD	DYVLEVRHFO	1320
	CPKWFNDPS	ISKTFELISV	IKEEAANRDG	PMIVDEHGG	VTAGTFCALT	TLMHQLEKEN	1380
20	SVDVYQVAKM	INLMRPGVFA	DIEQYQFLYK	VILSLVSTRQ	EENPSTSLDS	NGAALPDGNI	1440
	AESLESVL						1448

Seq ID NO: C312 Protein Sequence
Protein Accession #: XP_031379

25	1	11	21	31	41	51	
	MRILKRFLAC	IQLLCVCRID	WANGYYRQQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNKKL	KPQGWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
30	FKASKITFHW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSFEBAV	KKGKLRALS	180
	ILFEVGTEEN	LDFAKIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYI	YNGSLTSPPC	240
	TDVDMWVFK	DTVSISESQL	AVPCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFPSSY	300
	TGKEEIHAEV	CSSEPENVQA	DPENYTSLLV	TWERPRVVD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLFFE	420
35	LIGTEEIIKE	EEEGKDIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	GKGDVNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPT	VEGTASLND	540
	GSKTVLRSPH	MNLSTGAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPTITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLEM	PHYSTPAYFP	720
	TEVTPHAPT	SSRQQLVST	VNVVYSQTTQ	PVYNGETPLQ	PSYSSEVPFL	VTPLLLNQI	780
40	LNTTPAASSS	DSALHATPVF	PSVDVSPESI	LSSYDGAPLL	PFSSASPSSE	LFRHLTVSQ	840
	ILPQVTSATE	SDKVPLHSL	PVAGGDLLLE	PSLAQYSDVL	STTHAASETL	EFGSESGVLY	900
	KTLMFSPQEP	PSSDAMMHAR	SSGFEPSTAL	SDNEGSHIF	TVSYSSAIPV	HDSVGVTYQG	960
	SLPFGSPSHIP	IPKSSLITPT	ASLLQPTHAL	SGDGEWSGAS	SDSEFLLEPT	DGLTALNISS	1020
45	PVSAEFTYTT	TSVPGDDNKA	LKSEIYIGN	ETELQIPSPN	EMVYPSESTV	MFNMYDNVVK	1080
	LNASLOETSV	SISSTKGMFP	GSLAHTTTKV	FDHEISQVPE	NNFSVQPTHT	VSQASGDTSL	1140
	KPVLANSSEP	ASSDPASSEM	LSPSTQLLFY	ETSASFSTEV	LLQPSFQASD	VDTLTKTVLP	1200
	AVPSDPIVLE	TPKVDKISST	MHLIVSNSA	SSENMLHSTS	VPVFDVSPTS	HMSASLQGL	1260
	TISVASEKYE	PVLLKSESSH	QVPSLYSND	ELFQTANLEI	NQAEPPKGRH	VFATPVLSID	1320
50	EPLNTLNLK	IHSDEILTST	KSSVTGKVFA	GIPTVASDTF	VSTDHSPVIG	NGHVAITAVS	1380
	PHRDGVSST	KLLPFSKATS	ELSHSAKSDA	GLVGGGEDGD	TDDDDDDDD	DRGSDGLSIH	1440
	KCMSCSSYRE	SQEKVMNDSO	THENSIMDQN	NPISYSLSEN	SEEDNRVTSV	SSDSQTGMDR	1500
	SPGKSPSANG	LSQKHNKGKE	ENDIQTGSAL	LPLSPESKAW	AVLTSDSEBS	SGQGTSDSLN	1560
	ENETSTDFSF	ADTNEKDADG	ILAAQDSBIT	PGFPQSPSTSS	VTSENSEVFH	VSEAEASNS	1620
55	HESRIGLAEG	LESEKKAVIP	LVIVSALTFI	CLVLVVGILI	YWRKCFQTAH	FYLEDSTSPR	1680
	VISTPPTPIF	PISDDVGAIP	IKHFPKHVAD	LHASSGFTTE	FETLKRFYQE	VQSCVVDLGI	1740
	TADSSNHFDN	KHKRYNINIV	AYDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	1800
	QGPKLKTHAV	FMWMIWENH	EVIVMITNLV	EKGRRKCDQY	WPADGSEERY	NFLVTQKSVL	1860
	VLAYTYTRNF	TLRNKTIKKG	SQKGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFVRKAAV	1920
60	AKRHAVGPV	VECSAGVGR	GTIVVLDLML	QQIQHEGTVN	IPGFLKHRS	QRNYLVQTEE	1980
	QYVFIHDTLV	EAILLSKETEV	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFOLL	SQSNIQQSDY	2040
	SAALKQCNRE	KNRTSSIIIP	ERSRVGIISS	SGEGTDYINA	SYIMGYQSN	EFIITQHPLL	2100
	HTIKDFWRMI	WMHNAQLVVM	IPDQGNMAED	EFVYWPKNDE	PINCESFKVT	LMAREHKLCS	2160
	NBEKLIQDF	ILEATQDDYV	LEVREHFCPK	WPNFDPISK	TFELISVIKE	EAANRDGPMI	2220
65	VDEHGGVTA	GTFCALTFLM	HQLEKENSVD	VYQVAKMINL	MRPGVFAIDIE	QYQFLYKVIL	2280
	SLVSTRQEN	PSTSLDSNGA	ALPDGNIAES	LESVL			2315

Seq ID NO: C313 Protein Sequence
Protein Accession #: NP_002842

70	1	11	21	31	41	51	
	MRILKRFLAC	IQLLCVCRID	WANGYYRQQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNKKL	KPQGWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
75	FKASKITFHW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSFEBAV	KKGKLRALS	180
	ILFEVGTEEN	LDFAKIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYI	YNGSLTSPPC	240
	TDVDMWVFK	DTVSISESQL	AVPCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFPSSY	300
	TGKEEIHAEV	CSSEPENVQA	DPENYTSLLV	TWERPRVVD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLFFE	420
80	LIGTEEIIKE	EEEGKDIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	GKGDVNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPT	VEGTASLND	540
	GSKTVLRSPH	MNLSTGAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPTITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLEM	PHYSTPAYFP	720
	TEVTPHAPT	SSRQQLVST	VNVVYSQTTQ	PVYNASNS	HESRIGLAEG	LESEKKAVIP	780

5 PLVIVSALTFL ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGA 840
 PIKHPFHGVA DLHASSGFTE EFETLKEFYQ EVQSCVTDLG ITADSSNHPD NKHKRYINI 900
 VAYDHSRVKL AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAB DFWRMINEHN 960
 VEIVMITNL VEGRRKCDQ YWADGSEY GNFLVTQKSV QVLAYYTVRN FTLRNTKIKK 1020
 GSQGRPSGR VVTQYHYTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCSAGVGR 1080
 TGTIYVLD SM LQIQHEGTV NIPGFLKHIR SQRYNLVQTE EQYVFIHDTL VEALLSKETE 1140
 VLDSHIHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200
 VERSRVGISS LSGEGTDYIN ASYIMGYVQS NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260
 10 MIPDQGNMAE DEFVYVFNKD EPINCESPKV TLMABEHKCL SNEEKLIQD FILEATQDDY 1320
 VLEVRHFQCP KWNPDSPIS KTFELISVIK BEAANRDGPM IVHDEHGGVT AGTFPCALTTL 1380
 MHQLEKENSV DVYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440
 AALPDGNIAB SLESIV 1456

15 Seq ID NO: C314 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 20 MRILKRFAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGA LNQKNWG KKYPTCN SPK 60
 QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
 MYPKASKITP HMKCNMSDGS GSEHSLGQKFP LEMQIYCFDA DRPSSFEAV KKGKLRALS 180
 LSLFEVGTEN LDPKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240
 PCTDWDIVFK DTVSISESQL AVFCEVLTMO QSGYVMLMDY LQNNFREQY KFSRQVPSY 300
 25 TGTIYVLD SM LQIQHEGTV NIPGFLKHIR SQRYNLVQTE EQYVFIHDTL VEALLSKETE 1140
 VLDSHIHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200
 VERSRVGISS LSGEGTDYIN ASYIMGYVQS NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260
 30 MIPDQGNMAE DEFVYVFNKD EPINCESPKV TLMABEHKCL SNEEKLIQD FILEATQDDY 1320
 VLEVRHFQCP KWNPDSPIS KTFELISVIK BEAANRDGPM IVHDEHGGVT AGTFPCALTTL 1380
 MHQLEKENSV DVYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440
 AALPDGNIAB SLESIV 1456

45 Seq ID NO: C315 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 50 MRILKRFAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGA LNQKNWG KKYPTCN SPK 60
 QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
 FKASKITFW GKNMSDGS EHSLEGQKFP LEMQIYCFDA DRPSSFEAV KKGKLRALS 180
 ILFEVGTEN LDPKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240
 TDTVDWIVFK DTVSISESQL AVFCEVLTMO QSGYVMLMDY LQNNFREQY KFSRQVPSY 300
 55 TGTIYVLD SM LQIQHEGTV NIPGFLKHIR SQRYNLVQTE EQYVFIHDTL VEALLSKETE 1140
 VLDSHIHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200
 VERSRVGISS LSGEGTDYIN ASYIMGYVQS NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260
 60 MIPDQGNMAE DEFVYVFNKD EPINCESPKV TLMABEHKCL SNEEKLIQD FILEATQDDY 1320
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 MHQLEKENSV DVYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440
 AALPDGNIAB SLESIV 1456

75 Seq ID NO: C316 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 80 MRILKRFAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGA LNQKNWG KKYPTCN SPK 60
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 FKASKITFW GKNMSDGS EHSLEGQKFP LEMQIYCFDA DRPSSFEAV KKGKLRALS 180
 ILFEVGTEN LDPKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240

5 TDTVDWIVFK DTVSISESQL AVFCEVLTMO QSGYVLMMDY LQNNFREQQY KFSRQVFSY 300
 TGKEEIEHAV CSSEPEENVQA DPENYTSLLV TWERPRVVDY TMIEKFAVLV QQLDGEDQTK 360
 HEFLTDGYQD LGAILNLLP NMSYVLQIVA ICTNGLYGYK SDQLIVDMPT DNPEASNSH 420
 ESRIGLAELG ESEKKAVIPL VIVSALTFIC LVVLVGILYI WRKCFQTAHF YLEDSTSPRV 480
 10 ISTPPTPIFP ISDDVGAIPI KHFPKHVADL HASSGFTTEF ETLKEFYQEV QSCTVDLGIT 540
 ADSNHNPDNK HKNRYINIVA YDHSRVKLAQ LAEKDGLKTD YINANYVDGY NRPKAYIAAQ 600
 GPLKSTAEFDP WRMIWEHNV VIVMITNLVE KGRRKCDQYW PADGSEBYGN PLVTQKSVQV 660
 LAYYTVRNF LNTKIKKGS QKGRPSGRV TQYHYTQWPD MGVPEYSLEF LTFVRKAAYA 720
 KRHAVGPPVV HCSAGVGRG TYIVLDSMLQ QIQHEGTVNI FGFLKHRSQ RNYLVQTEBQ 780
 YVFIHDTLVE AILSKETEVL DSHIHAYVNA LLIPGPAGKT KLEKQFQLLS QSNIQQSDYS 840
 AALKQCNREK NRTSSIIIPVE RSRVGISLS GEGTDYINAS YIMGYQSNF FIITQHPLH 900
 TIKDFWRMIW DHNAQLVVM PDGQNMMAED FVYWPKNDEP INCESFKVTL MAEEHKCLSN 960
 15 EEKLIQDFI LEATQDDYVL EVRHFQCPKW PNPDSPISK FELISVIEKE AANRDGPMIV 1020
 HDEHGGVTAQ TFCALTILMH QLEKENSVDV YQVAKMINLM RGVFADIEQ YQFLYKVLIS 1080
 LVSTRQENP STSLDSNGAA LPDGNIAESL ESL 1113

Seq ID NO: C317 Protein Sequence
Protein Accession #: Eos sequence

20 1 11 21 31 41 51
 MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGAHQKNWG KKYPTCNSPK 60
 QSPINIDEDL TQVNVNKLKL KFGQWDTSL ENTPIHNTGK TVEINLTNDY RVSGGVSEMV 120
 25 FKASKITPHW GKCNMSDGS EHSLEGQKFP LEMQIYCFDA DRFSFEAV KKGKLRALS 180
 ILFEVGTEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240
 TDTVDWIVFK DTVSISESQL AVFCEVLTMO QSGYVLMMDY LQNNFREQQY KFSRQVFSY 300
 TGKEEIEHAV CSSEPEENVQA DPENYTSLLV TWERPRVVDY TMIEKFAVLV QQLDGEDQTK 360
 HEFLTDGYQD LGAILNLLP NMSYVLQIVA ICTNGLYGYK SDQLIVDMPT DNPELDLPE 420
 30 LIGTEEIIKE EBEKDIIEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN 480
 RSPTRGSEFS KGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPHPT VEGTSASLND 540
 GSKTVLRSPH MNLSTAESL NTVSITEYEE ESSLTSFKLD TGAEDSSGSS PATSAIPFIS 600
 ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPMEG NVWFPSTDI 660
 TAQPDVSGSR ESFLQNTYVE IRVDESEKTT KSFSAGPVMS QGPSVTDLME PHYSTFAYFP 720
 35 TEVTPHAFIP SSRQDDLST VNVVYSQITQ PVYNEASNS HESRIGLAEG LESEKKAVIP 780
 LVIVSALTPI CLVVLVGILI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAI 840
 IKHFPKHVAD LHASSGFTTE FETLKEFYQE VQSCVDLGI TADSSNHPDN KKNRYINIV 900
 AHDHSRVKLA QLAEKDGLT DYINANYVDG YNRPKAYIAA QGPLKSTAD FWRMIWEHNV 960
 EVIVMITNLV EKGRRKCDQY WPADGSEBYG NPLVTQKSVQ VLAYYTVRNF TLNTRIKKGS 1020
 40 SQKGRPSGRV VTQYHYTQWP DMGVPEYSLP VLTFRKAAY AKRHAVGPPV VHCAGVGRG 1080
 GTYIVLDSML QIQHEGTVNI IFGFLKHRS QRNYLVQTEE QYVFIHDTLV BAILSKEDEV 1140
 LDHSHIAYVN ALLIPGPAGK TKLEKQFQGL TSLPRLECRG TISAHCNLPL PGLTDPPTSA 1200
 SRVARTILLS QSNIQQSDYS AALKQCNREK NRTSSIIIPVE RSRVGISLS GEGTDYINAS 1260
 YIMGYQSNF FIITQHPLH TIKDFWRMIW DHNAQLVVM PDGQNMMAED FVYWPKNDEP 1320
 45 INCESFKVTL MAEEHKCLSN EEKLIQDFI LEATQDDYVL EVRHFQCPKW PNPDSPISK 1380
 FELISVIEKE AANRDGPMIV HDEHGGVTAQ TFCALTILMH QLEKENSVDV YQVAKMINLM 1440
 RGVFADIEQ YQFLYKVLIS LVSTRQENP STSLDSNGAA LPDGNIAESL ESL 1493

Seq ID NO: C318 Protein Sequence
Protein Accession #: Eos sequence

50 1 11 21 31 41 51
 MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGAHQKNWG KKYPTCNSPK 60
 QSPINIDEDL TQVNVNKLKL KFGQWDTSL ENTPIHNTGK TVEINLTNDY RVSGGVSEMV 120
 55 FKASKITPHW GKCNMSDGS EHSLEGQKFP LEMQIYCFDA DRFSFEAV KKGKLRALS 180
 ILFEVGTEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240
 TDTVDWIVFK DTVSISESQL AVFCEVLTMO QSGYVLMMDY LQNNFREQQY KFSRQVFSY 300
 TGKEEIEHAV CSSEPEENVQA DPENYTSLLV TWERPRVVDY TMIEKFAVLV QQLDGEDQTK 360
 HEFLTDGYQD LGAILNLLP NMSYVLQIVA ICTNGLYGYK SDQLIVDMPT DNPELDLPE 420
 60 LIGTEEIIKE EBEKDIIEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN 480
 RSPTRGSEFS KGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPHPT VEGTSASLND 540
 GSKTVLRSPH MNLSTAESL NTVSITEYEE ESSLTSFKLD TGAEDSSGSS PATSAIPFIS 600
 ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPMEG NVWFPSTDI 660
 65 TAQPDVSGSR ESFLQNTYVE IRVDESEKTT KSFSAGPVMS QGPSVTDLME PHYSTFAYFP 720
 TEVTPHAFIP SSRQDDLST VNVVYSQITQ PVYNEASNS HESRIGLAEG LESEKKAVIP 780
 LVIVSALTPI CLVVLVGILI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAI 840
 IKHFPKHVAD LHASSGFTTE FETLKEFYQE VQSCVDLGI TADSSNHPDN KKNRYINIV 900
 AYDHSRVKLA QLAEKDGLT DYINANYVDG YNRPKAYIAA QGPLKSTAD FWRMIWEHNV 960
 70 EVIVMITNLV EKGRRKCDQY WPADGSEBYG NPLVTQKSVQ VLAYYTVRNF TLNTRIKKGS 1020
 SQKGRPSGRV VTQYHYTQWP DMGVPEYSLP VLTFRKAAY AKRHAVGPPV VHCAGVGRG 1080
 GTYIVLDSML QIQHEGTVNI IFGFLKHRS QRNYLVQTEE QYVFIHDTLV BAILSKEDEV 1140
 LDHSHIAYVN ALLIPGPAGK TKLEKQFQGL QSNIQQSDY SAALKQCNRE KNRSSIIIPV 1200
 ERSRVGISL SGEGTDYINA SYIMGYQSN EFIITQHPL HTIKDFWRMI WDHNAQLVVM 1260
 75 IPDQNMMAED FVYWPKNDE PINCESFKVT LMAEEHKCLS NEEKLIQDFI LEATQAWRS 1320
 DGRNPLCDN PYAPTRKRKP RGCLPGSQDD QSDEARSLC 1359

Seq ID NO: C319 Protein Sequence
Protein Accession #: XP_002914.4

80 1 11 21 31 41 51
 MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKPRR TRPLEQDAL ETAARAEGLS 60
 LDASMSQSLR ILDEEHPKKG YHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSLAR 120
 VAHKKGELSM EDVWSLSKHE SSDVNCRLLE RLWQEELNEV GPDAASLRV VWIFCRTLRI 180

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LSIVCLMITQ LAGFSGPAPM VKHLEYTQA TESNIQYSL LVLGLLLEI VRSWSLALTW 240
 ALNYRTGVRL RGAILTMAFK KILKLNKIE KSLGELINIC SNDGQRMFEA AAVGSLLAGG 300
 PVVAILGMIY NVIILGPTGF LGSASFILFY PAMMFASRLT AYFRKCVAA TDERVQKME 360
 VLTYYIKPIKM YAWVKAPSQS VQKIREEERR ILEKAGYFQS ITVGVAPIVV VIASVVTFSV 420
 HMTLGFDLTA AQAFVTVTVF NSMTFALKVT PPSVKLSSEA SVAVDRPKSL FLMEEVHMIK 480
 NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKDK RASRGKKERV RQLQRTTEHQ 540
 VLAQKQGHLL LDSDERPSPS EEECKHIHLG HLRLQRTLHS IDLEIQEGKL VGICGSGVSG 600
 KTLISAILG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS 660
 CCLRFDLAIL PSSDLTEIGE RGNLSGGQR QRISLARALY SDRSIYILDD PLSALDAHVG 720
 NHIFNSAIRK HLKSKTVLTV THQLQYLVD CDEVIPMKEGC ITERGTHEEL MNLNGDYATI 780
 FNNLLGGETP PVEINSKKE TSGSKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKQGS 840
 VPWSVYGVYI QAAGGLPLAF VIMALPMLNV GSTAFSTWML SYWIKQSGSN TTVTRGNETS 900
 VSDSMKDNPH MQYASIALY SMVAMLILKA IRGVVPVKG TLRASSRLHDE LFRILRLSPM 960
 KFFDTTPTGR ILNRPFSKMD EVDVRLPFQA EMFIQNVILV PFCVGMIAGV FFWFLVAVGP 1020
 LVILFSLVLI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLEHRYQEL 1080
 LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT 1140
 GLPQFTVRLA SETEARFTSV ERINHVIKTL SLEAPARIKN KAPSPDWPE GEVTFENAEM 1200
 RYRENLPVLV KKVSTFIKPK EKIGIVGRTG SGKSSLGML FRLVELSGGC IKIDGVRISD 1260
 IGLADLRSLK SIIPQEPVLF SGTVRSNLD PNOYTEDQIW DALERTHME CIAQLPLKLE 1320
 SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLIQE TIREAFADCT 1380
 MLTIAHRLHT VLGSDRIMVL AQGVVVEFDT PSVLLSNDSS RPYAMPAAAE NKVAVKQ 1437

Seq ID NO: C320 Protein Sequence
 Protein Accession #: NP_005679.1

25
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1 11 21 31 41 51
 MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKPRR TRPLECQDAL ETAARAEGLS 60
 LDASHQSRLR ILDEEHPKPK YHGLSALKP IRTTSKHQHP VDNAGLPSCM TFSWLSLAR 120
 VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLMQBELNEV GPDAASLRV VWIFCRTRLI 180
 LSTVCLMITQ LAGFSGPAPM VKHLEYTQA TESNIQYSL LVLGLLLEI VRSWSLALTW 240
 ALNYRTGVRL RGAILTMAFK KILKLNKIE KSLGELINIC SNDGQRMFEA AAVGSLLAGG 300
 PVVAILGMIY NVIILGPTGF LGSASFILFY PAMMFASRLT AYFRKCVAA TDERVQKME 360
 VLTYYIKPIKM YAWVKAPSQS VQKIREEERR ILEKAGYFQS ITVGVAPIVV VIASVVTFSV 420
 HMTLGFDLTA AQAFVTVTVF NSMTFALKVT PPSVKLSSEA SVAVDRPKSL FLMEEVHMIK 480
 NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKDK RASRGKKERV RQLQRTTEHQ 540
 VLAQKQGHLL LDSDERPSPS EEECKHIHLG HLRLQRTLHS IDLEIQEGKL VGICGSGVSG 600
 KTLISAILG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS 660
 CCLRFDLAIL PSSDLTEIGE RGNLSGGQR QRISLARALY SDRSIYILDD PLSALDAHVG 720
 NHIFNSAIRK HLKSKTVLTV THQLQYLVD CDEVIPMKEGC ITERGTHEEL MNLNGDYATI 780
 FNNLLGGETP PVEINSKKE TSGSKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKQGS 840
 VPWSVYGVYI QAAGGLPLAF VIMALPMLNV GSTAFSTWML SYWIKQSGSN TTVTRGNETS 900
 VSDSMKDNPH MQYASIALY SMVAMLILKA IRGVVPVKG TLRASSRLHDE LFRILRLSPM 960
 KFFDTTPTGR ILNRPFSKMD EVDVRLPFQA EMFIQNVILV PFCVGMIAGV FFWFLVAVGP 1020
 LVILFSLVLI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLEHRYQEL 1080
 LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT 1140
 GLPQFTVRLA SETEARFTSV ERINHVIKTL SLEAPARIKN KAPSPDWPE GEVTFENAEM 1200
 RYRENLPVLV KKVSTFIKPK EKIGIVGRTG SGKSSLGML FRLVELSGGC IKIDGVRISD 1260
 IGLADLRSLK SIIPQEPVLF SGTVRSNLD PNOYTEDQIW DALERTHME CIAQLPLKLE 1320
 SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLIQE TIREAFADCT 1380
 MLTIAHRLHT VLGSDRIMVL AQGVVVEFDT PSVLLSNDSS RPYAMPAAAE NKVAVKQ 1437

Seq ID NO: C321 Protein Sequence
 Protein Accession #: NP_005553.1

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1 11 21 31 41 51
 MPALWLGCC LPSLLPAAR ATSRREVDC NGKSRQCIFD RELHRTQNG FRCINCNENT 60
 DGIHCECKN GFYRHRERDR CLPCNCNSKG SLSARCDNSG RCSCKPGVTG ARCDRLPGF 120
 HMLTDAGCTQ DQRLDLSKCD CDPAGIAGPC DAGRCVCKPA VTGERCDRCR SGYNNLDGNN 180
 PEGCTQCFYC GHSASCRSSA EYSVEKITST FHQDVVGWKA VQRNGSPAKL QWSQRHQDV 240
 SSAQRLDFVY FVAPAKPLGN QQVSYGQSL FQYRVDRGR HPSADHILE GAGLRITAPL 300
 MRLGKTLPCG LTKYTYFRLN EHPNNWSPQ LSYFEYRLL RNLTLALIRA TYGEYSTGYI 360
 DNVTLISARP VSGAPAPWE QCICPVGYKG QPCQDCASGY KRDSARLPGF GTCIPNCQG 420
 GGACDPDTGD CYSGDENPDI ECADCPIGFY NDFHDPSCCK PCPCNGPSC SVMPTERHV 480
 CINCPCPGVTG ARCELADG YPGDPFGERGP VRPCQPCQCN NNVDPSASGN CDRLTGRCCLK 540
 CIHNTAGIYC DQCKAGYFGD PLAPNPADKC RACNCNPMGS EPVGCSDGT CVCKPGFGSP 600
 NCEHGAFCSP ACYQVQIKQM DQFMQQLQRM EALISKAQGG DGVVPDTELE GRMQQAEQAL 660
 QDILRDAQIS EGASRSLGLQ LAKVRSQENS YQSRLLDLKM TVERVRALGS QYQNRVRDTH 720
 RLITQMLSL ABSEASLGNT NIPASDHYVG PNGFKSLAQE ATRLAESHVE SASNMEQLTR 780
 ETEDYSKQAL SLVRKALHEG VSGSGSPDG AVVQGLVEKL ETKTSLAQQL TREATQAEIE 840
 ADRSYQSLR LLDVSYRLQG VSDQSPQVEE AKRIKQKADS LSTLVTRHMD EPKRTQKNLG 900
 NWKEBAQQL QNGKSGREKS DQLLSRANLA KSRQAQALSM GNATPYEVES ILKNLEFDEL 960
 QVDNRKAEAE EAMKRLSYIS QKVSDASDKT QQAERALGSA ADAQRAKNG AGEALEISSE 1020
 IEQIGSLNL EANTADGAL AMEKGLASLK SEMREVEGEL ERKELEFDTN MDAVQMVITE 1080
 AQKVDTRAKN AQVTQDTLN TLDGLHLMD QPLSVDEBGL VLEQLKSLRA KTQINSQLRP 1140
 MMSELEERAR QQRGHLHLE TSIDGILADV KNLENIRDNL PPGCYNTQAL EQ 1193

80
 Seq ID NO: C322 Protein Sequence
 Protein Accession #: NP_066924.1

1 11 21 31 41 51
 MANAGLQLLG FILAPLGNIG AIVSTALPQW RIYSYAGDNI VTAQAMYEG LWMSCVSQSTG 60

QIQCKVFDLS LNLSTLQAT RALMVVGILL GVIAIFVATV GMKCMKLED DEVQKMRMAV 120
 IGGAFLLAG LAILVATAWY GNRIVQEFYD PMTPVNARYE FGQALFTGWA AASLCLLGA 180
 LLCCSCPRKT TSYTPRPYP KPAOSSGKDY V 211

5 Seq ID NO: C323 Protein Sequence
 Protein Accession #: AAM77876

10 1 11 21 31 41 51
 MSSWIRWHGP AMARLWGFCW LVVGFWRAP ACPTSCKCSA SRIWCSDPSP GIVAFPRLEP 60
 NSVDPENITE IFIANQKRL EINEDDVEAY VGLRNLITVD SGLKPVAKHA FLKNSNLQHI 120
 NFRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180
 SKNIPLANLQ IPNCGLPAN LAAPNLTVEE GKSITLSCSV AGDPVPMYV DVGNLVSKHM 240
 NETSHTQSSL RITNISSDDS GKQISCVAEV LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
 15 WCIPFTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
 DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF HKIPLDG 477

20 Seq ID NO: C324 Protein Sequence
 Protein Accession #: NP_006171.1

25 1 11 21 31 41 51
 MSSWIRWHGP AMARLWGFCW LVVGFWRAP ACPTSCKCSA SRIWCSDPSP GIVAFPRLEP 60
 NSVDPENITE IFIANQKRL EINEDDVEAY VGLRNLITVD SGLKPVAKHA FLKNSNLQHI 120
 NFRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180
 SKNIPLANLQ IPNCGLPAN LAAPNLTVEE GKSITLSCSV AGDPVPMYV DVGNLVSKHM 240
 NETSHTQSSL RITNISSDDS GKQISCVAEV LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
 30 WCIPFTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
 DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF HKIPLDG 477
 LHISNGSNT PSSSEGGFDA VIIGMTKIPV IENPQYFGIT NSQLKPDFTV QHIKRNHIVL 540
 KRELGEAGFC KVFLEACYNL CPEQDKILVA VKTLKADSDN ARKDFHREAE LLTNLQHEHI 600
 VKFYGVCEVG DPLIMVFEYM KHGDLNKLFR AHGPDVAVLMA EGNPPTLTQ SOMLHIAQOI 660
 35 AAGMVLASQ HFVHRDLATR NCLVGENLLV KIGDPGMSRD VYSTDYRVG GHTMLPIRNM 720
 PPESIMYRKF TTESDVWSLG VVLWEIFTYG KQFWYQLSNV EVIECITQGR VLORPRTCPQ 780
 EYELMLGCW QREPHMRKNI KGIHTLLQNL AKASPVYLDI LG 822

40 Seq ID NO: C325 Protein Sequence
 Protein Accession #: Eos sequence

45 1 11 21 31 41 51
 MSSWIRWHGP AMARLWGFCW LVVGFWRAP ACPTSCKCSA SRIWCSDPSP GIVAFPRLEP 60
 NSVDPENITE IFIANQKRL EINEDDVEAY VGLRNLITVD SGLKPVAKHA FLKNSNLQHI 120
 NFRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180
 SKNIPLANLQ IPNCGLPAN LAAPNLTVEE GKSITLSCSV AGDPVPMYV DVGNLVSKHM 240
 NETSHTQSSL RITNISSDDS GKQISCVAEV LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
 50 WCIPFTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
 DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF HKIPLDG 477

55 Seq ID NO: C326 Protein Sequence
 Protein Accession #: NP_570843.1

60 1 11 21 31 41 51
 MPLKHYLLLL VGCQAWGAGL AYHGCPSSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI 60
 LNTHITELNE SPFLNISALI ALRIEKNELS RITPGAFRNL GSLRYLSLAN NKQLVLPGL 120
 FQGLDSLES LLSSNQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAFF HLVLTKLNL 180
 GKNSLTHISP RVFQHLNLQ VLRLYENRIT DIPMGTFDGL VNLQELALQI NQIGLLSPGL 240
 PHNNENLQRL YLSNNHISQL PPSIFMQLFP LNRLTLFGNS LKELSLGIFG PMPNLRRLNL 300
 YDNHISLFP NVFSNLRQL VLILSRNQIS FISPGAFNGL TELRELSLET NALQDLQDNV 360
 FRMLANLQNI SLQNNRLRQL PGMIPANVNG LMAIQQLNNQ LENLPLGIFD HLKGLCELRL 420
 65 YDNPRCDS ILPLRNWLL NQPRLGITDV PVCFSANVR GQSLIIINVN VAVPSVHVPE 480
 VPSYPETPWY PDTPSYFDTT SVSSTTELTS FVEDYDILT IQVTDDRSWV GMTQAQSGLA 540
 IAAIVIGIVA LACSLAACVG CCOCKERSQA VLMQMKAPNE C 581

70 Seq ID NO: C327 Protein Sequence
 Protein Accession #: NP_002649.1

75 1 11 21 31 41 51
 MRALLARLLL CVLVVSDSKG SNELHQVPSN CDCLAGGTCV SNKYPSNIHW CNCPKKGQ 60
 HCEIDSKTC YEGNGHYRG KASTDTMGRP CLPWNATV L QQTYHAHRSD ALQLGLGKH 120
 YCRNPNRRR PWCVQVGLK PLVQECMVHD CADGKPPSP PEEELFCQCG KTLRPRFKII 180
 GGEEFTIENQ FWFPAIYRRE RGGSVTYVCG GSLISPCWVI SATHCFIDYP KKEDIYVILG 240
 RSRINSNTQG EMKFEVENLI LHKDYSADTL AHNNDIALK IRSKEGRCAQ PSRTIQTICL 300
 80 PSMYNDPQFG TSCBITGFGK ENSTDYLYPE QLKMTVVKLI SHRECCQPHY YGSEVTTML 360
 CAADPQWKT SCQGDSSGGL VCSLQGRMTL TGISVSGRG ALKDKPGVYT RVSHPLPWIR 420
 SHTKEENGLA L 431

Seq ID NO: C328 Protein Sequence
 Protein Accession #: XP_087254.1

1 11 21 31 41 51
 5 MQFRECSING MKYQEINGRL VPEGPTPDSS EGNLSYLSL SHLNLSHLT TSSSFRTSPE 60
 NETELIKEED LFPKAVSLCH TVQISNVQTD CTGDGPMQSN LAPSQLEYA SSPDEKALVE 120
 AAARIGIVPI GNSBETMEVK TLQKLERYL LHILEFDSR RRMSVIVQAP SGKLLFAKG 180
 AESSILPKCI GGEIEKTRIH VDEPALKGLR TLCIAYRKPT SKEYEIDKR IFEARTALQQ 240
 REEKLAAVPO FIEKDLILLG ATAVEDRLQD KVRRTIRALR MAGIKVWVLT GDXHETAVSV 300
 10 SLSCGHFHT MNILELINQK SDSECAEQRL QLARRITEDH VIQHGVLVVDG TSLSLALREH 360
 EKLFWVFCRN CSAVLCCRMA PLQKAKVIRL IKISPEKPT LAVGDGANDV SMIEAHVGI 420
 GIMGKEGRQA ARNSDYAIAI FKFLSKLLPV HGHFYIIRIA TLVQYFFYKN VCPITPQPLY 480
 QFYCLPSQQT LYDSVYLTLY NICPTSLPIL IYSLLEQHV DPHVLQNKPTL YRDISKNRLL 540
 SIKTPLYWTI LGFSHAPIFP FGSYLLIGKD TSLGNGQMP GWTFTGLVFP TVMVTITVTK 600
 15 MALETHFTW INELVTWSSI IFYFVPSLFY GGILWPFPLGS QNMYPFVFIQL LSSGSANFAI 660
 ILMVVTCLFL DIKKVFDHR LHPTSTRKAQ LTETNAGIKC LDSMCCPPEG EAACASVGRM 720
 LERVIGRCSP THISRWSAS DPFTYNDRSI LTLSTMDSSST C 761

Seq ID NO: C329 Protein Sequence
 Protein Accession #: XP_087461.1

20 1 11 21 31 41 51
 25 MLPLLAALLA AACPLPPVRG GAADAPGLLG VPSNASVNAS SAASPSPRGC WPRRPPGPPS 60
 ARARRRRRR RLNCNISVQR QMLSSLLVRW GRPRGFQCDL LLFSTNAHGR AFFAAAFHRV 120
 GPPLLIHHLG LAAGQAQDQL RLCVGCWVR GRRTGRLRPA AAPSAATA GAPALPAYP 180
 AAEPFGPLWL QGEPLHFCCL DFSLEELQGE PGWRLNRKPI ESTLVACFMT LVIVVWSVAA 240
 LIWPVPIIAG FLPNGMBCRR TTASTTAATP AAVPAGTTAA AAAAAAATA AVTSGVATK 299

Seq ID NO: C330 Protein Sequence
 Protein Accession #: XP_051522.2

30 1 11 21 31 41 51
 35 MDLHLFDYSE PGNFSDISWP CNSSDCIYVD TVMCPNMPNK SVLLYTLSPY YIFIFVIGMI 60
 ANSVVVWNI QAKTGTGYDTH CYILNLAIAD LWVVLITPVW VVSLVQHNQW PMGBLTCKVT 120
 HLIFSINLFG SIFFLTCMSV DRYLSITYFT NTPSSRKKMV RRVVCILVWL LAFCVSLPDT 180
 YYLKTVTAS NNETYCRSFY PEHSIKEWLI GMELVSVVLG FAVPFSTIAV FYFLLARAI 240
 ASSDQEKHSS RKIIFSYYVV FLVCWLPYHV AVLLDIPFSL HYIPFTCRLE HALPTALHVT 300
 40 QCLSLVHCCV NPVLYSFNR NYRYELMKAP IPKYSAKTGL TKLIDASRV S ETEYSALBQS 360
 TK 362

Seq ID NO: C331 Protein Sequence
 Protein Accession #: NP_000341.1

45 1 11 21 31 41 51
 50 MGFVRQIQLL LWKNWTLRKR QKIRFVVELV WFLSLFLVLI WLRNANFLYS HHECHFPNKA 60
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 HLGRITWELH ILSQFMDTLR THPERIAGRG IRIRDILKOE ETLTLFLIKN IGLSDSVVYL 180
 LINSQVRPEQ FARGVFDLAL KDIACSEALL ERFIIPSQRR GAKTVRYALC SLSCQTLQNI 240
 EDTLYANVDF FKLFRLVPTL LDSSRSQGINL RSWGGILSDM SPRIQEFIRH PSMQDLWVT 300
 RPLMQGGPPE TPTKLMGILS DLLCGYPEGG GSRVLSFNWY EDNMYKAFGL IDSTRKDFIY 360
 SYDRRTTFFC NALIQSLEEN PLTKIANRAA KPLLMGKILY TPDSPAARRI LKNANSTFEE 420
 55 LEHRVRLVKA WEEVGPIWY PFDNSTQNMN IRDTLGNFTV KDFLNRQLGE EGITAEAILN 480
 FLYKGPRRSQ ADDMANFDWR DIFNITDRTL RLNVQYLECL VLDKFESYND ETQLTQRALS 540
 LLEENMFAG VVFPDMYPMT SSLPPHVKYK IRMDLDVVEK TNKIKDRYWD SGPRADPVED 600
 FRYIWGGLPAY LQDMVEQGIT RSQVQAEAPV GIYLQQMFPY CFVDDSFMI I LNRCPPIPMV 660
 LANIYVSMT VRSIVLEKEL RLKETLKNQG VSNVWICTW FLDSFSIMSM SIFLLTIFIM 720
 60 HGRILHYSDF FILFLPLAP STATIMLCPL LSTPFSKASL AAACSGVIYF TLYLPHILCF 780
 AQQDRMTAEL KKAVALSLSPV APFGFTEYLV RFEEQGLGLQ WSNIGNSPTE GDEPSPFLSM 840
 QMMLDAACY GLAWYLDQV FPGDYGTPLP WYFLQLQESYV LSGEGCSTRE ERALEKTEPL 900
 TEETEDPEHP EGIHDSFFER EHPGWVPGVC VKNLVKIFEP CGRPVADRIN ITFYENQITA 960
 FLGHNGAGKT TTLSILTGLL PPTSGTVLVG GRDIETSLDA VRQSLGMCPO HNILFPHLTV 1020
 65 AEHMLPYAQL KGKSQBEAQL EMEAMLEDTG LHHKRNBAQ DLSGGMQRKL SVALAFVGDA 1080
 KVVILDEPTS GVDPSRRSI WDLLKYRSG RTIIMPTHM DEADHQDRI AIIAQGRLYC 1140
 SGTFLFLKNC FGTGLYTLV RKMKNISQR KGSEGTCSGS SKGFSTTCPA HVDDLTPBQV 1200
 LDGDNELMD VVLHVPPEAK LVECIQELI FLLPNKNFKH RAYASLFREL EETLADLGLS 1260
 SFGISDTPLB EIFLKVTEGS DSGPLFAGGA QQRKNVNP RHPCLGREKA GQTPQDSNVC 1320
 70 SPGAPAAHPE GQPPPEPECP GPQLMTGTQL VLQHVQALLV KRFQHTIRSH KDFLAQIVLP 1380
 ATFVFLALML SIVLPPGEY PALTLHPMIY GQYTFPSMD EPGSEQFTVL ADVLLNKPGF 1440
 GNRLKKEGWL PEYPCGNSTP NKTSPVSPNI TQLPQKQKWT QVNPSPSCRC STREKLTMLP 1500
 ECPBGAGLPE FQRTORSTE ILQDLTDENI SDPLVKTYPA LIRSLKSKF WNEQRYGGI 1560
 SIGGKLPVVE ITGALVGFL SDLGRIMVS GGPITREASK EIPDFLKHLE TEDNIKWVFN 1620
 75 NKGWHALVSP LNVAHNAIL ASLPKDRSPE HYGITVISQP LNLTKQLSE ITVLTTSDVA 1680
 VVAICVIFSM SPVPASVLY LIQERVNKS KQFISGVSP TTYWNTNFM DIMNYSVSAG 1740
 LVVGIFIGQ KKAATSPENL PALVALLLY GWAVIPMYP ASFLPDVPT AYVALSCANL 1800
 FIGINSAIT FILELFDNMR TLLRPNVLR KLLIVFPFHC LGRGLIDLAL SQAVTDVYAR 1860
 PGEHSANPP HNDLIGKNLP AMVVEGVVYF LTLVLVQRFH FLQWIAEPT KEPIDVEDDD 1920
 80 VASERQRIIT GONKTDILRL HELTKIYLG SSPAVDRICV GVRPGECFGL LGVNGAGKTT 1980
 TFMLTGDTT VTSGDATVAG KSILTNISEV HQNMGYCPQ DAIDELLTGR EHLVLYARLR 2040
 GVPAEIEKV ANWSIKSLGL TVYADCLAGT YSGGNKRKLS TAILIGCPP LVLLDEPTTG 2100
 MDPAARMLW NVVSIIRKG RAVVLTSHM BECEALCTRL AIMVKGAFRC MGTIQLKSK 2160
 PGDGYIVTMK IKSPKDDLLP DLNPFVEQFPQ GNPPGSVQRE RHYNMLQPVQ SSSSLARIFQ 2220
 LLLSHKDSLL IBEYSVTQTT LDQVFNPAK QQTESHDLPL HPAAGASRQ AQD 2273

Seq ID NO: C332 Protein Sequence
Protein Accession #: NP_006662.2

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5      1      11      21      31      41      51
|      |      |      |      |      |
MVPHAILARG RDVCRNGLL ILSVLSVIVG CLLGFFLRTR RLSPQEISYF QPPGELLMRM 60
LKMMLPLVVV SSLMSGSLASL DAKTSSRLGV LTVAYYLWTT FMAVIVGIFM VSIHFGSAA 120
QKETTEQSGK PIMSSADALL DLIRNMFFAN LVEATFKQYR TKTFPVVKSP KVAPEEAPPR 180
10    RILIYGVQEE NGSHVQNPFAL DLTPPPEVVY KSEPGTSDGM NVLGIVFFSA TMGIMLCRMG 240
DSGAPLVSFC QCLNESVMKI VAVAVWYFPF GIVFLIAGKI LEMDDPRAVG KKLGFYSVTV 300
VCGLVLHGLF ILPLLYFFIT KKNPIVFIRG ILQALLIALA TSSSSATLPI TPKCLLENNH 360
IDRRIRAFVL FVGATINMOG TALYEAVAAI FIAQVMNYEL DFGQIITISI TATAASIGAA 420
GIPQAGLVTM VIVLTSVGLF TDDITLIIAV DWALDRFRTM INVLDALAA GIMAHICRKO 480
15    FARDTGTEKL LPECETKPVSL QEIVAAQONG CVKSVARASE LTLGPTCPHH VPVQVERDEE 540
LPAASLNHCT IQISELETNV 560

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Seq ID NO: C333 Protein Sequence
Protein Accession #: NP_005680.1

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20    1      11      21      31      41      51
|      |      |      |      |      |
MVTVGNYCEA EGPVGPANWQ DGLSPCFFFT LVPSTRMALG TLALVLALPC RRRERPAAGD 60
SLSMGAGPRI SPYVLQLLLA TLQAALPLAG LAGRVGTARG APLPSYLLLA SVLESAGAC 120
25    GLLWLLVVERS QARQLAMGI WIKFRHSPGL LLLWTVAFAA ENLALVSWNS PQHWWARADL 180
GQQVQFSLWV LRYVVSGLF VLGLWAPGLR PQSYTLQVHE EDQDVERSQV RSAAQQSTWR 240
DPGRKLRLLS GYLWPRGSPA LQLVVLICLG LMGLERALNV LVPIFYRNIV NLLTEKAPWN 300
SLAWTVTSYV FLKFLQGGGT GSTGFVSNLR TFLMIRVQQF TSRRVELLIF SHLHELRLW 360
HLGRRTGEVL RIADRTGSSV TGLLSYLVEN VIPTLADIII GIIFYSMFFN AMFGLIVFLC 420
30    MSLYLTLTIV VTEWRTKFRR AMNTQENATR ARAVDSLLNF ETVKYNAES YEVEERYREI 480
IKYQGLEWKS SASLVLLNQT QNLVIGLGLL AGSLLCAYFV TEQKLQVGDY VLFGTYYIQL 540
YMPIANFGTY YRMIOQTNFID MENMFDLLKE ETEVKDLPGA GPLRFQKRI EFENVHFSYA 600
DGRETLQDVS FTVMPGQTLA LVGPGSAGKS TILRLLEFPY DISSGCIRID QDISQVTOA 660
35    SLRSHIGVVP QDVLVFNMTI ADNIYRGRVT AGNDEVEAAA QAAGIHDAIM APFEGYRTQV 720
GERGLKLSGG EKQRVAIART ILKAPGIILL DEATSALDTS NERAIQASLA KVCANRTTIV 780
VAHRLSTVNV ADQILVIKDG CIVERGRHEA LLSRGGVYAD MWQLQQQEE TSIEDTKPQTM 840
ER 842

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Seq ID NO: C334 Protein Sequence
Protein Accession #: NP_000667.1

```

40    1      11      21      31      41      51
|      |      |      |      |      |
MLLETQDALY VALELVIAAL SVAGNVLVCA AVGTANTLQT PTNYFLVSLA AADVAVGLFA 60
45    IFFAITISLG FCTDFYGCLE LACFVLVLTQ SSIFSLAVA VDRYLAICVP LRYKSLVIGT 120
RARGVIAVWV VLAPGIGLTP FLGWSKDSA TNNCTEPWDG TTNESCCLVK CLFENVVPM 180
YMWVFNFFGC VLPPLIMLV IYIKIFLVAC RQLQRTLM D HSRTTLQREI HAAKSLAMIV 240
GIFALCWLFP HAVNCVTLFP PAQGNKPKFN AMNMAILLSH ANSVNPNIVY AYRNDRFRYT 300
50    FHKIISRYLL CQADVKSNG QAGVQPALGV GL 332

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Seq ID NO: C335 Protein Sequence
Protein Accession #: NP_443164

```

55    1      11      21      31      41      51
|      |      |      |      |      |
MGLGARGAWA ALLGLTLQVL ALLGAHESA AMAETLQHPV SDHTNETSNS TVKPPTSVA 60
DSSNTTIVTM KPTAASNTT PGMVSTNMTS TTLKSTPKTT SVSQNTSQIS TSTMTVTENS 120
SVTSAASSVT ITTTMHSEAK KGSKFDTGSP VGGIVLTGLV LSILYTGCM YSRRGIRYR 180
60    TIDEHDAII 189

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Seq ID NO: C336 Protein Sequence
Protein Accession #: NP_004186.1

```

65    1      11      21      31      41      51
|      |      |      |      |      |
MAQHGMAGAF RALCGLALLC ALSLGQRPTG GPGCGPGRLL LGTGTARCC RVHTTRCCRD 60
YPGEKCCSEW DCMCVQPEFH CGDPCCTTCR HHPCPPGQGV QSQGFSGFG QCIDCASGTF 120
SGGHEGHCKP WTDCTQFGFL TVFFGNKTHN AVCVPGSPPA EPLGWLTVVL LAVAACVLL 180
70    TSAQLGLHIW QLRSQCMWPR ETQLLLEVFP STEDARSCQF PEERGERGSA BEKGRLGDLW 240
V 241

```

Seq ID NO: C337 Protein Sequence
Protein Accession #: BAC03767.1

```

75    1      11      21      31      41      51
|      |      |      |      |      |
MGCDGRVSGI LRRNLQPTLT YMSVFFSFGI CIAFLGPTLL DLRCQTHSSL PQISWVFFSQ 60
QLCLLLGSAL GGVFKRTLQ SLWALFTSSL AISLVFAVIP FCRDVKVLAS VMALAGLAMG 120
80    CIDTVANMQL VRMYQKDSAV FLQVLHFFVG FGALLSPLIA DPFLSEANCL PANSTANTIS 180
RGHLFHVSRV LGQHEVDAPK WSNQTFPGLT PKDGAGTRVS YAFWIMALID LPVPMVIML 240
LSKERLLTCC PORRPLLLSA DELALETQPP EKEDASSLPP KFSHLGHEED LPSCCQREN 300
RGAPYSFFAI HITGALVLFM TDGLTGAYSA FVYSYAVEKP LSVGHKVAGY LPSLFWGFIT 360
LGRLLSIPIS SRMKPATMVF INVVGUVVTF LVLLIFSINV VFLFVGTASL GLFLSTFP 420
MLAYTEDSLQ YKGCATTVLV TGAGVGEMVL QMLVGSIFQA QGSYSFLVCG VIFGCLAFTF 480

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YILLFPFHRM HPGLPSVPTQ DRISIGMENSE CYQR

514

Seq ID NO: C338 Protein Sequence
Protein Accession #: NP_002194.1

5
10
15
20
25

1	11	21	31	41	51	
MGPERTGAAP	LPILLVLALS	QGIILNCCLAY	NVGLPEAKIP	SGPSSEBQFGY	AVQQPINPKG	60
NWLLVGPWS	GFPENRMGDV	YKCPVDLSTA	TCEKLNQTS	TSIPNVTEMK	TNMSLGLILT	120
RNMTGSGFLT	CGPLMAQQCG	NQYTTGVCS	DISPDFQLSA	SFSPATQPCP	SLIDVVVVCD	180
ESNSIYPMDA	VKNFLKFFVQ	GLDIGPTKTQ	VGLIQYAMNP	RVVFMNTYK	TKKEMIVATS	240
QTSQYGGDLT	NTPGAIFYAR	KYAYSAAAGG	RRSATKVMVV	VTDGESHGGS	MLKAVIDQCN	300
HDNILRFGIA	VLGYLNRNAL	DTKNLIKEIK	AIASIPTRY	PFNVSDAAL	LEKAGTLGEQ	360
IFSGIEGTVGQ	GDNFQMEMSQ	VGFSADYSSQ	NDILMLGAVG	AFGWSGTIVQ	KTSGHGLIFP	420
KQAFDQILQD	RNHSSYLGY	VAAISTGEST	HFVAGAPRAN	YTGQIVLYSV	NENGNTIVIQ	480
AHRGDQIGSY	FGSVLCSVDV	DKDTITDVL	VGAPMYMSDL	KKEEGRVYLF	TIKKGILQGH	540
QPLEGPEGIE	NTRPGSAIAA	LSDINMDGFN	DVIVGSPLFN	QNSGAVIYN	GHOOTIRTKY	600
SQKILGSDGA	FRSHLQYFGR	SLDGYGDLNG	DSITDVSIGA	FGQVVQLWSQ	SIADVAIEAS	660
FTPEKITLVN	KNAQILKLC	FSAKFRPTKQ	NNQVAIVYNI	TLDADGFSR	VTSRGLFKEN	720
NERCLQKNMV	VNAQSCPEHF	IYIQEPSDV	VNSLDLRVDI	SLNPGTSPA	LEAYSETAKV	780
PSIPPHKDCG	EDGLCISDLV	LDVRQIPAAQ	EQPFIVSNQN	KRLTFSVTLK	NKRESAYNTG	840
IVVDPSENLF	FASFSLFVDG	TEVTCQVAAS	QKSVACDVGY	PALKREQQVT	FTINFDFNLQ	900
NLQNAASLSE	QALSESQEEN	KADNLVNLKI	PLLYDABHL	TRSTNINPYE	ISSDGNVPSI	960
VHSFEDVVGQ	FIFELKVTG	SVPVSMATVI	IHIPQYTKK	NPLMYLTGVQ	TDKAGDISCN	1020
ADINPLKIQQ	TSSSVSFKE	NFRHTKELNC	RTASCNVTC	WLDVHMKGE	YFVNVITRIW	1080
NGTFASSTFQ	TQVLTAAAEI	NTYNPEIYVI	EDNTVTIPLM	IMKPDEKAEV	FTGVIGSII	1140
AGILLLLALV	AILWKLGFPP	RYKEMTKNP	DEIDETTELS	S		1181

30 Seq ID NO: C339 Protein Sequence
Protein Accession #: NP_113648.1

35
40

1	11	21	31	41	51	
MYRPRARAAP	BGRVRCGAVP	STVLLLLAYL	AYLALGTGVF	WTLEGRAAQD	SSRSFQDKM	60
ELLQNTCLD	RPALDSLIRD	VVOAYKNGAS	LLSNTTSMGR	WELVGSFFFS	VSTITTIGYG	120
NLSPNTMAAR	LFCIFYFALVG	IPLNLVVLNR	LGHLMQGVN	HWASRLGGTW	QDPDKARWLA	180
GSGALLSGLL	LFLLPLPLLF	SHMEGWSYTE	GFYFAPITLS	TVGFGDYVIG	MNPSQRYPLW	240
YKMWVSLWIL	FGMAWLALII	KLILSQLETP	GRVCSCHHS	SKEDFKSQSW	RQGFDRBPES	300
HSPQGGCYPE	GPMGIQHLE	PSAHAAGCGK	DS			332

40 Seq ID NO: C340 Protein Sequence
Protein Accession #: NP_004145.1

45
50

1	11	21	31	41	51	
MEWDNGTQQA	LQLPPTTCVY	RENFKQLLLP	PVYSAVLAAG	LPLNICVITQ	ICTSRRALTR	60
TAVYTLNLAL	ADLLYACSLP	LLIYNYAQGD	HWPFQDFACR	LVRPLFYANL	HGSILPLTCI	120
SFQRYLGICH	PLAPWHKRG	RRAAMLVCVA	VWLAVTTQCL	PTAIFPATGI	QRNRTVCYDL	180
SPPALATHYM	PYGMALTVIG	FLLPFAALLA	CYCLLACRLC	RQDGPAPFVA	QERRGKAARM	240
AVVVAAPAFI	SFLPFIHTKT	AYLAVRSTPG	VPCIVLEAFA	AAKGTREPPA	SANSVLPDIL	300
FYFTQKFR	RPHELLQKLT	AKWQRQGR				328

55 Seq ID NO: C341 Protein Sequence
Protein Accession #: NP_009128.1

60
65

1	11	21	31	41	51	
MQRPGFRLWL	VLQVMGSCAA	ISSMDMERPG	DGKCQPIEIP	MCKDIGYNTM	RMPNLMGHEH	60
QREAAIQLHE	FAPLVEYGCH	GHLRFPLCSL	YAPMCTEQVS	TPIPACRVMC	EQARLKCSPI	120
MEQFNFKWPD	SLDCRKLPNK	NDPNYLCMEA	PNNGSDEPTR	GSGLFPPPLFR	PQRPHSAQEH	180
PLKDGPGPRG	GCDNPGKPHH	VEKSASCAPL	CTPGVDVYWS	REDKRFAVWV	LAIWAVLCFF	240
SASFTVLTFL	IDPARFYPPE	RPIIFLSMCY	CVYSVGYLIR	LPAGASSIAC	DRDSGQLYVI	300
QBGLESTGCT	LVFLVLYYFG	MASSLWVVVL	TLTWFLAAGK	KMGHEATEAN	SSYPHLAANA	360
IPAVKITILIL	VMRRVAGDEL	TGVCYVGSMD	VNALTGPFVLI	PLACYLVIGT	SPILSGFVAL	420
PHIRRVMTKG	GENTDKLEKL	MVRIGLFSVL	YTVPATCVIA	CYFYERLWMD	YWKILAAQHK	480
CKMNNQTKTL	DCLMAASIPA	VEIPMVKIFM	LLVVGITSGM	NIWTSKTLQS	WQVCSRRLLK	540
KSRRRKPAFV	ITSGGIYKKA	QHPQKTHHGK	YEIPAQSPTC	V		581

70 Seq ID NO: C342 Protein Sequence
Protein Accession #: NP_005752.1

75
80

1	11	21	31	41	51	
MEVSRRAKAP	RPFRPAAPLP	LLAYLLALAA	PGRGADEFVW	RSEQAIGAIA	ASQEDGVFVA	60
SGSCLDQLDY	SLEHSLRLY	RDQAGNCTEP	VSLAPPARPR	PGSSFSKLLL	PYREGAAGLG	120
GLLTGTWTFD	RGACEVRPLG	NLSRNSLRNG	TEVVSCHPQG	STAGVVYRAG	RNNRWYLAVA	180
ATYVLPPEPT	ASRCNPAASD	HDIAIALKOT	EGRSLATQEL	GRKLCEGAG	SLHFDVAFW	240
NGSIYFPYYP	YNYTSGAATG	WPSMARIAQS	TEVLFQGGAS	LDCGHGHPDG	RRLLLSLSSIV	300
EALDVWAGVF	SAAAGEQGER	RSPTTALCL	FRMSEIQARA	KRVSWDFKTA	ESHCKEGDQP	360
ERVQPIASST	LIHSDLSVY	GTVMNRTVL	PLGTGDGQLL	KVILGENLTS	NCPEVIYBIK	420
EETPVFYKLV	PDPVKNIYII	LTAGKEVRR	RVANCNKHK	CSECLTATDF	HCGNCHSLQR	480
CTPQDCVHS	ENLENWLDIS	SGAKKCPRIQ	IIRSSKERTT	VTMVGSPSPR	HSKCMVKNV	540
SSRELQNKNS	QNRCTCTCSI	PTRATYKDV	VNVMPSPGS	WNLSDRFNFT	NCSLKECPA	600
CVETGCANCK	SARRCIHFPT	ACDPSDYERN	QBQCPVAVEK	TSGGGRPKEN	KGNRTNQALQ	660
VFYIKSIEPQ	KVSTLGRSNV	IVTGANPTRA	SNITMILKGT	STCDKQVIQV	SHVLNDTHMK	720

5 FSLPSSRKEM KDVCIQFDGG NCSSVGSLSY IALPHCSLIF PATTWISGGQ NITMMGRNFD 780
 VFDNLIIISHE LKGNINVSEY CVATYCGFLA PSLKSSKVRT NVTVKLRVQD TYLDCGTLQY 840
 REDPRFTGYR VESEVDTELE VKIQKENDNF NISKKDIEIT LPHGENGQLN CSPENITRNQ 900
 DLTTILCKIK GIKTASTIAN SSKKVRVVLG NLELYVEQES VPSTWYFLIV LPVLLVIVIF 960
 AAVGVTRHKS KELSRRQSQQ LELLESELAK EIRDGPALQ MDKLDVVDSF GTVPFLDYKH 1020
 FALRTFFPES GGFTHIPTED MNRDANDKN ESLTALDALI CNKSFLVTVI HTLEKQKNPS 1080
 VKDRCLFASF LTIALQTKLV YLTSILEVLT RDLMEQCSNM QPKMLLRTE SVVEKLLTNW 1140
 MSVCLSGFLR ETVGEPFYLL VTTLNQKINK GPVDVITCKA LYTLNEDWLL WQVPEFSTVA 1200
 LNVVFEKIPK NESADVCRNI SVNVLDCDTI GQAKEKIFQA FLSKNGSPYG LQLNEIGLEL 1260
 10 QMGTRQKELL DIDSSSVILE DGITKLNTIG HYBISNGSTI KVPFKIANFT SDVEYSDDHC 1320
 HLLLPDSEAF QDVQGRHRG KHKFKVKEMY LTKLLSTKVA IHSVLEKLFK SIWSLPNSRA 1380
 PPAIKYFPDF LDAQAKKKI TDPDVVHINK TNSLPLRFVW NILKNPQFVF DIKKTPIHIG 1440
 CLSVAIAQFM DAFSLTEQQL GKEAPTINKL YAKDIPTYKE EVKSYKAIK DLPLSSSEM 1500
 15 EEFLTQESKK HENEFNEEVA LTBIIYKIVK YFDEILNKLK RERGLEBAQK QLLHVKVLFD 1560
 EKKKCKWM 1568

Seq ID NO: C343 Protein Sequence
 Protein Accession #: NP_002176.1

20 1 11 21 31 41 51
 | | | | | |
 MTILGTTFGM VFSLQLQVVG ESGYAQNGDL EDAELDDYSF SCYSQLEVNG SQHSLTCAFE 60
 DDPVNTNLE FEICGALVEV KCLNFRKLQE IYFIETKKFL LIGKSNICVK VGEKSLTCKK 120
 IDLTTIVKPE APFDLSVIYR EGANDFVVT NTSHLQKKYV KVLMDVAYR QEKDENKWT 180
 25 VNLSSSTKLTL LQRKLQPAAM YEIKVRSIPD HYFKQFWESE SPSYYFRTP EINNSSGEMDP 240
 ILLTISILSF FSVALLVILA CVLAKKRIK IVWPSLPDHK KTLHLCKKP RKNLNVSNFP 300
 ESPLDQIHR VDDIQARDEV BGFLODTFPQ QLEESERQRL GGDVQSPNCP SEDVVVTPES 360
 FGRDSSLTCL AGNVSACDAP ILSSSRSLDC RESGKNGPHV YQDLLLSLGT TNSTLPPPPFS 420
 30 LQSGILTLNP VAQQPILTS LGSNQEEAYV TMSSFYQNG 459

Seq ID NO: C344 Protein Sequence
 Protein Accession #: NP_002713.1

35 1 11 21 31 41 51
 | | | | | |
 MAAARLCLSL LLLSTCVALL LQPLLGAQGA PLEPVYPGDN ATPEQMAQYA ADLRRYINML 60
 TRPRYGRKHK EDTLAFSEWG SPHAAVPREL SPLDL 95

40 Seq ID NO: C345 Protein Sequence
 Protein Accession #: NP_115934.1

45 1 11 21 31 41 51
 | | | | | |
 MIWRHVRLL FTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRQSP LNWTSSEHFE 60
 VTGSAEGWGP EEPLEYSRAF GEGASARPC CRNGGTCVLG SFCVCPAHFT GRyceHDQR 120
 SECGALEHGA WTLRACHLCR CIPGALHCLP LQTPDRCDPK DFLASHAHGP SAGGAPSLLL 180
 LLPCALLHRL LRPDAPAHPR SLVPSVLQRE RRPOGRPGLG HRL 223

50 Seq ID NO: C346 Protein Sequence
 Protein Accession #: NP_006524.1

55 1 11 21 31 41 51
 | | | | | |
 MARSLVCLGV IILLAPSGP GVRGGPMPKL ADRKLCADQE CSHPISMAVA LDYMAPDCR 60
 FLTIHRGQV YVFSKLKGRG RLPWGGSVQG DYYGDLAARL GYFPSSIVRE DQTLKPGKVD 120
 VKTDKWDYFC Q 131

60 Seq ID NO: C347 Protein Sequence
 Protein Accession #: Bos sequence

65 1 11 21 31 41 51
 | | | | | |
 MTQVTEKSTE HPEKTTSTTE KTRTPPEKPT LYSEKTICTK GRNTPVPEKP TENLGNTILT 60
 TETIKAPVKS TENPEKTA AV TKTIKPSVKV TGDKSLTTS SHLNKTEVTH QVPTGSPFTLI 120
 TSRTKLSSIT SEATGNESH YLNKDGSKQG IHAGQMGEND SFPANAIVIV VLVAVILLV 180
 FLGLIFLVSY MMTRRTLTQ NTQYNDAEDE GGPNSYPVYL MEQQNLGMGQ IPSR 235

70 Seq ID NO: C348 Protein Sequence
 Protein Accession #: NP_543146.1

75 1 11 21 31 41 51
 | | | | | |
 MTQVTEKSTE HPEKTTSTTE KTRTPPEKPT LYSEKTICTK GRNTPVPEKP TENLGNTILT 60
 TETIKAPVKS TENPEKTA AV TKTIKPSVKV TGDKSLTTS SHLNKTEVTH QVPTGSPFTLI 120
 TSRTKLSSIT SEATGNESH YLNKDGSKQG IHAGQMGEND SFPANAIVIV VLVAVILLV 180
 FLGLIFLVSY MMTRRTLTQ NTQYNDAEDE GGPNSYPVYL MEQQNLGMGQ IPSR 235

80 Seq ID NO: C349 Protein Sequence
 Protein Accession #: FGENSEH predicted

1 11 21 31 41 51
 | | | | | |

	MMPRLAFCCW	GLALVSGNAT	FQOMSPSRNF	SFRLFPETAP	GAPGSIPAPP	APGDEAAGSR	60
	VERLQAPFRR	VRLLRLRLSE	RLELVFLVDD	SSSVGEVNF	SELMFVRKLL	SDPFVVPTAT	120
	RVAIVTFSSK	NYVVPVRVDYI	STRRARQHKC	ALLLQEIPI	SYRGGGTYTK	GAPQQAQIL	180
5	LHARENSTKV	VPLITDGYSN	GGDPRIPIAAS	LRDSGVEIFT	PGIWQGNIRE	LNDMASTPKE	240
	SHCYLLHSFE	EFBALARRAL	HEDLPSGSFI	QDDMVHCSTL	CDEGKDCDDR	MGSCCKOHT	300
	GHFECICEBK	YVGKGLQYEC	TACPSGTYKP	EGSPGGISSC	IPCDEHNTS	PPGSTSPEDC	360
	VCREGYRASQ	QTCELVHCPA	LKPPENGYFI	QNTONNHFWA	ACGVRCHPGF	DLVGSSIIIC	420
	LPNGLWSSSE	SYCRVTRCPH	LRQPKHGHS	CSTRMLYKT	TCLVACDEGY	RLEGSDEKLT	480
10	QGNQWDGPE	PRCVERHCST	FQMPKDVII	PHNCGKQPAK	FGTICVYSCR	QGFILSGVKE	540
	MLRCTTSGKW	NVGVQAQVCK	DVEAPQINCP	KDIBAKTLEQ	QDSANVTWQI	PTAKDNGSEK	600
	VSVHVHPAFT	DPYLFPTIGDV	AIVYTATDLS	GNQASCIPI	KVIDAEPFVI	DWCRSPFPVQ	660
	VSEKVAASH	DEPQSDNSG	AELVITRSH	QGDLPQGET	IVQYTATDPS	GNNRTCDIHI	720
	VIKGSPCBIP	FTPVNGDPIC	TPDNTGVNCT	LTCLEGYDFT	EGSTDKYICA	YEDGVWKP	780
15	TTEWPDCAK	RFANHGPKSF	EMFYKAARCD	DTDLMKKFSE	AFETTLGKRV	PSFCSDAEDI	840
	DCRLEENLTK	KYCLEYNDY	ENGFAIGPGG	WGAANRLDYS	YDDFLDTVQE	TATSIGNAKS	900
	SRIKRSAPLS	DPYLFPTIGDV	TASVPLPDER	NDTLEWENQ	RLLTLETIT	NKLKRTLNKD	960
	PMYSFQLASE	ILIADSNLE	TKKASPPCRP	GSVLRGRMCV	NCPLQTYYNL	EHTFCBSCRI	1020
	GSYQDEBQGL	ECKLCPSGMY	TEYIHSRNI	DCKAQCKQGT	YSYSGLETCE	SCPLGTYQPK	1080
20	FGSRSLCSCP	ENTSTVHKRA	VNISACGVPC	PEGKFSRSL	MPCHPCPRDY	YQPNAGKAPC	1140
	LACPFYGTTP	FAGSRITESC	STSVLNITIF	GGFGHLELLN	CPSEVFHECF	FNPCHNSGTC	1200
	QQLGRGVCL	CPYLFPTIGDV	ETDIDECSPL	PCLNNGVCKD	LVGEFICECP	SGYTQGRCEE	1260
	NINECSSSPC	LKNGICVDGV	AGYRCTCVKG	FVGLHCSTEV	NECQSNPCLN	NAVCEQVGG	1320
	FLCKCPGFL	GTRCGNVDE	CLSQPCNGA	TCKDGANSPR	CLCAAGFTGS	HCELNINECQ	1380
25	SNPCRNQAT	EDLSTVHKRA	CQPGFSGRKC	ETEQSTGFLN	DFEVSIGIYG	VMDGLMPSL	1440
	HALTCTFMK	SDDDMYGTP	ISYAVDNGSD	NTLLLTIDYNG	WVLYVNGREK	ITNCPVNDG	1500
	RWHIAITWT	SANGINKVYI	DGKLSGGAG	LSVGLPIPGG	GALVLQEQD	KKGGFSPAE	1560
	SFVGSISQLN	LWDYVLSPPQ	VKSLATSCPE	ELSKGNVLAW	PDFLSGIVGK	VKIDSKSIFC	1620
	SDCPRLGGSV	PHLRTASEDL	KPGSKVNLFC	DPGQPLVGNP	VQYCLAQGMQ	TQPLPHCERI	1680
30	SCGVFPPLGS	ENTSTVHKRA	GSTVTYQCN	GYVLLGDSRM	FCTDNGSWNG	VSPCLDVE	1740
	CAVGSDCSEH	ASCLNVDSGY	ICSCVPPYTG	DGKNCAEPIK	CKAPGNPENG	HSSGEIYTVG	1800
	AGVTFSCQEG	YQLMGVTKIT	CLESSEWNHL	IPYCKAVSQG	KPAIPENGCI	EELAFTEGSK	1860
	VTYRCNKGYT	LAGDKESSCL	ANSSWSHSP	VCEPVKCSPP	ENIDNGKYL	SGLTYLSTAS	1920
	YSCDTGYSLQ	GPSIIECTAS	GIMDRAPPAC	HLVPCGEP	IKDAVITGN	FTFRNTVTTY	1980
35	CKEYTLTAGL	DTIECLADGK	WSRSDQCLA	VSCDEPPIVD	HASPTAHRL	FGDIAFYCS	2040
	DGYSLADNSQ	LLCNAQKQWV	PPGQDMPRC	IAHFCEKPPS	VSYSILESVS	KAKFAAGSVV	2100
	SFKCMGPFVL	NTSAKIECMR	GGQWNPSPMS	IQCIFVRCE	PFSIMNGYAS	GSNYSFGAMV	2160
	AYSCKNGFYI	KGEKSTCEA	TGQWSSPIPT	CHPVSCGEP	KVENGFLHT	TGRIFESEVR	2220
	YQCNPGYKSV	GSPVFCQAN	RHWHSSEPLM	CVPLDCGKPP	PIQNGPMKGE	NFEVGSKVQF	2280
40	FCNTEGYELV	DSSWTQCKSG	KWKKSNPKC	MPAKCPEPPL	LENQLVLKEL	TTEVGVVTF	2340
	CKGSHVLQGP	SVLKCLPSQ	WNSDFPVCKI	VLCTPPPLIS	PGVPIPSAL	HFGSTVYSC	2400
	VGGFFLRGNS	TTLCPDGTW	SSPLPECVPV	ECPPQEEIPN	GIIDVQLAY	LSTALYTCRP	2460
	GFELVNTTT	LCGEGHMLG	GKPTCKAIEC	LKPKBILNGK	FSYTDLHYGQ	TVTYSCNRGF	2520
	RLBEGSALTC	LETGWDVDA	PSCAIHCD	PQPIENGFEV	GADYSYGAI	IYSCFPQFQV	2580
45	AGHAMGDEFS	SGWSSSIPTC	MPIDCGLPPH	IDFGDCTKLK	DDQGYFEQED	DMMEVPVPT	2640
	HPYPHLAGVA	KTWENTKESP	ATHSSNFLYC	TMVSYTCNPG	YELLGNPVLI	CQEDGTWNGS	2700
	APSCISIEDC	LPTAPENGFL	RPTETSMGSA	VQYSCKPGHI	LAGSDLRCL	ENRKWSGASP	2760
	RCEAISCKPK	NPVMNGSIK	SNYTYLSTLY	YECDPGYVLN	GTERRTQDD	KNWDEBPI	2820
50	IPVDCSSPPV	SANGQVRGDE	YTPQKEIET	CNEGFLLGGA	RSRVCLANGS	WSGATPDCVP	2880
	VRCATPQLA	NGWTEGLDYG	PMKEVTFHCH	EGYILHGAPK	LTCQSDGNWD	ASIPLCFVN	2940
	CGPPEDLAHL	PPNGFSPHIG	GHIQYQCFPG	YKLHGNSSRR	CLSGNSWGS	SPSCLPCRC	3000
	TFVIEYGTVN	GTDFDCGKAA	RIQCFKGFKL	LGLSEITCEA	DQWSSSGFPH	CBTSCGSLP	3060
	MIPNAPISBT	SSWKENVITY	SCRSGYVIQ	SSDLICTEKG	VNSQPYPVCE	PLSCGSPSV	3120
	ANAVATGEAH	TYSESEKRLC	LEGYTMDDT	DTFTCQKQGR	WFERIKSCSP	KKCPLPENIT	3180
55	HILVHGDEFS	SGWSSSIPTC	EGYTFEGVNI	SVCQLDGTWE	PPFSDSCSP	VSCGKPSPE	3240
	HGFVVSQKIT	FESTIIYQCE	PGVELEGNRB	RVCQENRQWS	GGVAICKETR	CSTPLEPLNG	3300
	KADIERNTTG	PNVYVSCNRG	YSLBGPSEAH	CTENGWSEHP	VPLCKPNPCP	VPPVIPENAL	3360
	LSEKEPYVDQ	NVSIKCREGP	LIQGHGIITC	NPDETWQTS	AKCEKISCGP	PAHVENAIAR	3420
	GVHYQYQDMI	TYSCYSGYML	EGFLRSVCL	NGTWTSPPIC	RAVCRPPCQ	GGICQRPNAC	3480
60	SCPEGMGRL	CEEPICILPC	LNGGRCVAPY	QDCPPGWTG	SRCHTAVCQS	PCLNGGKCVR	3540
	PNRCHCLSSW	TGHNC					3557

Seq ID NO: C350 Protein Sequence
Protein Accession #: FGENESH predicted

65	1	11	21	31	41	51	
	MRPVSQGMRT	DYPRSVLAPA	YVSVCLLLLC	PREVIAPAGS	EPWLQCPAPR	CGDKIYNPLE	60
	QCCYNDAIVS	LSETRQCGPP	CTFWPCFELC	CLDSFGLTND	FVVKLVQGV	NSQCHSSPIS	120
70	SKCERGRIC						129

Seq ID NO: C351 Protein Sequence
Protein Accession #: AAH35671.1

75	1	11	21	31	41	51	
	MVPGARGGGA	LARAAGRGLL	ALLLAVSAPL	RLQAEELG	CGHLVITYQDS	GTMTSKNYPG	60
	TYPNHTVCEK	TITVFKGKRL	ILRLGDLDE	SQTCASDYLL	FTSSSDQYGP	YCGSMTVPKE	120
	LLLNSTSEVT	RFESSGSHIS	RGFLITYASS	DHPDLITCLE	RASEYLTKEY	SKFCPAGCRD	180
	VAGDISGNMV	DGYRDTSLLC	KAAIHAGIIA	DELGGQISVL	QRKGISRYEG	ILANGVLSRD	240
80	GLSLDKRFLP	TSNGCSRLS	FEPDQIRAS	SSWQSVNESG	DQVHWSFGQA	RLQDQGPSWA	300
	SGDSNNHKP	REWLIDLGE	KKKITGIRTT	GSTQSNPNFY	VKSPVMNPN	NNSKWTKYK	360
	IVNNEKVPQ	QNSNFRDPVQ	NNFIPPIVAR	YVRVVPQIWH	QRIALKVELI	CQITQGNDS	420
	LWVRKTSQST	SVSTKKEDET	ITRPIPSBET	STGINTTVA	IFLVLLVVLV	PAGMGIFAAP	480
	RQKKKKGSPY	GSAAEQRTDC	WQIKYFPAR	HQSAEPTISY	DNEKEMTQKL	DLITSDMAG	539

Seq ID NO: C352 Protein Sequence
Protein Accession #: Eos sequence

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1	11	21	31	41	51	
MGFGAGQRLR	PVPAPRSSAE	EAARPGQLRL	GIRRGAEALA	KLAPSGVMVP	GARGGGALAR	60
AAGRGLLALL	LAVSAPLRQ	AEELGDGCGH	LVTYQDSGTM	TSKNYPGTYP	NHTVCEKTIT	120
VPGKRLILR	IGDLDIESTQ	CASDYLLFTS	SSDQYGPYCG	SMTVPKELL	NTSEVTVRFE	180
SGSHISGRGF	LLTYASSDHP	DLITCLERAS	HYLKTEYSKF	CPAGCRDVAG	DISGNMVDGY	240
RDTSLLCKAA	IHAGIADDEL	GGQISVLQRK	GISRYEGILA	NGVLSRDGSL	SDKRFLFTSN	300
GCSRSLSFEP	DGQIRASSSW	QSVNESGDQV	HWSPGQARLQ	DQGPSWASGD	SSNNHKPREW	360
LEIDLGEKKK	ITGIRTGST	QSNFNFYVKS	FVMNFKNNNS	KWKTYKGIVN	NEEKVFQGNS	420
NFRDPVQNNF	IPPIVARYVR	VVPQTHQRI	ALKVELIGCQ	ITQGNDSLWN	RKTSQSTSVS	480
TKKEDETITR	PIPSEETSTG	INITTVAIPL	VLLVVLVFAV	MGIFAARFKK	KKKGSPLYGSA	540
EAQKTDCKWQ	IKYFFARHQS	AEPTISYDNE	KEMTQKLDLI	TSDMAG		586

Seq ID NO: C353 Protein Sequence
Protein Accession #: FGENESH predicted

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1	11	21	31	41	51	
MFQRQERFLD	LSSAEAAVAH	ILHQHPDIIN	KDGGCGHLVT	YQDSGMTSK	NYPGTYPNHT	60
VCEKTIITVPK	GKRLILRLGD	LDIESQTCAS	DYLLFTSSSD	QYGMQKEEET	EVLCCLSVAGA	120
QRVDIPVQLL	PSFLBEGWGH	ADARGPYCGS	MTVPKELLN	TSEVTVRFES	GSHTSGRGFL	180
LTVASSDHPD	LITCLERASH	YLKTEYSKFC	PAGCRDVAGD	ISGNMVDGYR	DTSLCKAAI	240
HAGIADDELG	GGQISVLQRK	ISRYEGILAN	GVLSRDGSL	DKRFLFTSNG	CSRSLSFEED	300
GQIRASSSWQ	SVNESGDQVH	WSPGQARLQD	QGPSWASGDS	SSNNHKPREWL	EIDLGEKKKI	360
TGIRTGTGSTQ	SNPNFYVKSF	VMNFKNNNSK	WKTYKGIVNN	EEKVFQGNNS	FRDPVQNNFI	420
PPIVARYVRV	VQTHQRI	LKVELIGCQI	TQGNDSLVMR	KTSQSTSVST	KKEDETITRP	480
IPSEETSTDA	MPVQIVGDHT	QMISQRENLG	PDEGKIPFKG	TAESMVRVVF	AVVNDLGML	540
FLAHTPEEDI	DRYCNKQIKY	PPARHQSARF	TISYDNEKEM	TQKLDLITSD	MADYQQPLMI	600
GTGTVTRKGS	TFRPMDTDAE	EAGVSTDAOG	HYDCPQRAGR	HEVALPLAPP	EPEYATPIVE	660
RHVLRAHTFS	AQSGYRVPGP	QPGHKHSLSS	GGFSPVAGVG	AQDGDYQRP	SAQPADRGYD	720
RPKAVSALAT	ESGHFDSQKP	PTHPGTSDSY	SAPRDCLTPL	NQTAMTALL		769

Seq ID NO: C354 Protein Sequence
Protein Accession #: NP_004607.1

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1	11	21	31	41	51	
MAGVSACIKY	SMFTFNFLFW	LCGILILALA	IWVRVNSDSQ	AIFGSEDVGS	SSYVAVDILI	60
AVGAIIMILG	FLGCCGAIKE	SRCHLLFFI	GLLLILLIQV	ATGILGAVPK	SKSDRIVNET	120
LYENTKLLSA	TGESEKQFQE	AIIVFQEEFK	CCGLVNGAAD	WGNPNQHYPE	LCACLDKQRP	180
CQSYNGKQVY	KETCISFIKD	FLAKNLIIVI	GISFGLAVIE	ILGLVFSMVL	YQIQGNK	237

Seq ID NO: C355 Protein Sequence
Protein Accession #: NP_004608.1

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1	11	21	31	41	51	
MCTGGCARCL	GGTLIPLAPP	GPLANILLFP	PGKVIDDND	HLSQRIWFFG	GILGSGVLM	60
FPALVFLGLK	NNDCCGCCGN	EGCGKRFAMP	TSTIPAVVGF	LGAGYSPIIS	AISINKGPKC	120
LMANSTWGYF	PHDGYLND	ALMNKCREPL	NVVPWNLTFL	SILLVVGIGQ	MVLCAIQVVN	180
GLLGLTLCGDC	QCCGCCGGDG	FV				202

Seq ID NO: C356 Protein Sequence
Protein Accession #: NP_002372.1

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1	11	21	31	41	51	
MPRPAPARRL	PGLLLLLLWPL	LLLPASAPDP	VARPGFRRLE	TRGPGGSPGR	RPSAPAPDGA	60
PASGTSEPGR	ARGAGVCKSR	PLDLVFIIDS	SRSVRPLEFT	KVKTFSVRII	DTLDIGPADT	120
RVAVVNYAST	VKIRFQLQAY	TDKQSLKQAV	GRITPLSTGT	MSGLAIQTAM	DEAFTVEAGA	180
REPSSNIPKV	AIIVTDGRPQ	DQVNEVAARA	QASGIELYAV	GVDRADMASL	KMMASEPLEE	240
HVFVVTYGV	IEKLSSRFQE	TFCALDPCVL	GTHQCQHVCI	SDGEGKHCE	CSQGYTLNAD	300
KKTCALDR	ALNTHGCEHI	CVNDRSGSYH	CECYEGYTLN	EDRKTCQAQD	KCALGTHGCO	360
HICVNDRTGS	HHCECYEGYT	INADKKTCSV	RDKCALGSHG	CQHICVSDGA	ASYHCDYCPG	420
YTLNEDKKT	C SATEEARLV	STEDACGCEA	TLPQDKVSS	YLQRLATKLD	DILEKLKINE	480
YQIHR						486

Seq ID NO: C357 Protein Sequence
Protein Accession #: NP_057723.1

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1	11	21	31	41	51	
MARGSLRRL	RLVLGLWLA	LLRSVAGEQA	PGTAPCSRGS	SWSADLDKCM	DCASCRRARH	60
SDFCLGCAAA	PPAPFRLWLP	ILGALSITF	VIGLLSGFLV	WRCRRREKXP	TTPTESTGGE	120
GCPAVALIQ						129

Seq ID NO: C358 Protein Sequence
Protein Accession #: NP_001810.1

	1	11	21	31	41	51	
	MQPTLLLSLL	GAVGLAAVNS	MPVDNRNHN	GMVTRCIIEV	LSNALSKSSA	PPITPECRQV	60
	LKTSRKDVND	KETTENTNK	FBVRLLRDPA	DASEAHSSSS	RGEAGAPGB	DIQGPTKADT	120
5	EKWABGGHS	REKADPEQWS	LYPSDSQVSE	EVKTRHSEKS	QREDEEEEG	ENYQKGERGE	180
	DSSEKHLSE	PGETQNAFLN	ERKQASAIKK	BEIVARSETH	AAGHSQEKTH	SREKSSQESG	240
	EEAGSQENHP	QESKQPRSQ	EESEEGEEDA	TSEVDKRRTR	PRHHHGRSRP	DRSSQGGSLP	300
	SEKKGHPQEE	SEESNVSMAS	LGEKRDHHST	HYRASESEPE	YGEEIKGYPG	VQAPEDLEWE	360
10	RYRGRGSEFY	RAPRPQSEES	WDEEDKRNYP	SLELDKMAHG	YGEESEEREG	LEPGKGRHHR	420
	GRGGEPRAYF	MSDRREKRF	LGEHGHVRQE	NQMDKARRHP	QGAWKELDRN	YLNYGEEGAP	480
	GKMQQQGDLQ	DTKENREBAR	FQDKQYSSHH	TAZKRLRGE	LPNFPYDPLQ	MKSSHFERED	540
	NMNDNPLEGE	EENELTLNEK	NFFPEYNYDW	WEKPFSESDV	NWGYEKRLNA	RVPKLDLRQ	600
	YDRVAQLDLQ	LHYRKKSAEF	PDFYDSKEPV	STHQBAENK	DRADQTVLTE	DEKKELENLA	660
15	AMDLQLKIA	EKPSQRG					677
	Seq ID NO: C359 Protein Sequence						
	Protein Accession #: XP_093082.1						
	1	11	21	31	41	51	
20	MKLLCEGLKQ	PNCVLQTLRW	YRCLISSASC	GALAAVLSTS	QWLTELEPSE	TKLEASALKL	60
	LYGGLKDPNC	KLQKLNLPFS	LSVTAALKLV	GMVNCSCGFS	GSLVQSHFGY	CQSSSPKCDL	120
	CKLLWPSTRV	AAAKDCGSPK	SFLSEGLNWA	GRLEAVEEVL	GLGLVLQPGD	PASQGGHCE	180
	NYGSPRDLVD	LEVKAEPSLR	KGGMDLQRP	LQVLLCKIF	SLKFLFLIAL	PNSPGGVSVV	240
25	QVTIPDGFVN	VIVGNSVTIL	CIYTTIVASR	EQLSIQWSPF	HKKEMEPISS	PWEEGKWPDV	300
	EAVKGLDGG	QAEQLIYFSQ	GGQAVAIQF	KDRITGSNDP	GNASITISHM	QPADSGIYIC	360
	DVNNPPDFLG	QQGLILNVSV	LVPKSKPLCS	VQGRPETGHT	ISLSCLSALG	TPSPVYVWHK	420
	LEGRIIVFVK	ENFNPTTGIL	VIGNLTNFEQ	GYQCTAINRL	LGNSSCEIDL	TSSHPEVGII	480
	VGALIGSLVG	AAIIISVVCV	ARNKAKAKAK	ERNKTIKINP	EPMTKINPRG	ESEAMPREDA	540
30	TQLEVTLPSS	IHETGPDITQ	EPDYEPKPTQ	EPAPPEPAPG	EPMAVFDLDI	ELELEPETQS	600
	ELEPEPEPEP	ESEPGVVVEP	LSEDEKGVVK	A			631
	Seq ID NO: C360 Protein Sequence						
	Protein Accession #: FGENESH predicted						
	1	11	21	31	41	51	
	MVPFAFWKVL	ILSLCAGQVS	VVQVTIPDGF	VNVIVGNSVT	LICIYTTTVA	SREQLSIQWS	60
	FPHKMEMEPI	SSPWREGKWP	DVEAVKOTLD	GQQAELQIYF	SQGGQAVAIQ	QFKDRITGSN	120
40	DPGNASITIS	HMQPADSGIY	ICDVNNPPDF	LQNNQGIILN	SVLVKPSKPL	CSVQGRPETG	180
	HTISLSCLSA	LGTSPSPVYV	HKLEGRDIVP	VKNFNPTTGG	ILVIGNLTNF	BQGYIYQCTAI	240
	NRLGNSSCEI	DLTSSHPFVG	IIVGALIGSL	VGAIIISVIV	CFARNKAKAK	AKERNKTIKIN	300
	ELEPMKINP	RGESEAMPRE	DATQLEVTLP	SSIHETGPD	IQEPDYEPKP	TQEPAPPEPAP	360
45	GSEPMVAVDL	DIELELEPET	QSELEPEPEP	EPSEPGVVV	EPLSEDEKGV	VKA	413
	Seq ID NO: C361 Protein Sequence						
	Protein Accession #: NP_003011.1						
	1	11	21	31	41	51	
50	MVSRMVSTML	SGLLFWLASG	WTPAPAYSFR	TFDRVSEADI	QRLHGVMEQ	LGIARPRVEY	60
	PAHQAMNLVG	PQSIIEGGAHE	GLQHLGPFNG	IPNIVAEITG	DNIPKDFSED	QGYPDPPNFC	120
	PVGKTDGGL	ENTPDAEFS	REFQLHQHLE	DPEHDYPLGL	KWNKLLYEK	MKGGERRKRR	180
55	SVNPYIQQQR	LDNVVAKKSV	PHPSDEKDP	B			211
	Seq ID NO: C362 Protein Sequence						
	Protein Accession #: NP_076926.2						
	1	11	21	31	41	51	
60	MTMQGMEQA	MPGAGPGVPQ	LGNMAVIRSH	LWKGLQEKFL	KGEPKVLGVV	QILTALMSLS	60
	WGIITMMQAS	NTYGSNPISV	YIGYTIWGSV	MPIISGSLSI	AAGIRTTKGL	VRGSLGMNIT	120
	SSVLAASGIL	INTFSLAFYS	FHHPYCNVYG	NSNNCHGTMS	ILMGLDQMV	LLSVLEPCIA	180
65	VSLAPGCKV	LCCTPGGVVL	ILPSSHMAE	TASPTPLNEV			220
	Seq ID NO: C363 Protein Sequence						
	Protein Accession #: NP_002082.1						
	1	11	21	31	41	51	
70	MRGSELPLVL	LALVLCAPR	GRAVPLPAGG	GTVLTKMYPR	GNHWAVGHIM	GKKSTGESSES	60
	VSEKSGIKQ	LREYIRWEEA	ARNLLGLIEA	KENRNEQPPQ	PKALGNQQPS	WSEDSNNFK	120
	DVSGKGVGR	LSAPGSQREG	RNPQLNQ				148
75	Seq ID NO: C364 Protein Sequence						
	Protein Accession #: NP_036393.1						
	1	11	21	31	41	51	
80	MDLQGRGVPS	IDRLRVLLML	FHTMAQIMAE	QEVENLSGLS	TNPEKDIPVV	RENGTTCLMA	60
	EPAAKFIIVP	DVMAENYVDL	ITEQADIALT	RGAEVKGRGC	HSQSEIQVFW	VDRAIALKML	120
	FPKESHNMK	GPEATWRLSK	VQFVYDSSEK	THFKDAVSAG	KHTANSHHLS	ALVTPAGKSY	180
	EQQAQQTISL	ASSDPQKTVT	MILSAVHIQ	FDIISDFVFS	BEHKCPVDER	EQLEETPLPI	240
	LGLILGLVIM	VTLAIYVHH	KMTANQVQIP	RDRSQYKHM			280

Seq ID NO: C365 Protein Sequence
Protein Accession #: NP_003217.1

5 1 11 21 31 41 51
MLGLVLALLS SSSAEEYVGL SANQCAVPK DRVDCGYPHV TPKECNNGRC CFDSRIPGVP 60
WCFKPLTRKT ECTF 74

10 Seq ID NO: C366 Protein Sequence
Protein Accession #: NP_002984.1

15 1 11 21 31 41 51
MSLPSSRAAR VPGPGSLCA LLALLLLLT PGLASAGPV SAVLTELRCT CLRVTLRVNP 60
KTIGKLQVFP AGPQCSKVEV VASLKNKGQV CLDPEAPFLK KVIQKILDSG NKKN 114

20 Seq ID NO: C367 Protein Sequence
Protein Accession #: NP_005233.2

25 1 11 21 31 41 51
MRSPSAWLL GAAILLAAAL SCSGTIQGTN RSSKGRSLIG KVDGTSHTVG KGVTVETVFS 60
VDEFSASVLT GKLTIVFLPI VYTIIVFVGL PSNGMALWVF LFRTKKKHPA VIYMANLALA 120
DLGSVIWFPL KIAYHIHANN WIYGEALCNV LIGFFYGNMY CSILEMTCLS VQRYWVIVNP 180
MGHSRKKANI AIGSLAIWL LILLVTIPLY VVKQITFIPA LNTTCHDVL PEQLLVGDMF 240
NYFLSLAIGV FLPPAFITAS AYVLMIRMLR SSAMDENSEK KRKRAIKLIV TVLAMYLICF 300
TSMNLLLVVH YFLIKSQQS HVYALYIVAL CLSTLNSCID PFVYVFSHD FRDHAKNALL 360
CRSVRTVKQM QVSLTSKHS RKSSSYSSSS TTVKTSY 397

30 Seq ID NO: C368 Protein Sequence
Protein Accession #: NP_003460.1

35 1 11 21 31 41 51
MAEAKTHWLG AALSILPLIF LISGAEEASF QRNQLLQKEP DLRLNVQKP PSPEMIRALE 60
YIENLRQAH KEESFPDYNP YQGVSVPLQQ KENGDESHLP ERDSLSEEDW MRIILEALRQ 120
AENEPQSAEP ENKPYALNSE KNFPMDSDD YETQWPERK LKHMQPPMY EENSNDNPFK 180
RTNEIVEEQY TPQSLATLES VPQELGKLTG PNNQKRERMD BEQKLYTDD EDDYKANNIA 240
YEDVVGEDW NPVEEKIESQ TQEEVRDSKE NIGKNEQIND EMKRSQGLGI QEEDLRKESK 300
DQLSDDVSKV IAYLKLRLVA AGSGRLQNGQ NGERATRLFE KPLDSQSIYQ LIEISRLQI 360
PPEDLIEMLK TGEKPNGSVE PERELDLPVD LDDISEADLD HPDLFQNRML SKSGYPKPTG 420
RAGTEALPDG LSVEDILNLL GMESAANQKT SYFFNPYNQE KVLPRLPYGA GRSRSNQLPK 480
AAHIVHVENR QMAYENLNDK DQELGEYLAR MLVKYPEIIN SNQVKRVPGQ GSSEDDLQEE 540
EQIEQAIKEH LNQGSSQETD KLAPVSKRFP VGPPKNDTTP NRQYWEDELK MKVLEYLNQE 600
KAEGGREHIA KRAMENM 617

50 Seq ID NO: C369 Protein Sequence
Protein Accession #: NP_112217.1

55 1 11 21 31 41 51
MPCAQRSMWA NLSVVAQLLN FGALCYGRQP QPGPVRFPPDR RQEHFIKGLP EYHVVGPRV 60
DASGHFLSYG LHYPITSSRR KRDLDSSEDW VYYRISHEEK DLFFNLTVNQ GFLSNSYIME 120
KRYGNLSHVK MMASSAPLCH LSGTVLQOQT RVGTAALSAC HGLTGFFQLP HGDFFIEPVK 180
KHPLVEGGYH PHIVYRRQKV PETKBPCTGL KDSVNISQKQ ELWREKWERH NLPSSRLSRR 240
SISKERWVET LVVADTKMIE YHGSENVESY ILTIMNMVTG LFHNPSIGNA IHIVVRLIL 300
LEEBEQGLKI VHAHEKTLSS PCKWQKSINP KSDLNPFVHD VAVLLTRKDI CAGFNRPCT 360
LGLSHLSGMC QPHRSNINE DSGLEPLAFTI AHELGHSEFI QHDGKENDCE FVGRHPIYMS 420
RQLQYDPTPL TWSKCEEYI TRFLDRGWGP CLDDIPKKKG LKSKVIAPGV IYDVHQCQL 480
QYGNATFCQ EVENVQTLW CSVKGFCRSK LDDAADGTQC GEKKWCMAK CITVKGKPE 540
IPGQWGRWSP WSHCSRTCGA GVQSAERLCN NPEPKFGGKY CTGERKRYRL CNVHPCRSEA 600
PTFRQMCSE FDTVPYKNEL YHWFPFNPFA HPCELYCRPI DGQFSEKMLD AVIDGTPCFE 660
GGNSRNVGIN GICKMVGCDY EIDSNATEDR CGVCLGDGSS CQTVRKMFQ KBGSGYVDIG 720
LIPKGARDIR VMEIEGAGNF LAIRSEDPEK YYLNGGPIIQ WNGNYKLAGT VFQYDRKGD 780
EKLMAFGPTN ESWIQLLPQ VTNPGIKY EY TIQKDGLND VBQMYFMQYG HWTECSVTC 840
TGIRRTAHK IKKGRGMVKA TPCDPETQPN GRQKKCHEKA CPFRNWAGW EACSATCGPH 900
GEKKRTVLCI QTMVSDQAL PPTDCQHLK PKTLLSCNRD ILCPSDWTVG NWSECSVSCG 960
GGVIRSRVTC AQNHDEPCDV TRKPNRSLC GLQCCPSSRR VLKPNKGTIS NGKNPPTLKP 1020
VPPPTSRPRM LTPPTGPESM STSTPAISSP SPTTASKEGD LGGKQWQDSS TQPELSSRYL 1080
ISTGSTSQPI LTSQSLSIQ SEENVSSSDT GPTSEGLVA TITSGSGLSS SRNPITWPVT 1140
PFYNTLTGKP EMEIHSGSGE EREQPEDKDE SNFVIWTKIR VPGNDAPVES TEMPLAPPLT 1200
PDLRESWMP PFSTVMEGLL PSQRPTTSET GTPRVEGMVT EKPANTLLPL GGDHQPPEPSG 1260
KTANRNHLK PNMNQTKSS EPVLTEEDAT SLITBGLLN ASNYKQLTNG HGSANHIVGN 1320
WSECSTTCGL GAYWKRVECT TQMSDCAAI QRPDPKRCR LRPCAGWKV NWSKSGRNC 1380
GGFKIREIQC VDSRDHRLR PFHCQFLAGI PPPLSMSCNP EPCBANQVEP WSQCSRSCGG 1440
GVQERGVPFC GGLCDWTKRP TSIMSCNEHL CCHWATGNWD LCSTSCGGGF QKRIVQCVPS 1500
EGNKTEDQDQ CLCDHKPRPP EFKKCNQAC KKSADLLCTK DKLSASFQCT LKAMKCSVP 1560
TVRABCCFSC PQTHITHYQR QRRQLLQKS KEL 1593

80 Seq ID NO: C370 Protein Sequence
Protein Accession #: NP_001053.1

1 11 21 31 41 51

	1	11	21	31	41	51	
	MRQSHQLPLV	GLLLFSPFIP	QLCEICEVSE	ENYIRLKLPL	NTMIQSNYNR	GTSAVNVVLS	60
	LKLVGIIQIT	IMQMIQKIR	YNVKSRLSDV	SSGELALIL	ALGVCRNAEE	NLIYDYHLTD	120
5	KLENKFAEI	ENMEAHNGTP	LITNYQLSLD	VIALCLFNGN	YSTAEVVNHF	TPENKNYYPG	180
	SQFSVDTGAM	AVLALTCVKK	SLINGQIKAD	EGSLKNISYI	TKSLVEKILS	EKKENGLIGN	240
	TFSTGBAMQA	LFVSSDYNE	NDWNCQQTIN	TVLTEISQGA	FENPNAAQV	LPALMGKTFL	300
	DINKDSSCVS	ASGNFNISAD	EPITVTPFDS	QSYISVNVSV	RINETYFTNV	TVLNGSVFLS	360
	VMEKAQKMD	TIFGFTMEER	SWGPIYTCIQ	GLCANNNDRT	YWELLSGSEP	LSQAGAGSVV	420
	RNGENLEVRW	SKY					433
10	Seq ID NO: C371 Protein Sequence Protein Accession #: NP_004582.1						
	1	11	21	31	41	51	
15	MCCTKSLLLA	ALMSVLLLHL	CGESEASNF	DOCLGYTDRI	LHPKFIVGFT	RQLANEGCDD	60
	NAIIFHTKKK	LSVCANPKQT	WVKYIVRLLS	KKVKNM			96
20	Seq ID NO: C372 Protein Sequence Protein Accession #: NP_037403.1						
	1	11	21	31	41	51	
25	MAGSPLLWGP	RAGGVGLLVL	LLGLFRPPP	ALCARPVKEP	RGLSAASPL	AETGAPRRFR	60
	RSVPRGEAAG	AVQELARALA	HLLEAERQER	ARAEAEAEED	QQAARVLAQLL	RVWGAPRNSD	120
	PALGLDDDFD	APAAQLARAL	LRARLDPAAL	AAQLVPAPVP	AAALRPRPFV	YDDGPAGPDA	180
	EEAGDETVDV	DPELLRYLLG	RILAGSADSE	GVAAPRRLRR	AADHDVGSEL	PPEGVLGALL	240
	RVKRLTAPAP	QVPARRLLFP					260
30	Seq ID NO: C373 Protein Sequence Protein Accession #: NP_002236.1						
	1	11	21	31	41	51	
35	MLQSLAGSSC	VRLVERHRSA	WCFQFLVLGY	LLYLVFGAVV	FSSVELPYED	LLRQELRKLK	60
	RRFLEEHECL	SEQQLEQPLG	RVLEASNYGV	SVLEASNGNW	NWDFTSALFP	ASTVLSTTGY	120
	GHTVPLSDGG	KAPCIYISVI	GIPFTLLFLT	AVVQRITVHV	TRRPVLYPHI	RWGFPSKVVA	180
	IVHAVLLGFV	TVSCFFFIAP	AVPSVLEDDW	NFLESFYPCF	ISLSTIGLGD	YVPGEGYNQK	240
	FRRLYKIGIT	CYLLGLLIAM	LVVLETFCEL	HELKKFRKMF	YVKKDKDEDQ	VHIIEHDQLS	300
40	FSSITDQAAG	MKEDQKQNEP	FVATQSSACV	DGPANH			336
	Seq ID NO: C374 Protein Sequence Protein Accession #: NP_005463.1						
	1	11	21	31	41	51	
45	METTINGTETW	YESLHAYLKA	LNATLHSNLL	CRPGPGLGPD	NQTEERRASL	PGRDDNSYMY	60
	ILFVMPFLFAV	TVGSLILGYT	RSRKVDKRSO	PYHVYIKNRV	SMI		103
50	Seq ID NO: C375 Protein Sequence Protein Accession #: NP_005236.1						
	1	11	21	31	41	51	
55	MGRHLALLLL	LLLLFQHFQD	EDGSQRLEQT	PLQPTHLEYN	VTVQENSAAK	TYVGHFVKMG	60
	VYITHPAWEV	RYKIVSGDSE	NLPKABEYIL	GDPCPLRIRT	KQNTAILNR	EVKDHYYTLIV	120
	KALEKNTNVE	ARTKVRVQVL	DTNDLRPLFS	PTSYSVSLPE	NTAIRTSTIAR	VSATDADIGT	180
	NGEYFYSFKD	RTDMFAIHPT	SGVIVLTGRL	DYLETKLYEM	EILAADRGMK	LYGSSGIISSM	240
	AKLTVHIEQA	NECAPVITAV	TLSPSELORD	PAYAIPTVDD	CDQAGANGIA	SLSIVAGDLL	300
60	QQFRTVRSFP	GSKEYVKVKA	GDIDWDSHPP	GYNLTLQAKD	KGTTPQPFSSV	KVIHVTSPOF	360
	KAGPVKFEKD	VYRAEISEFA	PNTPTVVMVK	AIPAYSHLRY	VFKRTPGKAK	PSLNNTGLI	420
	SILEPVKRQQ	AAHFELEVTT	SDRKASTKVL	KVVLGANSNP	PRFTQTAYKA	AFDENVPIGT	480
	TIMLSAVDP	DEGENGYVTY	SIANLNVHVP	AIDHPTGAVS	TSENLDYELM	PRVYTLRIRA	540
	SDWGLPYRRE	VEVLATITLN	NLNDNTPLFE	KINCEGTIPR	DLGVGEQITT	VSADADELQ	600
65	LVQYQIEAGN	ELDLFSLNPN	SGVLSLKRSL	MDGLGAKVSF	HSLRITATGD	ENFATPLYIN	660
	ITVAASHKLV	NLQCBETGVA	KMLAEKLLQA	NKLNQGEVE	DIFFDSSHVN	AHIPQFRSTL	720
	PTGIQVKENQ	PVGSSVIFMN	STDLDTGFGN	KLVAVSNGN	EDSCFMIDME	TGMLKILSPL	780
	DRETTDKYTL	NITVYDLGIP	QKAAWRLLEV	VVDANDNPP	EPLQESYFVE	VSEDKEVHSE	840
	IIQVEATDKD	LSPNGHVTYS	ILTDITDTSI	DSVTGVVNIA	RPLDRELQRE	HSCLKIARDQ	900
70	AREKPQLFST	VUVKVSLEDV	NDNPPTFIPP	NYRVKVRDEL	PEGTVIMWLE	AHDFDLGQSG	960
	QVRYSLLDHG	EGNFVDVDELS	GAVRIVQQLD	FEKKQVYNLT	VRADKRGKPV	SLSSTCYVEV	1020
	EVVDVNENLH	PPVSSPVKEK	GTVKEDAPVG	SLVMTVSAHD	EDAGRDGEIR	YSIRDGSGVG	1080
	VEKIGESTGV	IETSDRLDRE	STSHYWLTVF	ATDQGVVPLS	SPIEIYIEVE	DVNDNAPQTS	1140
	BVVYYPIME	NSPKDVSUVQ	IEAFDPDSSS	NDKLMYKITS	GNPQGFBSIH	PKTGLITTTTS	1200
75	RKLDREQQDE	HILEVTVDN	GSPFKSTIAR	VIVKILDEND	NKPQFLQKPY	KIRLPEREKP	1260
	DRENNARREP	LYRVIAATDK	EGPNABISYS	IEDGNEHGKF	PFBPKTGVVS	SKRFSAAQGY	1320
	DLISIKAVDN	GRPQKSSSTR	LHIEMISKPK	QSLPISFEE	SFFTFTVMS	DPVAHMIGVI	1380
	SVEPPGIPLW	FDITGGNYDS	HPDVKGTGT	IIVAKPLDAB	QKSNYNLTVE	ATDGTITILT	1440
	QVPIKVIDTN	DHRPQFSTSK	YEVVIPEDTA	PETEILQISA	VQDEKRNKLI	YTLQSSRDPL	1500
80	SLKKFRLDPA	TGSLTYSEKL	DHEAVSFAHL	TMVVRQDVP	VGRNFARIVV	NVSDTNDHAP	1560
	WFTASSYKGR	VYESAAVGSV	VLQVTALDKD	KGKNAEVLVS	IESGNIGNIG	NSFMIDPVLG	1620
	SIKTAKELDR	SNQASYDLMV	KATDKGSPPM	SEITSVRIFV	TIADNASPKF	TSKEYSVELS	1680
	ETVSGSFVQ	MYTAHSQSSV	VYEIKDGN TG	DAFDINPHSG	TIITQKALPD	ETLPITTLII	1740
	QGTNNAGLST	NTTVLVHLQD	ENDNAPVFMQ	AETVGLISES	ASINSVVLTD	RNVPLVIRAA	1800

DADKDSNALL VYHIVEPSVH TYFAIDSSTG AIHTVLSLDY EETSIFHFTV QVHDMGTPLR 1860
 FAEYAAENVTV HVIDINDCFP VFAKPLYEAS LLLPTYKGVK VITVNATDAD SSAFSQLIYS 1920
 ITEGNIGKEF SMOYKTGALT VQNTTQLRSR YELTVRASDG RFAGLTSVKI NVKESKESHL 1980
 KFTQDVYSAV VKENSTEAEET LAVITAIGSP INEPLFYHIL NPDRRPKISR TSGVLSTTGT 2040
 PFDREQQEAF DVVVEVIEEH KPSAVAHVVV KIVEDQNDN APVFNLPYV AVVKVDETVG 2100
 HVIRYVTAVD RDSGRNGEVH YYLKEHHEHF QIGPLGEISL KKQFELDTLN KEYLVTVVAK 2160
 DGGNPAFSAE VIVPITVMNK AMPVFEKPFY SAEIAESIQT HSPVVHVQAN SPEGLKVYYS 2220
 ITDGDFFSQF TINFNTGVIN VIAPLDFAH PAYKLSIRAT DSLTGAHAHV FVDIIVDDIN 2280
 DNPPVFAQQS YAVTLSEASV IGTSVVQVRA TDSSEPNRG ISYQMFNGHS KSHDHFHVD 2340
 STGLISLLRT LDVEQSRQHT IFVRAVDGGM PTLSSDVIVT VDVTDLNGNP PLFPEQIYEA 2400
 RISEHAPHGH FVTCVKAYDA DSSDIDKLQY SILSGNDHKK FVIDSATGII TSLNLRHAL 2460
 KPFYSLNLSV SDGVFRSSTQ VHVTVIGGNL HSPAFLQNEY EVELAENAPL HTLVMEVKT 2520
 DGDSGIYGHV TYHIVNDFAK DRPYINERGQ IPTLEKLDRE TPAEKVISVR LMAKDAGGKV 2580
 AFCTVNVLIT DDNDNAPQFR ATKYEVNIGS SAAKGTSVVK SASDADEGSN ADITYAIEAD 2640
 SESVKENLEI NKLSGVITTK ESLIGLENEF PTFVRAVDN GSPSKESVVL VIVKILPEM 2700
 QLPKFSEPPY TFTVSEDPV GTEIDLIRAE HSGTVLYSLV KGNTPESTRD ESFVIDRQSG 2760
 RLKLEKSLDH EHHYQFQSI LARCTODDHE MVASVDVSIQ VKDANDNSPV FESSPYEAFI 2820
 VENLPGGSRV IQIRASDADS GTNGQVMYSL DQSQSVIEIE SFAINMETGW ITTLKELDHE 2880
 KRDNVQIKVV ASDHGEKIQI SSTAIVDVTV TDVNDSPFRF TABIYKGTVS EDDPGGVIA 2940
 ILSTTDADSE BINRQVTYFI TGGDFLGQFA VETIQNEWKV YVKKPLDREK RDNVLLTITA 3000
 TDGTFSSKAI VEVKVLDAAND NSPVCETLY SDTIPEDVLP GKLIHQISAT DADIRSNAEI 3060
 TYTLGSGAE EHVKNPTDGE LKTSTPLDRE EQAVYHLLVR ATDGGGRFCQ ASIVVTELDV 3120
 NDNAPEFSAD PYAITVPENT EPGTLLTRVQ ATDADAGLNR KILYSLIDSA DQGFINSIELS 3180
 GIIQLEKPLD RELQAVYTL S LKAVDQGLPR RLATATGTIV SVLDINDNPP VFEYREYGAT 3240
 VSEDILVTE VLQVYAASRD IEANAETYS IISGNEHGKF SIDSKTGAVF IENLDYESS 3300
 HEYILTVEAT DGGTSLSDV ATNVNVNVDI NDNTPVFSQD TYTIVISEDA VLEQSVITVM 3360
 ADDADGPNHS HHYHSDIDGN QGSSFTIDPV RGEVKVTKLL DRETISGYTL TVQASDNGSP 3420
 PRVNTTIVNI DVSDVNDNAP VFSRGNYSVI IQENKPVGFS VLQVVTDED SSHNGPPFF 3480
 TIVTGNDEKA FEVNPQGVLL TSSAIKRKEK DHYLLQKVA DNGKPLSSL TYIDIRVIEE 3540
 SIYPPAILPL EIFITSSGEE YSGGVIGKI ATDQDVYDTL TYSLDPOMDN LFSVSSSTGK 3600
 LIAHKKLDIG QYLLNVSTVD GKFTTVADIT VHIRQVTQM LNHTIAIRFA NLTPESEFVD 3660
 YWRNQRSLR NILGVRNDI QIVSLQSEP HPHLDVLLFV EKPGSAQIST KQLLHKINS 3720
 VTDIEEYIGV RILNVFQKLC AGLDCPWKFC DEKVSVDSEV MTHSTARLS FVTPRHHRAA 3780
 VCLCKEGRCP PVHGCEDDP CPEGSECVSD FWEKHTCVC PSGRFGQCPG SSMMLTNGS 3840
 YVKYRLTENE NKLEMKLTMR LRTYSTHAVV MYARGTDYSI LEIHGRLQY KFCGSGPGI 3900
 VSVQSIQVND GQWHAVALVE NGNYARLVLD QVHTASGTAP GTLKTNLNLDN YVFFGGHIRQ 3960
 QGTRHGRSTQ VGNFRGCMO SIYNGQELP LNSKPRSYAH IEESVDVSPG CFLTATEDCA 4020
 SNPCQNGVC NPSPAGGYC KCSALYIGTH CEISVNPCCS NPCLYGGTCV VDNGGFVQC 4080
 RGLYTQGRQ LSPYCKDEPC KNGGTCFDSL DGAVCQCDG FRGERCQSDI DECSGNPCLH 4140
 GALCENTHGS YHCNCSHEFR GRHCEAAPN QYVSTPNWIG LABGIGIVVF VAGIFLLVV 4200
 FVLCKMIRSR KKHQAEPKD KHLGPATAPL QRPYFDSKLN KNIYSDIPPQ VPVRPISTY 4260
 SIPEDSRNML DRNSFEGSAI PEHPEFSTFN PESVHGHRKA VAVCSVAPNL PPPPPNSPS 4320
 DSDSIQKPSW DFDYDTKVVD LDPCLSKKPL BEKPSQPYSA RESLSEVQSL SSFQSESCDD 4380
 NGYHWDTSW MPSVPLFDIQ EFPNYEVIDE QTPLYSADPN AIDTDYYPGG YDIESDFPPP 4440
 PEDFPAADEL PPLPPEFSNQ FESIHPPRDM PAAGSLGSSS RNRQRFNLNQ YLPNFYPLDM 4500
 SEPTKTGTGE NSTCREPHAP YPPGYQRHFE APAVESMPMS VYASTASCSD VSACCEVESE 4560
 VMMSDYESGD DGHFEVTTIP PLDSQQHTEV 4590

Seq ID NO: C376 Protein Sequence
 Protein Accession #: NP_055035.1

1 11 21 31 41 51
 1 MCYKGCARCI GHSVLGLALL CIAANILLYF FNGETKYASE NHLRFRVWFF SGIVGGGLLM 60
 55 LLPAFVPIGL EQDDCCGCG HENCGKRCAM LSSVLAALIG IAGSGYCVIV AALGLABGPL 120
 CLDSLQWNY TPASTEGQYL LDTSTWSECT EPKHIVEWNV SLFSILLALG GIEFILCLIQ 180
 VINGVLGGIC GPCCSHQQY DC 202

Seq ID NO: C377 Protein Sequence
 Protein Accession #: NP_003750.1

1 11 21 31 41 51
 65 1 MSTENVEGKP SNLGERGRAR SSTFLRVVQP MFNHSIFTSA VSPAERIRF ILGEEDSPA 60
 PPQLFTELDE LLAVDGQEME WKETARWIKF EEKVEQGER WSKPHVATLS LHSLEFELTC 120
 MEKGSIMLDR EASSLPQLVE MIVDQIETG LLKPELKDKV TYTLRKHRR QTKKSNLRL 180
 ADIGKTVSSA SRMFTNPONG SPAMTHRNLT SSSLNDISDK PEKQDLKNKF MKKLPRDAA 240
 SNVLGVEVDF LDTPIAPVR LQAVMLGAL TEVVPVTFRL FILLGPKGA KSYHEIGRAI 300
 70 ATLMSEVDFH DLAAYAKDRH DLIAGIDEFL DEVIVLPPGE WDPAIRIEPP KSLPSSDKRK 360
 NMYSGGENVQ MNGDTPHDG HGGGEGDCE ELQRTGRFCG GLIKDIKKA PFFASDFYDA 420
 LNIQALSAIL FIYLATVNA ITFGGLGDA TDNMQGVLES FLGTAVSGAI FCLFAGQPLT 480
 ILSTGFLVIV FERLLNFSK DNNFDYLEFR LWIGLWSAFL CLILVATDAS FLVQYFTRFT 540
 BEGFSSLSIF IFIYDAFKDM IKLADYYPIN SNFKVGYNTL PSCTCVPPDF ANISISNDTT 600
 75 LAPEYLPMS STDMYHNTTF DWAFSLKKEC SKYQGNLVGN NCNFVVDITL MSFILELGT 660
 TSSMALKKFK TSPYPTTAR KLISDPAIL SILIFCVIDA LVGVDTFKLI VPSEFKPTSP 720
 NRGWFPVPPG ENPWVCLAA AIPALLVITL IFMDQGITAV IVNRKEKKLK KGAGYHLDLF 780
 WVALPVIACS LMALPFWAA TVISIAHIDS LKMETETSAP GEQPKFLGVR BQVVTGLVF 840
 80 ILTGLSVFMA PILKPIPMV LYGVFLYMGV ASLNGVQFMD RLKLLMLPLK HQPDFIYLRH 900
 VPLRRVHLPT FLQVCLALL WILKSTVAAT IFFVMILALV AVRKGMDYLF SQHDLSDLDD 960
 VIPEKDKKKK EDEKDKKKK GSLSDNDDSD DCPYSEKVPV IKIPMDIMEQ QPFLSDSKPS 1020
 DRERSPTFLE RHTSC 1035

Seq ID NO: C378 Protein Sequence
 Protein Accession #: NP_000949.1

1 11 21 31 41 51
 5 MSTPGVNSSA SLSFDRLNSP VTIPAVMFIF GUVGNLVAIV VLCKSRKEQK ETTFTYTLVCG 60
 LAVTDLLGTL LVSPVTIATY MKGQWPGGQP LCEYSTFILL FFSLSGLSII CAMSVERVLA 120
 INHAYFYSHY VDKRLAGLTL FAVYASNVLP CALPNMGLGS SRLQYPTDWC FIDWTTNVTA 180
 HAAYSVMYAG FSSFLILATV LCNVLVCGAL LRMHRQPMRR TSLGTBQHEA AAAASVASRG 240
 HPAASPALPR LSDFRRRRSF RRIAGAEIQM VILLIATSLV VLICSIPLVV RVFVNQLYQP 300
 SLEREVSQNP DLQAIRIASV NPILDPMIYI LLRKTIVLSKA IEKIKCLPCR IGGSRRRERSG 360
 10 QHCSDSQRTS SAMSGHSRSP ISRELKBISS TSQTLLPDLS LPDLSENGLG GRNLLPGVPG 420
 MGLAQEDTTS LRLTRISETS DSSQGDSES VLLVDEAGGS GRAGPAPKGS SLQVTFPSET 480
 LNLSEKCI 488

15 Seq ID NO: C379 Protein Sequence
 Protein Accession #: NP_002650.1

1 11 21 31 41 51
 20 MGHPPILLPLL LLLHTCVPAS WGLRCMQCKT NGDCRVEECA LGQDLCRTTI VRLWBEGEEL 60
 ELVEKSCTHS EKTNRITLSYR TGLKITSLTE VVCGLDLCNQ GNSGRAVTYS RSRYLECISC 120
 GSSDMSCERG RQSLQCRSP EEQCLDVVTH WIQEGEEGRP KDRHLRGCQ YLPGCFGSNG 180
 FHNNDTFHFL KCCNTTKCNE GPILLEENLP QNGRCYSCK GNSHGCSSE ETLIDCRGP 240
 MNQCLVATGT HEPKQSYMV RGCATASMCQ HAHLGDAFSM NHIDVSCCTK SGCNRPDLGV 300
 25 QYRGAAPQP GPAHLSTTIT LLMTARLMGG TLLWT 335

25 Seq ID NO: C380 Protein Sequence
 Protein Accession #: BAB55406.1

1 11 21 31 41 51
 30 MDEFSGQVDP LASVILPPNL LENLSPEDSV LVRRQAFTFF NKTGLFQDVG PQRKTLVSYV 60
 MACSIGNITI QNLKDPVQIK IKHTRTQEVH HPICAFWDLN KNKSPGGWNT SGCVAHRDSD 120
 ASETVCLQNH FTHPGVMDL PRSASQLDAR NTKVLTPISY IGCGISAIYS AATLLTYVAF 180
 35 EKLRRDYPK ILMNLSTALL FLNLLFLLDG WITSPNVLDG CIAVAVLLHF FLATPTWVG 240
 LEAHHMYAL VKVFNTYIRR YILKFCIIGW GLPALVVSUV LASRNNNEVY GKESYKKEKG 300
 DEFQNIQDPV IFYVTCAGYF GVMFFNLIAM FIVVMVQICG RNGKRNRITL REEVLRNLS 360
 VVSLTFLLGM TWGFAFFAWG PLNIPFMYLF SIFNSLQGLF IFIFHCAMKE NVQKQMRRL 420
 CQGRFRLADN SDWSKTATNI IKKSSDNLKG SLSSSSISGN STYLTSKSKS SSTTYFKRNS 480
 40 HTDNVSYEHS FNKSGSLRQC FHGQVLVKTG PC 512

40 Seq ID NO: C381 Protein Sequence
 Protein Accession #: NP_000565.1

1 11 21 31 41 51
 45 MTVARPSVPA ALPLLGLPRL LLLVLLCLP AVWGDCGLPP DVPNAQPALE GRTSFPEDTV 60
 ITYKCESEFV KIPGEKDSVI CLKGSQWSDI EFCNRSCEV PTRLNSASLK QPYITQNYFP 120
 VGTVVEYECR PGYRRBPSSL PKLTCLQNLK WSTAVEPCKK KSCPNPGBIR NGQIDVPGGI 180
 50 LFQATISFSC NTQYKLPGST SSPCLISGSS VQWSDPLPEC REIYCPAPPQ IDNGIIQGER 240
 DHYGYRQSVT YACNKGFTMI GEHSIYCTVN NDEGEWSGPP PECRGKSLTS KVPPTVQKPT 300
 TVNVPTTEVS PTSQKTTTIT TTPNAQATRS TPVSRTTKHF HETTPNKQSG TTSQTTRLLS 360
 GHTCFTLTGL LGTLVTNGLL T 381

55 Seq ID NO: C382 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 60 MDTSLRLGVLL SLPVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60
 PSNLSVFTSY LDLSMNNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLN 120
 LQNNQLRHVP TEALQNLRLS QSLRLDANHI SYVPPSCPSG LHSRLHMLD DNALTEIPVQ 180
 AFRSLALQA MTLALNKHIIH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLTLD 240
 LNNNLDDEFF TAIRTLNLSK ELHFYDNPIQ FVGRSAFQHL PELRTLTNG ASQITEPDL 300
 65 TGTANLESLL LTGAQISLPL QTVCNQLPNL QVLDLSYNLL EDLPSEFSVQ KLQKIDLRHN 360
 EIYEIKVDTF QLLSLRLSLN LAWNKIAIHH PNAFTLPSL IKDLSSNLL SSFPTGLHG 420
 LTHLKLGNH ALQSLISSEN FPFLKVIEMP YAYQCCAFGV CENAYKISNQ WNKGDNSMD 480
 DLHKKDAGMF QAQDERDLED PLLDFEEDLK ALHSVQCSFS PGFFKPCEHL LDGWLIRIGV 540
 WTIIVLALTC NALVTSTVPR SPLYISPIKL LIGVIAAVNM LTGVSSAVLA GVDAPTFGSF 600
 70 AREGAWENG VGCHVIGFLS IFASESSVFL LTLAALERG SVKYSKAPET KAPFSSLRVI 660
 ILLCALLALT MAAVPLGGS KYGASPLCLP LPFGEPTMG YMVALLILNS LCFIMMTIAY 720
 TKLYCNLDKG DLENIWDCSM VKHIALLLFT NCILNCPVAP LSPSSLINLT PISPVEIKFI 780
 LLVVVPLPAC LNPLLYILFN PHFKEDLVSL RKQTYVWTRS KHPSLMSINS DDVEKQSCDS 840
 TQALVTFTSS SITYDLPPSS VPSPAYPVTE SCHLSSVAFV PCL 883

75 Seq ID NO: C383 Protein Sequence
 Protein Accession #: NP_003658.1

1 11 21 31 41 51
 80 MDTSLRLGVLL SLPVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60
 PSNLSVFTSY LDLSMNNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLN 120
 LQNNQLRHVP TEALQNLRLS QSLRLDANHI SYVPPSCPSG LHSRLHMLD DNALTEIPVQ 180
 AFRSLALQA MTLALNKHIIH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLTLD 240
 LNNNLDDEFF TAIRTLNLSK ELGPHSNNIR SIPEKAPVGN PSLITTIHFYD NPIQFVGRSA 300

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FOHLPELRLT TLNGASQITE FFDLTGTANL ESLTLTGAQI SSLPQTVCNQ LPNLQVLDLS 360
YNLEEDLPSP SVCCQKQKID LRHNEIYBIK VDTFQQLLSL RSLNLAWNKI AIHPNAPST 420
LPSLIKLDLS SNLSSFPPI GLHGLTHLKL TGNHALQSLI SSENFPPELV IEMPAYQCC 480
AFGVCENAYK ISNQWNGKDN SSMDDLHKKD AGMPQAQDER DLEDPLDPE EDLKALHSVQ 540
CSPSPGPFPR CEHLDDGLI RIGVNTIAVL ALTGNALVTS TVFRSPLYIS PIKLLIGVIA 600
AVNMLTGVS AVLAGVDAFT FGSFARHGAW WENGVGCHVI GFLSIFASES SVFLTLAAL 660
ERGPSVKYSA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGSSKYGASP LCLPLPPGEP 720
STMGYMVALI LLNSLCFIMM TIAYTKLYCN LDKGDLENIV DCSMVKHIAL LLFTNCILNC 780
PVAFSPSSL INLTIFISPEV IKFILLVVVP LPACLNPLLY ILFNPHFKED LVSLRKQTYV 840
WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PPSSVPSPAY PVTESCHLSS 900
VAFVPC 907

Seq ID NO: C384 Protein Sequence
Protein Accession #: NP_003497.1

1 11 21 31 41 51
MEMPTFLITC IFPLLRGHS LFTCEPITVP RCMQKAYNMT FFPNLMGHYD QSIAAVEMEH 60
FLFLANLECS PNLETFLCKA FVPTCIEQIH VVPPCRKLCE KVSQDCKLI DTFGIRWPEE 120
LECDRLQYCD ETVPTTFDPH TEFGLGPKKT EQVQRDIGFW CPRHLKTSQG QGYKPLGIDQ 180
CAPPENMYF KSELEFAKS FIGTVSIFCL CATLPTFLT LIDVRRFRYP ERPIIYVSVC 240
YSIVSLMYFI GFLLDGSTAC NKADEKLELG DTVVLGSQNK ACTVLFMLLY FFMAGTVWV 300
VILTTWFLA AGRWKSCAI EQKAVWFHAV AWGTPGFLTV MLLALNKVEG DNISGVCFVG 360
LYDLASRYF VLLPLCLCVF VGLSLLLAGI ISLNHVRQVI QHDGRNQEKL KKFMRIGVF 420
SGLYLVPLVT LLGCYVYEQV NRITWEITWV SDHCRQYHIP CPYQAKAKAR PELALFMKY 480
LMTLIVGISA VFVVGSKKTC TEWAGFFKRN RKRDPISER RVLQESCEFF LKHNSKVHKH 540
KKHYKPSHK LKVISKSGT STGATANHGT SAVAITSHDY LGQETLTETI TSPETSMREV 600
KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD 660
TGLAQSNLIQ VPSSEFSSL KGSTSLLVHP VSGVRKEQGG GCHSDT 706

Seq ID NO: C385 Protein Sequence
Protein Accession #: NP_000573

1 11 21 31 41 51
MRIAIVICFL LGITCAIPVK QADSGSSEK QLYNKYPDAV ATWLNPDPSQ KQNLAPQTL 60
PSKSNESHSH MDDMDDEDD DHVDSQDSID SNDSDDVDDT DSDHQSDSH HSDESEDLVT 120
DFPTDLPATV VFTPVVPTVD TYDGRGDSV YGLRSKSKKF RRPDIQYPA TDEDITSHME 180
SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDQS AEHSHKQSR LYKRKANDES 240
NEHSDVIDSQ ELSKVSREFH SHEPHSHEDM LVVDPKSKEE DKHLKFRISH ELDSASSEVN 300

Seq ID NO: C386 Protein Sequence
Protein Accession #: NP_002812

1 11 21 31 41 51
MGAARGSPAR PRLPLLSVL LLPLLGQTQT AIVFIKQPS QDALQRRAL LRCEVEAPGP 60
VHVYWLDDGA PVQDTERFPA QGSSLSFAAV DRLQDSGTFQ CVARDDVTGE BARSANASFN 120
IKWIEAGPVV LKHPASEABI QPQTQVTLRC HIDGHPRTY QWFRDGTPLS DGQSNHTVSS 180
KERNLTLRPA GPEHSGLYSC CAHSAFGQAC SSQNTFLSIA DESFARVVLA PQDVVVARVE 240
EAMFHQPSA QPPPSLQWLF EDETPITNRS RPPHLRRATV FANGSLLLTQ VRPRNAGIYR 300
CIGQGQRPPI IILEATLHIA EIEDMPLFEP RVFTAGSEER VTCLPPKGLP EPSVWWEHAG 360
VRLPETHGRVY QKGHELVLAN IAESDAGVYT CHAANLAGQR RQDVNITVAT VPSWLKQPD 420
SQLEEGKPGY LDCLTQATPK PTVVWYRNQM LISEDSRFEV PKNGTILRNS VEVDGTWYR 480
CMSSTPAGSI EAQARQVLE KLKFTPPQP QCCMEFDKRA TVPCSATGRE KPTIKWERAD 540
GSSLPFWVD NAGTLHFAFR TRDDAGNYTC IASNGPQQI RAHVQLTVAV FITPKVEPER 600
TTVYQGHIAL LQCEAQGDPR PLIQWKGKDR ILDPKLGPR MHIFQNGSLV IHDVAPEDSG 660
RYTCIAGNSC NIKHTEAPLY VVDKPVPEBS EGPGSPPPYK MIQTIGLSVG AAVAYILAVL 720
GLMEYCKKRC KAKRLQKPE GEPEMECLN GGPLQNGQPS AEIQEEVALT SLGSGPATN 780
KRHSTSDKMH FPRSSLPIT TLGKSEFGEV FLAKAQGLEB GVAETLVLVK SIQTKDEQQQ 840
LDPRRELEMF GKLNHANVVR LLGLCREAEP HYMVLEYVDL GDLLQFLRIS KSKDEKLKSK 900
PLSTKQKVAL CTQVALGMEH LSNNRFVHKD LAARNCLVSA QRQVKVSALG LSKDVYNSEY 960
YHFRQAWVPL RWMSPEAILE GDFSTKSDVW AFGVLMWEVF THGEMFEGGQ ADDEVVLADLQ 1020
AGKARLPQPE GCPKSLYRLM QRCWALSFKD RPSFSEIASA LGDSTVDSKP 1070

Seq ID NO: C387 Protein Sequence
Protein Accession #: NP_002300.1

1 11 21 31 41 51
MKVLAAGVVP LLLVLHWKHG AGSPLPITPV NATCAIRHPC HNNLMNQIRS QLAQLNGSAN 60
ALFILIYTAQ GEPPFNNDK LCGPNVTDFF PPHANGTEKA KLVELYRIVV YLSTSLGNIT 120
RDQKILNPSA LSLHSLKINAT ADILRGLLSN VLCRLCSKYH VGHVDVITYGP DTSGKDVFK 180
KILGCOLLKG YKQIIVAVLAQ AF 202

Seq ID NO: C388 Protein Sequence
Protein Accession #: XP_097508

1 11 21 31 41 51
MGRPRLTLVC HVSIIISARD LSMNNLTQL PGLFHHLRFL EELRLSGNHL SHIPGQAFSG 60
LYSLKILMLQ NNQLGIPAE ALWELPSLQS LRLDANLISL VPERSFEGLS SLRHLWLDN 120
ALTEIPVRAL NNLPAIQAMT LALNRISHIP DYAFQNLISL VVLHLENRI QHLGTHSFEG 180
LHNLLETDLN YNKIQEFPVA IRTLGRIQEL GFHNNNIKAI PEKAFMGNPL LQTHFYDNP 240

5 IQPVGRSAFO YLPKLHTLSL NGAMDIQEFPL DLKGTTSLEI LTLTRAGIRL LPSGMCQQLP 300
 RLRVLELSHN QIEELPSLHR CQKLEELGLQ HNRIMEIGAD TFSQLSSLOA LDLSWNAIRS 360
 IRPEAFSTLE SLVKLDELTON QLTTLFLAGL GGLMHLKLG NLALSQAFSK DSFPKLRILE 420
 VPYAYQCCPY GMCASFPAKAS QMWEARDLHL DDESSSKRPL GLLARQAENH YDQDLDELQL 480
 EMEDSKPHPS VQCSPTPGPF KPCEYLFESW GIRLAVMAIV LLSVLNGLV LLTVFAGGPFV 540
 PLFPVKPVVG AIAGANTLTG ISCGLLASVD ALTFQGFSEY GARWETGLGC RATGFVAVLG 600
 SEASVLLLT AAVQCSVSVS CVRAYGKSPS LGSVRAGVLG CLALAGLAAA LPLASVGEYG 660
 ASPLCLPYAP PEGQPAALGF TVALVMNSF CFLVVAGAYI KLYCDLPRGD FEAVMDCAMV 720
 10 RHVAWLIFAD GLLYCPVAPL SFASMLGLFP VTPEAVKSVL LVVLPPLACL NPLLYLLFNP 780
 HFRDDLRLRL PRAGDSGLA YAAAGELEKS SCDSTQALVA FSDVDLILEA SEAGRPPGLE 840
 TYGFPVSTLI SCQPGAPRL BGSHCEVEEG NEFGNPQPSM DGBLLLRABG STPAGGGLSG 900
 GGGFQPSGLA FASHV 915

15 Seq ID NO: C389 Protein Sequence
 Protein Accession #: NP_570901

20 1 11 21 31 41 51
 MASLVSELEL LLLAVLVVTA TASPPAGLLS LITSQQCALD QEALGGLINT LADRVHCTNG 60
 PCGKCLSVED ALGLGEPEGS GLPPGPVLEA RYVARLSAAA VLYLSNPEGT CEDTRAGLWA 120
 SHADHLLALL ESPKALTPLG SWLLQRMQAR AAGQTFKTAC VDIPQLLEEA VGAGAPGSAG 180
 GVLAAALLDV RSGSCFHALP SPQYFVDFVF QQHSSEVFMT LAELSALMQR LGVGREAHSD 240
 HSHRHQASS RDPVPLISSS NSSSVWDTVC LSARDVMAAY GLSEQAGVTP BAWAQLSPAL 300
 25 LQQQLSGACT SQSRPPVQDQ LSQSERLYLG SLATLLICLC AVFGLLLTC TGCGRVARIYI 360
 LQTFLSLAVG ALTGDVAVHL TPKVLGLHSH SEGLSPQPT WRLLAMLAGL YAFFLFFENLF 420
 NLLLPDPED LEDGFCGHSS HSHGHSHGV SLQAPSELR QPKPREGSR ADLVAESPE 480
 LLNPEPRRLS PELRLPYMI TLGDVHNFA DGLAVGAAPA SSWKTGLATS LAVFCHELPH 540
 ELGDFALHL AGLSVRQALL LNLASALTAF AGLYVALAVG VSESEBAIL AVATGLFLYV 600
 30 ALCDMLPAML KVRDPRPWL FLHNVLGLL GWTVLLLSL YEDDITP 648

35 Seq ID NO: C390 Protein Sequence
 Protein Accession #: NP_061844

40 1 11 21 31 41 51
 MANASEPGGS GGGEAAALGL KIATLSLLLC VSLAGNVLPA LLIVRERSLH RAPPYLLLDL 60
 CLADGLRALA CLPAVMLAAR RAAAAAGAPP GALGCKLLAF LAALFCFHAA FLLLVGVVTR 120
 YLAIAHRFPY AERLAWPCA AMLVCAANAL ALAAAPFPVL DGGDDDEDAP CALEQRPDGA 180
 PGALGFLLL AVVVGATHLV YLRLLFFIHD RRMKRPARLV PAVSHDWTFH GPGATQAAAA 240
 45 NWTAGFGRGP TTPALVGIRP AGPGRGARRL LVLEEFKTEK RLCKMFYAVT LLFLLWGPY 300
 VVASYLRLV RPAVQPAYL TASVWLTFAQ AGINPVVCFPL FNRELDRCFR AQFPCCQSPR 360
 TTQATHPCDL KGIGL 375

50 Seq ID NO: C391 Protein Sequence
 Protein Accession #: NP_005622

55 1 11 21 31 41 51
 MAAARPARGP ELPLGLLLLL LLLGDPGRGA ASSGNATPGP PRSAGGSARR SAAVTGPPPP 60
 LSHCGRAAPC EPLRVNVCGL SVLPYGATST LLAGDSDSQE BAHGKLVLS GLRNAPRCWA 120
 VIQPLLCAVY MPKCENDRVE LPSRTLQCAT RGPCAIVERE RGWDFLRCT PDRFPEGCIN 180
 EVQNIKFNSS QCCEVPLVRT DNPKSWEDEV EGCGIQCCNP LFTBAHQDM HSYIAAFGAV 240
 TGLCTLPTLA TFVADWRNSN RYPAVILFYV NACFPVGSIG WLAQFMDGAR REIVCRADGT 300
 60 MRLGEPTNE TLSCVIFVI VYALMAGVW WFWVLTAYNH TSFKALGTTY QPLSGKTSYF 360
 HLLTWSLPFV LTVAILAVAQ VDGDVSGIC FVGKYNRYR AGFVLAPIGL VLVGGYFLI 420
 RGVMTLPBKI SNHPGLLSEK AASKINETML RLIGIPGLAP GFVLITFSCH PYDFPNQAEW 480
 ERSFRDYVLC QANVTIGLPT KQIPDCEIK NRPGLLVEKI NLFAMFGTGI AMSTWVWTKA 540
 TLLIWRRTWC RTGQSDDEP KRIKSKMIA KAFSKREHLL QNPQQLSFS MHTVSHDGPV 600
 65 AGLAFDLNRP SADVSSAWAQ HVTMVARRG AILPDISVT PVATPVPPPE QANLWLVBAE 660
 ISPELQKRLG RKKKRRKRRK EVCPLAPPE LHPPAPAPST IPRLPQLPRQ KCLVAAGAWG 720
 AGDSCRQGAN TLVSNPFCPE PSPPDQFFLP SAPAPVAWAH GRRQQLGPIH SETNLMDET 780
 MDADSDP 788

70 Seq ID NO: C392 Protein Sequence
 Protein Accession #: BAC04382

75 1 11 21 31 41 51
 MGARSARGA LLLALLLWCD PRLSQAGRKR SGEVLDPDSFP SAPAEPLPYF LQEPQDAYIV 60
 KNPVELRCR APPATQIYFK CNGEWSQND HVTQEGLEDA TLGARGGLRV REVQIEVSRQ 120
 QVEELFGLD YWCQCAWSS AGTKSRRAY VRIAYLRKNF DOEPLGKEVP LDHEVLLQCR 180
 PPEGVPAEV EWLKNEVDID PTQDTNFLT IDHNLIRQA RLSDTANYTC VAKNIVAKRR 240
 STTATVIVV NGWSSWAEW SPCSNRCGRG WQKTRTCTN PAPLNGGAF C EQAQPQRTAC 300
 80 TTICFVDGAW TEWSKWSACS TECAHWSRE CNAPPPQNGG RDCSGTLLDS KNCDTGLCMQ 360
 NKRTLSDFNS HLEASGDA LYAGLVVAIF VVAILMAGV VVVYRRNCRD FDTDITDSSA 420
 ALTGGPHFVN FKTRARPENQ LHPSPVPDL TASAGIYRGV VYALQDSTDK IPMTNSPLLD 480
 FLPSLKVVEY SSSTTSGSPG LADGADLLGV LPPGTYPSPD ARDTFLHLR SASLGSQQLL 540
 GLPRDPGSSV SGTFGCLGGR LSIPGTGVSL LVPGNAIPQG KPYEMYLLIN KAESTLPLSE 600
 GTQTVLSPV TCGPTGLLLC RPVILTMFHC AEVSARDWIP QLKTOAQGH WEEVVTLDSE 660
 TLNTPCYCQL EPRACHILL QLGTVVPTGE SYRSBAVKRL QLAVFAPALC TSLEYSLRVY 720
 CLEDTFVALR EVLBLERTLG GYLVEEPKPL MFKDSYHNLR LSLHDLPHAH WRSKLLAKYQ 780
 BIPFYHIWSG SQKALHCTPT LERHSLASTE LTCKICVRQV EGEGQIPQLH TTLAETPAGS 840
 LDTLCSAPGS TVTQLGPYA FKIPLSIRQK IONSILDAFNS RGNDRWMLAQ KLSMDRYLNY 900
 FATKASPTGV ILDLWEALQQ DDGDLNSLAS ALBEMKSEM LVAVATGDGC 950

Seq ID NO: C393 Protein Sequence
Protein Accession #: NP_004616

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5      1      11      21      31      41      51
|      |      |      |      |      |
MNRKARRCLG HLFSLGVMV LRIGGFSSVV ALGASTICNK IPGLAPRQRA ICQSRPDAIL 60
VIGEGSQMGL DECCQFQFRNG RWNCSALGER TVFGKELKVG SREAAPTYAI IAAGVAHAIT 120
AACTQGNLSD CGCKEKQGG YHRDEGKWKW GCSADIRYGI GFAKVFPDAR EIKQNARTLM 180
10     NLHNEAGRK ILEENMKLEC KCHGVSGSCT TKTCTWTLFQ FRELGYYLKD KYNEAVHVEP 240
VRASRNKRPV FLKIKKPLSY RKPMDTDLVY IEKSPNYCEE DPVTGSGVTQ GRACNKTAPO 300
ASGCDLMCCG RGYNTHQYAR VHQCNCKFWH CCYVKQNTCS ERTENYTKC 349

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Seq ID NO: C394 Protein Sequence
Protein Accession #: NP_003777

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15     1      11      21      31      41      51
|      |      |      |      |      |
MDALCGSGEL GSKFWDNLS VHTENPDLT CPQNSLLAWV PCIYLWVALP CYLLYLRRHC 60
20     RGYIILSHLS KLMVGLVLL WCVSWADLFY SPHGLVHGRA PAPVFPVTPV VVGVTMLLAT 120
LLIYERLQGG VQSSGVLIIF WFLCVVCAIV PFRSKILLAK AEGEISDPFR FTFYIHFAL 180
VLSALILACF REKPPPPSAK NVDPNPYPET SAGFLSRLEFF WFTKMAIYG YRHPLEEKDL 240
WSLKEEDRSQ MVVQQLLEAW RKQEKQTARH KASAAPGKNA SGEDEVLLGA RPRPKPSFL 300
KALLATFGSS FLISACFKLI QDLISFINPQ LLSILIRFIS NPMAPSWWGF LVAGLMFLCS 360
25     MMQSLILQHY YHYIFVTGVK FRTGIMGVIY RKALVITNSV KRASTVGETV NLMASVDAQRF 420
MDLAPFLNLL WSAPIQLILA IYPLWQNLGP SVLAGVAFMV LLIPLNGAVA VKMRAFQVKQ 480
MKLWDSRIKL MSBILNGIKV LKLYAWEPSE LKQVEGIRQG ELQLLRTAAY LHTTTFTTWM 540
CSPFLVTLIT LNVVYVVDPN NVLDAEKAFV SVSLFNILRL PLNMLPOLIS NLQASVSLK 600
RIQQLSQEE LDPQSVERIT ISPGYAITIH SGTFTNAQDL PPTLHSLDIQ VPKGALVAVV 660
30     GPVCGGKSL VSAALGEMEK LEGKVHMKGS VAYVQQAWI QNCTLQENVL PGKALNPKRY 720
QQTLEACALL ADLEMLPGGD QTEIGEKGIN LSGGQRQVRS LARAVYSDAD IFLDDPLSA 780
VDSHVAKHIF DHVIGPEGVL AGKTRVLVTH GISFLPQTFD IIVLADGQVS EMGPYPALLQ 840
RNGSFANFLC NYAPDEDQGH LEDSWTALEG AEDKEALLIE DTLSNHTDLT DNDPVTVVWQ 900
KQFMRLQSLAL SSDGEGGGRP VPRRHLPSE KVQTEAKAD GALTQEEKAA IGTVELSVFV 960
35     DYAKAVGLCT TLAICLLYVG QSAALIGANV WLSAWTNDAM ADSRQNTSL RLGVYAALGI 1020
LQGLVLMMAA MAMAAGIOA ARVLHQALLH NKIRSPQSFF DTPSGRIILN CFSKDIYVVD 1080
EVLAFVILML LNSFNAIST LUVIMASTPL FTVVILPLAV LTYLVORFYA ATSRQLKRL 1140
SVSRSPYISH FSETVTGASV IRAYNRSRDF EIIISDTKVA NQSCYPYII SNRWLSIGVE 1200
FVGNCVLVFA ALFAVIGRSS LNPGLVGLSV SYSLQVTFAL NNMIRMSDLS ESNIVAVERV 1260
40     KEYSKTETEA PWVVGSRPP EGWPPRGEVE FRNYSVRYRP GLDLVLRDLS LHVHGGEKVG 1320
IVGRTGAGKS SMTLCFLRIL EAKGEIRID GLNVADIGLH DLRSQLTIIIP QDPILPSGTL 1380
RMNLDPFGSY SEEDINWALE LSHLHTFVSS QPAGLDQFCS EGGENLSVQG RQLVCLARAL 1440
LRKSRILVLD BATAAIDLET DNLIQATIRT QFDTCTVITI AHRILNTIMDY TRVLVLDKGV 1500
45     VAEFDSANL IAARGIFYGM ARDAGLA 1527

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Seq ID NO: C395 Protein Sequence
Protein Accession #: NP_004617

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50     1      11      21      31      41      51
|      |      |      |      |      |
MRARPQVCEA LLFALALQTG VCYGIKWLAL SKTFSALALN QTQCKQLEG LVSAQVQLCR 60
SNLELMHTVV HAAREVMKAC RRAFADMWVN CSSIELAPNY LLDLERTRE SAFVYALSA 120
AISHAIARAC TSGDLPGSCS GPVPGEPGP GNRNGGCADN LSYGLMGAK FSDAPMKVK 180
TGSQANKLMR LHNEVGQA LRASLEMKCK CHGVSGSCSI RTCKWGLQEL QDVAADLKTR 240
55     YLSATKVVRH PMGTRKHLVP KDLDIRPVKD SELVYLQSSP DFCMKNEKVG SHGTODRQCN 300
KTSNGSDSCD LMCCGRGYNP YTDVVERCH CKYEWCCYVT CRRCERTVER YVCK 354

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Seq ID NO: C396 Protein Sequence
Protein Accession #: NP_114072

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60     1      11      21      31      41      51
|      |      |      |      |      |
MEMGYLLEVT SLLAALALLQ RSSGAAAASA KELACQBITV PLCKGIGYNY TYMPNQFMHD 60
TQDEAGLEVH QFWPLVEIQ SPDLKFFLCS MYTPICLEDY KKPLPPCRSV CERAKAGCAP 120
LMRQYGFAMP DRMRCDRLPE QGNPDTLCDM YNRTDLTTAA PSPRRLPFP PPGEQFSGS 180
GHGRPPGARF PHRGGRGGG GGDAAAPPAR GGGGGKARP PGGAAPCEP GCQCRAPMV 240
VSSERHPLYN RVKTQIANC ALPCHNPFPS QDERAFTVFW IGLWSVLCFV STFATVSTPL 300
IDMERFKYPE RPIIFLSACY LFVSVGYLVR LVAGHEKVAC SGGAPGAGGA GGAGGAAAGA 360
GAAGAGAGGP GGRGEYEEGL AVEQHVRYET TGPALCTVVF LLVYFFGMAS SINWVLSLT 420
70     WFLAAGMKNG NEALAGYSQY PHLAANLVPS VKSIAYLALS SVDGDPVAGI CYVGNQSLDN 480
LRGEVLAPLV IYLFITMPL LAGFVSLFRI RSVIKQDGP TKYHKLKLM IRLGLFTVLY 540
TVPAAVVAC LFYEQRNRP WEATHNCPL RDLQPDQARR PDYAVFMKY FMCLVVGITS 600
GVWVWSGKTL ESWRSLCTRC CWASKGAAGV GGAGATAAGG GGGPGGGGG GPGGGGGPGG 660
75     GGGSLYSDVS TGLTWSGTA SSVSYPPQMP LSQV 694

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Seq ID NO: C397 Protein Sequence
Protein Accession #: XP_050625

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80     1      11      21      31      41      51
|      |      |      |      |      |
MLQGGPSLLL LFLASHCLG SARGLELFGQ PDFSYKRSNC KPIPANLQLC HGIEYQNMRL 60
PNLLGHETMK EVLEQAGAWI PLVMKQCHPD TKKFLCSLFA PVCLDDDET IQPCHSLCVQ 120
VKDRCAVMS AFGFPWPDML ECDRFPQDND LCIPLASSDH LLPATERAPK VCEACKNKND 180
DDNDIMETLC KNDPALKIKV KBITYINRDT KIILETKSKT IYKLVGVSER DLKKSVLWLK 240

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DSLQCTCEEM NDINAPYLVM GQKQGGELVI TSVKRWQKGQ REFKRISRSI RKLQC 295

Seq ID NO: C398 Protein Sequence
Protein Accession #: NP_001297.1

5
10
1 11 21 31 41 51
MSMGLBITGT ALAVLGLWGT IVCCALPMWR VSAPIGSNII TSQNIWEGWL MNCVVQSTGQ 60
MQCKVYDLSL ALPQDLQAAR ALIVVAILLA AFGLLVALVG AQCTNCVQDD TAKAKITIVA 120
GVLFLLAALL TLVPVWSAN TIIRDFYNFV VPEAQKREMG AGLYVGWAAA ALQLLGGALL 180
CCSCPPEKK YTATKVVYSA PRSTGPGASL GTGYDRKDYV 220

Seq ID NO: C399 Protein Sequence
Protein Accession #: NP_036581.1

15
20
1 11 21 31 41 51
MESRKDITNQ EELWKMKPRR NLEEDDYLHK DTGETSMLKR FVLLHLHQTA HADEFDCPSE 60
LQHTQELFPQ WHLPKIAAAI IASLTFLYTL LREVIHPLAT SHQQYFYKIP ILVINKVLPM 120
VSITLLALVY LFGVIAAIVQ LHNGTKYKFP PHWLDKMWLT RKQFGLLSFF FAVLHAIYSL 180
SYPMRRSYRY KLLNWAYQQV QQNKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS 240
VSDSLTWREP HYIQSKLGIV SLLLOTIHAL IFAMNWKIDI KQFVWYTPPT FMAVFLPIV 300
VLIFKSLFLP CLRRKKILKI RHGWEDVTKI NKTEICSQL 339

Seq ID NO: C400 Protein Sequence
Protein Accession #: NP_001766.1

25
30
1 11 21 31 41 51
MANCEFPFVS GDKPCCRLSR RAQLCLGVSI LVLILVVVLA VVPRWRQTW SGPGTTKRFP 60
ETVLARCVMY TEIHPEMRHV DCQSVMDAPK GAFISKHPCN ITEEDYQPLM KLGQTQVPCN 120
KILLWSRIKD LAHQPTQVQR DMPTLEDTLG GYLADDLTWC GBFNTSKINY QSCPDWRKDC 180
SNNPVSVFWK TVSRFPABAA CDVVHVMLNG SRSKIFDKNS TFGSVSVHNL QPEKVVQTLA 240
WVIHGGREDS RDLQCDPTIK ELESIIKRN IQPSCNITYR PDKFLQCVKN PEDSSCTSEI 300

Seq ID NO: C401 Protein Sequence
Protein Accession #: XP_120513.2

35
40
45
1 11 21 31 41 51
MVSCTFSGPL RETNENVKKF YALRAFMRM SSEAAMLGES RTPKPRKHRA TTRAKIFKRF 60
FSEGESNSR LVEELAVIHT YSDDPAPTTS PSSVQPREFG VMQAPRARF GSRTPPAAAE 120
ASSPHLGIGE AACQSGARAA APRAGARRCQ PQRQAAAAA TAQHTLPHA RTRADPAGRR 180
RRHPRSPAPG GSGTCSGPA PRRRMSEEMQ PAEGGPSVPK IYKQSPFYSV LKTFPSKRPA 240
LAKRYERPTL VELPHGLRT PAQPPPASPA ASSSSSFAAV VRLGAPPRFP RRGFRAGTI 300
PPLLAPGVA GTLLPPTTS SPPSPRPFRW HAAAPRGOTS HTHMWSQST LFGSDTMVSF 360
FGLMAQRWQV HRSLLKQFEGW ILGSGWTWPC QDWLEKEBQ VAVLLPRSEG NTAPKKSRMI 420
LDAFAQQCSR VLSLNCGGK LLDNSHSQSM ISCVKQEGSS YNERQEHCHI GKGVHSQTSF 480
NVDIEMQYMQ RKQQTSAFLR VFTDSLQNYL LSGSFPTPNP SSASEYGHIA DVDPLSTSPV 540
HTLENISLDS TASLCKSRHL SREPPVKSDF FNPLQALAG GASRPFSGAQ QSIAYRVNSE 600
LEDGIRSFVP LSCEALEMDL TSLGSKQLLN NYPVYITSKQ WDEAVNSSKK DGRLLRLYLI 660
RFVFTTDLK YSCGLGKRKR SVQSGETGPE RRPLDPVKVT CLRGTASPRS VSPSVISFHR 720
IGGSPRTSV QPSVF 735

Seq ID NO: C402 Protein Sequence
Protein Accession #: BAA92562.1

55
60
65
1 11 21 31 41 51
METTVLSGIN FEYKGMTGWE VAGDHIYTA GASDNDFMIL TLVVPGRFP QSVMDATEN 60
EVARITPVFE TICSVMCELY FMVGVNSRTN TPVETWKGSK GKQSYTYIIE ENTITSPTWA 120
PQRTTFEAS RKYTNDVAKI YSINVTVNMN GVASYCRPCA LEASDVGSSC TSCPAGYYID 180
RDSGTCHSCP PNTILKAHP YGVQACVPCG PGITNNKIHS LCYNDCTFSR NTPTRTFNIN 240
FSALANTVIL AGGFSPTSKG LKYFHHFTLS LCGNQGRKMS VCTDNVTDLE IPEGESGFSK 300
SITAYVQCAV IIPPEVTGYK AGVSSQPVSL ADRLIGVTTD MTLDGITSPA ELPHLESGLI 360
PDVIFPYRDN DVYQSCSSGR STTIRVRCSP QKTVPGSLLL PGTCSGDTCD GCMFPLMES 420
AAACPLCSVA DYHAIIVSSCV AGIQKTTYVM REPKLCSGGI SLPEQRVTIC KTIDFWLKVG 480
ISAGTCTAIL LTVLTCTYFWK KNQKLEYKYS KLVNATLKD CDLPAADSCA IMEGEDVEDD 540
LIFTSKSLP GKIKSPTSKQ PAPVTISLSE DS 572

Seq ID NO: C403 Protein Sequence
Protein Accession #: NP_055139.1

75
80
1 11 21 31 41 51
MALQGISVVE LSGLAPGRXC AMVLADFGAR VVRVDRPQSR YDVSRLGRGK RSLVLDLKQP 60
REPRAAASVQ AVCAAGALP PRCHGETPAG PRDSAAAGSK AYLCQAEWIV PVQESFCRLA 120
GHIDNYLALS GVLSKIGRSG ENPYAPLNLV ADFAGGGLMC ALGIIMALFD RTRTDKQVI 180
DANNVBGTAY LSSFLWKTQK SSLWEAPRGQ NMLDGGAPFY TTYRTADGEP MAVGAIEPQP 240
YELLIKGLGL KSDSLFNQMS TDDWPEMKKK FADVFAKTKK AEWQIFDGT DACVTPVLTF 300
EEVVHHDENK ERGSFITSEB QDVSPRLAPL LIANTPAIPSS KGDPPFIGBT EBILEBFGPS 360
REBIYQLNSD KIIESNKVKA SL 382

Seq ID NO: C404 Protein Sequence

Protein Accession #: XP_091332.1

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1      11      21      31      41      51
5      |      |      |      |      |      |
MQRNTLWAA FLTLHSAQAF PQTDISISPA LPPELPLPSLC PLFWMEFKGH CYRFFPLINKT 60
WAEADLYCSE FSVGRKSAKL ASIHSWEEHV FVYDLVNSCV PGIPADVWTG LHDHRQEGGF 120
EWTGSSSYDY SYWDGSSQPD GVDHDPDEED CVQIWRPPTS EQLQAPPEQL PLSISEATDV 180
YLPEDFPAEP KLMDQSWVSR KSLKPSKSHL MEPPTPAVAK QKAKTRHRSR RGVMWPSGKA 240
GSWKERMNAD YGRRKRSAPR QEGRLRCRER RLRAASQGR PEGQRKQRQQ ERQERGWEEL 300
GGVSPMRGAQ AQWQHGLGAGS QRGAAPCEGE NHQAPELGST WRGQRLOPQT AALCHFALRK 360
LPGNAHGLAA AFVQPALQVQ EENNRNTRFS GAYFTMSDPT CDQDSKEQSL RRHGREAED 420
GPYRLVKKKR GPVACPSSFE LQSGGEVCLD FPVELRAGTW IAREPP 466

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Seq ID NO: C405 Protein Sequence
Protein Accession #: XP_054869.2

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1      11      21      31      41      51
20     |      |      |      |      |      |
MHTCCPPVTL EQDLHRMHS WMLQTLAPAV TSLVLSCAET IDYYGEICDN ACPCEEKDDGI 60
LTVSCENRGI ISLSEISPPR FPIYHLLLSG NLLNRLYPNE FVNYTGASIL HIGSNVIQDI 120
ETGAFHGLRG LRRHLNANNK LELLRDDTFL GLENLEYLQV DYNYSIVIEP NAFGKLHLIQ 180
VLILNDNLLS SLPNMLFRFV PLTHLDLRGN RLKLLPYVGL LQHMCKVVEL QLEENPWNC 240
CELISLKDML DSISYSALVG DVVCEPFLRL HGRDLDEVSK QELCPRLIS DYEMRPQTPL 300
STTGYLHTTP ASVNSVATSS SAVYKPLKP PKQTRQPNKP RVRPTSRQPS KDLGYSNYGP 360
SIAYQTKSPV PLECPACSC NLQISDLGLN VNCQERKIES LAELQPKFYN PKKMYLTENY 420
IAVVRRTDFL EATGLDLHL GNNRISMIDQ RAFGDLTNLR RLYLNGNRIE RLSPFLFYGL 480
QSLQYLFQY NLIREIQSGT FDPVFNQLL FLNNLLQAM PSGVFSGLTL LRLNLRNHF 540
TSLPVSGLVD QLSLIQIDL HDNPNWCTCD IVGMKLVVEQ LKVGVLVDEV ICKAPKFAE 600
TDMRSIKSEL LCPDYSDDVV STTPSSIQV PARTSAVTPA VRLNSTGAPA SLGAGGASS 660
VPLSVLILSL LLVFMVSFV AAGLFLVMK RRRKNQSDHT STNNSDVSSF NMQYSVYGGG 720
GGTGHHFAH VHRGPALPK VRTPAHVYE YIPHLGHMC KNPYRSREG NSVEDYKDLH 780
ELKVYSSNH HLQQQQQPP PPQQPQQQPP PQLQLQPGEE ERRESHLRS PAYSVSTIEP 840
REDLLSPQD ADRFVRGILE PDKHCSTTPA GNSLPEYKPF PCSAPAYTFS PNYDLRRPHQ 900
YLHPGAGDSR LREPVLVSPP SAVFVEPNRN EYLELKAKLN VEPDYLEVLE KQTTFSQF 958

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Seq ID NO: C406 Protein Sequence
Protein Accession #: NP_000784.2

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1      11      21      31      41      51
40     |      |      |      |      |      |
MGILSVLLI TLQILFVFFS NCLFLALYDS VILLKHVVLL LSRKSTRGE WRRMLTSEGL 60
RCVWKSFLLD AYKQVKGED APNSSVVHVS STEGGDNNGN GTQEKIAEGA TCHLLDFASP 120
ERPLVNVFSG ATUPPPTSGL PAFRKLVEEF SSVADFLVY IDEAHPSDGN AIPGSSSLSP 180
EVKKHQHQB RCAAAQQLLE RFSLLPQCRV VADRMNNAN IAYGVAFERV CIVQRQKIAY 240
LGGKGFPSYN LQEVHRLBK RFSKRUKTR LAG 273

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Seq ID NO: C407 Protein Sequence
Protein Accession #: NP_006540.2

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1      11      21      31      41      51
50     |      |      |      |      |      |
MSSCVSQPS SNRAAPQDEL GGRGSSSSSES QKPCEALRGL SLSIHLGME SFIVVTECEP 60
GCAVDLGLAR DRPLEADQE VPLDSSGSA RPHLSGRKLS LQERSQGLA AGGLDMNGR 120
CICPSLPYSP VSSPQSSPRL PRRPTVESHH VSITGMQDCV QLNQYTLKDE IGKGSYGVVK 180
LAYNENDMTY YAMKVLKSKK LIRQAGFPFR PPPRGTAPAP GGCQIPROPI EQVQOEIAL 240
KKLDHFNVVK LVEVLDDPNE DHLVMVFLV NQGPVMEVPT LKPLSEDQAR FYFQDLIKGI 300
EYLYHQIHH RDIKPSNLLV GEDGHIKIAD PGVSNFPGS DALLNTVGT PAFMAPESLS 360
ETRKFISGKA LDVWAMGVTL YCFVFGQCPF MDERIMCLHS KIKSQALEFP QDPDIARDLK 420
DLITRMIDKN PESRIVVPEI KLHPWVTRHG AEPLPSEDEN CTLVEVTEEE VENSVKHIPS 480
LATVILVKIM IRRKSPGNPF EGSRREERSL SAPGNLLTKK PTRCESELSE LKEARQRRQP 540
PGERPAPRG GGSALVRGSP CVESCWAPAP GSPARMHPLR PEEAMEPE 588

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Seq ID NO: C408 Protein Sequence
Protein Accession #: NP_061116.2

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1      11      21      31      41      51
65     |      |      |      |      |      |
MGLSLPKEKG LILCLWSKFC RWFQRRESWA QSRDEQNLLQ QKRIWESPLL LAAKNDVQA 60
LNKLKYEDC KVRQRGAGE TALHIAALYD NLEAAMVME AAPVLVFEPM TSELYEGQTA 120
LHIAVVNQNM NLVRALLARR ASVSARATGT AFRRSPCNLI YPGEHPLSFA ACVNSKEIVR 180
LLIEHGADIR AQDSLGNLTVL HILILQPNKT FACQMYNLLS SYDRHGDLQ PLDLVFNHQQ 240
LTPFKLAGVE GNTVMFQHLM QKRKHTQWY GPLSTLYDL TEIDSSGEDEQ SLELEITTK 300
KREARQILDQ TPKVELVSLK WKRYGRPYFC MLGAIYLLYI ICTPMCCYR PLKPRNTNRT 360
SPRDNLTQQ KLLQRAYMTP KDDIRLVGEL VTVIGAIIL LVEVPDIFEM GVTFRFGQTI 420
LGGPFHVLII TYAFMVLVTM VMRLISASGE VVPMSPALVL GWCNMVYFAR GFQMLGPFTI 480
MIQKMFQEDL MRFCNLMVAV ILGFASAFYI IFQTEDPREL GHFYDYPMAL FSTFELFLTI 540
IDGPANYVD LPFMYISITYA AFALIIATLLM LNLIIAMGD THWRVAHERD ELWRAQIVAT 600
TVMLERKLEP CLWPRSGICG REYGLGDRWF LRVEDRQDLN RQRIQRYAQA FHTRGSEDL 660
KDSVEKLELG CPPSPHLSL MPSVSRSTSR SSANWERLRQ GTLRDLRGI INRGLEDGES 720
WEYQI 725

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Seq ID NO: C409 Protein Sequence
Protein Accession #: NP_068710.1

1 11 21 31 41 51
 MQKVTGLGLLV FLAGPFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSEW 60
 RSSGQAGRG WGSPPPLTTQL SPTGAKCKCK PGQKSGHHPG ETPPLITPGS AQS 113

Seq ID NO: C410 Protein Sequence
 Protein Accession #: NP_005962.1

1 11 21 31 41 51
 MQKVTGLGLLV FLAGPFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSAK 60
 CKCKPGQKSG HHPGETPPLI TPGSAQS 87

Seq ID NO: C411 Protein Sequence
 Protein Accession #: NP_004952.1

1 11 21 31 41 51
 MLSKVLPLVLL GILLILQSRV BGPQTESKNE ASSRDVVYGP QPQPLENQLL SEETKSTETE 60
 TGSRVGKLPE ASRIINTILS NYDHLKLRPGI GEKPTVVTVF IAVNSLGLPLS ILDMETITDI 120
 IFSGTYWDER LCYNDTFESL VLNQNVVSQ L WIPDTFFRNS KRTHEHEITM PNQMVRIYKD 180
 GKVLTYTIRM IDAGCSLHML RFPMDSHSCP LSPSSPSYPE NEMIKYKWFN KLEINERKNSW 240
 KLFQDFDTGV SNKTEIITP VGDFMVTIIF PNVSRFPYV AFQNYVPSSV TMLSWVSFW 300
 IKTESAPART SLGITSVLTM TILGTFSRKN PFRVSYITAL DFYLAICFVP CFCALLEFAV 360
 LNFLLIYNQTK AHASPKLRHP EINSRAHART RARSACARQ HQEAFVCQIV TTEGSDGEER 420
 PSCSAQQPS PGSPGPRSL CSKLACCEWC KRPKKYFCW PDCBGSSTWQ GRLCIHVYRL 480
 DNYSRVVPV TFFPFFNVLYW LVCLNL 506

Seq ID NO: C412 Protein Sequence
 Protein Accession #: NP_068819.1

1 11 21 31 41 51
 MEYTIIDIFS QTWYDERLCY NDTFESLVLN GNVVSQWLIP DTFPRNSKRT HEHEITMPNQ 60
 MVRIYKDGKV LYTIIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSPYENEM IYKWFNFKLE 120
 INEKNSWKLQ QDFTGVSNNK TEIITTPVGD FMVMTIFFNV SRRPGYVAFQ NYVPSSVTIM 180
 LSWVSFWIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDFY IACFVFCFC 240
 ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQB AFVCQIVTTE 300
 GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCENCKRF KKYFCMVDC EGSTWQQARL 360
 CIHVYRLDNY SRVFPVTFP FPNVLYWLVC LNL 393

Seq ID NO: C413 Protein Sequence
 Protein Accession #: NP_068822.1

1 11 21 31 41 51
 MEYTIIDIFS QTWNSKRTH HEITMFNQMV RIYKDGKVLV TIRMTIDAGC SLHMLRFPMD 60
 SHSCPLSPSS FSYPENEM IYKWFNFKLE EKNWKLQF DFTGVSNKTE IITTPVGD 120
 VMTIFFNVSR RFGYVAFQNY VPSSVTIMLS WVSFWIKTES APARTSLGIT SVLMTTLGT 180
 FSRKNFPRVS YITALDFYIA ICFVFCFCAL LEFAVLNFI YNQTAKAHSP KLRHPRINSR 240
 AHARTRARS ACARQHQB AFVCQIVTTE GSDGEERPSC QPPSPGSPE GPRSLCSKLA 300
 CCEWCKRFPK YFCMVDCBEG STWQQGRLCI HVYRLDNYSR VFPVTFPFF NVLYWLVCNL 360
 L 361

Seq ID NO: C414 Protein Sequence
 Protein Accession #: NP_068830.1

1 11 21 31 41 51
 MEYTIIDIFS QTWYDERLCY NDTFESLVLN GNVVSQWLIP DTFPRNSKRT HEHEITMPNQ 60
 MVRIYKDGKV LYTIIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSPYENEM IYKWFNFKLE 120
 INEKNSWKLQ QDFTGVSNNK TEIITTPVGD FMVMTIFFNV SRRPGYVAFQ NYVPSSVTIM 180
 LSWVSFWIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDFY IACFVFCFC 240
 ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQB AFVCQIVTTE 300
 GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCENCKRF KKYFCMVDC EGSTWQQGRL 360
 CIHVYRLDNY SRVFPVTFP FPNVLYWLVC LNL 393

Seq ID NO: C415 Protein Sequence
 Protein Accession #: NP_068591.1

1 11 21 31 41 51
 MPAVSGPGFL FCILLLLLDL HSPETGCPPL RRFYKLSFK GPRALPGAG IPFWSHHGA 60
 ILGLEVRIT PSMRNRSGAV WSRASVFFSA WEVEVQMRVT GLRRGAHGM AVWYTRGRGH 120
 VGSVLGLAS WDGIGIFPDS PAEDTQDSPA IRVLASDGI PSEQPGDGAS QGLGSCHNDF 180
 RNRPHFRAR ITYWGQRLRM SLNSGLTPSD PGFPCVDVGP LLLVPGGFFG VSAATGTLD 240
 DHVLSPLTF SLSESPFV PPFLEMQQL RLARQLEGLW ARLGLGTRED VTPKSDSEAG 300
 GEGERLFDLE ETLCRHRRIL QALRGLSKQL AQARQWKKQ LGPPQARPD GGWALDASCQ 360
 IPSTPGRGH LMSGLNDSA KVGALLHGOW TLLQALQEM DAARMAAEA QVSYLEVIGIE 420
 HHFLZLDHIL GLLQELRGP AKAAKAPRP PQQPRASSC LQGFIFLYL LIQTVGPFY 480
 VHFQELNKS LQELCTSGSL PLGPAPHTPR ALGILRRQPL PASMPA 526

Seq ID NO: C416 Protein Sequence
 Protein Accession #: XP_117036.1

1 11 21 31 41 51
 5 MERRTRGALG SRRPPPLPA LRHLCTGLQA AGMAWPGTLW RHTCQGRAXA AEGPWGLFRP 60
 HRCPREAGQA PVGPSPETQG VAHVCSRARV SVDEREPGGG AYAMHVTFRW KGCHRHSGRT 120
 VRGSVSWKRP EQAAPETGRG PAVARGSGDG NECGWG 156

Seq ID NO: C417 Protein Sequence
 Protein Accession #: XP_167803.2

1 11 21 31 41 51
 10 MPKGQRKTA TNKPGGLPGA PGVGIGGHCL YVLECKCFIK NKTKTHHHK KNFAAKRNEE 60
 15 KLGKKKKQEK KNHTKFFHHT YPLSQQDFLF AKSYFCGNPG CFLWQGLF 108

Seq ID NO: C418 Protein Sequence
 Protein Accession #: NP_079056.1

1 11 21 31 41 51
 20 MFRLVERYEM PRHEVYVLLI RNIFLKISII GILCYWLTNT VALSGEECWE TLIGQDIYRL 60
 LLMDFFVSLV NSFPLGEFLR IIGMQLITSL GLQEFDIARN VLELIYAQTL VWIGIFFCPL 120
 LPPIQMIMLE IMPYSKNISL MMNFQPPSKA WRASQMMTFF IFLFPSPST GVLCTLAITI 180
 25 WRKLPADCG PFRGLPLFIH SIYSWIDTSL TRPGYLMVVW IYRNLIQSVH PFFILTILVL 240
 IITYLWQIT EGRKIMIRLL HEQIINEGKD KMFLIEKLIK LQDMEKKANP SSLVLERREV 300
 EQQGFHLHGE HDGSLDLRSR RSVQEGNPRA 330

Seq ID NO: C419 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 30 MLSDDHVNEI IQVENVSSG VQSHFPSSNQI PQEKVLLDSS INMVLISIDI DVIDSQTIVSK 60
 RNDQKGNQVL RFSTSLNESM SQTLSLECM GIDTPGSSHE TVQGKLIAS LIPMTSRDRI 120
 35 KAIRNQPRIM EEKRNLRKIV DKEKSKQTHR ILQLNCCIQC LNSISRAYRR SKNSLSEILN 180
 SISLWQRTLK IIGGKFGTSV LSYFNFLRWL LKFNIPSPIL NFSPIIIPQF TVAKKNTLQF 240
 TGLEFFTGVG YPRDTVMYIG FYTNSTIQHG NSGASYNMQL AYIFTIGACL TTCFSLLS 300
 MAKYFRNNFI NPHIYSGGIT KLIFCWDFTV THEKAVKLKQ KNLSTEIREN LSELQENSK 360
 40 LTFNQLLTRF SAYMAVWVS TGVAIACCAA VYLAAYNLE FLKTHSNPGA VLLLPVVSC 420
 INLAVPCIYS MFRLVERYEM PRHEVYVLLI RNIFLKISII GILCYWLTNT VALSGEECWE 480
 TLIGQDIYRL LLMDFFVSLV NSFPLGEFLR IIGMQLITSL GLQEFDIARN VLELIYAQTL 540
 VWIGIFFCPL LPPIQMIMLE IMPYSKNISL MMNFQPPSKA WRASQMMTFF IFLFPSPST 600
 45 GVLCTLAITI WRKLPADCG PFRGLPLFIH SIYSWIDTSL TRPGYLMVVW IYRNLIQSVH 660
 FFFILTILVL IITYLWQIT EGRKIMIRLL HEQIINEGKD KMFLIEKLIK LQDMEKKANP 720
 SSLVLERREV EQQGFHLHGE HDGSLDLRSR RSVQEGNPRA 760

Seq ID NO: C420 Protein Sequence
 Protein Accession #: NP_002241.1

1 11 21 31 41 51
 50 MGGLDLVLGL ALRRRKRLLR QEKSLAGWAL VLAGTGIGLM VLHAEMLWFG GCSWALYLF 60
 VKCTISISTE LLLCLIVAFH AKEVQLFMTD NGLRDWRVAL TGRQAAQIVL ELVVCGLHPA 120
 PVRPPPCVD LGAPLTSQPF WPGFLQGGEA LLSLAMLRL YLVPRAVLLR SGVLNLSYR 180
 55 SIGALNQVRP RHWPVAKLYM NTHPGRLLG LTLGLWLTAL VWLSVAERQA VNATGHLSDT 240
 LWLIPITFLT IGYGDVVPQT MWGKIVCLCT GVMGVCTAL LVAVVARKLE FNKAERKVN 300
 PMMDIQYTKK MKESAARVLQ EAMMFYKHTR RKESHAARRH QRKLLAANA PRQVRLKHRK 360
 60 LREQVNSMVD ISKMHMILYD LQQNLSSSHR ALEKQIDTLA GKLDALTELL STALGPRQLP 420
 EPSQSK 427

Seq ID NO: C421 Protein Sequence
 Protein Accession #: NP_079533.1

1 11 21 31 41 51
 65 MGKQRDEDD EAYGKPVKYD PSFRGPIKNR SCTDVICCVL FLLFILGYIV VGIVAWLYGD 60
 PRQVLYPRNS TGAYCGMGEN KDKPYLLYFN IFSCILSSNI ISVAENGLQC PTPQVCVSSC 120
 PEDPWTVGKN EFSQTVGEVF YTKNRNFCPL GVPWMTVIT SLQQLCPSPF LLPSAPALGR 180
 70 CFPWNITFP ALPGITNDTT IQQGISGLID SLNARDISVK IFEDFAQSWY WILVALGVAL 240
 VLSLEPILL RLAVAGPLVLV LILGVLGVLA YGIYYCWESE RVLKDKGASI SQLGFTNLS 300
 AYQSVQETWL AALIVLAVLE AILLVLIFL RQRIRIAIAL LKEASKAVGQ MMSTMFYPLV 360
 TVVLLICIA YWAMTALYPL PTQPATLGYV LWASNISSPG CEKVPIINTSC NPTAHLVNSS 420
 CPGLMCVFQG YSSKGLIQRS VFNLIYGVV GLFWTLNWWL ALGQCVLAGA FASFYWAFHK 480
 75 PDITFPPLI SAFITRLRYH TGSALFGALI LTLVQIARVI LEYIDHKLGR VQNPVARCIM 540
 CCFKCCLWCL EKFIKPLNRN AYIMIAIYK NPCVSAKNAP MLLMRNIVRV VWLDKVTDL 600
 LFFGKLLVVG GVGVLSEFFF SGRIPGLGKD FKSPLHLYYW LPINTSILGA YVIASGFFSV 660
 PGMCVDTLFL CFLEDLERNN GSLDRPYYS KSLKILGKK NEAPPDNKGR KK 712

Seq ID NO: C422 Protein Sequence
 Protein Accession #: NP_057264.1

1 11 21 31 41 51
 80 MGSNSGQAGR HIYKSLADDG PFDSEVPPKR PTSRLIMHSM AMPGREFCYA VEAAYVTFVL 60

5
10
15
20
25

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LSVGLPSSLY SIVWFLSPIL GFLLQPVVGS ASDHCRSRWG RRRFYILTLG VMMLVGMALY 120
LNGATVVAAL IANPRRLKLV AISVTMIGVV LPDFAADPID GPIKAYLFDV CSHQDKKGL 180
HYHALFTQFG GALGYLLGAI DMAHLELGRL LGTEPQVMFF PSALVLTLCF TVHLCISIEA 240
PLTEVAKGIP PQOTPDPPPL SSDGMYEYGS IEKVKNGYVN PSLAMQGAQN KNHAEQTRRA 300
MTLKSLLRAL VMPPHYRYL CISHLIGMTA FLSNMLFFTD FMGQIVYRGD PYSAHNSTEP 360
LIYERGVEVG CMGFCINSVF SSLYSYFQKV LVSYIGLKGL YFTGYLLFGL GTGFIGLFPN 420
VYSTLVLCSL FGVMSSTLYT VPFNLITEYH REEKEKROQA PGDPDMSVR GKGMDCATLT 480
CMVQLAQILV GGGGLFLVNT AGTVVVVVIT ASAVALIGCC FVALFVRYVD 530

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Seq ID NO: C423 Protein Sequence
Protein Accession #: NP_003264.1

1 11 21 31 41 51

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MEGFGGVGGR GTRGFAAKGV WRGRAEBGPV LGAAERGFMV STGSRRRVFE GPGGGGLRWT 60
PGKGTGRQRG AMGPRAEDGV RRTLCMPRG SRRDVRAPCG PAGSWGARGG RRRDGPSSRR 120
RGSATAAARH KVPPAPCGPF GPRAPAGSTR VPARAGGAVE PTGAAAVARL ARPAGGALPT 180
AGAQQAGPAR GRSGEGSEWA RRGKGRPGFY QSLGPAVAE GQELKDKSRL RYPINGPQAL 240
VLTALLVGLG MSAGLPLGAL PEMLLPLAFV ATLTAFIFSL FLYMKAQVAP VSALAPGGSN 300
GNPIYDFPLG REINLPRICFF DFKYFCELRP GLIGWVLINL ALLMKEAELR GSPSLAMWLV 360
NGPQLLYVGD ALMHEEAVLT TMDITHDGF FMLAFGDMAN VPFTYSLQAG FLLHHPQPLG 420
LPMASVICLI NATGYYIFRG ANSQKNTFRK NPSDPRVAGL ETISTATGRK LLVSGWGMNV 480
RHPNYLGDLI MALAWSLPG VSHLLPYFYLY LYPTALLVHR EARDERSACR STAWPGRSTA 540
GVCLTASCTP STEAAPPPQV GHVPTHPPAH PGPGASTHLG LKGLHPTQP 589

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Seq ID NO: C424 Protein Sequence
Protein Accession #: NP_056535.1

30
35
40

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MGRLLRAARL PPLLSPLLL LVGGAFLGAC VAGSDEPGPE GLTSTSLDL LLPTGLEPLD 60
SEEPSETMGL GAGLGAPGSG FPSENEESR ILQPPQYFWE EEEELNDSSL DLGPTADYVF 120
PDLTEKAGSI EDTSQAELE NLPSPFLPMN LVPEPPWHMP EEEEEEEEEE EEREKEEVEK 180
QEEEEEEELL PVNGSQBEAK PQVRDPSLTS SSQTPGATKS RHEDSGDQAS SGVEVESSMG 240
PSLLLPSTVP TTVTPGQDS TSQAEATVL PAAGLGVEFE APQEAASEAT AGAAGLSGQH 300
EEVPALPSPF QTTAPSGAEH FDEDPGSR T SASSPLAPGD MELTPSATL GQEDLNQQLL 360
EGQAAEAQSR IPWDSTQVIC KDWSNLAGKN YIILNMTENI DCEVFRQHRG PQLLALVBEV 420
LPRHSGSGHG AWHISLSKPS EKEQHLLMTL VGBQGVVPTQ DVLMLGLDIR RSLERIGIQN 480
YSTSSCQAR ASQVRSYGT LFFVLLVIGA ICIIILALGL LYNCRQRLP KLKEVSHGEE 540
LRFVENGCHD NPTLDVASDS QSEMQRKPS LMGGLALNGP GSWGALMGK RDPEDSDVFE 600
EDTHL 605

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Seq ID NO: C425 Protein Sequence
Protein Accession #: NP_001188.1

45
50

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MSEVRPLSRD ILMETLLYEQ LLEPPTMEVL GMTDSEEDLD PMEDPDSLEB MEGSDALALR 60
LACIGDEMVD SLRAPRLAQL SEVAMHSLGL AFYIDQTEI RDVLRSMFDG FTTLKENIMR 120
PWRSPNPGSW VSCEQVLLAL LLLLALLLPL LSGGLHLLK 160

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Seq ID NO: C426 Protein Sequence
Protein Accession #: AAF76225.1

55
60

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MATPLPPSP RHLRLRLRL SGLVLGAALR GAAAGHPDVA ACPGSLDCAL KRRARCPPGA 60
HACGCLQPF QEDQGLCVP RMRRFPGGGR PQPRLEDEID FLAQELARKE SGQSTPPLPK 120
DRQLPEPAT LGFSARGQL ELGLPSTPGT PTPTPHTSLG SPVSSDPVEM SPLEPRGGGQ 180
DGLALVLILA PCVAGAAALS VASLCNCRIL REIRLTQKAD YATAKAPGSP AAFRISPGDQ 240
RLAQSAEMYH YQHQKQMLC LERHKEPPKE LDTASSDEEN EDGDTFVYEC PGLAPTGEHE 300
VRNPLFDHAA LSAPLPAPSS PPALP 325

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65
70

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Seq ID NO: C427 Protein Sequence
Protein Accession #: NP_004436.1

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1 11 21 31 41 51

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MVCSLMVLVL VSSVLALBEV LLDITGETSB IGWLTYPGG WDEVSVLDDQ RRLTRTFEAC 60
HVAGAPPCTG QDNWLQTHFV ERGAQRAHI RLHFSVRACS SLGVSGGTCR EFTFLYRQA 120
EEPSPDSVS SWHLKRWTKV DTIAADESFP SSSSSSSSSS SAAMAVGPHG ACQRAGLQLN 180
VKERSFGPLT QRGFYVAFQD TGACALAVAV RLFSYTCFV LRSFASFPET QASGAGGASL 240
VAAVGTCAVA AEPEEDGVGG QAGGSPFRLH CNBEGKMWVA VGGCRCQPGY QPARGDKACQ 300
ACPRGLYKSS AGNAPCSPC ARSHAENPAA PVCPCLEGFY RASSDPPEAP CTGPSPAPQE 360
LWPEVQGSAL MLHWRLPREL GGRGDLFPV VCKECEGRQE PASGGGTCH RCRDEVHFD 420
RQRGLTESRV LVGGLRAHVP YILEVQAVNG VSELSPDPQ AAAINVSTSH EVPSAVPVVH 480
QVSRASNSIT VSWFPDQTN GNILDYQLRY YDQAEDESHS PTLTSETNTA TVTQLSPGHI 540
YGFQVARTTA AGHGYGGKV YFOTLPQGL SSQLEPRLSL VIGSILGALA FLLLAATVL 600
AVVFQKRRG TYGTEQLQY SSPGLGVKYY IDPSTYEDPC QAIRLAREV DPAYIKIEEV 660
IGTGSFGEVR QGRLPQGRR EQTVAIQALW AGQAESLQMT FLGRAAVLGQ FOHPNILRE 720
GVVTKSRPLM VLTEFMBLGF LDSFLRQREG QFSSLQLVAM QRGVAAAMQY LSSFAFVHRS 780
LSAHSVLVNS HLVCVKVARLG HSPQGPSCLL RWAAPVIAH GKHTTSSDGV SPQILMWEVM 840
SYGERPYWDM SEQEVNLAE QEFRLPPFP CPGGLHLLML DTWQKDRARR PHFDQLVAAP 900
DKMIRKPDTL QAGGDGGERP SQALLTPVAL DFPCLDSFQA WLSAIGLECY QDNFSKPLC 960

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TFSDVAQLSL EDLPALGITL AGHQKLLHH IQLLQQLHRQ QGSVEV

1006

Seq ID NO: C428 Protein Sequence

Protein Accession #: XP_043340.2

1121314151

MPFDFFRFDI YRKVPKDLTQ PTYTGAIIIS CCLPILFLP LSELTGFITT EVVNELYVDD

PKDSDGGKID VSLNISLPNL HCELVGLDIQ DEMGRHEVGH IDNSMKIPLN NGAGCRFEGQ

FSINKVPGNF HVSTHSATAQ PQNPDMTHVI HKLSFGDTLQ VQNIHGAFNA LGGADRLTSN

PLASHDYRLK IVPTVYEDKS GKQRYSYQYT VANKEYVAYS HTGRIIPAIW FRYDLSPITV

KYTERRQILY RFITTICAI I GGTFTVAGIL DSCIPTASEA WKKIQLGKMH

60120180240290

Seq ID NO: C429 Protein Sequence

Protein Accession #: NP_002142.1

11121314151

MAQKEGGRTV PCCSRPKVAA LTAGTLLLLT AIGAASWAIW AVLLRSQDEP LYPVQVSSAD

ARLMVFDKTE GTWRLLCSSR SNARVAGLSC EEMGFRLALT HSELDVRTAG ANGTSQFFCV

DEGRLEHTQR LLEVISVCDQ PRGRFLAAIC QDCGRRKLPV DRIVGGRDTS LGRWPNQVSL

RYDGAHLGG SLLSGDWILT AAHCFPERNR VLSRWRVPAG AVAQASPHGL QLGVQAVVYH

GGYLPFRDPN SEENSNDIAL VHLSSPLPLT EYIQPVCLPA AGQALVDGKI CTVTGWNQNT

YVGQAGVLIQ EARVPIISND VCNAGADFCYN QIKPKMFCAG YPEGGIDACQ GDGSGPFVCE

DSISRTFRWR LCGIVSWGTG CALAQKPGVY TKVSDPREWI FQAIKTHSEA SGMVTQL

60120180240300360417

Seq ID NO: C430 Protein Sequence

Protein Accession #: BAA92562.1

11121314151

METTIVLSGIN FEYKGMTGWE VAGDHIYTAA GASDNDFMIL TLVVPGFRPP QSVMDATENK

EVARITVFPE TLCSVNCELY FMVGVNSRTN TPVETWKGSK GKQSYTYIIE ENTITTSFTA

FORITTFHEAS RKYINDVAKI YSINVTNVMN GVASYCRPCA LEASDVGSSC TSCPAGYYID

RDSGTCHSCP PNTILKAHQY YGVQACVPCG PGTKNKKIHS LCYNDCTFSR NTPTRTFTFN

FSALANTVTL AGGSPFTSKG LKYFHHFTLS LCGNQGRKMS VCTDMVTDLR IPEGESGFSK

SITAYVCOQAV IIPPEVTGYK AGVSSQPVSL ADRLIGVTTD MTLDGITSFA ELFHLESLSGI

PDVIPPFRYSN DVTQSCSSGR STTIRVRCSF QKTVPGLSLP PGTCSDGTCG GCNHFHLMES

AAACPLCSVA DYHAIVSSCV AGIQKTTYVW REPKLCSGGI SLPEQRVTIC KTIDFWLKVQ

ISAGTCTAIL LTVLTCYFWK KNQKLEYKYS KLVMMNATLKD CDLPAADSCA IMEGEDVEDD

LIFTSEKSLF GKIKSFTSKQ PAPVTISLSE DS

60120180240300360420480540572

Seq ID NO: C431 Protein Sequence

Protein Accession #: NP_004855.1

11121314151

MPQQLRTVYN GSQMLLVLLV LSWLPHGGL SLAEASRAS PGPSELHSED SRPRELRKRY

EDLLTRLRAN QSWEDSNTDL VPAPAVRIIT PEVRLGSGGH LHLRISRAAL PEGLPPEARSL

HRALFRLSPT ASRSWDVTRP LRRQLSLARP QAPALHLRLS PPPSQSDQLL AESSSARPOL

ELHLRPPQAR GRRRARARNG DDCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTC

IGACPSQFRA ANMBAQIKTS LHRLKPDTEP APCCVPASYN PMVLIQKTD TGVSLQTYDDL

LAKDCHCI

60120180240300308

Seq ID NO: C433 Protein Sequence

Protein Accession #: NP_443090.1

11121314151

MEDPSGAREP RARPRERDPG RRPHPDQGR HDRPRDRPGD PRKRSSDGN RRRDGDGRDPK

RDQERDGNRD RNRDRERERE RERDPDRGPR RDTHRDAGPR AGEHGVWEKP RQSRTRDGAR

GLTWDAAP GPAPWEAPEP PQPQRKQDPG RRRPESEPPS ERYLPSTPRP GREEVEYYQS

EAEGILLECHK CRYLCTGRAC QMLEVLLNL LILACSSVSY SSTGGYTGIT SLGGIYYYP

GGAYSGFDGA DGEKAQQLDV QFYQLKLMV TVAMACSGAL TALCCLFVAM GVLRVPHWCP

LLLVTEGLLD MLIAGGYIPA LYFYFHYLSA AYGSPVCKER QALYQSKGYS GFGCSFHGAD

IGAGIFALG IUVFALGAVL AIKGYRKVRK LKEKPAEMPF

60120180240300360401

Seq ID NO: C435 Protein Sequence

Protein Accession #: Eos sequence

11121314151

MGAAGRQDFL FKAMLTISWL TLTCFPGATS TVAAGCPDQS PELQPNWPGH QDQHHVHIQ

GKTLILLTSSA TVYSIHISEG GKLVIKDHDE PIVLRTRHIL IDNGGELHAG SALCPFGQNF

TIILYGRADE GIQDPPIYGL KYIGVGKGA LELEGQKLS WTFNLKTLHP GGMAEGGYFF

ERSWGHGRVI VHVIDPKSGT VIHSDRFDTY RSKKESERLV QYLNAPVDGR ILSVAVNDEG

SRNLDDMARK AMTLGSKHF LHLGFRHPWS FLTVKGNPSS SVEDHIEYHG HRGSAAARVP

KLFQTEHGY FNVSLSSSEW QDVWTEWFD HDKVSQTKGG EKISDLWKAH PGKICNRPID

IQATTMDGVN LSTEVVYKGS QDYRFACYDR GRACRSYRVR FLCGKPVPRK LTVTIDTNVN

STILNLEDNV QSWKPGDTLV IASTDYSMYQ AESEQVLPCK SCAPNQVKA GKPMYLIHGE

EIDGVDNRAB VGLLSRNIIV MGEMEDKCYF YRNHICNFFD FDTFGGHIEF ALGFKAHLE

GTELKMGQGG LVGQYPIHPH LAGDVDERGG YDPTTYIRDL SIHTFTSRVC TVHGSNGLLI

KDVVGYNLSG HCFPTEDGPE ERNTFDHCLG LLVKSGLTLP SDRDSKMKCM ITEDSYPGYI

PKPRQDCNAV STFWMANPNN NLINCAAAGS EETGFWPIPH HVPTGSPVGM YSPGYSEHIP

60120180240300360420480540600660720

LGKFYNNRAH	SNYRAGMIID	NGVKTTEASA	KDKRPFLSII	SARYSPHQDA	DPLKPREPAI	780
IRHFLAYENQ	DHGANLRGGD	VWLDSCFPRG	EAQEGPLLTG	MKAGGILLGG	DEAASGMAQG	840
FSPPCRCLLK	LVTGTGSPFAH	VSLAHS				866

5

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein
5 incorporated by reference as if each individual publication, accession number, or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method for determining the presence or absence of a pathological cell in a
2 patient, said method comprising detecting a nucleic acid comprising a sequence at least 80%
3 identical to a sequence as described in Tables 2A-80 in a biological sample from said patient,
4 thereby determining the presence or absence of said pathological cell.
- 1 2. The method of Claim 1, wherein:
2 a) said pathology is described in Table 1, including a cancer; and/or
3 b) said biological sample comprises isolated nucleic acids.
- 1 3. The method of Claim 1, wherein said biological sample is tissue from an organ
2 which is affected by said pathology of Table 1, including a cancer.
- 1 4. The method of Claim 2, wherein said nucleic acids are mRNA
- 1 5. The method of Claim 2:
2 a) further comprising a step of amplifying nucleic acids before said step of detecting
3 said nucleic acid; or
4 b) where said detecting is of a protein encoded by said nucleic acid.
- 1 6. The method of Claim 1, wherein said nucleic acid comprises a sequence as
2 described in Tables 2A-80.
- 1 7. The method of Claim 2, wherein:
2 a) said detecting step is carried out by:
3 i) using a labeled nucleic acid probe;
4 ii) utilizing a biochip comprising a sequence at least 80% identical to a sequence
5 as described in Tables 2A-80; or
6 iii) detecting a polypeptide encoded by said nucleic acid; or
7 b) said patient is:
8 i) undergoing a therapeutic regimen to treat said pathology of Table 1; or
9 ii) is suspected of having said pathology or cancer.
- 1 8. An isolated nucleic acid molecule comprising a sequence as described in
2 Tables 2A-80.

- 1 9. The nucleic acid molecule of Claim 8, which is labeled.
- 1 10. An expression vector comprising the nucleic acid of Claim 8.
- 1 11. A host cell comprising the expression vector of Claim 10.
- 1 12. An isolated polypeptide which is encoded by a nucleic acid molecule
2 comprising a sequence as described in Tables 2A-80.
- 1 13. An antibody that specifically binds a polypeptide of Claim 12.
- 1 14. The antibody of Claim 13:
2 a) conjugated to an effector component;
3 b) conjugated to a detectable label, including a fluorescent label, a radioisotope, or a
4 cytotoxic chemical;
5 c) which is an antibody fragment; or
6 d) which is a humanized antibody.
- 1 15. A method for specifically targeting a compound to a pathological cell in a
2 patient, said method comprising administering to said patient an antibody of Claim 13,
3 thereby providing said targetting.
- 1 16. A method for determining the presence or absence of a pathological cell in a
2 patient, said method comprising contacting a biological sample with an antibody of Claim 13.
- 1 17. The method of Claim 16, wherein:
2 a) said antibody is conjugated to:
3 i) an effector component; or
4 ii) a fluorescent label; or
5 b) said biological sample is a blood, serum, urine, or stool sample.
- 1 18. A method for identifying a compound that modulates a pathology-associated
2 polypeptide, said method comprising the steps of:

- 3 a) contacting said compound with a pathology-associated polypeptide, said
- 4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence
- 5 at least 80% identical to a sequence as described in Tables 2A-80; and
- 6 b) determining the functional effect of said compound upon said polypeptide.

1 19. A drug screening assay comprising the steps of:

- 2 a) administering a test compound to a mammal having a pathology of Table 1 or a
- 3 cell isolated therefrom; and
- 4 b) comparing the level of gene expression of a polynucleotide that selectively
- 5 hybridizes to a sequence at least 80% identical to a sequence as described in
- 6 Tables 2A-80 in a treated cell or mammal with the level of gene expression of said
- 7 polynucleotide in a control cell or mammal, wherein a test compound that
- 8 modulates said level of expression of the polynucleotide is a candidate for the
- 9 treatment of said pathology.

10

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60/359,077	20 February 2002 (20.02.2002)	US
60/368,809	29 March 2002 (29.03.2002)	US
60/370,110	4 April 2002 (04.04.2002)	US
60/372,246	12 April 2002 (12.04.2002)	US
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(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/36810

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12Q 1/68; C07H 21/02, 21/04

US CL : 435/6; 536/23.1, 24.3

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6; 536/23.1, 24.3

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
WEST, PubMed

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	SATO, H. et al., Cloning and Expression of a Plasma Membrane Cystine/Glutamate Exchange Transporter Composed of Two Distinct Proteins, J. Biol. Chem. 23 April 1999, Vol. 247, No. 17, pp. 11455-11458.	1-7
A	KIM, J. Y. et al., Human cystine/glutamate transporter: cDNA cloning and upregulation by oxidative stress in glioma cells, B.B. Acta. June 2001, Vol. 1512, pp. 335-344.	1-7



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:		"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"B"	earlier application or patent published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Z"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

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INTERNATIONAL SEARCH REPORT

International application No.

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Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-7, SEQ ID NO: 19

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.
No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

PCT/US02/36810

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-7, drawn to a special technical feature of a method for determining presence or absence of a pathological cell in a patient, said method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a biological sample from said patient, thereby determining the presence or absence of said pathological cell.

Group II, claim(s) 8-11, drawn to a special technical feature of an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80, expression vector comprising the nucleic acid and a host cell comprising the expression vector.

Group III, claim(s) 12, drawn to a special technical feature of an isolated polypeptide which is encoded by an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80.

Group IV, claim(s) 13, 14, drawn to a special technical feature of an antibody which specifically binds to polypeptide of claim 12.

Group V, claim(s) 15, drawn to a special technical feature of a method for specifically targeting a compound to a pathological cell in a patient, comprising administering to a patient an antibody of claim 13.

Group VI, claim(s) 16, 17, drawn to a special technical feature of a method for determining the presence or absence of a pathological cell in a patient, comprising contacting a biological sample with an antibody of claim 13.

Group VII, claim(s) 18, drawn to a special technical feature of a method for identifying a compound that modulates a pathology-associated polypeptide by contacting the compound with a pathology-associated polypeptide encoded by a polynucleotide which selectively hybridizes to a sequence at least 80% identical to a sequence described in Tables 2A-80 and determining the functional effect of the compound on the polypeptide.

Group VIII, claim(s) 19, drawn to a special technical feature of a drug screening assay comprising the steps of: administering a test compound to a mammal having pathology of Table 1 or a cell isolated therefrom; comparing the level of gene expression of a polynucleotide which selectively hybridizes to a sequence at least 80% identical to a sequence described in Tables 2A-80 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal.

The inventions listed as Groups I-VIII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: claim 8 is anticipated by a sequence with accession No. BE440042 (Table 2A, first entry) (July 25, 2000), therefore there is no contribution of claim 8 over prior art.

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(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.

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